‘For a quart of ale is a dish for a king’?[1]

Malting, brewing and beer in the Mid Anglo-Saxon period: a case study of Sedgeford

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[1] This quotation is taken from Shakespeare’s ‘The Winter’s Tale’, Act IV, scene ii.

Abstract

Primary documentary sources attest to 'oceanic' beer drinking in Anglo-Saxon England; however, corresponding archaeological and archaeobotanical evidence has, to date, been conspicuously lacking. Archaeobotanical and structural evidence have together recently been used to designate a crop-processing complex, securely radiocarbon dated to the Mid Saxon era, at the site of Sedgeford in northwest Norfolk as, more specifically, a malting complex (comprising a steeping tank, and multiple germination floors and kilns): the earliest known in Anglo-Saxon England.

The key archaeobotanical criterion signifying malting is abundant germinated cereal grains. The malting complex assemblage is, unusually, dominated by rye grains, and secondarily, free-threshing wheat. New methods for assessing germination in 'naked' grains such as rye and free-threshing wheat, based on external morphology as visible under a light microscope, are presented. Results are 'triangulated' with other novel analyses -- geometric morphometric analysis and scanning electron microscopy – for assessing germination in malting complex grains. Coherence in these results provides multi-stranded evidence for widespread germination, and hence malting, at Sedgeford.

This study sets the malting complex in its broader socio-economic and cultural context: describing Sedgeford's place in the contested Mid Saxon 'agricultural revolution'. Stable isotope analysis and functional weed ecology together evidence all three components of the mooted 'mouldboard plough package': heavy plough use, extensification and, perhaps, early crop rotation, in the arable land supplying the malting complex. Further, results suggest Sedgeford may have been a 'collection centre' for harvested crops from surrounding arable land. Cultural continuity between the 'eastern zone' of England and northwest continental

Europe in the era is increasingly recognised, and evidenced at the site. Rye was then commonly cultivated on the continent. Importation of rye-husbanding and -malting customs by recent immigrants to Sedgeford from littoral northwest Europe is tentatively hypothesised.

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Dedicated to the memory of Dr Lisa Lodwick (1988-2022) – brilliant archaeobotanist and friend.

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Abbreviations and Notes

EHD	English Historical Documents (Whitelock, 1979)
TEH	The English Housewife (Markham, 1631)
FWE	Functional Weed Ecology
GMM	Geometric Morphometric analysis
SEM	Scanning Electron Microscopy
MNI	Minimum Number of Individuals
FTIR	Fourier Transform Infrared Spectroscopy

All dates are AD, unless otherwise stated.

Following FeedSax convention[2] (Hamerow et al., in prep) date ranges for periods of English history are defined as:

Early Saxon (420-670)

Mid Saxon (670-880)

Late Saxon (880-1030)

medieval (1030-1500)

post-medieval (post-1500)[2]

'East Anglia' is defined as comprising modern Cambridgeshire, Essex, Norfolk and Suffolk.

[2] Due to peculiarities of the set of radiocarbon dates obtained by FeedSax, the FeedSax group 'period H' is defined as post-1400. However, the 'post-medieval' period is conventionally dated to post-1500 – this convention is here adopted.

1 INTRODUCTION

1.1 Research outline

This work focuses on a Mid Saxon (670-880)[3] malting complex at the site of Sedgeford in northwest Norfolk, and features a thorough examination of charred plant material recovered therein. The study aims to understand the role of Mid Saxon Sedgeford and its malt in the wider socio-economic and cultural context of this time and place.

The opening chapter begins to position the study by critically summarising current scholarship on agriculture and rural life in Mid Saxon England; thought on Mid Saxon East Anglia specifically is also examined. **Chapter 2** continues to 'set the scene' by outlining key concepts relating to malting, brewing and beer, including biochemical processes implicated in brewing; thus facilitated, it evaluates ways in which malting and brewing have been, to date, discerned in the archaeological record. **Chapter 3** explores the history of beer production and consumption - in Anglo-Saxon England and in early medieval Europe more broadly - based on examination of textual, archaeological and archaeobotanical evidence.

Chapter 4 introduces the archaeological site at Sedgeford, its malting complex, and the ongoing archaeological excavations there taking place, whilst **Chapter 5** describes the methodologies used to recover, assess, and analyse the malting complex's assemblage of charred plant material. The findings of these assessments and analyses are reported in the subsequent two chapters. **Chapter 6** characterises the archaeobotanical assemblage, including

[3] The Mid Saxon era is conventionally dated 650-850. However, recent research by the FeedSax group concludes, based on the configuration of the IntCal 20 radiocarbon calibration curve, that the dates 670-880 are more empirically verifiable in terms of radiocarbon dating (Reimer et al., 2020; Hamerow et al., in prep.). 'Mid Saxon' is hereafter assumed to imply a 670-880 date range. Other periods (e.g., 'Early Saxon'), are in this work also defined as per FeedSax convention (see **Abbreviations and Notes**).

evidence for germination amongst cereal grains therein and examination of methods used to process crops malted at Sedgeford. **Chapter 7** focuses on methods of crop cultivation and arable land management. These results are synthesised with all the foregoing discussion in **Chapter 8**. Finally, concluding thoughts and some potential avenues for future research are presented in **Chapter 9**.

1.2 Why malting at Sedgeford?

What wider purposes might researching Mid Saxon malt, brewing and beer - with a focus on Sedgeford's malting complex - fulfil? There exists a rich body of primary literary sources from the era attesting that the Anglo-Saxons drank beer on (what Finberg has called) an 'oceanic' scale (1972, 422). However, as recently noted by Carruthers and Hunter Dowse (2019, 107), corresponding archaeobotanical evidence for beer production and consumption in the period is conspicuously lacking. It is hoped that the current study will partially right this imbalance.

It will here be argued that Sedgeford's is the oldest yet discovered malting complex in Anglo-Saxon England – as such, a detailed study of the site's archaeology and the archaeobotanical assemblage recovered therein is lent extra significance within the wider corpus of Anglo-Saxon archaeology. Further, charred plant material at Sedgeford comprises primarily cereal species with so-called 'naked' grains, whose morphology makes discerning evidence for germination, (a key stage of malting), in the grains, particularly challenging. To date, evidence for use of naked grains in malting has only rarely been found at archaeological sites. For each of these reasons, no methods have yet been devised for diagnosing

germination from the external morphology of naked grains. A set of three novel methods for so doing have been developed and these are here presented.

Finally, this project represents the first comprehensive study of malting, brewing and beer in mid Anglo-Saxon England, both incorporating the results of an in-depth review of primary and recent literature and employing a suite of scientific methods to examine closely and quantitatively a specific rich archaeobotanical assemblage as a case study. This combination of qualitative review and quantitative analysis is utilised for the first time to thoroughly investigate the production, exchange and consumption of beer on geographical and chronological scales from fine-grained (Mid Saxon Sedgeford) to broad (medieval Europe), and all in between.

1.3 Research Questions

This study aims to respond to the following questions:

1. ***What is the nature of the archaeobotanical assemblage at Sedgeford?***
2. ***What evidence is there for malting and brewing at Sedgeford and beyond?***
3. ***How were the cereals from which beer was malted and brewed at Sedgeford and beyond likely cultivated?***
4. ***What can be discerned about how beer was malted and brewed at Sedgeford and beyond?***
5. ***How may the beer malted and brewed at Sedgeford and beyond have been consumed?***
6. ***What was the role of Mid Saxon Sedgeford and its malt in the wider socio-economic context?***

1.4 Characterising Mid Anglo-Saxon England

Full response to these questions requires first a 'framing' of Mid Saxon Sedgeford and its malting complex in time and space.

1.4.1 Socio-political transformation

Mid Saxon times are widely recognised as an era of transformation in English society (e.g., Hansen and Wickham, 2000; Rippon, 2010, 121; McKerracher, 2018). The traditional view is that this was a period, otherwise known as the 'long eighth century',[4] when the population - augmented by Germanic immigration - emerged from the early Saxon 'dark ages' following the end of Roman occupation; and when the stage was set in many ways for further developments in later parts of the Medieval period. Sweeping transitions occurred in politics, with the emergence of both royal and ecclesiastical elites; in settlement structure, with, *inter alia*, proto-urban *emporia* being established on coastal trade routes, alongside inland 'productive sites'; and in the economy – including what has (at times) been termed a 'revolution' in agriculture (White, 1940; Duby, 1954; Scull, 1993; Ulmschneider, 2000; Yorke, 2002; Blair, 2005; Loveluck and Tys, 2006; Williamson, 2018).

The establishment of kingdoms across England, with a shift from warrior-leaders (characteristic of the 'migration period') to dynastic rule had far reaching implications for every level of society, and was associated with creation of a land-owning aristocracy (e.g.,

[4] Archaeologists have traditionally called the period 650- 850 'Mid Saxon', whilst historians Hansen and Wickham have recently termed an overlapping period (680-830) the 'long eighth century' e.g., (2000; Rippon, 2010, 44–45).

Hamerow, 2002, 87; Wickham, 2009, 157–161; Davies, 2010a, 95). Following Christianisation of much of the British Isles, the proliferation of monastic centres was arguably at least as influential – with rulers of successive kingdoms granting land, including (from the late 7th century) *bookland* (held in perpetuity) for the creation of monastic institutions, such that monasteries came to control large tracts of the English landscape, often investing heavily therein (Ulmschneider, 2000, 72; Pestell, 2003, 137; Rippon, 2010, 47; see Blair, in press). Hamerow notes that the 'security and stability' afforded by such land ownership - also awarded to noble families from the 770s - was amongst the encouragements[5] for major capital investment projects by both secular and ecclesiastical elites, such as construction of watermills, corn-dryers; and rare canals[6] and malting houses, during the period (Watts, 2002, 72–82; Hamerow, 2012, 164; Blair, 2014, 4; Faulkner and Blakelock, 2020; Caroe, 2022).

1.4.2 Agriculture

The entirety of Anglo-Saxon society depended intimately on crop and animal husbandry; and for the vast majority of the population, the rhythm of their daily lives was dictated by the demands of field and herd (e.g., Hamerow, 2002, 125; McKerracher, 2018, 119). The nature of a supposed agricultural 'revolution' in Mid-Saxon England (e.g., White, 1940, 151; Williamson, 2018)[7] has recently been the focus of a multi-proxy study focusing on bioarchaeological remains, conducted by the University of Oxford's 'Feeding Anglo-Saxon England' (hereafter, FeedSax) group (Hamerow et al., 2019; McKerracher and Hamerow,

[5] Increased arable productivity was a further powerful motivation for construction of cereal-processing infrastructure: including corn-dryers, malthouses and watermills (**section 1.4.2**).
[6] The earliest tentative evidence for canal-building in Anglo-Saxon England dates to the early 9th century (Blair, 2014, 4).
[7] Such a 'revolution' has been theorised to have also taken place in early medieval Europe (e.g., Duby, 1954)

2022; Hamerow et al., in prep.). Some of the group's key findings, (along with additional pertinent research), are here explored. Yet first, understandings of English farming prior to this era are examined.

The 'received wisdom' is that in post-Roman Britain, agriculture 'retracted to come to rest in an almost pre-Roman state of operation', as part of an extended economic decline (Fowler, 2002, 285; Hamerow, 2002, 152). Further, whilst Roman husbandry methods may have been continued in some areas, with the collapse of urban centres and military garrisons these were, it is claimed, outlasted by a characteristically 'Early-Saxon' type of farming typified by unspecialised animal and plant husbandry with production of only small surpluses – appropriate in a socio-economic system with very local, minimal goods exchange (e.g., McKerracher, 2018, 119). Farming essentially became again (as it had been in the pre-Roman age), autarkic and shifting – or so has been believed.

FeedSax's work (and that of others) somewhat questions conventional understandings of Early Saxon 'retraction' as well as Mid Saxon 'revolution'. For example: palynological (pollen) studies, arguably providing the best available organic evidence for shifts in vegetation cover and agricultural land use over expanses of time and space (e.g., Forster and Charles, 2022, 61), reveal, contrary to expectations, no significant woodland regeneration in the immediate post-Roman era (Dark, 2000, 150–154; Rippon et al., 2015, 335; Forster and Charles, 2022, 72).

Significantly, pollen sequences across Anglo-Saxon England, including from East Anglia, evidence expansion in land under cultivation from the late 7th century (Rippon, 2010, 57–60; Hamerow, 2012, 147–148; Forster and Charles, 2022, 77). For instance, increased frequencies of cereal pollen coincide with signs of sedimentation (indicative of soil erosion and hence arable cultivation) in sequences securely radiocarbon dated to the Mid Saxon era at

both Micklemere in Suffolk and the Oakley palaeochannel, Scole, on the Norfolk/Suffolk border (Wiltshire, in Murphy, 1994, 29; Wiltshire, in Ashwin and Tester, 2014, 405–421). A similar trend in cereal pollen, plausibly datable to the 7th century, is apparent at Hockham Mere, Norfolk (Sims, 1978, 58–59 Figure 2).

Increased abundance of cereal pollen indicates a wider trend of 'cerealisation' – a shift in emphasis from pastoral to arable farming which has been claimed to characterise the Mid Saxon period (e.g., Hamerow, 2012, 147–149). The agricultural revolution 'story' suggests that the long 8th century saw, across the British Isles and beyond, a pervasive shift in agrarian practices, with general reversal of early Medieval trends; heavy clay and fenland soils, abandoned in the immediate post-Roman period, again brought into cultivation – implying novel, and widespread, use of the mouldboard plough; concurrent with widespread adoption of systematic crop rotation (e.g., White, 1940, 151–152; Williamson, 2003, 120–122; Robinson, 2007, 30–31).

Comprehensive research by the FeedSax project suggests this 'story' requires some adjustment. The group find that no one period of the English medieval era saw 'revolutionary' changes in agriculture (McKerracher and Hamerow, 2022). Rather, cerealisation and associated transitions took place in a piece-meal, regionally-varied manner over several centuries, 'punctuated by periods of innovation and rapid change', of which the late 7th to 9th centuries were one (Hamerow, 2022, 24).

Shifts in agricultural practice associated by FeedSax with the Mid Saxon period include not only cerealisation but also an increase in arable productivity attested by the post-Roman

era's first dense archaeobotanical assemblages[8] and other new developments including large-scale centralised cereal processing and storage facilities (Hamerow, 2002, 139; McKerracher, 2016a, 97–98; 2016b; 2018, 90–92). For instance, there is no evidence for construction of purpose-built corn-dryers in the 5th to 7th centuries but (as noted), these begin to re-appear in the Mid Saxon period (Moffett, 1994a, 62; Hamerow, 2012, 151; 2022, 18), along with granaries (evidencing surplus production) and watermills (Watts, 2002, 72–82; McKerracher, 2016a, 97).

Mid Saxon shifts in animal husbandry are also indicated, including by the earliest post-Roman sets of ditched plots, seemingly paddocks for livestock. McKerracher (2018, 39–42) suggests these aimed to protect expanding arable land from free-ranging herds. Further – (dairy cattle will be female, such that) an increase in the proportion of male cattle from about seven per cent in the 5th to 7th centuries to ~23 per cent by *c.* 750 implies increased use of cattle (oxen) for ploughing – additional evidence for a shift to arable (Hamerow, 2022, 19; Holmes, 2022). This 'picture' of heavy plough use from an early date, at least in some areas, is bolstered by the recovery of a distinctive mouldboard plough coulter dated to the 7th century at the royal monastic site of Lyminge, in Kent, (Thomas et al., 2016).

Arable 'extensification' has been recognised as characterising medieval England and beyond (Hamerow et al., 2021, 157; Hamerow, 2022, 4). Extensification is defined by FeedSax as increase in crop productivity achieved through increasing land area under cultivation, concomitant with a decline in inputs of manure and labour (weeding and tillage) per unit of land area (Hamerow, 2022, 13). Research based on the functional ecological traits of arable

[8] 'Dense' assemblages are here defined as comprising more than 30 grains per litre of sediment (Hamerow, 2022, 18).

weeds associated with cereal assemblages (**section 5.6**) implies a shift from higher to lower input arable farming beginning across England from the 8th century (Bogaard et al., 2022, 29–31; Bogaard et al., in Hamerow et al., in prep.).

Further, specialisation, for instance in wool production,[9] begins to be evident in Mid Saxon England, along with increasing selection of crops well-adapted to local environments (McKerracher, 2018, 106). These trends were accompanied by associated patterns of exchange and trade: for example, inhabitants of the English *emporia* are recognised as having depended on large-scale importation of cattle, through a system of food renders, for their meat consumption (O'Connor, 1994, 139; Crabtree, 1996b, 64). Hence archaeological (structural), zooarchaeological and archaeobotanical evidence - the latter from both micro-(pollen) and macro-fossil (weed seed and grain) remains - cohere in suggesting that the late 7th to 9th centuries were a time of significant transition in English agriculture.

However, 'transition' does not equal 'revolution'. The FeedSax project has identified a triumvirate of features often associated with early medieval agricultural revolution – extensification, use of the mouldboard plough (both discussed above), and crop rotation – and dubbed this the 'mouldboard plough package' (Hamerow, 2022, 11–12). Contrary to long-held views, the group's work shows that these three phenomena – which ultimately coalesced in the established open-field system – are not inextricably linked, either to each other or to particular forms of field system (ibid.)

Commencing with crop rotation, in its 'classic' i.e., communal, systematic form, this involved two or three 'courses' (usually fields), with one remaining fallow while the other(s)

[9] This is suggested by age and sex profiles of sheep comparing, for instance, Brandon (a probable Mid Saxon monastic site) and early Saxon West Stow (Crabtree, 1996a, 72).

were cultivated.[10] In three-field rotation, one field will be sown with an autumn-sown crop (generally wheat, or, more rarely, rye or barley), one with a spring-sown crop (often barley or oats, although wheat can be spring-sown). The third would lie fallow and be grazed by livestock (in 'traditional' medieval crop rotation, all fields, including the fallow, would be ploughed); in subsequent years, use would 'rotate', such that each course spent every third year lying fallow (Hall, 2014, 36). Evidence in an archaeobotanical assemblage for patterning in crop-sowing times (i.e., a consistent association of a particular crop with a particular sowing season); for much soil 'disturbance', indicating regular ploughing; or for different crops being cultivated in equivalent environmental conditions (and therefore, arguably, the same field), is thus consistent with crop rotation (Bogaard et al., in Hamerow et al., in prep.). FeedSax research suggests complex trends, with much regional and inter-site variation; overall patterns are compatible with three-course rotations being adopted by the late 9th and early 10th centuries in parts of southern and central England (ibid.). Certainly, there is no clear evidence to support the significant, country-wide 'dark ages' shift to this field system that some have advocated (e.g., White, 1940, 151–152).

Regarding extensification, whilst, as has been established, low-input arable farming is evidenced from the 8th century, weed ecology suggests an ongoing decline in fertility across England until at least 1250 – implying long-term use of low-input farming, (Bogaard et al., in Hamerow et al., in prep.). As for the mouldboard plough, which famously permitted expansion of cultivated land onto heavy clay soils; whilst the Lyminge coulter clearly evidences use at isolated locations as early as the 7th century, zooarchaeological data

[10] Significantly, other forms of crop rotation e.g., unregulated cultivation by individual landholders in enclosed fields, were likely also in use (e.g., Bogaard et al., in Hamerow et al., in prep.).

(particularly, evidence for pathologies in cattle foot-bones, indicating heavy traction) suggest use of this eponymous component of the 'package' was itself rare until the mid-9th century (Holmes, 2022, 100). Further, (although arguably unsurprisingly, considering how little textual evidence of any kind remains from this early period) there is minimal documentary evidence for the mouldboard plough pre-10th century (ibid., 94).[11]

A mouldboard plough and oxen team were an expensive resource for local farmers, likely requiring collective organisation and decision-making (Hamerow, 2022, 15; Holmes, 2022, 107). The mouldboard plough has long been considered necessarily associated both with reorganisation of field systems i.e., the onset of crop rotation and communal 'open field' farming (where fields are divided into strips or *selions*, and a different local cultivator takes responsibility for each strip), and with novel 'nucleated' settlement patterns; however these phenomena did not invariably coincide (Dyer, 1990, 111; Williamson, 2022, 222–223; Hamerow, 2022, 15). Certainly, whilst there is evidence for 'precocious' mouldboard plough use and crop rotation in the long 8th century, 'true' nucleated settlements did not begin to emerge until the later 11th century (Hamerow, 2022, 20).

Returning to changes which, it is suggested, *did* occur in Mid-Saxon agriculture: cerealisation, increased productivity, specialisation and exchange: what caused these significant transitions? Population changes during this period are notoriously difficult to adduce (Hamerow, 2002, 139); however, a meta-analysis of radiocarbon dated stratigraphies evidences slow but continual population growth in early medieval Britain (Bevan et al., 2017, 10525). Such growth would have increased both supply of produce (through an expanded labour

[11] Amongst the earliest known references to oxen-pulled ploughing occurs in late 10th century Ælfric's Colloquy (Swanton, 1975, 108), whilst the first explicit mention of a mouldboard plough is found in the (likely late 10th century) Exeter Book (Riddle 21, Muir, 2000 I, 300; II, 624).

force) and demand for food (McKerracher, 2018, 121).[12] More specifically, population increase was linked to the growth of proto-urban areas and inland markets, and of the non-agricultural population – including craftspeople, merchants, and members of ecclesiastical communities – wholly dependent on trade in surplus crops and animals (ibid., 121). Though evidently not 'revolutionary', I posit that the scale of change in Mid Saxon agriculture was such that McKerracher is not unjustified in claiming (2018, 125), that the period witnessed 'from the cornfield to the king…a story of farming transformed'.

1.4.3 Rural settlement hierarchy and structure

Although nucleated villages post-date this era, 'sweeping transitions' in late 7th to 9th century England also implicated the hierarchy and structure of settlements. The most notable 'proto-urban' areas were the aforementioned *emporia*, established in Mid Saxon times at sites including (in East Anglia), *Gipeswic* (Ipswich) (e.g., Hamerow, 2007; McKerracher, 2016a, 91). Excavated to varying degrees, these were major national and international trading sites – marking the post-Roman re-emergence of a market economy in Anglo-Saxon England – with an easily taxable population of craftspeople and merchants (Davies, 2010a, 89; Naylor, 2012; Crabtree, 2014, 107; Blair, 2018, 45; Crabtree, 2018). There is 'ample evidence' that the *emporia* were provisioned from the surrounding rural landscape (Hamerow, 2007, 219). Trade with the rural hinterland was two-way: wheel-turned 'Ipswich ware', mass-produced in the East Anglian *emporium*, was clearly marketed long-distance across the kingdom, occurring near

[12] Broadberry *et al.* estimate English medieval population increased from ~1.7 million in 1086 to ~4.8 million by *c.* 1290 (2015, 20).

ubiquitously at contemporary settlements in the region (Wade, 1988, 95–96; Scull, 1997, 277–278; Blinkhorn, 2012) .

Emerging evidence implies that exchange was also occurring at inland market settlements – 'productive sites' –initially identified by numismatists from the abundance of metal-detector finds, particularly of silver *sceatta* coins, by which they are characterised (Ulmschneider, 2000; Davies, 2010a). Productive sites must have focused primarily on exchanging agricultural goods from their rural hinterland; and contributed to provisioning of the coastal *emporia* (Hamerow, 2007, 228; Crabtree, 2014, 107). The broad distribution of *sceatta* across England[13] evidences much of the landscape (including rural regions) being incorporated into networks of trade and exchange by the latter Mid Saxon period (Blackburn, 2003, 20–22).

How can these and smaller rural settlements be characterised? The hypothesised 'Mid Saxon shift' is here relevant. A dislocation between the position of many Mid Saxon settlements as revealed archaeologically and in the 1086 Domesday book has long been recognised, (Hunter Blair, 1963, 269–270; Arnold and Wardle, 1981, 145–148). Hodges (1989, 62) claims that settlement shifts, such as at West Stow, Suffolk, were largely from lighter, poorer soils onto heavier and more fertile ones. Further, J. Blair has found striking evidence that rural settlements were consistently aligned on standardised grid-plan axes (2013; 2018, 148–149; Blair et al., 2020).

It is difficult to ascribe directionality to shifts in Mid Saxon society. McKerracher, however, boldly claims farming to be 'the force behind kingdom-formation and economic resurgence in the age of Bede' (2018, 2). Examining medieval Stafford, Hamerow *et al.* posit

[13] There is a bias in the distribution of *sceatta* to the east and southeast of the country (Metcalf, 2003).

(2020, 1) that, in the period *c.* 800-1200, changes in agriculture 'fuelled population growth and underpinned the expansion of towns and markets as well as the rise of lordship'. Moreland's related argument (2000, 69, 81, 97) that agrarian innovation may have preceded and even precipitated development of coastal *emporia* is supported by Crabtree (2014, 107), focusing more closely on East Anglia.

1.4.4 Cereals

Turning now, in this plant-focused work, to Anglo-Saxon cereal crops. All those most commonly cultivated and consumed in England at this time were so-called *free-threshing* (relating to the way in which grains are relatively easily detached from their encapsulating 'glumes' during crop-processing) (e.g., Stevens, 2011, 98).

Wheat

Free-threshing bread wheat – *Triticum aestivum* L. (a *hexaploid* cereal)[14] – was the most-cultivated wheat in the Saxon period, all but replacing the glume-wheat spelt, favoured in Roman-occupied Britain (see below) (e.g., Moffett, 2006, 47; van der Veen, 2016, 808). Bread wheat is also traditionally regarded as the most prestigious cereal of the Saxon period (e.g., Moffett, 1997, 81). In Ireland, where barley and oat dominated, the 8th century law tract *Bretha Déin Chécht* still records wheat as the cereal with highest status (followed by rye, barley and lastly oats) (Kelly, 1997, 219, as cited in McClatchie et al., 2015, 180). In the 11th century, wheat was used as an index of living costs in the Anglo-Saxon chronicle, (*EHD,* 258 I. no.1 §1040), the text implying wheat's higher price than other cereals (Hagen, 2006, 30).

[14] Hexaploidy/tetraploidy refers to the cereal's chromosome complement.

Notably, other forms of free-threshing wheat, variously identified, and to date distinguishable from *Triticum aestivum* subsp. *aestivum* only by their chaff,[15] have been identified at some Mid Saxon sites. These include club wheat, *Triticum aestivum* subsp. *compactum* L. (part of the aestivum hexaploid group) and also *tetraploid* forms: rivet wheat *T. turgidum* subsp. *turgidum* L., as identified at Gloucester and Hamwic, and durum wheat, *T. turgidum* subsp. *durum* L (Monk, 1977, 294, 321; Roushannafas, in prep, 112). It is widely held, but cannot be assumed, that *Triticum aestivum* subsp. *aestivum* is the predominant form across Anglo-Saxon England (e.g., van der Veen et al., 2013, 172; Robinson, 2018). Throughout this work, *Triticum aestivum* L. refers to free-threshing wheat of either member of the aestivum hexaploid group (club wheat or bread wheat).

Barley

It has long been assumed that barley was the commonest crop in Early Saxon England, with a shift in prominence to bread wheat in Mid Saxon times (e.g., Hagen, 2006, 35). However, McKerracher (2016a) critiques this 'bread wheat thesis', based on comprehensive examination of charred grain assemblages from sites across East Anglia and the Thames Valley, arguing rather that barley remained common throughout the Mid Saxon period.

Varieties of barley include 'six-rowed', 'two-rowed' and 'hulled' or 'naked' types. Archaeobotanical evidence suggests Mid Saxon peoples primarily cultivated hulled, six rowed barley – *Hordeum vulgare* subsp. *vulgare* L. (Moffett, 2011, 251). Processing hulled varieties for

[15] A preliminary study suggests geometric morphometric analysis can be used to distinguish between these taxa based on grain morphology (see **section 5.8** and Roushannafas, in prep.)

baking involves (arduous) grain dehusking: Hagen suggests barley was therefore largely cultivated for brewing, which does not necessitate dehusking (2006, 34). Modern beer-making relies largely on hulled (two-rowed) barley (**section 2.3.1**), with a hulled rather than naked form favoured for malting now as (presumably) in Mid Saxon times since grain embryos better survive harvesting, facilitating germination (Banham and Faith, 2014, 30). Documentary evidence also suggests barley was primarily grown for beer: with frequent reference to use of barley for malting (e.g., Kelly, 1997, 245), whilst barley bread was nominated by the East Anglian hermit Guðlac (Goodwin, 1848, 27) and by a fasting Oxford noblewoman (Turner, 1828 III, 27), as next-best to starvation.

Barley survives on poorer quality soils than bread wheat (e.g., Moffett, 2006, 48), including damp and saline substrates, and is archaeobotanically frequently attested in the East Anglian fens, perhaps an agrarian adaptation to the local environment (McKerracher, 2016a, 95). The social significance of barley is indicated in its being more frequently referenced than wheat in *leechdoms* (collections of medical remedies) from the period, and in the prevalence of Mid Saxon place names incorporating reference to *here* (barley) (Cockayne, 1864; Banham and Faith, 2014, 27–28).

Oats

McKerracher's meta-analysis of Mid Saxon archaeobotanical assemblages finds evidence (2016a, 95) for rye 'and perhaps oat' becoming increasingly prevalent from the 7th century (though neither ever rivalled bread wheat or barley in abundance); he notes that oats may not have always been purposely farmed. Both rye (*Secale cereale* L.) and oat (*Avena sativa* L.) are thought to have originally been weeds in fields of other deliberately cultivated species

(Behre, 1992, 141; Evans, 1995, 167–168; Thomas, 1995, 134). The wild relatives of *Avena sativa*: *Avena. fatua* L. and *Avena sterilis* L. remain common crop-weeds to this day (Clapham et al., 1987, 636; Banham and Faith, 2014, 30). Unless the entire floret is preserved, it is not archaeobotanically possible to distinguish between cultivated and wild oats (Jacomet, 2006). Thus, whilst Moffett claims that cultivated oats occur frequently at medieval sites (2006, 352), their true prevalence is uncertain. However, these are sufficiently abundant at some Mid Saxon sites to clearly substantiate their status as a crop (ibid.). Interestingly, few English place-names refer to oats, implying the crop was not symbolically significant for Saxon peoples (Hagen, 2006, 37).

Rye

Initially a crop weed, in the 5th and 6th centuries rye cultivation spread rapidly across continental northern Europe, with rye becoming the free-threshing cereal which replaced Roman-era hulled types as chief bread crop (whilst, as described – in England – bread wheat assumed this role) (Behre, 1992, 152; Hamerow, 2002, 135–136). Rye is resilient and able to survive drought, due to its extensive root system (up to 1.8 metres) and early ripening (Behre, 1992, 149; Moffett, 2011b, 352; Zohary and Hopf, 2012, 64–65). The only cross-pollinating cereal species, rye thus has in general high disease resistance (however it is the cereal most prone to infection by the poisonous fungus ergot – *Claviceps purpurea*) (Moffett, 2006, 48). Schroeder describes widespread adoption of this cereal on the continent as a 'bio-innovation', permitting cultivation of new (drought-prone or infertile) ecological settings (Schroeder, 2022, 202).

Moffett argues that rye was introduced to England in the early Saxon era by immigrants from Germany (2011, 351), whilst Hagen posits that more favourable conditions in Britain enabled farmers to rather grow their preferred crops: a reason – along with ergot likely becoming common in rye crops in the damp British climate – for rye never rivalling medieval dominance on the continent (2006, 38; McClatchie et al., 2019, 71; Comeau and Burrow, 2021, 116, 130). However, McKerracher's research clearly reveals that rye became increasingly prevalent over time in Anglo-Saxon England (2019, 94). Archaeobotanical data suggest a particular 'focus' of Mid Saxon rye cultivation in parts of East Anglia (Rippon et al., 2015, 172; McKerracher, 2018, 105). This likely represents an adaptation of farmers to local conditions since rye would be the 'ideal crop' (Hagen, 2006, 37) for dry, sandy soils as occur in much of the region.

Rye was clearly symbolically important: in the laws of Wihtred of Kent (690-725), a month (possibly August) is given the name *Rugern*, 'rye harvest' (Liebermann, 1898, i, 12) whilst many places – particularly in East Anglia – have 'rye' related place-names (Banham and Faith, 2014, 31). Rye straw, referred to in a 10th century leechdom (Bald's leechbook, II.72, para.2 as cited in Cockayne, (1864)), is tall and strong and may have been used for thatching and fuel (Campbell, 1994, 67; Moffett, 2011, 351). Finally, it should be noted that there is (tentative) evidence – both documentary[16] and archaeobotanical – for rye and wheat occasionally being grown together in Mid Saxon England as a *maslin* (Banham, 2004, 22; Banham and Faith, 2014, 36).

[16] The Ancient Laws and Institutes of Wales (encoded in the *c.* mid-10th century) record the price of a thrave of maslin (Hagen, 2006, 38).

Glume wheats

The commonest wheat (as noted) and, with six-row barley, one of the most widely cultivated cereal species in Roman-occupied Britain, was spelt, *Triticum spelta* L, (van der Veen, 2014, 808). Although occasional spelt cultivation is evidenced even into the Mid Saxon era (e.g., at Gloucester, Winchester and probably *Hamwic*) (Monk, 1977, 294, 302), Hagen conjectures (2006, 32) that spelt is entirely absent in eastern England by the Mid Saxon period. However, in apparent contradiction, spelt has been identified in Late Saxon phases – dated after *c.* 800 – at Harston Mill, Cambridgeshire (Scaife, 2016, 189).

1.4.5 Corn-dryers

Corn-dryers and malting kilns – a type of corn-dryer – are specific features of the Anglo-Saxon built landscape, intimately associated with cereal cultivation, and pertinent to this study. A 'corn-dryer' (alternatively, 'drying kiln' or 'grain oven') has been defined by McKerracher (2014a, 82) as, 'a purpose-built structure for the drying or malting of cereal grain, and possibly other crops too'. Traditional uses of corn-dryers include drying ears or sheaves of corn after a wet harvest, to prevent unintentional germination or insect-attack; 'parching' of glume wheats and hulled grains to facilitate crop processing; drying grains to facilitate milling; or 'kilning' of intentionally germinated grains during malting (van der Veen, 1989, 303; Fosberry and Moan, 2018, 25; Comeau and Burrow, 2021, 112).

Corn-drying requires gentle heat, and conventional archaeological understanding has been that all corn-dryers comprise a drying chamber in which crops are lain, separated by a flue (to channel heat and reduce the risk of accidental conflagration) from a hearth where a fire was lit and 'worked' from a stoking area (Rickett, 1975, 19–28; Monk and Kelleher, 2005,

80). Working a corn-dryer (supplying fuel and removing ash, as well as watching for accidental fire) necessitated 'considerable' labour (Moffett, 2006, 52).

Corn-dryers were common in Roman Britain (Lodwick, 2017, 55–68). However, as noted, there is scant evidence for use or construction of purpose-built drying kilns in 5th to 7th century England (Hamerow, 2012, 151). The Mid Saxon 'renaissance' in English corn-dryer construction is widely recognised as indicating increasing agricultural productivity and the concomitant need to process, and dry, larger volumes of crops than was feasible using domestic hearths (**section 1.4.2**) (Hamerow, 2012, 151–152). Comeau and Burrow (2021, 114) extrapolate further, linking early medieval corn-dryer construction with, 'developments in agricultural distribution, tax, tribute and trade, so that they are effectively indicators of changing social complexity'.

Rickett's (1975) seminal work on medieval 'drying kilns' suggests these were stone-lined. With developments in archaeological methods, many non-stone corn-dryer structures from the era have now been discovered (McKerracher, in Rickett, 2021, 3). Various types of corn-dryer have been identified, based on morphology; it is suggested that the most common of these in medieval Ireland is the 'classic' keyhole-shaped structure (Monk and Kelleher, 2005, 81). A recent comprehensive study of corn-dryers in Wales identified six corn-dryer 'types' including pear-shaped and oval (**Figure 1.1**) (Comeau and Burrow, 2021, 113).

McKerracher (2014a) presents evidence for a particular sub-set of English Mid Saxon corn-dryers which he terms 'monumental grain ovens'. Those at Higham Ferrers, Northamptonshire; Feltham, Middlesex; and Gillingham, Dorset, have striking commonalities: stone-lined, with substantial, ~2m square drying chambers (ibid., 82); he conjectures these may result from standardised construction by itinerant specialists (ibid., 83).

Also remarkable is a set of 14 corn-dryers revealed at the ecclesiastical centre of Hoddom in Dumfriesshire, the earliest perhaps constructed in the 7th century, which evidence several 'episodes' of accidental fire, with structures destroyed, re-built and again burnt down (Holden, 2006a, 154; Lowe, 2006; Hamerow, 2012, 152). Documentary sources (including early Irish laws) attest that, owing to the risk of accidental fire, corn-dryers were often constructed some distance from dwellings (Lowe, 2006, 102; Hamerow, 2012, 155).

Distance from other buildings has almost certainly reduced the frequency of archaeological corn-dryer 'finds' (Lowe, 2006, 102; Hamerow, 2012, 155). In 1975, Rickett (1975/2021, 35) argued that early medieval documentary evidence implies an abundance of corn-dryers in England far greater than archaeological evidence would suggest (admittedly, many more corn-dryers have been excavated since this time).

Of the Anglo-Saxon corn-dryers that *have* been recovered to date, only a very small proportion include archaeobotanical evidence for malting; the author's thorough review has identified only six sites in England with archaeobotanically-attested malting kilns securely dated to the Anglo-Saxon era (see the **Descriptive Catalogue**); an extensive assessment of all archaeological evidence for corn-dryers in Anglo-Saxon England is long overdue – but their frequency certainly far exceeds that of known malting kilns. Of the 42 fifth to tenth centuries corn-dryers identified in Comeau and Burrow's comprehensive study of such structures in Wales, only a single site (South Hook) shows clear evidence for malting (2021, 122, 130). No archaeobotanically-attested malting kilns have yet been discovered in Ireland (McClatchie, *pers. comm.*).[17] In seeming contrast, it has been posited that later medieval English documents refer

[17] It is of course the case that, among the many 'standard' corn-dryers excavated to date in the British Isles, many may, at least at times, have also been used as malting kilns, but be without preserved plant material or, alternatively, where such material is to be found, this may yet to have been analysed for evidence of (germination,

far more frequently to malting than to corn-drying (Moffett, 2006, 52). This may indicate something of the respective cultural significance each held in contemporary society.

Rickett was the first to suggest that medieval corn-dryers were likely often either opportunistically used, or purpose-built, to fulfil more than one function at different times (e.g., both malting and drying crops) (Rickett, 1975/2021, 20). Methods used in the medieval era for 'kilning' malt in a corn-dryer, specifically, are described in **section 3.2.3**. Corn-dryers purpose-built for malting are hereafter termed 'malting kilns'.

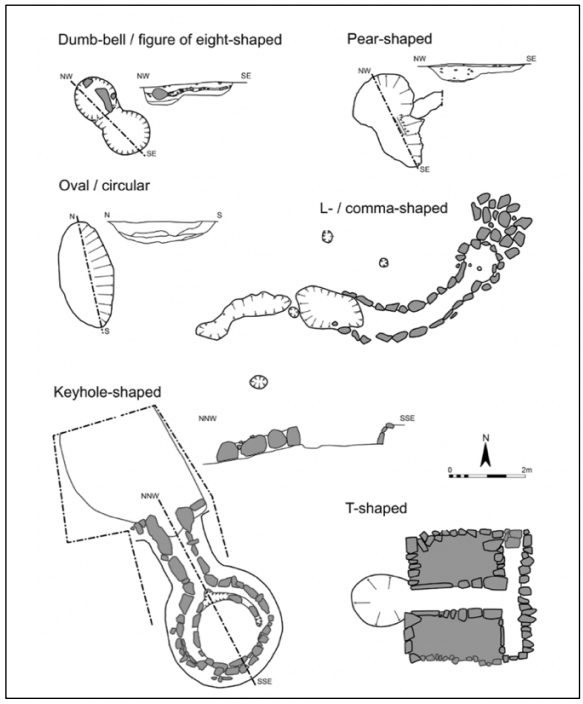

Figure 1.1 Corn-dryer 'morphology-types' occurring in Wales between the later prehistoric era and the 16th century, as identified by Comeau and Burrow (2021). Reproduced, (adapted), with kind permission from Comeau and Burrow (2021, Figure 1, p.113)

and thus) malting. Thus, even among structures revealed to date, the frequency of malting kilns will almost certainly be underestimated.

At Sedgeford, cereal crops as described above are likely to have been locally cultivated and dried, perhaps as malt, in the several corn-dryers there. Positioning Sedgeford firmly in time and space requires a closer examination of Mid Saxon East Anglia.

1.5 Anglo-Saxon East Anglia

Pestell (2017, 193) has called the Anglo-Saxon East Anglian kingdom (bordered by sea to the north and east, and partially cut-off to the west by the fens), 'an almost island-like territory…on England's east coast'. It is widely construed that, in the 5th century, East Anglia was the first area of Britain to be settled by Anglo-Saxon immigrants (e.g., Carver, 1989, 147–148; Scull, 1992, 10). Indeed, there is a growing consensus in favour of ongoing connection between East Anglia and Scandinavia, as evidenced, for example, in the famous princely ship burial at Sutton Hoo in modern Suffolk, dated to the early 7th century – these being the only areas in Europe where boat burials occur in the period, and with stylistic parallels in grave goods buried, (along with the kingly *Wuffingas*) at Sutton Hoo, and in Vendel period Scandinavia (Hines, 1984, 286–288; Yorke, 2002, 61; Wareham, 2005, 7). Hines and others note the abundance of objects from early medieval Scandinavia[18] found across the East Anglian kingdom (1984, e.g., 376 Map 6.1; Pestell, 2017, 199–205).

In striking contrast to other Anglo-Saxon kingdoms, virtually no written records exist from the time of the kingdom of East Anglia,[19] limiting present knowledge of its history (J. Blair has therefore termed Mid Saxon East Anglia 'pre-historic', Blair, in press). However it is

[18] These include brooches, bracteates and pendants.
[19] The most widely-cited reason for this is destruction of written records during 9th century Viking raids (Yorke, 2002, 58; Blair, in press).

widely believed that the kingdom was firmly established by *c.* 600 (Yorke, 2002, 58, 61; Rogerson, 2003, 120). The *emporium* at Ipswich (**Figure 1.2**), a significant international trading and craft-making centre (and the source of 'Ipswich ware'), was established by *c.* 720 (Hodges, 1982, 70–73; Blinkhorn, 2012). A number of putative 'productive sites' (**section 1.4.3**), established by the late 7th century, have been identified in East Anglia, with six recognised in northwest Norfolk (Rogerson, 2003; Davies, 2010a) (**Figure 1.2**). These were likely implicated in trading relationships with both the rural hinterland and Ipswich's *emporium* (Hutcheson, 2006, 79–80; Hamerow, 2007, 228; Crabtree, 2014, 107).

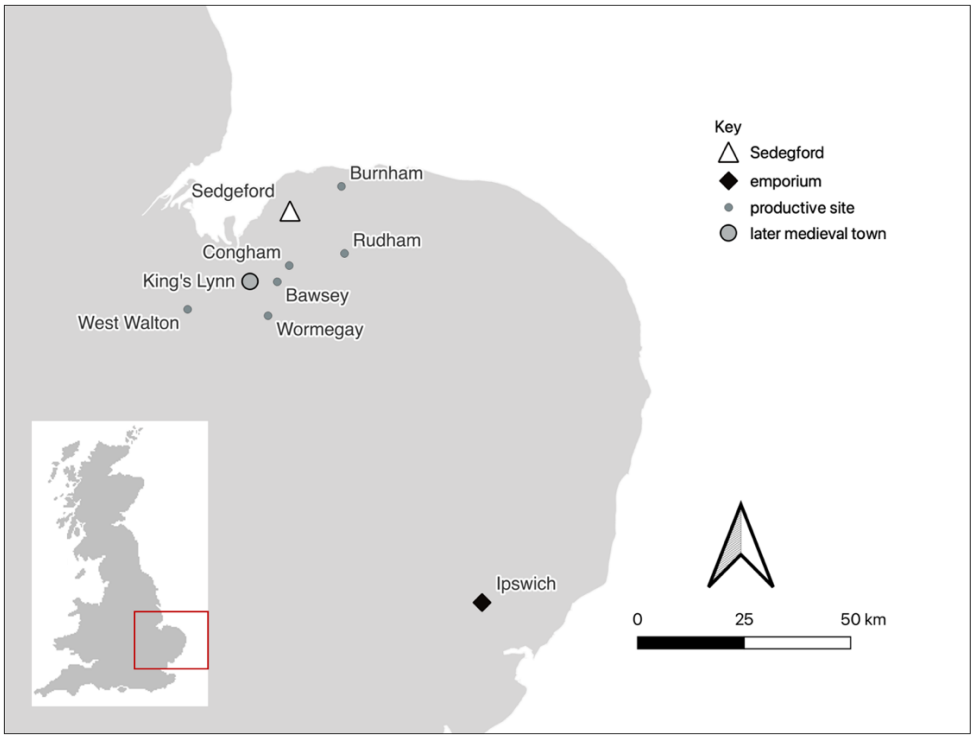

Figure 1.2 Map of Mid Saxon East Anglia locating Sedgeford, the emporium at Ipswich, 'productive sites' in northwest Norfolk (as identified by Rogerson, 2003) and the later medieval town of King's Lynn. Contains Ordnance Survey Open Data © Crown copyright and database right 2017, under the Open Government licence. Map created with QGIS (http://www.qgis.org; accessed 22/09/2022). Inset map (adapted) by Xeyarlear – Own work, CC BY-SA 4.0, https://commons.wikimedia.org/w/index.php?curid=50520413

Despite a high population density, west Norfolk remained without an urban (or proto-urban) area until the emergence of King's Lynn in the 12th century (Davies, 2010a, 95, 118). Arguably, Norfolk as a whole was a later addition to the early Saxon East Anglian kingdom, centred on the Suffolk coast (Yorke, 2002, 70). However, according to Wareham (2005, 115), East Anglia entire was the wealthiest and second-most-populous area (after London) of England in the medieval period. Northwest Norfolk was not socio-economically marginalised in the Mid Saxon period. On the contrary, and significantly, as Blair writes, 'northwestern Norfolk and Lincolnshire… we now know to have been a powerhouse of the seventh- to tenth-century economy' (Blair, 2018, 44). Others have advanced similar arguments (Hayes, 1988; Murphy, 2005; Davies, 2010a; Wright, 2015). In support of this statement, Blair cites the density of rich settlement evidence from the few as-yet excavated archaeological sites dated to this period (referencing North Elmham, Fishtoft, Shipdham and Gooderstone, as well as Sedgeford), along with frequent field-walking finds,[20] in the region. Western Norfolk (but not East Anglia entire) forms part of Blair's distinctive Mid Saxon 'eastern zone', characterised by a notable density of settlement and cemetery sites, and finds including Ipswich Ware and *sceatta* coinage, along with a characteristic building culture (**Figure 1.3**) (Blair, 2018, e.g., 29, 31, 33). Further, he asserts that, as a result mostly of long-term penetration through trade and by merchants, northwest Norfolk and the 'eastern zone' were connected to Scandinavia not only culturally but also socio-economically in the era. He writes, 'Scandinavian and English farming communities [in this region]…belonged to the same socioeconomic world' (parenthesis mine) (ibid., 306).

[20] References are: North Elmham Park (Wade-Martins, 1980a; Wright, 2015, 161–163); Fishtoft (Cope-Faulkner, 2012); Shipdam (Ames et al., 2009); Gooderstone (Weston and et al., 2007). Field walking evidence is discussed in Wade-Martins (1980b).

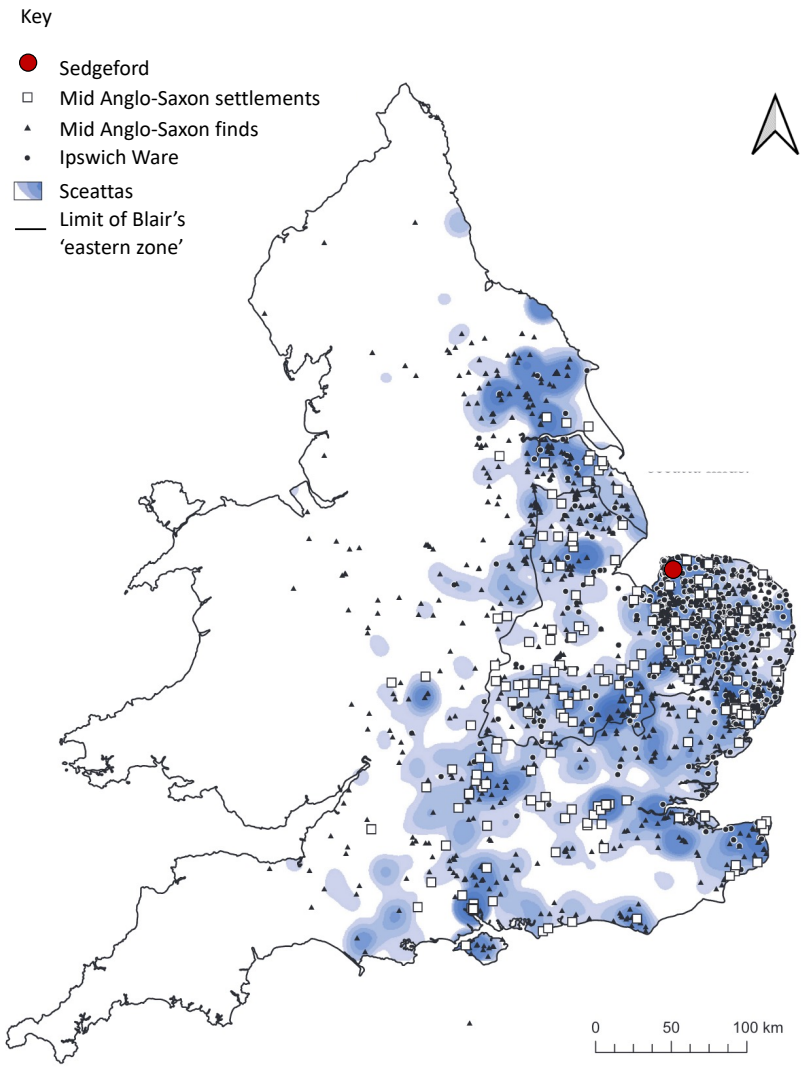

Figure 1.3 J. Blair's 'eastern zone' showing distribution of settlements dated c. *600-850, (data from the Archaeology Investigations Project), single finds of metal objects from the same era (data from Portable Antiquities Scheme), Ipswich Ware finds (data from P. Blinkhorn), and the density of* sceatta *finds (blue shading). Reproduced, adapted, with kind permission from Blair (2018, 33, Figure 6).*

…

This opening chapter has, it is hoped, partially 'set the scene' by locating Mid Saxon Sedgeford and its malting complex geographically and chronologically.

2 MALTING, BREWING AND BEER: KEY CONCEPTS

2.1 Introduction

This chapter introduces malting, brewing and beer: describing the biochemical processes involved in beer production, and, building upon this, the forms of evidence (archaeological, archaeobotanical, and archaeochemical) which have been used to justify claims for malting, brewing and beer consumption in the archaeological record.

2.2 Introducing beer and brewing

Beer can be defined as an alcoholic drink produced from a starch source – generally germinated cereal grains – involving enzymatic conversion of starch to fermentable sugars, followed by yeast-based fermentation (e.g., Stika, 2011, 41; Shellhammer, 2014, 4; Heiss et al., 2020, 2). Brewing commences with the soaking of cereal grains (steeping) in water: which initiates germination (e.g., Hough, 1985, 8–18; Shellhammer, 2014, 4–5) involving the growth of a sprout (or *coleoptile*), root sheaths (*coleorhizae*) and the release of *diastase* enzymes, within the grain body (e.g., Briggs, 1998, 154). After four to six days, the grains are 'kilned' or dried in an oven at a relatively low temperature (initially about 50-70°C): sufficient to stop the process of germination without denaturing the diastase enzymes (e.g., Briggs, 1998, 439–472; Hornsey, 2013, 45–46). These are the three stages of malting and concern us most here. Grain malting can also be used to create sweet-tasting foods or drinks (e.g. Stika, 2011b, 56; Valamoti, 2018, 619).

Where malt is used for brewing, the grains are milled, and added to warm water during *mashing*, facilitating the enzymatic conversion of starches in the grain bodies to sugars. The liquid mixture, or *wort*, is boiled, during which additives (flavourings and/or preservatives) e.g., hops (*Humulus lupulus* L.), are introduced. Finally, during *fermentation*, yeast is added to the mixture and causes the conversion of sugars to alcohol (e.g., Hornsey, 2013, 163–176). A simplified scheme, summarising the stages of brewing, is presented in **Figure 2.1**, whilst **Table 2.1** summarises the physical and biochemical processes affecting grains during beer-making; opportunities during brewing for grains to become charred by fire are also indicated.

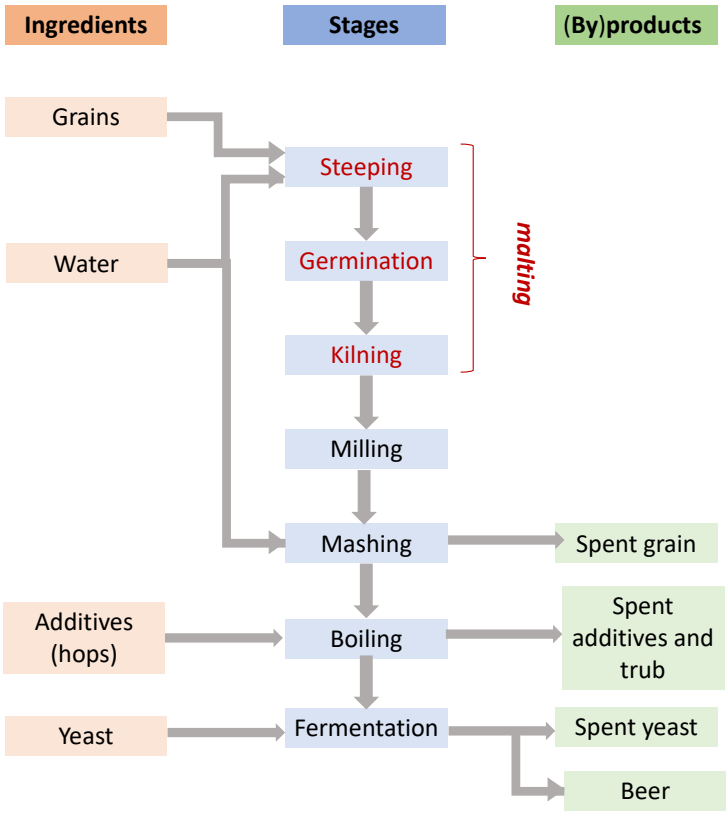

Figure 2.1 Schematic summarising the stages of brewing. Stages of malting are highlighted.

Table 2.1 Processes (physical and biochemical) affecting grains, and potential opportunities for grain charring,[21] *during the early stages of traditional brewing*

Stage of brewing		Processes affecting grains		Exposure to fire?
		Physical	(Bio)chemical	
Malting	Steeping	Sink to bottom of steeping tank, absorb water	Grain becomes metabolically active	
	'Couched' onto germination floor	Saturated grains germinate, visibly indicated by growth of sprout and rootlets	*Diastase* enzymes released and begin to break down starch and proteins in endosperm	
	Kilning	Dried, causing germination to stop	Germination processes suspended without denaturing key enzymes. *Maillard* reactions	**FIRE**
Brewing	Milling	Ground to grist (fragmented)		Risk of explosion and **FIRE** in dusty atmosphere
	Mashing	Grain husks form a filter bed, permitting extraction of wort during *lautering*. Spent grains separated from wort and used, e.g., as animal fodder	Starches enzymatically converted to fermentable sugars	**FIRE**

2.3 Biochemistry of malting and brewing

The following describes brewing as practiced today, with associated biochemical processes. However much malting and brewing methods have changed between Mid Saxon

[21] Risks of fire are identified by Inskipp (1893, 144) and Cairns (1915, 183–186). Kilning is the major fire-risk in a malting complex.

and modern times (and Dineley (2015, 65) argues that 'floor malting traditions and techniques seem to have remained unchanged across the millennia'), the biochemical processes involved are unchanged.

2.3.1 Malting

The purpose of *malting* is to create, after the succeeding process of *mashing*, a *wort* (sugary liquid) containing a balance of all the essential metabolites required to support the growth of yeast (Hornsey, 2013, 38). Malting causes biochemical changes in grains – in modern commercial brewing, almost invariably two-row hulled barley: *Hordeum vulgare* subsp. *distichum* L. – known as *modification processes* (Briggs, 1998, 7). The first stage of malting is *steeping*, in which grains are soaked in water in a steeping tank for up to 48 hours (e.g., Holl and Lindell, 2012, 564). In modern brewing, air is bubbled through the water to ensure the process remains aerobic and thus to maximise grain germination rate. 'Wet stands' are alternated with air-breaks. After 24 hours, 'extensive reprogramming of gene expression occurs' (Hornsey, 2013, 40).

The grain is then permitted to germinate: traditionally (and still amongst many craft brewers today), turned onto a *germination floor* (**Figure 2.2**) at between 10 and 16°C and constantly turned; to encourage sprouting and dissipation of heat by convection and to reduce rootlet tangling. Turning also permits the oxygen necessary for biochemical processes to diffuse through the layer of grains, and prevents accumulation of carbon dioxide (Holl and Lindell, 2012, 564; Hornsey, 2013, 40).[22] Modern brewers maintain constant levels of humidity and temperature at this stage, to ensure even germination, (e.g., Stika, 2011, 44). Germination

[22] Many modern brewers use 'pneumatic' malting, with malt in rotating drums (Kilfoil, 2020).

is considered complete when the average length of the growing sprout (known in brewing as an *acrospire*) is between 3/4 and 7/8 of the grain length (Briggs, 1998, 60; Briggs et al., 2004, 16). This takes between four days and a week and creates so-called *green malt* (Kraus-Weyermann, 2012, 562).

Figure 2.2 Germination floor at a traditional (19th century) floor maltings at Crisp Malt, Great Ryburgh, northwest Norfolk (photograph: August 2019)

Biochemical processes occurring during germination are as follows: essentially, enzymes – with those which degrade starch known collectively as diastase (Briggs, 1998, 154) – alter the structure of the grain *endosperm* (where nutrients for the growing embryo are stored) by causing disintegration of cell walls and of the endosperm's protein matrix (e.g., Hough, 1985, 4). Modification begins at the grain's embryo end and moves towards the apex (Heiss et al., 2020, 6).

Ungerminated grains contain latent β-amylase, which is solubilised and becomes available during malting (Hornsey, 2013, 43). Further, the plant hormone gibberellic acid produced by the embryo during germination is transported to the *aleurone* layer of the grain,

where it causes production of enzymes including α-amylase, endo-β-glucanases, pentosanases, endo-proteases and limit dextranase – these are all *lytic* enzymes (i.e., they degrade cell walls), and are translocated to the endosperm, where they modify the structure of cell wall starches; including that of β-glucans and arabinoxylans (types of polysaccharide), leading to exposure of the protein matrix surrounding starch granules to action by proteases (protein-degrading enzymes) (Bamforth and Martin, 1983, 303; Han and Schwarz, 1996, 216; Gubler et al., 2002; Hornsey, 2013, 44).

The subsequent stage of malting is *kilning*, during which green malt is dried at temperatures over 50°C,[23] halting growth of the sprout and stopping germination (Thomas, 2012, 517). The sequence of temperatures and length of kilning employed (usually between 16 and 60 hours) determines the type of malt produced (Hornsey, 2013, 45). Temperature must be carefully controlled, with kilning aiming to reduce grain moisture content as rapidly as possible, from ~45% to ~2.5-3%, without denaturing all the diastase enzymes (ibid., 45-46). The colour of the malt is governed by so-called *Maillard* reactions between amino acids and sugars, which produce *melanoidins* (Coghe et al., 2006).

After kilning, the malt is cooled and grain rootlets removed (deculming (Briggs, 1998, 143)).[24] At this stage, the grains may be cleaned using sieving and pumping of air. If grain moisture content remains below 4%, malt can be stored for several months before further processing (Hornsey, 2013, 46). The subsequent stages of brewing will here be more briefly described.

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[23] Enzymes are most susceptible to denaturing caused by high temperatures when moist. In modern kilning, a kiln temperature of between 50-70°C is slowly increased to ~80°C, over ~20 hours, after which (generally) it is increased to ~100° C for between six and eight hours (Hornsey, 2013, 46).

[24] Since these have a high protein and low starch content, and hence are undesirable for brewing – R. Moody, *pers. comm.*

2.3.2 Milling

Following malting, the grain is milled, i.e., ground to *grist*. This aims to expose the grain cotyledon, containing most of the seed's carbohydrates and sugars, to enzymatic activity (Shellhammer, 2014, 18). Milling seeks also (where the cereal is hulled e.g., barley or oats) to separate the grain from its husk, since 'grits' facilitate filtering during *lautering* (see below) (ibid., 27).

2.3.3 Mashing

During mashing, starches liberated during malting are converted into fermentable sugars (ibid., 23) (*saccharification*); mashing involves the mixing of ground malt with water to produce a medium supportive to yeast growth (Buttrick, 2012, 576). The first stage of mashing involves combining milled grains with hot water in a mash tun, at approximately 63-69°C (Oliver, 2012, 488). In addition to degradation (*amylolysis*) of starch, ~35-40% of proteins are catalysed (Shellhammer, 2014, 20–21). In *infusion* mashing, temperature is maintained in the mash-tun for between 30 minutes and four hours (Hornsey, 2013, 109) The most modern mashing methods, so-called *decoction* mashing, involve reiterated removal of part of the wort, which is boiled and re-added to the mash tun (Shellhammer, 2014, 25–26). Following all forms of mashing, the sugary mashing liquor (*wort*) is filtered through the base of the mash tun: *lautering* (Parkes, 2012, 540).

Lautering is the physical separation of the mash (Hornsey, 2013, 111–114). Filtration enables the separation of solids from the liquid wort, and (where hulled grains are used) the husks form an important constituent of the filter bed (Shellhammer, 2014, 27). For some beers, ungerminated grains of other cereals (or other starch sources) are added during

mashing: known as 'solid adjuncts' these influence the final colour and flavour of the beer (Bamforth, 2012, 12).

2.3.4 Boiling

During boiling, additives, (flavourings and/or preservatives), today almost invariably hops, are introduced to the wort. The products of lautering are wort and spent, residual grain (**Figure 2.1**); the wort is added to a *brewing kettle* with additives, and boiled for at least 45 minutes (Hornsey, 2013, 122). Chemical reactions taking place during boiling include termination of enzyme activity, precipitation of proteins and sterilising and concentration of the wort (ibid., 125–129). Precipitation of proteins and tannins is key, since any remaining solubilised may be (detrimentally) incorporated into the final beer (Curioni et al., 1995, 2620). Boiling causes proteins to be permanently denatured – these react with polyphenols and precipitate out as *hot trub* sediment (Shellhammer, 2014, 30). Trub, spent grain, and spent hops have some nutritive value and may be used for animal fodder (e.g., Karlović et al., 2020, 88).

2.3.5 Fermentation

Fermentation involves the removal of 'hopped wort' to a fermentation vessel, and the *pitching* (addition) of yeast. The most used species of yeast in both modern and traditional brewing is *Saccharomyces cerevisiae*,[25] commonly known as 'top-fermenting' or 'ale' yeast (Shellhammer, 2014, 41). Yeast metabolises the various sugars in the wort, generating alcohol, in a particular order; the monosaccharides (glucose and fructose) are first to be utilised (D'Amore et al., 1989, 317).

[25] Yeasts have a complex taxonomy: (Briggs et al., 2004, 366–367; Kurtzman et al., 2011; Lachance, 2018).

Modern and likely Anglo-Saxon methods of beer-making are contrasted in **Table 3.2**. Understanding of brewing methods is next applied in examining evidence for beer-making in the archaeological record.

2.4 Evidence for malting and brewing in the archaeological record

The most commonly referenced archaeobotanical evidence for beer-making is modification in the morphology of preserved grains: particularly, the growth of a sprout from the embryo-end of the caryopsis – an indicator of germination in grains, and, arguably, of malting (Stika, 1996, 83; Moffett, 1997, 79; Helm and Carruthers, 2011, 363; Larsson et al., 2018, 5).

The sprout may itself be preserved, either attached to (**Figure 2.3**) or detached from the grain (**Figure 2.4**); attached sprouts are rare, since these readily detach with even gentle mechanical disturbance (Stika, 2011a, 45). In hulled grains, including hulled barley and oat, the sprout grows within the glumes (husk) along the dorsal side of the grain, often leaving a diagnostic channel or 'dorsal furrow'(e.g., Moffett, 1997, 79; Fosberry and Moan, 2018, 26). Husks generally become detached during charring and/or preservation such that this sign is visible under light microscopy (**Figure 2.5**). In 'naked' cereals including free-threshing wheat and rye, the sprouts and rootlets generally grow away from the grain endosperm, so cannot be expected to leave a dorsal furrow, and the sprout is more readily detached since it is not protected by a husk (**Figure 2.6)** (Ross-Mackenzie, 1934, 13; Fosberry and Moan, 2018, 26; Cordes et al., 2021, 2). For these reasons, it is widely considered difficult to discern evidence for germination in naked grains (e.g., Moffett, 1997, 79; Cordes et al., 2021, 2).

Figure 2.3 Germinated charred barley grains, retaining sprouts, from late medieval deposits at 'Fischerinsel', Berlin-Mitte. Reproduced with kind permission from Stika, 2011a (p.43 Figure 2)

Figure 2.4 Detached grain sprouts, probably of spelt wheat, from the Romano-British site of Over, Cambs. Reproduced with kind permission from Fosberry and Moan (2018, p.27 Figure8b) © Oxford Archaeology Ltd and Cambridge Antiquarian Society.

Figure 2.5 Germinated barley grains showing dorsal furrows from Iron Age Hochdorf, southern Germany,(dorsal view). Reproduced with kind permission from Stika, 2011 p.46 Figure 4

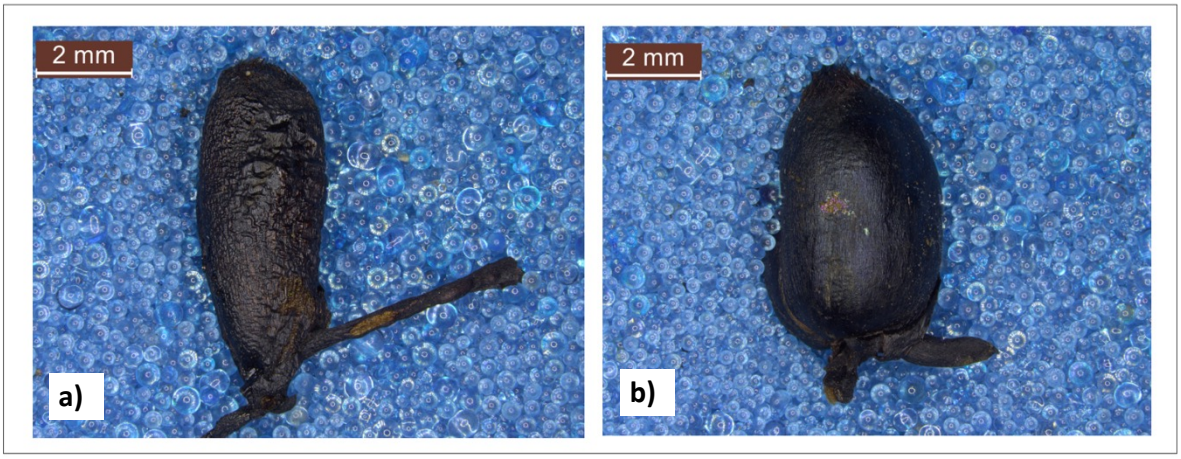

Figure 2.6 Experimentally germinated and charred a) rye grain (left) and b) bread wheat grain (right), both after three days of germination, (lateral view), showing sprout growing away from the 'body' of the grain

Other signs of germination in charred grains include damage to, or loss of, the embryo end of the grain where the endosperm has been 'used up' as germination progresses (Helm

and Carruthers, 2011, 363) – Stika (1996, 86) notes that damp germinated grain may break on charring such that the embryo end is lost. Additionally, germination may cause grain to have 'collapsed' or 'scooped-out' sides where the endosperm has been depleted (e.g., Helm and Carruthers, 2011, 363; R. Ballantyne, *pers. comm.*; G. Campbell, *pers. comm.*). Further detailed description of morphological features characteristic of germinated grains can be found in **section 5.3.**

Considering that grains can germinate because they are accidentally wetted, either during cultivation or in storage (Stika, 1996, 86), for example if stored in contact with damp soil (M. McClatchie, *pers. comm.*), arguably, a significant proportion – van der Veen specifies more than 75% (1989, 305) – of grains in a sample should show signs of germination for it to be reasonably determined that malting is occurring. However, at 5th to 7th century Uppåkra, in Sweden, Larsson *et al.* (2018, 7–8) claim malting is indicated based on up to only 29% of grains in given samples showing germination, suggesting that where grains are subject to occasional accidental charring rather than a single conflagration, less evidence of germination is to be expected.

At Iron Age Hochdorf, Stika found evenly-germinated barley grains and, with Hillman and G. Jones, argues that deliberately malted grain should show even germination (Hillman, 1982, 140; G. Jones, 1983, 3; Stika, 1996, 86). However, finding unevenly germinated grain at Uppåkra, Larsson *et al.* argue (2018, 69) that grains which represent a palimpsest of multiple malting events may well not show even germination, and, further that early brewers may have been less concerned than are modern maltsters about the need for uniform sprout length (see also, Moffett, 2006, 52).

Further archaeobotanical evidence for brewing includes remains of plants used as beer flavouring. Flavourings utilised in the early medieval era are discussed in **section 3.2.4**.

Additionally, it has recently been claimed that certain amorphous fragments of starchy substance found in archaeobotanical assemblages can be identified as by-products of brewing. For example, Valamoti (2018, 619), describing evidence from the Bronze Age site of Archondiko on mainland Greece, hypothesises that so-called starchy 'lumps' derive from cakes of mash by-product which may have been used to introduce yeast to the wort of subsequent brews. Amorphous fragments of milled grain from Iron Age sites in Cambridgeshire, studied under scanning electron microscopy (SEM) have also been claimed as evidence for ancient brewing.[26] The author contends that, pending further research, such material alone cannot be relied upon to signify brewing at a site.

Where former beer- or wort-containing vessels retain a preserved residue, this may include discernible chemical and biological indicators (e.g. Michel et al., 1993; Maksoud et al., 1994). Beer residues commonly contain 'beer-stone', of which calcium oxalate is a key component (e.g., Michel et al., 1992, 24; Michel et al., 1993, 412–413), detectable using archaeochemical techniques (e.g., Masár et al., 2003). However, calcium oxalate is commonly-occurring in both plants and animals, and can occur naturally in soils (Hornsey, 2003, 92; Tooulakou et al., 2016, 2577). Heiss (*pers. comm.*) suggests calcium oxalate in residues cannot reasonably be claimed as evidence for beer without other more reliable indicators. Potential microbiological indications of beer-derived residue include the presence of lactic acid bacteria (a sign of sugar fermentation), yeast grains, and starch granules showing characteristic altered morphology (Guerra-Doce, 2015, 759).

[26] These have been used as the basis for claims of the 'oldest beer in England' e.g., https://molaheadland.com/earliest-physical-evidence-of-beer-making-process-in-britain-discovered-on-the-a14c2h-improvement-scheme/ accessed 18.7.19.

Research suggests germination induces histological changes in grains which are visible under SEM: including amylolytic (enzyme-induced) pitting in starch granules in the endosperm at the embryo-end of germinated grains (**Figure 2.7**) (Palmer, 1995, 103, 108; Samuel, 1996a, 3; Samuel, 1996b, 488; Cordes et al., 2021). Further, Heiss *et al.* identify quantifiable (and statistically significant) thinning of cell walls, and appearance of intercellular spaces, in the aleurone layer (between the endosperm and the outer pericarp and testa), at the embryo-end of germinated caryopses (Heiss et al., 2020, 25). Finally, both Palmer (1995, 103) and Dineley (2015, 68) suggest that separation of the aleurone layer and testa from the endosperm is an additional feature (visible under SEM) characteristic of germinated grains.

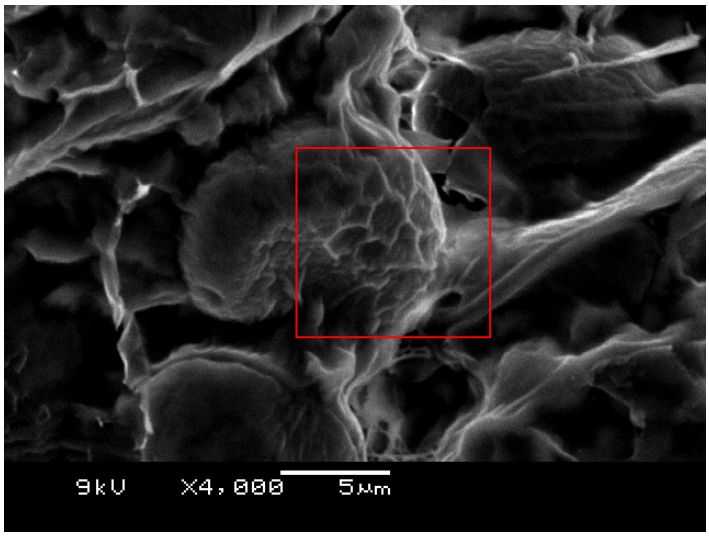

Figure 2.7 SEM image showing pitting in starch granules from a charred modern rye grain after five days of germination. Reproduced with kind permission from Y. Zhou.

Turning to archaeological evidence for malting and brewing; as noted by Cool (writing on Roman Britain), brewing generally leaves few characteristic architectural remains (2006,

142–143). Wooden vessels generally do not preserve.[27] Stika (2011a, 47) theorises that 'cooking stones' may have been used for heating the mash and potentially for wort boiling at Hochdorf, and at 10th-11th century Vinberg in Sweden, supposed 'fire-cracked stones' are cited as indicating brewing (Viklund, 2011, 242) – yet these may, for example, derive from a cooking pit (Hjulström and Lindeberg, unpublished) – and are certainly not alone sufficient evidence for beer-making. Further, structures such as ovens and tanks may represent malting kilns and steeping cisterns but can be otherwise interpreted. Lodwick observes that tanks may indicate industries 'from salt-making, to dyeing' (2017, 62) whilst malting kilns may be very difficult to distinguish from drying ovens – indeed ovens were likely often multi-purpose (**section 1.4.5**) (Hillman, 1982, 140; Rickett, 2021, 20). These considerations highlight the vital role for archaeobotanical analysis in identifying malting and brewing.

Final sources of evidence for beer-making and consumption are, firstly, iconographic or (in the historical period) documentary records, and, secondly, material culture associated with drinking, e.g., drinking vessels. Clearly, the case for beer being produced or consumed at a site is strengthened where multiple forms of evidence (for instance archaeobotanical, archaeochemical and documentary) coincide (e.g., Dietler, 2006, 233).

…

This chapter has developed understanding of forms of evidence which can be used to discern beer production and consumption in the archaeological record, including archaeobotanical and archaeochemical, as well as structural evidence.

[27] 'Beautifully preserved' (M. McClatchie *pers. comm.*) waterlogged wooden vessels, hypothesised to be have been used for brewing, have been found at early medieval Drumclay crannog in Ireland (Bermingham et al., 2013).

3 MEDIEVAL BEER PRODUCTION, CONSUMPTION AND EXCHANGE: A HISTORY

3.1 Introduction

Understandings of the archaeological record developed in **Chapter 2**, combined with a detailed review of primary documentary sources, are in this chapter applied in thoroughly examining the history of beer and beer making (production, consumption and exchange), focusing on the 7th to 9th centuries in Anglo-Saxon England and in medieval continental Europe. Evidence from 'mainland Europe' is here in places included to contextualise the beer 'story' in England. A thorough review reveals remarkable consistencies in brewing and drinking across early medieval Europe (including Anglo-Saxon England) in this period: it is considered justified to incorporate the 'story' on the continent as part of a combined region-wide assessment.

There is a notable lack of early medieval literary sources pertaining to brewing methods. It is here judged admissible to glean carefully from later- and post-medieval material; on the grounds that disparities between modern brewing methods and those described in such texts likely can be extrapolated back to the early medieval era (with early medieval brewing probably differing more from modern practices than those such later sources describe).

However, there was undeniably some geographical and chronological variation in malting and brewing methods, and in beer consumption practices, in the era (an important example being the transition from flavouring with gruit to hops-flavoured beer across Europe

which took place gradually from the 9th to 14th centuries, with spatial variation in the timing of this shift (**section 3.2.4**)).[28] A level of care must therefore be taken in interpretation of primary sources from later periods or from continental Europe – these cannot be unthinkingly applied to the 'beer story' of 7th to 9th centuries Anglo-Saxon England.

Primary sources referenced in this chapter are presented, chronologically, in **Table 3.1**. **Tables 3.2** and **3.3** summarise the stages of early medieval brewing as revealed in this chapter and compare these with modern brewing methods, presented in **Chapter 2**.

[28] A further example of variation in brewing practices across early medieval Europe: Glamann describes 'air-drying' - a practice used in 'pre-industrial' Danish malting seemingly unknown in Anglo-Saxon England (2005, 19).

Table 3.1 Primary sources referenced in Chapter 3

Period	Source(s)	Date (century)	Author	Place of origin	Source type	Reference(s)
Early Saxon	Praefatio de poenitentia Gildae	6th	attr. Gildas	Insular	Penitential	(Haddan and Stubbs, 1869)
	Cáin Aicillne	7th	anon.	Irish	Law text	(Hancock and O'Mahoney, 1869)
	The Laws of Ine	7th	attr. King Ine of Wessex	English	Law code	(*EHD*)
	Regula cuiusdam patris ad virgines	7th	attr. Jonas de Bobbio	French	Rule for monastic life	(Diem, 2021)
	Life of Abbot Columbanus	7th	Jonas de Bobbio	French	Hagiography	(O'Hara and Wood, 2017)
Mid Saxon	Maxims I	7th or 8th	anon.	English	Poetry (wisdom literature)	(Muir, 2000)
	Early English charters	7th to 10th	various	English	Royal charters	(Robertson, 1939; Finberg, 1972; The Electronic Sawyer: Online catalogue of Anglo-Saxon charters, n.d.)

Period	Source(s)	Date (century)	Author	Place of origin	Source type	Reference(s)
	Paenitentiale Ecgberhti	8th	attr. Archbishop Ecgberht of York	English	Penitential	(Haddan and Stubbs, 1869)
	The English correspondence of Saint Boniface	8th	Boniface	English	Collection of letters	(Tangl, 1955)
	Historia Ecclesiastica Gentis Anglorum	8th	Bede	English	History	(Colgrave and Mynors, 1969)
	Capitulare de Villis	Late 8th	attr. Charlemagne	French	Regulations for running royal estate	(Brühl, 1971; Loyn and Percival, 1975)
	St Gall plan	9th	anon.	Swiss	Plan of an idealised monastery	(Horn and Born, 1979)
	Les Statuts d'Adalhard	9th	attr. Adalhard	French	Statute book (for an abbey)	(Levillain, 1900)
	Un État de redevances dues à la mense conventuelle de Saint-Denis (832)	9th	anon.	French	List of royalties due to a monastery	(Levillain, 1909)
	The Gododdin	9th or later	anon.	Welsh	Epic poem	(Jackson, 1969)

Period	Source(s)	Date (century)	Author	Place of origin	Source type	Reference(s)
Late Saxon	Traditionen des Hochstifts Freising	9th to 13th	anon.	German	List of donations and privileges (for a bishopric)	(Bitterauf, 1967)
	The Exeter Book	10th	various	English	Collection of poems	(Muir, 2000)
	Ælfric's Colloquy	10th	Ælfric, Abbot of Eynsham	English	Conversation manual for language learning	(Garmonsway, 1991)
	The Will of Æthelgyfu	10th	Æthelgyfu	English	Will	(Whitelock, 1968)
	Bald's Leechbook	10th	attr. Bald and Cild	English	Book of medical remedies	(Cockayne, 1864)
	Beowulf	10th to 11th	anon.	English	Epic poem	(Liuzza, 2000)
	Ælfric's Lives of saints: being a set of sermons on saints' days formerly observed by the English church	11th	Ælfric, Abbot of Eynsham	English	Homilies	(Skeat, 1881)
	The sermon of the 'wolf' to the English…	11th	Wulfstan II	English	Homily	(Swanton, 1975)

Period	Source(s)	Date (century)	Author	Place of origin	Source type	Reference(s)
Medieval	The Letters of John of Salisbury	12th	John of Salisbury	English	Collection of letters	(Miller and Butler, 1986)
	Physica Sacra	12th	Hildegard of Bingen	German	Study of human body and medical practices	(von Berendes, 1896)
	Life of St Maedóc	Late 12th to early 13th	anon.	Welsh	Hagiography	(Plummer, 1910)
	King Horn	13th	anon.	English	Chivalric romance literature	(Herzman et al., 1999)
	The Treatise of Walter de Bibbesworth	Late 13th	Walter de Bibbesworth	English	Poem (for teaching children)	(Bickerdyke, 1886; Brears, 2008)
	Calendar of close rolls, Henry III, v.1, 1227-31, Calendar of close rolls, Edward I, v.5 1302-07	13th and 14th	compiled by royal chancery	English	Records of formal royal correspondence	(Maxwell-Lyte, 1902; Maxwell-Lyte, 1908)
	The Book of Taliesin	Early 14th	attr. Taliesin	Welsh	Collection of poems	(Williams and Lewis, 2019)

Period	Source(s)	Date (century)	Author	Place of origin	Source type	Reference(s)
	Vitae sanctorum Hiberniae ex codice olim Salmanticensi nunc Bruxellensi	14th	anon.	Irish	Hagiography	(Heist, 1965)
Post-medieval	Household Book	15th	Dame Alice de Bryené	English	Household records	(Redstone and Dale, 1984)
	The Boke of Husbandry	16th	Anthony Fitzherbert	English	Guide to farming	(Fitzherbert, 1540)
	Five hundred points of good husbandry	16th	Thomas Tusser	English	Instructional poem	(Tusser, 1576; Tusser, 1710; Tusser, 1812)
	The English Housewife	17th	Gervase Markham	English	Book of recipes / remedies	(*TEH*)

3.2 Production

3.2.1 Primary sources

It has well been said that, 'traditional, non-industrial methods of malting and brewing are not well documented, and even in the historical period, individual stages of malting are frequently glossed over' (Smith, 2011, 110; see also Doyle, 2022, 35). However, one key source for the British Isles, the likely 7th century Irish law text *Cáin Aicillne* summarises thus contemporary understanding of how malt ought to be prepared:

> *Malt of three fortnights: a day and a night steeping, and three days dripping, and nine days lying under its covering, and three days and three nights it shall lie exposed until it is raised in sods, and it should be a fortnight in sods without being raked, and in ridges after being raked until it is dried*
>
> (Translated from 7th century *Cáin Aicillne* (Hancock and O'Mahoney, 1869, 241))

Other sources are later. A late 13th century English collection of poems includes a set of instructions for malting and brewing (Walter de Bibbesworth, cited in Brears, 2008, 88) (reproduced in **Appendix A**); the Anglo-Norman couplets being juxtaposed with a 19th century translation (Bickerdyke, 1886, 49).

Whilst superficially these descriptions bear resemblance to the process of beer-making practiced today, as described in **Chapter 2**, in fact fundamental distinctions exist between early medieval and modern brewing.[29] These are here explored.

[29] *Senchus Mór* relates that malt, after grinding, was at times made into cakes so hard that these required breaking with a mallet (Hancock and O'Mahoney, 1869, 243).

3.2.2 Fundamentals of brewing

Whilst modern brewing relies heavily for its starch source on hulled, two-row barley – in fact, any cereal can be used to produce malt for brewing and barley was not widely established as the grain of choice for malting until the 16th century (e.g., Hornsey, 2003, 284).[30] Both documentary and archaeobotanical evidence attest that early medieval peoples across Europe malted and brewed using a variety of different cereals, including hulled six-row barley, oats, and bread wheat (e.g., Tusser, 1812, 46; Hoffman, 1956, 48; Simonsson, 1957, 282; Moffett, 1991; Moffett, 1994b; Campbell, 1994; Stika, 2011, 41). For instance, contemporary records suggest the canons of St Paul's Cathedral, London were in the year 1222 brewing 67,814 gallons of ale from 175 quarters of each of wheat and barley, and 708 of oat (Hale, 1858, 160–164). It was common to malt, and sometimes cultivate for malting (as a kind of mixed crop) more than one species of cereal together (e.g., Tusser, 1557 / 1812, 46; Stika, 2011, 41). A 15th century English text refers to ale composed from half wheat malt and half dredge (oats and barley cultivated together) (Redstone and Dale, 1984, 2, 31). Significantly, cereals grown for malting can include hulled cereals such as barley and oats alongside other, 'naked' crops, such as wheat and rye, since dehusking is not necessary prior to malting (i.e., all cereals in a mixed crop including hulled types can be processed together).

Seeming archaeobotanical evidence for malting cereals cultivated as a mixed crop has been identified in a 15th century hypothesised malting kiln at Burton Dassett, where mixed barley, oats and wheat were discovered, with over half the barley and some oats showing signs of germination (Moffett, 1991, 10). Kiln fills at the Late Saxon site of West Cotton,

[30] 'The German Reinheitsgebot, a brewing purity law established in 1516 and still in existence today, decreed that beer could be made only from barley…' (Shellhammer, 2014, 3).

Northamptonshire were similarly found to contain mixed oats and barley with up to one third of the grains germinated (Campbell, 1994, 69). However, Campbell notes Markham's 1631 recommendation that oats be added to malt only if the barley be found 'wanting', implying that, in his day, crops could be combined after harvesting (*TEH*, VII, 2; Campbell, 1994, 69). Markham further suggests that wild oats found with harvested grain should be tolerated for, 'both the wild oat and the perfect oat give a pleasant sharp relish to the drink' (*TEH,* VII, 4).

Unlike today, early medieval malting would have avoided the warmest months, since high summer temperatures were believed to cause overly rapid germination of grains (Underdown, 2003, 6; Hertrich, 2013, 133). Tusser advises that November and February, in particular, are months to 'go thresh out to malt' (Tusser, 1557/ 1812, 46, 112), whilst Markham suggests that malting in high summer will, 'breed loss and encumbrance' (*TEH,* VII, 7).

3.2.3 Stages of brewing

Steeping

Turning now to stages of brewing as practiced in early medieval times. Markham recommends for steeping a stone-lined cistern over a wooden vat, implying that both were in use by his era (*TEH*, VII, 22). The practice of creating a particularly potent beverage by using beer instead of water for steeping the grain, i.e., 'double-brewing', is recorded in Anglo-Saxon leechdoms (e.g., Cockayne, 1864 v. 2, Leechbook 1, xlvii, 3, 121).

Multiple sources attest that, once grains had been added to the steeping tank, weeds and remaining chaff were 'skimmed', floating, from the water's surface, rendering prior winnowing (or 'casting') unnecessary (Tusser, 1710, 161; Tusser, 1812, 47; Muspratt, 1860,

237; Krzywinski and Soltvedt, 1988, 62; Hertrich, 2013, 133). W. Mavor writes, 'In malting… (casting) is not necessary, as the light grains and seeds of weeds may be skimmed off in the cistern' (Mavor, in Tusser, 1812, 47). Later sources record, 'there will always be some light grains and other matter floating on the surface of the liquor, which must be skimmed off, otherwise…they would impair the quality… of the beer' (Muspratt, 1860, vol 1, 237), and, further, that, 'Emphasis was placed on cleaning barley in the steep by skimming chaff, light barley, and foreign seeds from the surface…of the steep tanks' (Hertrich, 2013, 133).[31]

Couching and germination

Markham describes couching of the steeped grain onto a germination floor as follows, 'and the thickness of this heap shall be answerable to the season of the year; for if the weather be extreme cold, then the heap shall be made very thick, as three or four foot, or more…but if the weather be temperate and warm, then shall the heap be made thinner,' (*TEH,* VII*,* 27). Nineteenth century Muspratt suggests that, in the English climate, grains couched onto a 'traditional malting floor' should be left to germinate for 14 days, until the malt is friable – crumbling between the fingers – and (for hulled grains) before the sprout, growing from the grains' embryo end, beneath the hull, becomes visible at the opposite, (apical) end of the grains (Muspratt, 1860, 238).[32]

[31] However, significantly, where harvested material is 'contained' during steeping, for instance suspended in sacking, 'skimming' will not be possible (see **section 5.4.3**) (Krzywinski and Soltvedt, 1988, 62).
[32] Germination experiments conducted by the author and others suggest a considerably shorter time period is required for grains to be 'germinated' – five to six days (e.g., Stika, 1996, 86). However, Markham seems to concur with Muspratt, suggesting malting requires at least three weeks (*TEH,* VII, 30).

Kilning

Grains, once deemed sufficiently germinated, are next kilned. The structure and use of corn-dryers (of which malting kilns are a type) in the Mid Saxon era are described in **section 1.4.5**. However, it is here worth noting evidence for the use of straw as a lining for the kiln floor (raised above the fire) on which germinated grains were laid. A review of Welsh historical buildings describes the use in corn-dryers and malting kilns of, 'two planks…placed at right-angles to each other… These served to support the sticks which were placed regularly over the kiln until it was covered. Over the whole clean straw was laid, upon which the corn was placed to be dried' (Wiliam, 1986, 180). Markham recommends the 'best, neatest and sweetest' of straw to be used for this purpose being of rye – even woven together as an 'Indian' mat (*TEH*, VII, 16; Markham, 1657, 163). Campbell, noting this, suggests the overabundance of rye rachises recovered from supposed Late Saxon malting kilns at West Cotton may be attributable to use of chaff, leftover from rye straw lining the drying chamber, as kiln-fuel (Campbell, 1994, 69). The use of a 'hair cloth' either in place of, or positioned over, the straw, on which germinated grains are lain, is often suggested (e.g., *TEH*, VII, 15, 27; Wiliam, 1986, 182).

There is consensus in both the literature and archaeobotanical findings that the preferred fuel for a malting kiln was straw and chaff, rather than wood. A review of inventories from the 17th century finds that straw is the most used fuel (Crosby, 2000, 41). According to Tusser, 'Some drieth with straw, and some drieth with wood / Wood asketh more charge, and yet nothing so good' (Tusser, 1557/1812, 258). Markham's view is that, as malting kiln fuel, 'wheat straw is the best…the next is rye straw, then oaten straw, and last barley straw' (*TEH*, VII, 18).

The danger of fire associated with use of all corn-dryers has been described in **section 1.4.5**. However, post-medieval sources refer to the need to watch the kiln carefully with specific reference to malting kilns: Tusser writing, (in a section entitled, 'malting'), 'Take heede to the kell, [kiln] / Sing out as a bell. / Be suer no chances to fier can drawe, / the wood, or the furzen, the brake or the strawe' (Tusser, 1557/1812, 258). Markham warns:, 'it is very possible that the kiln may be set on fire, to the great loss and often undoing of the owner' (*TEH*, VII, 12).

De-culming

There are many references to the need, following kilning, to remove 'rootlets' (including sprouts), believed to taint the beer's flavour, from the malted grains. Malt processing to this day involves 'de-culming' (Briggs, 1998, 8, 10; Neylon et al., 2020, 119), however 'traditional' methods for so doing differ from today's. Sources suggest Anglo-Saxons would commonly have removed rootlets by hand pounding, rubbing or vigorous stirring after kiln-drying, followed by winnowing and fine sieving (Smith, n.d., 7; Muspratt, 1860, 278; Krzywinski and Soltvedt, 1988, 62; Brears, 2008, 93). Markham describes, '… both those rubbings from the sieve and the chaff and dust which cometh from the winnowings…are very good swine's meat' (*TEH,* VII, 28). The use of 'rootlets' for animal fodder, or, indeed, as kiln fuel, is also referenced elsewhere (e.g., Smith, 2011, 110). Finally, on malting, Markham decrees, 'less than three weeks you cannot have to make good and perfect malt' (*TEH,* VII, 30).

Milling, mashing and boiling

In both modern and traditional brewing, the malt is, following kilning, coarsely ground in a mill such that husks of hulled grains are separated from the grains but left partially intact (forming a 'filter bed' during lautering). Early medieval times saw the first use of watermills to grind grain for malting, with the earliest such use in Europe recorded for *c.* 619 in Nendrum, Ireland (Rynne, 2015, 72). Mechanised milling (water- and wind-milling) for either flour making or malting was widespread in England by the 11th century (with ~6,000 mills recorded in Domesday), and further proliferated in the 12th to 14th centuries (Langdon, 2004; Watts, 2018, 167). However, domestic milling, heavily reliant on quern-stones, and often a source of ground grain for 'industrial' production, still accounted for 20% of all English grain milling in the 14th century, and was particularly common in East Anglia (Langdon, 1994, 31; Jervis, 2022, 283).

Water for mashing (or 'liquor') would be extracted from a local source (such as a river or spring), with the water's chemical properties influencing the beer's eventual characteristics (Hornsey, 2013, 103–104). Mixing, using paddles, would take place in a single vessel, the 'mash tun'. This is 'one step' or *infusion* mashing (ibid.). It is said that the temperature at which the liquid, 'best reflects the brewer's face' (around 65-70°C) was sought (ibid., 102). The mash would stand for approximately two hours before manual extraction (often by ladling) of the wort (Muspratt, 1860, 282). It is suggested that, prior to the use of hops (added during boiling) as a flavouring and preservative for beer, herbal flavourings were added to the wort during mashing, and the boiling stage would be wholly foregone – creating so-called *raw ale* (Nordlund, 1969, 190–194; Laitinen and Mosher, 2019; Verberg, 2020, 18). When used in the medieval period, boiling involved heating of a large leaded vessel over a fire (**Figure 3.1**).

Figure 3.1 A member of the Mendelsche Zwölfbrüderstiftung community, boiling wort in a lead vessel. Illustration can be dated to 1425/1426. Source: Hausbuch der Mendelschen Zwölfbrüderstiftung. Band 1, Nuremberg 1426–1549. Stadtbibliothek Nürnberg, Amb. 317.2°. Available from: https://commons.wikimedia.org/wiki/File:Jorg_Prewmaister,_Mendel_Band_I_(1437),_Seite_60r.jpg

Fermentation

It has long been claimed that the crucial role of yeast in the fermentation stage of brewing was not understood until the 19th century (e.g., Shellhammer, 2014, 3). However, C. Doyle (2022, 41) cites a recipe from Bald's Leechbook (II.51) in support of his claim that the Anglo-Saxons deliberately added yeast in ale-production. Certainly, Mid-Saxon brewers would have understood the need to skim yeast-containing foam (*barm*) from one fermentation vessel for re-use in the next (Shellhammer, 2014, 42). According to Kölling-Paternoga, yeast

'pitching' may have been aided by insect vectors such as *Drosophila melanogaster* (fruit-flies) (H.P. Stika, *pers. comm.*). Ethnographic evidence suggests Nordic brewers may have, for long centuries, used carefully-guarded 'totem sticks' to transfer yeast between brews (Jackson, 1993).[33]

3.2.4 Flavouring

Turning to flavourings: significantly, a key distinction between the 'stories' of brewing in Anglo-Saxon England and early medieval Europe is the earlier use of hops on the continent (e.g., DeLyser and Kasper, 1994, 169). Exactly when hops were first cultivated for brewing in England is a vexed question.

Prior to widespread use of hops, the most commonly-referenced flavouring and preservative in medieval literature was *gruit*, which likely comprised a mixture of herbs – most prominently sweet gale/bog myrtle, *Myrica gale* L. (Unger, 2007, 31), which has a natural range encompassing the British Isles and large parts of littoral western Europe (Behre, 1999, 36). Despite arguably being under-represented archaeobotanically, (Behre, 1999, 36), *Myrica gale* occurs in abundance in assemblages at several medieval sites in Europe, where its use for brewing seems incontestable. 469 fruitlets were discovered at ninth to 13th century Alte Boomborg in northwest Germany; 704 at 8th to 12th century Ribe in Denmark and 'nearly 700' accompanied by fire-cracked stones in two sunken-floored houses at late Viking Vinberg in Sweden (Jensen, 1986, 24; Behre, 1999, 38–39; Viklund, 2011, 236). Finds in England are rare, with some identifications being dismissed as naturally occurring; however, at 10th-12th century

[33] The Norwegian brewers interviewed by Jackson claimed their 'totem sticks' carried yeast cultures whose provenance was as early as the Viking period (Jackson, 1993).

Lincoln at least, *Myrica gale* remains are identified as 'possible ale-brewing waste' (Greig, 1989, 12).

In Europe until the 13th century, sweet gale was the flavouring of choice for brewers within the shrub's natural distribution, with hops favoured beyond this range: sweet gale beer does not preserve well and was not amenable to long-distance trade (Behre, 1999, 39, 44; Viklund, 2011, 239). Both archaeobotanical and documentary evidence attest that this flavouring was used from the 10th century in northwest Germany, Denmark and Sweden (Behre, 1999, 41–42). (German abbess) St Hildegard wrote of *Mirtelbaum*, (sweet gale), in the 12th century, 'If you want to brew beer, cook the leaves and fruits together, the drink will be healthier' (von Berendes, 1896, 62–63; Verberg, 2020, 10, 20).

Turning now to *Humulus lupulus* L.: the use of hops in brewing is first recorded in 822, in the statute of a Frankish abbey which intimates that these are gathered in local woods (Levillain, 1900, 384). However, archaeobotanical evidence, with 175 specimens recovered at Develier in Switzerland, dated to the 6th to 8th centuries, suggests hops were earlier implicated in brewing (Brombacher et al., 1997, 105). The earliest unambiguous references to purposeful cultivation of hops derive from Bavaria; orchards with hop-gardens are documented from 859 onwards at an abbey here (Bitterauf, 1967, I, 666–715). Indeed, in his comprehensive review, Behre finds the mean abundance of hop fruitlets per site increases from 1.3 in Roman times to 209.9 in the early medieval period: surely attributable only to the advent of hop cultivation for brewing (Behre, 1999, 38, 40).

The use of *Myrica gale* in brewing seems to begin declining from the 14th century in all parts of its natural range excluding Britain, with long-lasting hopped beer favoured, principally, for its significant commercial potential (Verberg, 2020, 15). By 1429 it is recorded

that nuns at a monastery in Roermond, (the Netherlands) 'now preferred to drink beer brewed with hop' (Verberg, 2018, 57; Municipal Archives of Roermond, 1429).

Considering the origins of hops' use for brewing in England: three sites in Norfolk are claimed to show an increase in hops / cannabis pollen (these being indistinguishable) in the Anglo-Saxon era; potentially indicating hops cultivation (R. E. Sims, *pers. comm.*, in Wilson, 1975, 637). Famously, a 10th century boat excavated at Graveney in Kent was found to contain abundant partial hop fruitlets (411 in total) and bracteoles (136), which are inferred to have been a part of the boat's cargo (Wilson, 1975, 628).

McKerracher's (2018, 115) comprehensive review of 96 sites with Mid Saxon archaeobotanical remains in the Thames Valley and East Anglia identified only a single occurrence of hops, in 8th to 9th century deposits at the Ipswich emporium, (**section 1.5**). It is plausible that these were imported: the same may be argued for the Graveney boat, in which were also found French or Belgian pottery and fragments of quern-stones from modern Germany – suggesting that the vessel may have been involved in overseas trade (ibid.; Wilson, 1975, 646). There is certainly no unambiguous archaeobotanical evidence for widespread cultivation of *Humulus lupulus*: in Mid Saxon Britain.

Other flavourings used by early medieval brewers likely regularly included fruits, honey and a range of herbs. More obscure substances reportedly utilised include alder tree bark, cinnamon and even fresh egg (Wilson, 1991, 373; Hagen, 2006, 212; Unger, 2007). Tastes of early medieval beers would have been very varied.

3.2.5 Brewing by whom?

It has been asserted, of 'brewing and beer traditions in Norway', that, 'ale brewing is an activity deeply integrated in peasant society' (Nordlund, 1969, 283). Archaeological

evidence for brewing in 3rd to 4th century Namur, in modern Belgium (Deckers, 1970, 448), is cited by Unger in support of his claim that household brewing activity continued unabated in Europe throughout and beyond Roman occupation. He claims, moreover, that, 'in the early Middle Ages, Europe knew virtually nothing other than household production' (Unger, 2007, 24, 26). There is little archaeobotanical evidence to support this, though brewing using household hearths would likely not leave an archaeobotanically detectable signature (Larsson, 2018, 1969)

The first large-scale production of beer in early medieval Europe commenced with the advent of monastic institutions in the 8th and 9th centuries (these were, according to Unger, 'nearly always centres of brewing') (2007, 26). The earliest known explicit reference to brewing in a monastic setting predates this period: a 7th century Frankish religious 'rule' decrees that nuns should daily be involved in manual labour including beer production; beer being their daily drink (Diem, 2021, 106, 115).

Horn and Born posit that, 'Before the twelfth and thirteenth centuries…the monastery was probably the only institution where beer was manufactured on anything like a commercial scale' (Horn and Born, 1979 II p.261). Unger concurs, arguing that monasteries were alone in having access to sizeable volumes of surplus grain and hence also in having capacities for large-scale beer making (2007, 27). The 'St Gall plan' of 820: an idealised design for a monastery, produced in St Gall, Switzerland (**Figure 3.2**), incorporates a malthouse, kiln, mill-room, three breweries and storage cellars (Urion and Eyer, 1968, 43; Horn and Born, 1979 II, 249-264) . It is suggested that three types of ale may have been intended for brewing here: for religious, lay and pilgrims.

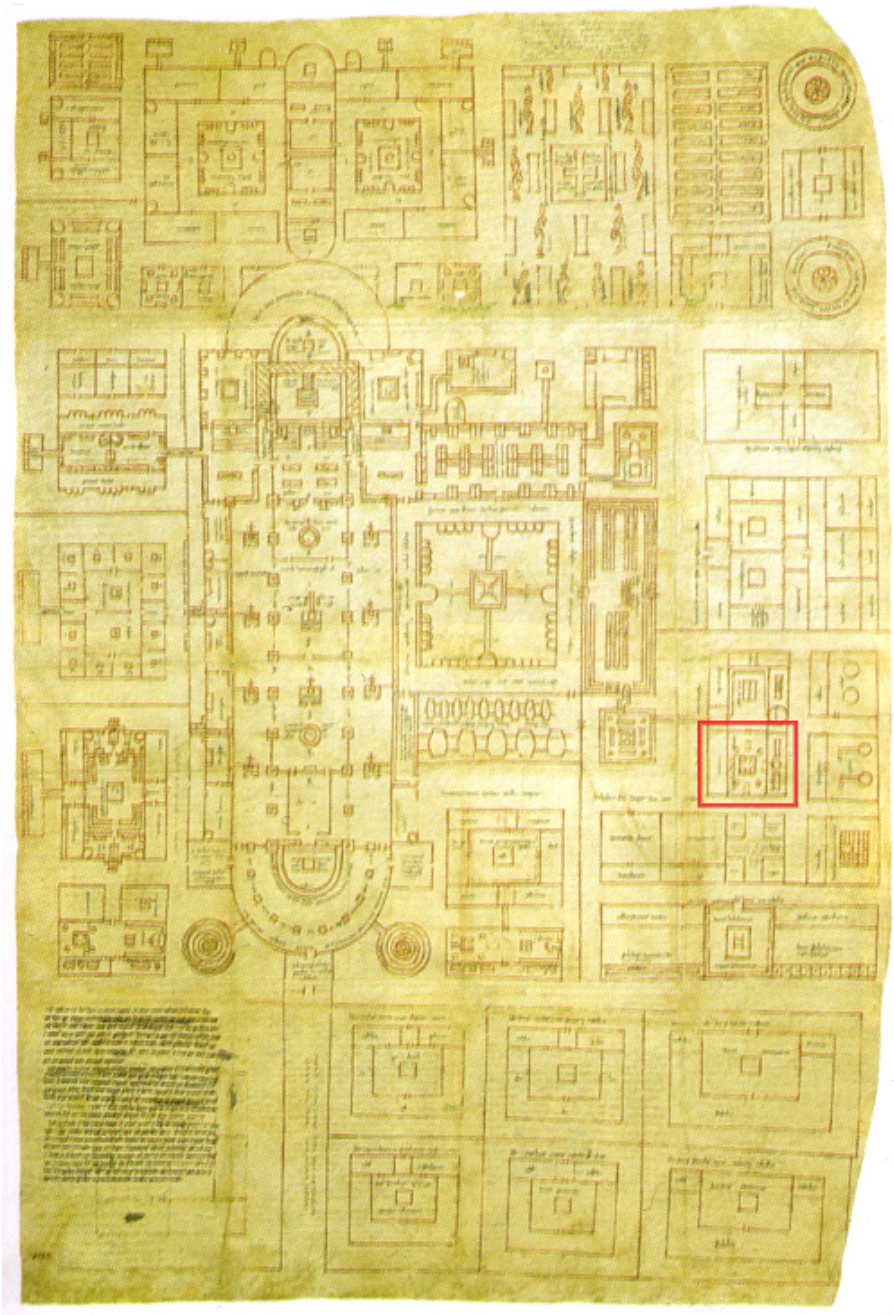

Figure 3.2 The St Gall Monastery Plan, with the brew-house highlighted. The text here reads 'hic fribus con fi ciat ceruisa' – 'here let the beer for the brothers be brewed' (Unger, 2007 p.28) (adapted from Public Domain, https://commons.wikimedia.org/wiki/www/index.php?curid=2259984, accessed:18.11.22)

However there is also much evidence for brewing at high status secular estates; at Higham Ferrers in Northamptonshire 'industrial-scale' brewing seems to have taken place at a

likely royal tribute site (Hardy et al., 2007, 204). A set of late 8th century Carolingian guidelines for the administration of a landed estate specifies that the estate's steward ought to have a brewer amongst his set of skilled labourers (Brühl, 1971 ch. 45). Indeed, Charlemagne himself announced in 778 a plan to expand his entourage to include a trained brewer (Salem, 1880, 15; Hoffman, 1956, 53). The undoubtedly high status (secular) regional centre at Uppåkra, southern Sweden, where kilns dated *c.* 400-685 contained abundant germinated barley grains, is argued to be a site of large scale beer production intended for feasting and potentially trade (Larsson et al., 2018, 1966, 1971).

It is widely held that large-scale brewing at monastic and other estates was by men, but evidence (the later medieval surnames 'Brewster' and 'Maltster' having female connotations) suggests that domestic brewing was undertaken by women (Fell, 1984, 49; Bennett, 1996, 18; Hagen, 2006, 211; Rickett, 2021, 36). Indeed, later medieval A. Fitzherbert refers to malting as a part of the wife's 'duty' (1540, 95). Ethnographic analogies suggest domestic brewing commonly uses between 15-30% of household grain supply (Dietler, 2006, 238).

Finally, early medieval peoples were quite willing to attribute beer-making prowess to supernatural influence. Contemporary records describe ritual practices used by brewers in medieval Sweden, (Salomonsson, 2000, 124), while late 6th century Colmán Elo, abbot of Muckamore, Ireland, apparently miraculously both caused beer to ferment and turned water into beer (Vit. Sanct. Colm., Heist, 1965, 215, 223).

A summary of the methods used for malting and brewing in this era in both the British Isles and continental Europe, compared with modern practices as described in **Chapter 2**, is presented in **Table 3.1**. **Table 3.2** displays, for each stage of the early medieval brewing process, a relevant descriptive quotation from a contemporary (or later pre-industrial) source.

Table 3.2 Summary of stages of brewing as practiced today and in early medieval era Europe (including the British Isles). The expected length of each stage is specified.

Modern methods		**Stage of brewing process**		**'Traditional' methods**		
Practice	**Length of time (days)**			**Practice**	**Length of time (days)**	
Grains pre-processed (cleaned) before steeping and alternately soaked in water and dried during 'air-breaks' when air is blown through.	c. 2[34]	**Malting**	**Steeping** - soaking grains in water	In stone or wooden cistern. Chaff and buoyant seeds 'skimmed' from the water's surface. 'Skimming by-product' may have been used as kiln fuel. Crop material may have been suspended in water using sacking, in which case skimming would not occur.	2.5[35]-3[36]	21[33]
Pneumatic malting, with grains in rotating drums.	4-6		**Germination** - waiting for wetted grains to germinate	Grains 'couched' (piled in small heaps) onto germination floor. Raking used to vary depth of piles according to ambient temperature. Grains regularly turned to give access to air.	14[37]	
Specified set of temperatures for fixed periods of time.	0.6 – 2.5[31]		**Kilning** - heating grains to stop germination	Kiln fuelled by straw and chaff. Grain layered on sticks and straw over hearth area. Kiln watched carefully because of fire risk.	2[34]	
Mechanical agitation	n/a		**De-culming** - removing sprouts and rootlets from germinated grains	'Rubbing' by hand and sieving. By-product (detached rootlets and small seeds) perhaps used as fuel or fodder.	n/a	

[34] I. Hornsey 2013
[35] Hancock and O'Mahoney, 1869
[36] *TEH*
[37] S. Muspratt 1882

Modern methods		Stage of brewing process		'Traditional' methods	
Practice	**Length of time (days)**			**Practice**	**Length of time (days)**
Wet or dry milling. Coarse grinding to leave barley husks intact.	n/a	**Brewing**	**Milling** - roughly grinding grain	By a water-powered malt mill? Coarse grinding to leave husks of hulled grains intact.	n/a
'Decoction' mashing, with a part of the wort at stages removed, boiled and re-added to the mash tun.	0.1[31]		**Mashing** - soaking ground grain (grist) in warm water	In a single mash tun vessel, regularly stirred using a paddle. Water from local source. Herbal flavourings e.g., sweet gale added. Barley/oat? husks form filter bed for lautering.	c. 0.1[38]
Heated using pressurised steam. Hops added.	0.03-0.1[35]		**Boiling** - and adding preservatives	Not performed prior to introduction of hops? Thereafter, in an iron cauldron over a fire.	c.0.05[33]
'Top-fermenting' yeast 'pitched' into hopped wort in fermentation vessel.	2.3-3.1[31]		**Fermentation** -yeast converts sugars to alcohol	Ambient yeast introduced e.g., using a 'totem' stick or by insect vectors. Further fermentations encouraged by skimming foam (barm) from batch and adding to next.	3-9[34]

Table 3.3 Stages of brewing illustrated by quotations from medieval or post-medieval literature, describing methods as then practiced in the British Isles ad continental Europe

Stage of beer-making		Primary source references
Malting	Steeping	'you shall from your pump or well convey the water into the cistern, till all the corn be drenched…and for the space of three nights you shall let the corn steep in the water.' (*TEH,* VII, 25) 'In malting…the light grains and seeds of weeds may be skimmed off in the cistern.' (Mavor, in Tusser, 1812, 47)
	Germination	'malt… is raised in sods, and it should be a fortnight in sods without being raked, and in ridges after being raked until it is dried' (Translated from 7th century Cáin Aicillne, (Hancock and O'Mahoney, 1869, 241)) *'…*but if the weather be temperate and warm, then shall the heap be made thinner…' (*TEH,* VII, 27)
	Kilning	'lay the malt as thin as may be (as about three fingers' thickness) upon the hair-cloth, and so dry it with a gentle and soft fire, ever and anon turning the malt (as it drieth on the kiln) over and over with your hand, till you find it sufficiently well dried' (*TEH*, VII, 27)
	De-culming	'Now…before the winnowing you shall rub it exceeding well between your hands to get the come or sproutings clean away... After it is well rubbed and winnowed, you shall then ree' it over in a fine sieve-… ' (*TEH*, VII, 28)
Brewing	Milling and Mashing	'your malt being well ground and put in your mash vat, and your liquor in your lead ready to boil, you shall then little by little with scoops or pails put the boiling liquor to the malt, and then stir it to the bottom exceeding well together' (*TEH*, IX, 5)
	Boiling	'then to every quarter of malt put a pound and a half of the best hops you can get, and boil them for an hour together' (*TEH*, IX, 5)
	Fermentation	'you shall in the bottom thereof set a great bowl with your barm and some of the first wort…mixed together, that it may rise therein, and then let your wort drop or run gently into the dish with the barm' (*TEH*, IX, 5)

3.3 Consumption

Unger argues that beer was known both to Britons prior to the 5th century (with beer in Wales and Ireland long retaining the non-Germanic names *cwrw* and *courmi,* respectively) and also, most certainly, to the Angles and Saxons arriving in England across the North Sea from the 5th century onwards (Unger, 2007, 23–24). Beer consumption continued unabated thereafter.

3.3.1 Scale of drinking

It has been claimed that the Anglo-Saxons consumed beer on an 'oceanic scale' (Finberg, 1972, 422), and that they were 'addicted to extreme drunkenness' (White, 1860, 12). The English were not alone in their heavy drinking habits. Based on the beer ration for paupers proposed by a 9th century West Francian abbot, Unger calculates consumption per head as in excess of 500 litres per year (Unger, 2007, 29), whilst Scandinavians in the era are described by Foote and Wilson as, 'men of some thirst' (Foote and Wilson, 1980, 166). Of Denmark, it is said, 'great quantities of beer were drunk in the Middle Ages' (Jørgensen, 1986, 69). However, by the close of the Anglo-Saxon period, England in particular was known across the continent for her peoples' heavy eating and over-consumption of drink (Knowles, 1963, 465; Thomas, 2003, 301). In the 8th century, Boniface saw drunkenness as a vice peculiar to the English, 'For neither the Franks, nor the Gauls, nor the Lombards, nor the Romans, nor the Greeks have it' (Tangl, 1955, 171 no. 78); whilst for 12th century John of Salisbury, 'indefatigable drinking has made the English famous among foreign nations' (Miller and Butler, 1986, 56–58).

Indeed, such was the scale of drinking in England that Bede felt led, in his 'Ecclesiastical History' to write disparagingly of, 'even our Lord's own flock, and its pastors...giving themselves over to drunkenness...and other such sins' (*HE* 1969 I. xiv). The church issued several edicts to control drunkenness amongst clergy and religious (Hornsey, 2003, 237). One late 8th century penitential specified that a religious found to vomit the Eucharist through drunkenness should do 60 days penance (Haddan and Stubbs, 1869, v.3, 427 XI no.7). The earliest surviving reference to beer in a Western monastic setting is found in a 6th century penitential, in which the punishment for a brother pilfering beer from the kitchen at night is to stand for three hours in darkness (ibid. v.1, 115, XXII).

Most certainly, however, heavy drinking was not limited to peoples of the cloth; ample beer consumption amongst secular elites is also well attested. Indeed, by the 11th century, bishop Wulfstan expressed in a sermon his conviction that over-eating and over-drinking were bringing about all England's destruction (Swanton, 1975, 122). A set of 14th century Welsh poems includes metaphorical reference to a corn-drying oven as a 'red-clawed' hen that begins the magical conversion of corn into beer *for a king* (Williams and Lewis, 2019, 53; poem 16), whilst the epic Saxon poem *Beowulf* contains four references to the elite retainers of Hrothgar and others being, 'druncen' (Hough, 2004, 303).

3.3.2 Symbolic significance and feasting

Not only was beer heavily consumed, it was across Europe symbolically significant: in old Norse mythology, warriors who reached Valhalla were plied with beer as fitting reward for

their heroism (Phillips, 2019, 97),[38] whilst in medieval Sweden, beer had great significance as a ceremonial drink, vital for marking occasions including political settlements, trading agreements, weddings and welcoming a child (Keyland, 1989, 72). In Swedish, sets of words concluding '-beer' (*-öl*) – including 'roof-topping' (Swedish *taklagsöl*) and 'wake' (Swedish *gravöl*) – were in use by the early Viking era (and remain current to this day), signifying the drink's ceremonial importance (Nylén, 1977, 57). The symbolic significance of beer (along with wine and mead) for the early medieval period's heroic feasting culture is illustrated in a poem describing events of the early 7th century in northern Britain[39] in which bands of warriors are described as fighting, 'in return for mead and ale', with a hero a, 'bedfellow of the beer-hall' (Jackson, 1969, 154, 157).

Ample supply of drink was an expected feature of the frequent and symbolically significant feasts laid on by secular elites across Europe to win favour from retainers and tenants (Hagen, 2006, 409); according to Hagen, feasting 'always involved the consumption of liquor' (ibid., 15) whilst, 'praiseworthy hospitality involv[ed] the supply of unlimited drink' (ibid., 240) (see **section 1.4.1** for discussion of ecclesiastical and secular elites in Anglo-Saxon society). Van der Veen (2003, 412), discussing the symbolic value of luxury foods, highlights that in medieval and other (pre-state) societies which were relatively little stratified,[40] 'luxury' consisted in consuming great quantities of common staples such as meat and beer. It has been said of a later period, but is surely applicable to early medieval times, that 'those who could, gorged themselves; those who couldn't, aimed to' (Weber, 1973, 202). In such a context,

[38] The divine leader of Valhalla, Óðinn, drank beer in the beer-hall, but also enjoyed wine and mead (Unger, 2007, 22).
[39] The surviving text containing this poem does not pre-date the 9th century.
[40] Anglo-Saxon society can be considered 'little stratified' compared to state-led societies.

hospitality featuring luxury foods was used to create or strengthen social relationships, and reify political position (van der Veen, 2003, 413).

Early medieval feasting was associated with a particular set of rituals and traditions. Feasts would take place in a great hall (or, in Old English, *sele/heall*). The significance of drink for feasting is demonstrated in the hall's regular naming as 'beer-' or 'ale-hall';[41] further, (*bēor* being an Anglo-Saxon term for beer) feasting was at times known in England as *Gebeorscipe* (Hagen, 2017, 174).

The order of seating and serving at a formal feast was strictly hierarchical, with drink being offered by a cup-bearer (or Old English *byrele*) according to a carefully prescribed order of precedence, establishing and cementing relative rank, and mutual obligations (Enright, 1988, 179). In a poem from the 10th century *Exeter Book*, it is the estate's lord who is first brought drink, whereas an 11th century hagiography relates that St Martin, as honoured guest, was served from the drinking goblet even before his host at a feast, the emperor himself (Skeat, 1881 St Martin, l.630; Muir, 2000, Maxims I ll.80-84).

In the early medieval period, *byrele* were typically female (Hagen, 2006, 237). Indeed, the 7th century laws of king Æthelbert refer to both *eorls* and *ceorls* having female cup-bearers (*EHD*, 391, no.29 §§14, 16). At Heorot (of *Beowulf* fame) it is the queen herself who bears the cup to king Hrothgar and his guests (Enright, 1988; Liuzza, 2000 lines 612-630).[42] It was not uncommon for an Anglo-Saxon woman at the time to be buried with a 'bucket' pendant –

[41] 'Mead-hall' and 'wine-hall' are also found in literature from the period (Hagen, 2017, 174).
[42] Queen *Wealhtheow* serves her husband, king Hrothgar and his guest the warrior Beowulf at Heorot in lines 612-630. Later, 'wise and discreet' queen *Hygd* similarly plies Beowulf and her husband Hygelac, king of Geat, with drink at their 'noble hall' in lines 1978-1981 (Liuzza, 2000)

perhaps symbolic of her role as a server of beer or ale (Meaney, 1981, 166–168).[43] Women's significance in the era's heroic drinking culture is further indicated in Scandinavian so-called 'valkyrie' amulets – each depicting a cup-bearing female; the pair recovered at Öland in southern Sweden, (dated to 950-1000), being typical examples.[44]

3.3.3 Burials and material culture

There are several known richly-furnished so-called 'princely' burials in England dated to between *c.* 580-630 containing drinking vessels and other feasting paraphernalia: best known examples include Sutton Hoo and also the recent excavations at Prittlewell (Geake, 1992, 85–86; Carver, 2017; Blackmore, 2019). Drinking and feasting paraphernalia from the near-iconic early 7th century burial mounds at Sutton Hoo (Suffolk) include silver and bronze bowls, cauldrons, dishes, a sizeable wooden tub, three buckets, two sets of wooden drinking vessels and, famously, a pair of drinking horns (e.g., Comey, 2013, 107). The Sutton Hoo horns, decorated with incised silver gilt, have been interpreted as Scandinavian in origin and argued to be royal regalia, for use in ceremonial settings (Neuman de Vegvar, 1992).

'Grave-goods', as they are often termed, have been understood symbolically to represent the deceased's identity during their life and at death, and to accompany the deceased into the unknown realm beyond (e.g., Dickinson, 2011, 1). 'Princes' buried with drinking and feasting equipment were likely communicating a lifetime of feast-hosting largesse, in hopes

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[43] T. Dickinson describes 12 miniature buckets identified with a female buried at Bidford-on-Avon, Warwickshire. These are interpreted as 'amuletic' with 'magical or symbolic functions' and the woman herself she terms a 'cunning woman' (Dickinson, 1999, 363–366)

[44] 'Valkyrie Pendant 266707', Historiska museet, 2011, https://mis.historiska.se/mis/sok/fid.asp?fid=266707&page=2&in=1 [accessed Feb 25, 2022]
'Valkyrie Pendant 108864', Historiska museet, 2011, https://mis.historiska.se/mis/sok/fid.asp?fid=108864&page=1&in=1 [accessed Feb 25, 2022]

that political and social consequence gained thereby somehow be sustained in life beyond death.

Not only do drinking vessels buried with the dead convey the significance of drinking to early medieval elites; they grant an invaluable 'window' for the study of material culture associated with the then consumption of beer and other drinks. 'Drinking horns, customarily filled with either mead or beer, occur across Europe in graves from at least the early Roman Iron Age (Splitter, 1952, 257; Klindt-Jensen, 1957, 123; Klingenberg et al., 2017, 134). An elaborately carved wooden flask recovered from a 6th century grave at Trossingen-Stohrenhof in southern Germany was found to contain a residue with abundant *Hordeum* pollen grains along with, tantalisingly, a single grain of *Humulus lupulus*; it was almost certainly used for beer (Rösch, 2008, 234–235).

To be proffered drink in a horn was arguably a sign of high status (Hagen, 2006, 238). In the 13th century Middle English romance *King Horn* a king's daughter is offering the ceremonial drinking horn to the assembled guests at her wedding feast, but, when approached by one she believes to be a beggar, presents him rather with drink in a bowl, as more befitting his status (Herzman et al., 1999, ln. 1131-1134).

3.3.4 Beer and ale

For, in early medieval society, beer was most certainly consumed not solely by elites. 'Beer', as understood today, and Anglo-Saxon *bēor* (or Old Norse *bior*) are not wholly equivalent. Though 'beer' and 'ale' are now used synonymously, it is widely recognised that in early medieval times there was a distinction between *bēor*/*bior*, believed to be a strong and sweet liquor consumed by the elite, and *ealu* (Old Norse *alu*) or ale, a less alcoholic drink widely imbibed, often as an alternative to water (Fell, 1975; Hornsey, 2003, 251–259; Hough,

2004; Unger, 2007, 22; Pajic, 2019, 285–286).[45] A distinction was drawn between beer and ale in Old Norse sagas: *bior* was a drink for the gods and *alu* for people (Hoffman, 1956, 42–44; Unger, 2007, 22). Across Europe, ale – drunk by everyone including children – was perceived as the inferior drink (e.g. Skaarup, 1993, 134; Brettell et al., 2012, 779). In his *Colloquy*, Anglo-Saxon abbot Ælfric is recorded as asking his 'schoolboy' charge, Ælfric Bata, what he drinks; the latter responds, 'Ale if I have it, or water if I have no ale' (Garmonsway, 1991, 47; see also Doyle, 2022, 47). Indeed, it is conjectured, for Anglo-Saxon England at least, based on a dearth of references in contemporary documents to *bēor* malt (when there are frequent mentions of ale malt) – that *bēor* in the era may generally not have been cereal-based (Hagen, 2006, 200–202).[46]

Old English includes an extensive list of compound terms which include *bēor* and *ealu*; including *bēorbyrde*, *bēorsceal, brydealu, ealuclyfac, ealugāl, ealuscop*; (translating, respectively, as 'cellerer', 'reveller', 'wedding feast', 'beer-cellar', 'drunk with ale', and 'singer in ale houses'). These 'emotive' words are cited as evidence of the high regard in which these drinks were held in the period (Fell, 1975, 79; Hagen, 2006, 234).[47] Ale (*ealu*) is the most commonly-mentioned liquid in Anglo-Saxon leechdoms, and was recognised at the time not only for sating thirst and treating maladies, but also as a source of nutrition (Cockayne, 1864 v. 2 leechbook 1, 78, 120, 136; Kelly, 1997, 133). Hildegard clearly perceived beer as both food and medicine – recommending barley or wheat beer for the treatment of lameness, whilst also voicing concerns about redness of face and fatty tissues caused by over-consumption

[45] Having to drink water alone was seen as a deprivation (Hagen, 2006, 197).
[46]It is possible that bēor is best translated as 'cider' (Hagen, 2006, 200–202).
[47] Similar compound terms existed for 'win' and 'meodu'.

(Schipperges, 1957, 191–195, 233). Evidently, beer was 'a drink of great social importance' (Kelly, 1997, 332).[48]

3.4 Exchange

In contrast to the dearth of documentary evidence from the time for brewing methods, there are frequent references (including in Anglo-Saxon royal charters) to ale and malt given as gifts, dues, and, above all, commanded as tributes by secular and ecclesiastical authorities (Hagen, 2006, 208–209; Hardy et al., 2007, 204; Unger, 2007, 24). For instance, Ine, a West Saxon king reigning from 688 to 726, issued an early set of laws with a clause specifying that a particular tenant, as rent for ten *hides* of land, should pay dues including, '12 "ambers" of Welsh ale, and 30 of clear ale' (*EHD* no.32 §70.1). Æthelwyrd, king of East Anglia, (living until 854), left one day's food rent to the monastic community at Bury St Edmund's (in modern Suffolk) every year, including forty *sesters* of ale. Royal food renders at Berkeley, Gloucestershire, in 883 consisted of – amongst other things – *bēor*, *ealu* and honey (S218; Finberg, 1972, 49–50). The many references to rents paid in malt include the following: Æthelgyfu, abbess of Shaftesbury, left land to Ælfwold on condition that he gives every lent, 'six *mittan* of malt' (Whitelock, 1968, 8) – equally, Leofsige, bishop of Worcester was required to pay annually either three days food rent to the abbey at St Alban's, or a set of items including sixteen *mittan* of malt (ibid., 10). Further, a will fragment from Bury St Edmunds afforded 'five ores for malt…for the first funeral feast' (Robertson, 1939, 253, VIII). Significantly, it has been suggested that the wording of renders and dues as recorded in Welsh

[48] In his review of literary references from the era, C. Doyle concludes that ale-houses, or '*ealahuses*' became a feature of the English landscape, 'only in the last century and a half before the Norman Conquest' (2022, 51).

charters from the 7th and 8th centuries onwards implies that early medieval estates were commonly classified based primarily on their beer-producing capacities (Comeau and Burrow, 2021, 116).

Concerning transporting beer and malt, the very great cost in the era of transporting bulky goods overland as opposed to by water is noteworthy (Unger, 2007, 59). Some transport must have taken place over land, however; 7th century Irish St Maedóc is recorded as driving a wagon full of beer (presumably made by local lay people) to his monastery (Plummer, 1910, I, 146, 299).

Across Europe, local exchange and trade in beer and its components was widely practiced. As St Maedóc's story tells us, early medieval monasteries in Europe often did not produce all their own malt and beer, but commonly purchased these from external local cultivators (Nelson, 2004, 65). For instance the monastery of St Denis (Francia) in 832 received from surrounding farmland more than 392 modii of malt (*bracis*) and 44.5 modii of hops (*umlonis*) – sufficient for the brewing of at least 55,000 litres of beer (Levillain, 1909, 87–88).

Arthur and Sindbaeck argue that evidence for long-distance trade – in bulk cargo such as grain (and we can, surmise, malt) – is 'inconclusive' before the 10th century (2007, 312). Intriguingly, an excerpt from the 7th century *Life of Abbot Columbanus* mentions a shipment of 'one hundred measures of wine, two hundred of (wheat) grain, and one hundred of beer' between northwest France, and Ireland; Doherty interprets this as suggesting regular sea-transport of beer and grain in the 7th century (O'Hara and Wood, 2017, 149; Doherty, 1980, 77). Strikingly, reviewing evidence on international trade from Mid Saxon emporia, Blair concludes, 'it was as channels for bulk exports that they really mattered' (2018, 166).

A final consideration: records from *Calendars of patent rolls* and *Calendars of close rolls* suggest King's Lynn (in northwest Norfolk, ~15 miles from Sedgeford), was 'shipping quantities of corn, together with malt and ale made from it, throughout the thirteenth century and even earlier' to Scotland, France, Belgium, Holland, Denmark and Norway (Carus-Wilson, 1962, 185; Maxwell-Lyte, 1902, 356. 397; Maxwell-Lyte, 1908, 247). Indeed, Lynn customs lists from *c.* 1300 demonstrate that malt was then the item after textiles most commonly exported from the port town to Norway (Blom, 1966, 305–308). Lynn was not founded until the 12th century; however one can speculate as to for how long 'Eastern zone' trading centres had been involved in exporting malt and ale. The question of whether malt and even beer or ale were exchanged via sea-routes in the era, specifically from the East coast of Anglo-Saxon England with littoral continental Europe, will be further considered (**section 8.6**).

3.5 Summary

Striking parallels in the 'stories' of beer in Anglo-Saxon England and early medieval continental Europe strongly suggest that beer production and consumption practices in Europe largely predate the 5th and 6th centuries dispersal of Germanic tribes and their associated customs across the continent (e.g., Ward, 2001, 1). To indicate the scale of both production and consumption of beer: by the other end of the Anglo-Saxon era (10th century), it is argued, based on evidence from Ælfric's *Colloquy* and elsewhere that (in England at least), cereals were the single most important component of daily diet – vitally important for both bread and beer (Garmonsway, 1991, 40; Hagen, 2006, 41). According to Salzman (1913, 185), ale was in medieval England judged so significant it was 'coupled with bread for purposes of

legal supervision';[49] quite rightly does he describe ale in the era (and surely also Anglo-Saxon times) as 'the people's food in liquid form' (ibid.).

[49] This is based partially on evidence for local courts holding the 'assize of bread and ale' (ibid.)

4 MID SAXON SEDGEFORD

4.1 Introduction

Having 'set the scene' for malting at Mid Saxon Sedgeford by examining the socio-political and economic life of Anglo-Saxon England (**Chapter 1**), some key concepts in beer-making and types of evidence for malting, brewing and beer drinking (**Chapter 2**) and the early medieval history of brewing, beer consumption and exchange in England and beyond (**Chapter 3**), this chapter introduces excavations and discoveries to date at the archaeological site of Sedgeford *per se*.

4.2 Sedgeford: a background, and excavations to date

The archaeological site which is the focus of this study lies in the southern part of the parish of Sedgeford, six km inland from the coast of northwest Norfolk, in East Anglia (**Figures 1.2** and **4.1-4.2**). The contemporary parish of Sedgeford lies on a low-lying north-south aligned escarpment (Davies, 2010a, 94). The region overlies Upper Cretaceous Middle Chalk bedrock (**Figure 4.3**), and 18th century Parliamentary Enclosure Acts record the soil at Sedgeford as poor[50] – due likely to its high sand content (Chatwin, 1961, 32).

[50]As noted in the 1795/97 Parliamentary Enclosure Committee report (sourced from Norfolk County Records Office).

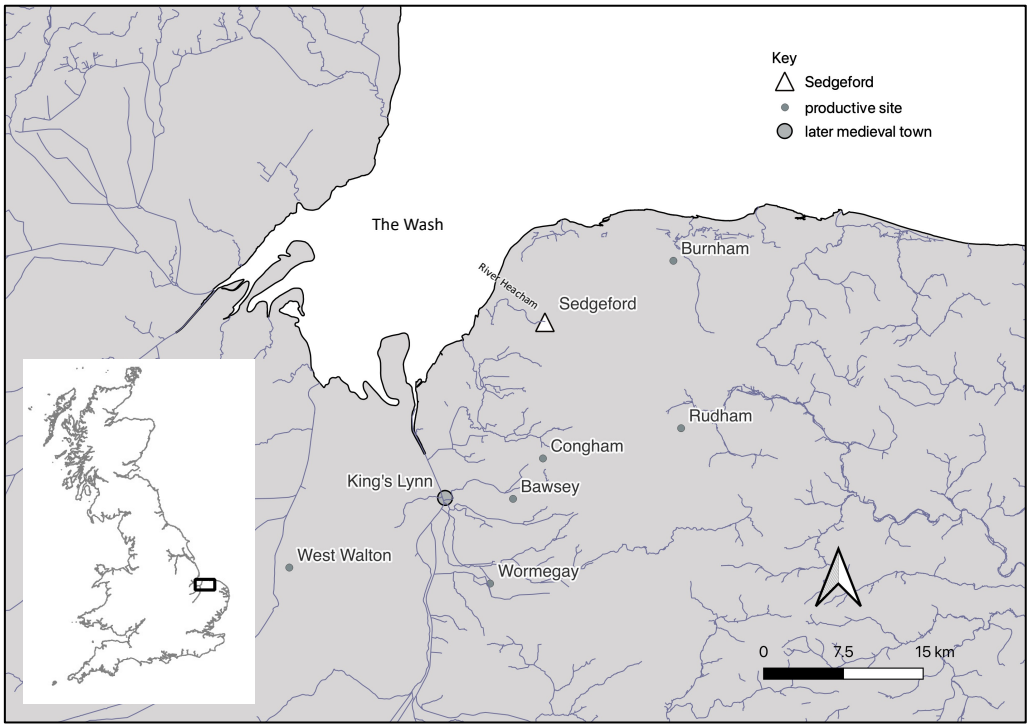


Figure 4.1 Sedgeford and surroundings, showing local water courses as at present. Contains Ordnance Survey Open Data © Crown copyright and database right 2017, under the Open Government licence. Map created with QGIS (http://www.qgis.org; accessed 4/01/2023).

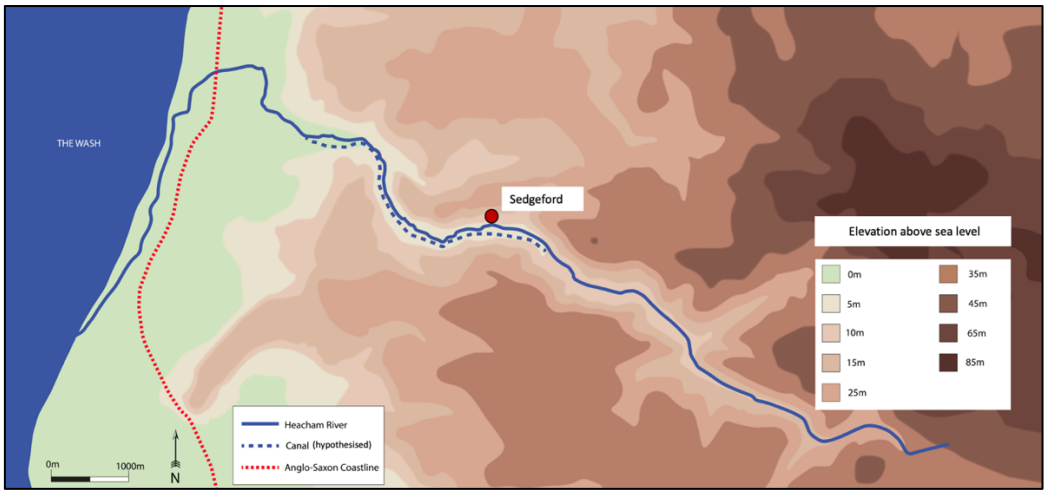


Figure 4.2 Sedgeford and surroundings (larger-scale) showing elevation, river Heacham, and hypothesised canal course. Adapted from image shared with kind permission by Gary Rossin, 2023.

The 'Western escarpment' is traversed by the valley of the Heacham River which flows to the coast through the parish (**Figures 4.1-4.2**) – an important east-west communication-route in Mid Saxon times (Faulkner et al., 2014, 13). There existed two north-south routeways in this part of Anglo-Saxon west Norfolk: the prehistoric Icknield Way and the once Roman military road Peddars Way, which bypasses contemporary Sedgeford (Gregory, 1982, 354; Faulkner et al., 2014, 13). In contrast, the extensive fenland to the southwest of Sedgeford would have represented a major barrier to movement (**Figure 4.3**) (Faulkner, 2022, 163 Figure 40).

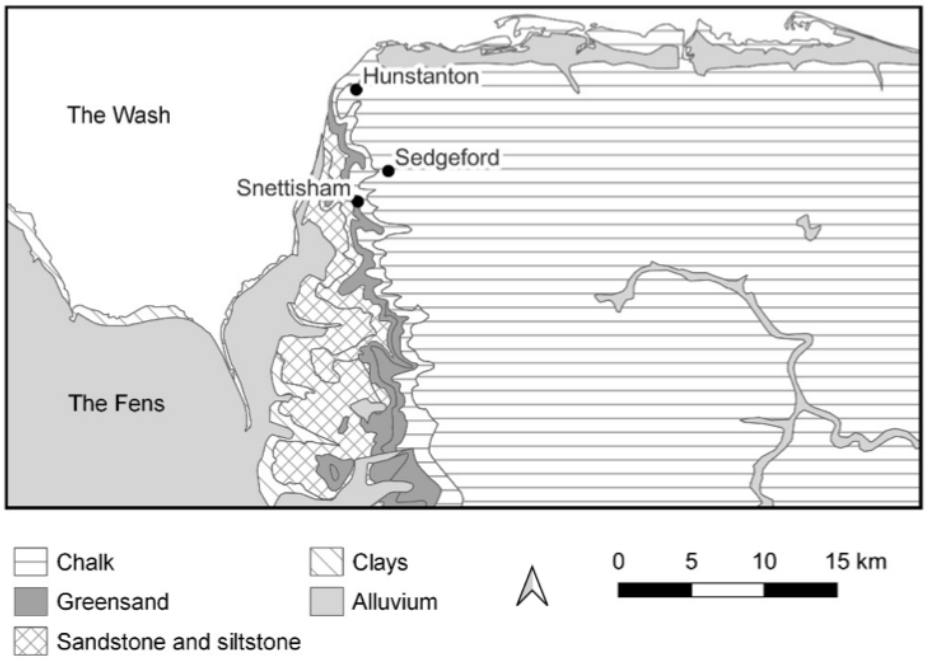


Figure 4.3 Geology of the area surrounding Sedgeford. Reproduced (adapted) with kind permission from Faulkner, (2022, 163, Figure 40). Contains BGS Geology 625K Data © UKRI 2021, sourced via BGS Digital Data under the Edina Licence; and Ordnance Survey Open Data © Crown copyright and database right 2017, under the Open Government licence.

Recent archaeological excavation began at Sedgeford in 1996, under the aegis of the Sedgeford Historical and Archaeological Research Project (SHARP). It should be noted that the excavations and interpretations described here are as of the 2021 season. Initially the project focused on the partial excavation of a Mid Saxon period cemetery, containing up to 1,000 inhumations (**Figure 4.4**) (Faulkner et al., 2014, 2; Jolleys et al., 2019, 75; Faulkner and Blakelock, 2020, 68). The graves were oriented east-west and, excepting two, were entirely without grave-goods; the conclusion that this was a Christian cemetery seems inescapable (Faulkner et al., 2014, 92).

From 2007, focus shifted south-wards, to an area where magnetometry survey (**Figure 4.5**) indicated a likely settlement (Faulkner and Blakelock, 2020, 68). Excavation at this 'settlement' site revealed likely occupation from the late 7th until the 11th centuries (Jolleys et al., 2019, 72), with several distinct phases. Significantly, phases 5 and 6 (the later 8th to early 9th centuries) seem to have witnessed a major re-organisation of the settlement, with construction of north-south aligned buildings of standard size, on rectilinear boundaried plots (Faulkner et al., 2014, 115). Post-holes for several of these imply substantial 'hall' structures (Faulkner and Blakelock, 2020, 68). Radiocarbon dating of two grain samples from contexts within the settlement area returned dates of cal. AD 774-887 (95.4% confidence) and cal. AD 800-896 (69.5%) respectively (McKerracher, 2022a).[51] Date ranges and associated plans for identified phases of the Mid Saxon sequence at Sedgeford are displayed in **Appendix B.**

[51] Calculated age BP for these samples is 1193±19 and 1174±20, respectively (McKerracher, 2022a, 1).

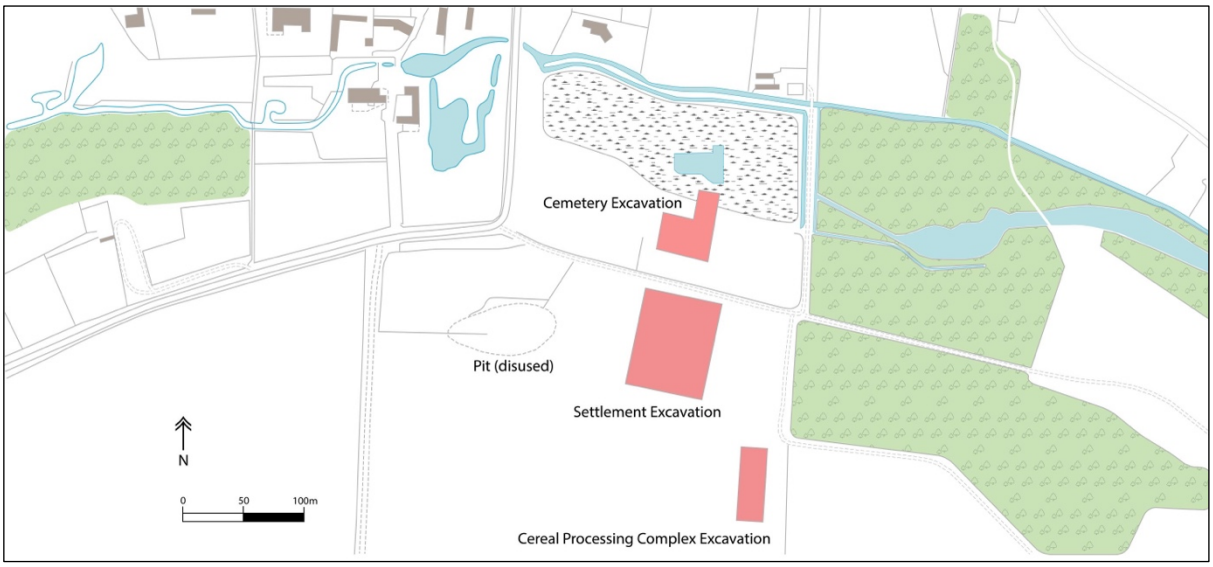


Figure 4.4 Approximate locations of key areas of excavation, 1996-present, as part of the SHARP (Image: Gary Rossin / SHARP)

In 2013, excavation in a gully southeast of the settlement site investigated magnetometry survey anomalies (**Figure 4.5** – Trench 23) (Jolleys et al., 2019, 73). Early evaluation here revealed rich deposits of charred grains, accompanied by kilns and associated structures, implying a cereal-processing complex.

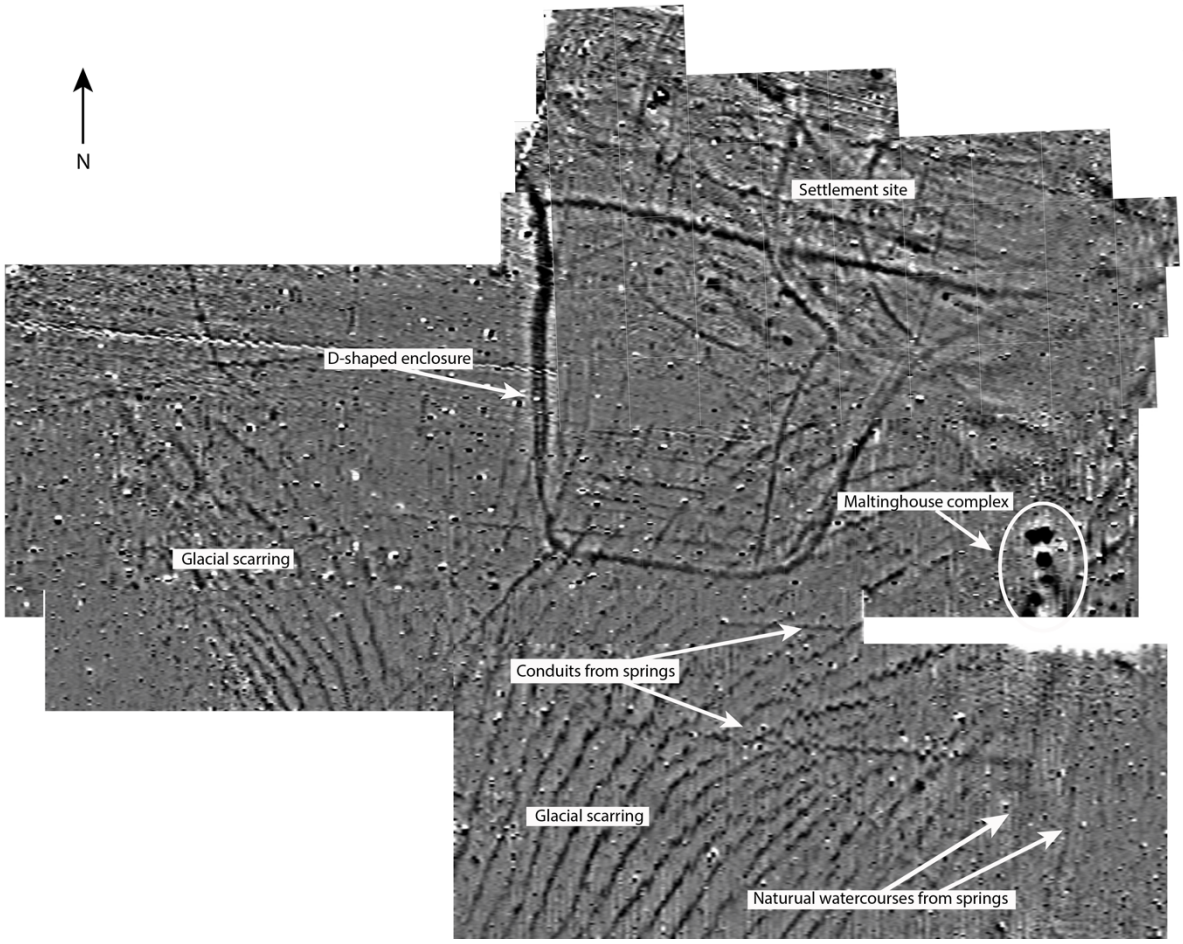


Figure 4.5 Results of geophysical survey of Lower Chalkpit field, Sedgeford, created using magnetometry. Key features, including the malting complex, are highlighted. (Image: D. Wood, M. Barham, SHARP 2007)

4.3 The Mid Saxon cereal processing complex at Sedgeford

Trench 23 lies in a relatively steep-sided, small gully at the bottom of a chalk hill, sloping slightly downhill to the north, and has a sand-gravel subsoil (Faulkner and Blakelock, 2020, 69). A complex of built structures here was covered by a layer what Faulkner and Blakelock contend is 'plough-soil', with both the features and plough soil layer characterised ceramically by Ipswich ware alone, and hence datable to the Mid-Saxon era (ibid.). The entire

gully was 'sealed', and these layers preserved, by what seems to be later medieval colluvial in-wash (ibid.). The excavators note a lack of vertical stratigraphy in this part of the site, and it has consequently been surmised that all features derive from the same phase of activity (N. Faulkner, *pers. comm.*).

Ongoing excavation at the complex has uncovered at least three kiln structures, with emerging evidence for further kilns. Early archaeobotanical analysis of charred plant material implied that a high percentage of grains here show signs of germination – indicative of malting (**section 2.4**) (Wolff, 2017). This led to the kilns being reinterpreted as, specifically, malting kilns, with associated features now understood to represent one or more steeping cisterns and several germination floors (up to six have been tentatively identified) (Caroe, 2022, 194). Kilns 1, 2 and 3, with associated features, are marked in the aerial photograph (**Figure 4.6**).

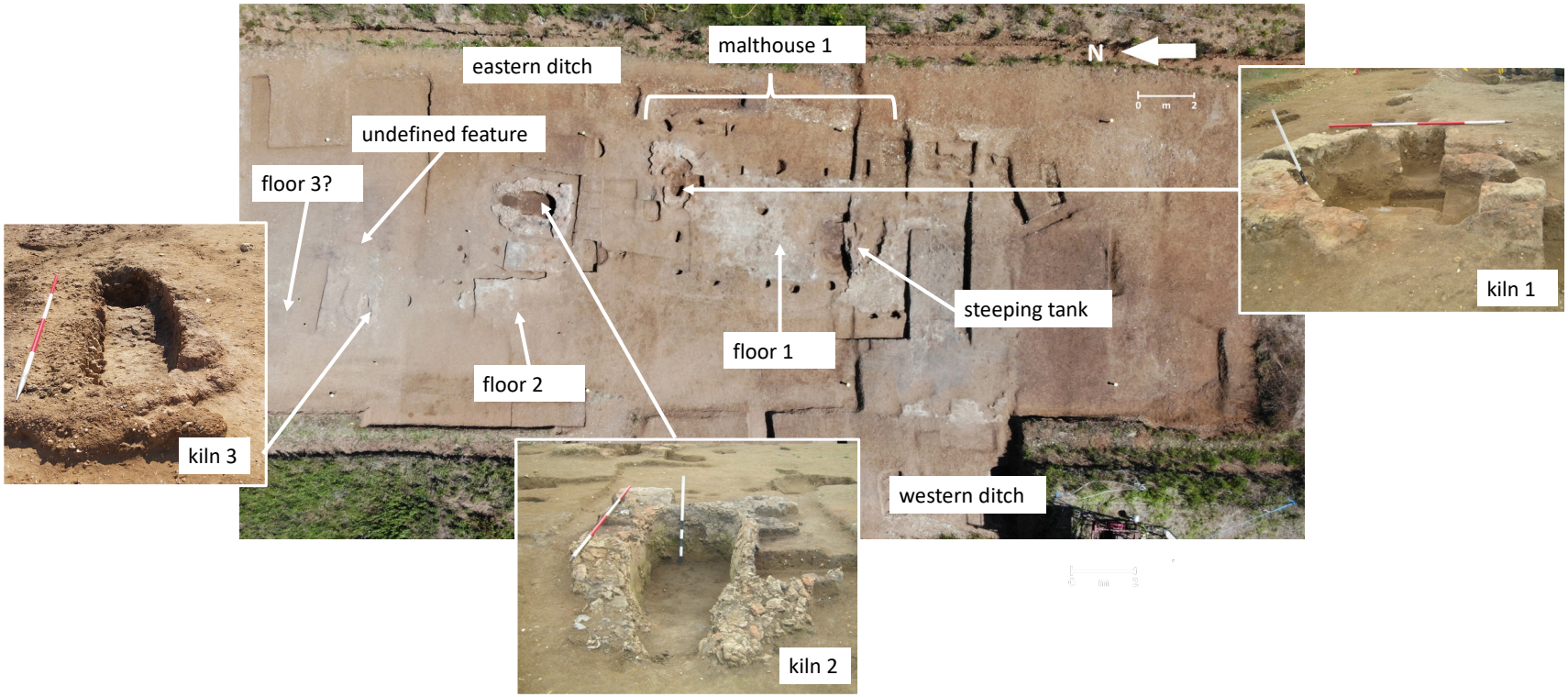


Figure 4.6 Aerial photograph of malting complex (taken 4.7.19), with primary features highlighted, and inset photographs of kilns 1, 2 (taken 6.8.19) and 3 (taken August 2021) (Image: Ian Drummond/ SHARP 2019)

Kiln 1, with a hypothesised steeping cistern and clay-lined germination floor – and associated post-holes – together comprise 'malthouse 1', as shown in **Figure 4.7**. Kiln 1 (**Figure 4.8**) is positioned east-west, and (as is each of the kilns) constructed from clay wattle-and-daub. Its outer dimensions are 3.0m x 2.1m, with the internal drying chamber oval shaped and measuring 2.1m x 1.9m, with a depth of at least 0.46m.[52] The kiln is argued to have been worked from a 1.0m opening on the western side. Daub remains and the configuration of the kiln suggest this was originally covered by a domed wattle-and-daub superstructure (Blakelock and Caroe, in prep.).

The hypothesised kiln 1 germination floor (**Figures 4.6** and **4.7**) comprises puddled grey clay up to 0.1m thick, and measures approximately 4.5m north-south and up to 3.5m east-west (Faulkner and Blakelock, 2020, 81).[53] The clay surface is raised by about 2.5cm on east and west sides (Jolleys et al., 2019, 73), forming a 'lip' where the floor met the surrounding wall. The supposed steeping tank feature to the south of the clay floor comprises a semi-circular depression, a rectangular structure in the depression – characterised by burnt daub and carbonised timbers, with a further clay floor (possibly a working surface) to the south and an adjacent clay 'ramp' to the west (Faulkner and Blakelock, 2020, 77).

Malthouse 1 is defined by several post holes (up to six) (**Figure 4.7**). The two postholes representing the eastern wall of the drying area are significantly larger than others (the smaller of these measuring 0.51m x 0.40m), and have been interpreted as having contained support posts for a raised floor, above the kiln, supporting the drying chamber in which the drying grain was lain (**section 1.4.5**) (Faulkner and Blakelock, 2020, 84–85). There

[52] The fill of the drying chamber may as yet not have been fully excavated.
[53] The entire extent of the germination floor may not yet have been excavated (Faulkner and Blakelock, 2020, 81).

is strong evidence – from carbonised in situ timbers and burnt wattle-and-daub in both the kiln walls and surrounding collapse (including infill in the supposed steeping cistern) – to suggest that malthouse 1 burnt down and was not replaced in the same location (Faulkner and Blakelock, 2020, 74).

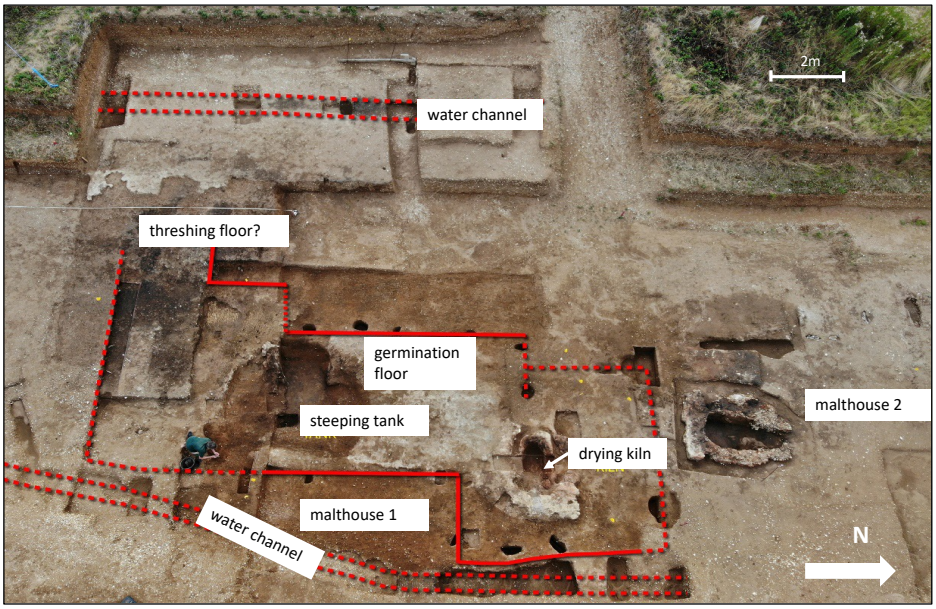


Figure 4.7 Photograph of malthouse 1showing interpretation of structural features as understood in 2019 (Image: Ian Drummond and Gary Rossin SHARP 2019)

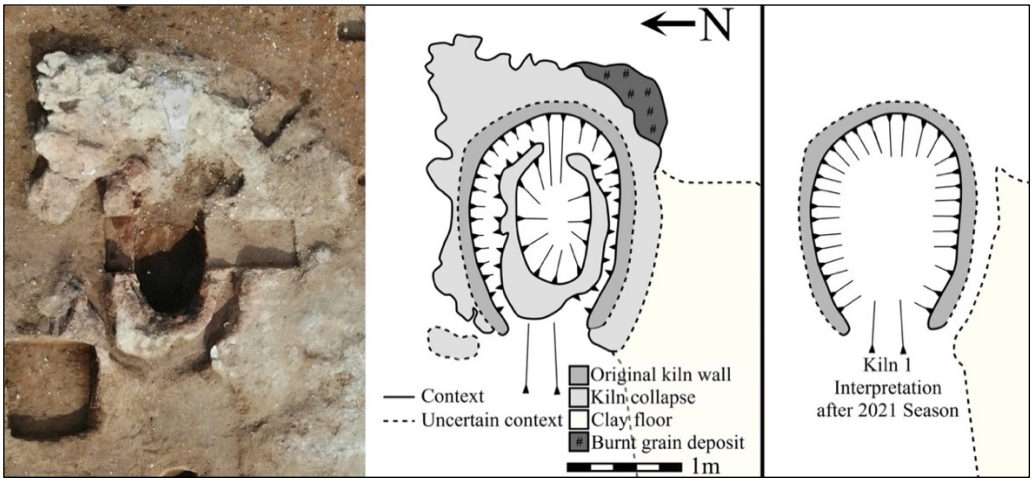


Figure 4.8 Photograph and plan showing kiln 1, with interpretation at close of 2021 season (Images: Eleanor Blakelock/SHARP 2022, Photo': August 2021)

Malting kiln 2 (**Figure 4.9**) lies to the north of malthouse 1, and is aligned north-south, with a stoking area to the north. The maximum dimensions of the interior are 2.4m by ~1.2m. The maximum chamber depth is 0.68m, (the kiln floor is considerably deeper than those for the other kilns). The broadest part of the clay daub wall lining the chamber is 0.55m in thickness; however, as shown in **Figure 4.9**, much of this 'wall' is surmised to be collapse of the kiln's wattle-and-daub superstructure. There is some evidence for daub re-use in the kiln's construction (Blakelock and Caroe, in prep.). Analysis of daub from kiln 2 implies use of relatively sophisticated techniques and equipment for the period – including a saw – in construction of the kiln – suggesting that, as hypothesised for 'monumental' drying ovens elsewhere in Mid Saxon England (**section 1.4.5**), the Sedgeford kilns were perhaps constructed by itinerant specialists (see McKerracher, 2014a; Faulkner and Blakelock, 2020, 85). An area of puddled clay to the west of the kiln is hypothesised to be an associated germination floor.

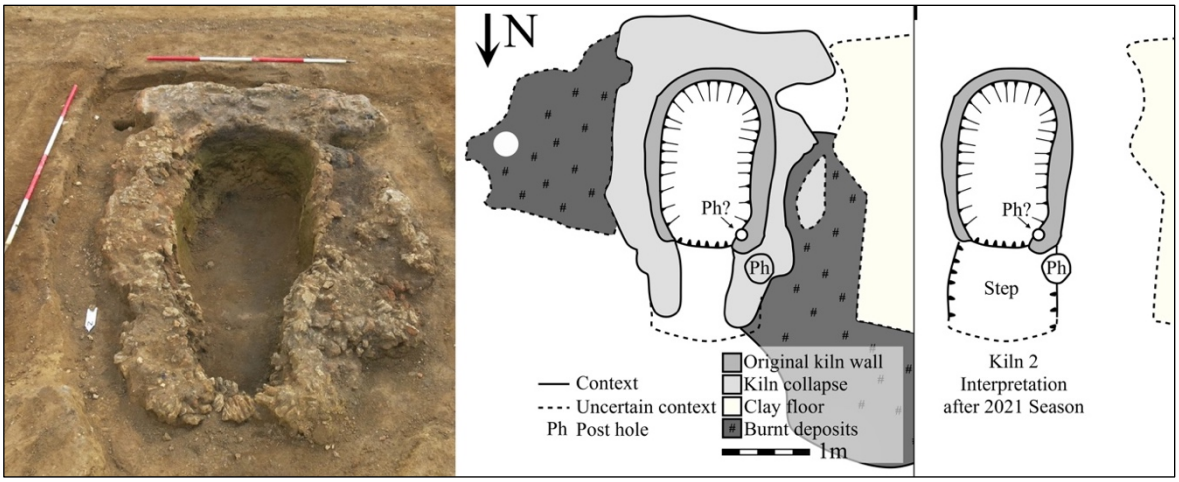


Figure 4.9 Photograph and plan showing kiln 2 , with interpretation following 2021 season (Images: Eleanor Blakelock/SHARP 2022, Photo': August 2021)

Concerted excavation of hypothesised kiln 3 (**Figure 4.10**), at the northern end of the trench, began in 2019. The inner drying chamber in this structure measures, at a maximum, 1.05m x 0.52m. The fill of the chamber has yet to be fully excavated. A clay-and-daub area to the north and east of the kiln structure was originally hypothesised to be an associated germination floor. Subsequent excavation (including of an overlying clay layer) has engendered a re-interpretation of this area, now understood to include a built structure – hereafter termed the 'undefined feature'. Further, a clay floor recently exposed to the north of kiln 3 is currently tentatively hypothesised to represent the malthouse 3 clay germination floor (**Figure 4.6** and **Figure 4.10**).

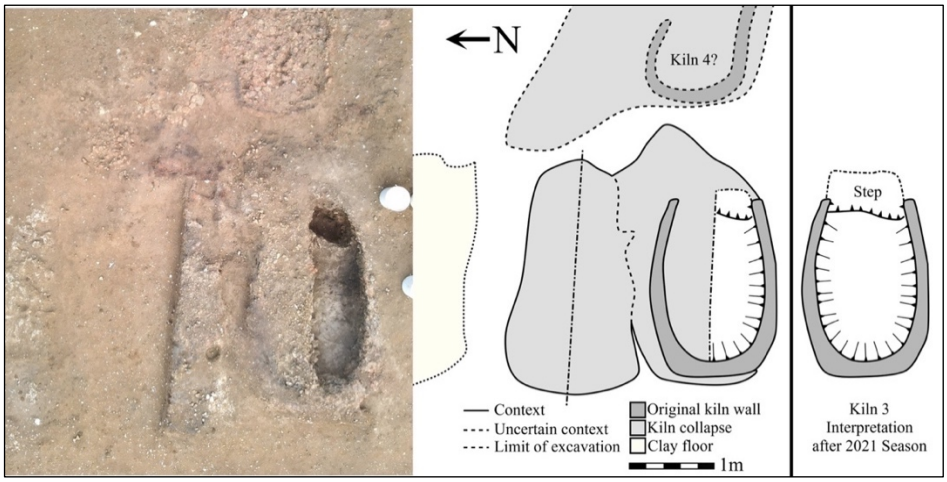


Figure 4.10 Photograph and plan showing kiln 3 , with interpretation following 2021 season (Images: Eleanor Blakelock/SHARP 2022, Photo': August 2021)

In terms of typology, all three kilns compare most favourably with the 'oval / circular' corn-dryer type as described by Comeau and Burrow (2021, 113; R. Comeau, *pers. comm.*) (**section 1.4.5**). According to Comeau and Burrow, this would suggest, for each of the Sedgeford kilns, that the firing area was in the kiln 'pit', with the drying area likely occurring over the shallow extension (ibid, 122, 125).

A final feature of Trench 23: two Mid Saxon ditches running down the east and west sides of the gully, respectively (**Figure 4.5**), are argued to represent features for management of water arriving from springs to the south (**Figure 4.4**). It is suggested that these were designed to protect the malting complex from flooding and colluvium deposition, and as a source of water for steeping (Faulkner and Blakelock, 2020, 75). Two distinct carbonised layers are apparent, most clearly in the western ditch, suggesting the malting complex experienced at least two distinct burning events (E. Blakelock, *pers. comm.*).

4.4 Material culture 'finds'

The malting complex is a 'clean' trench, with few material culture finds, whilst the site as a whole is, for the area, coin-poor with few 'high status' objects (Jolleys et al., 2019, 76). Certain of the finds are pertinent to this project. Firstly, the discovery of two large iron hooks close to the steeping tank in Trench 23 supports a hypothesis that sacks of grain were suspended for steeping in the water-filled cistern (**Figure 4.11**) (Jolleys et al., 2019, 73; Faulkner and Blakelock, 2020, 85; Blakelock and Caroe, in prep.). Secondly, two writing styli have been recovered from the cemetery area: fashioned from copper-alloy and iron respectively (Faulkner et al., 2014, 113; Jolleys et al., 2019, 76). Styli at other Mid Saxon sites, including Flixborough, have been associated with elite ecclesiastical oversight, although this is somewhat contentious (Loveluck, 2001, 100, 112–113).

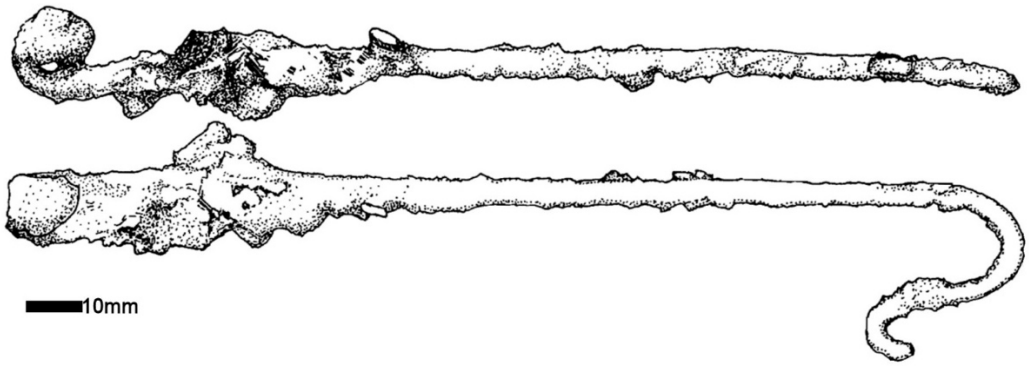


Figure 4.11 One of two iron hooks recovered from the vicinity of the Sedgeford steeping tank (Image: Ann Smith, SHARP 2021)

Three further categories of 'find' imply connections between Sedgeford and continental Europe in the era. Fragments of basaltic quern stone, recovered at the site, likely originated in Germany (Ogden, 2021). Further, 18 sherds of vessel glass, probably representing globular beakers, claw beakers, palm cups and perhaps bowls, and all surmised to date from the 8th century, have been recovered from the cemetery and settlement excavations (Faulkner et al., 2014, 114). Consensus suggests that western Europeans were not creating glass from raw materials in the era: rather, vessels were fashioned from ingots imported from the Near East or through recycling (sometimes Roman) glass. Faulkner *et al.* conjecture that some of the sherds may have been imported from northwest Europe (ibid.) Finally, and significantly, one among the sparse numismatic finds at the site is a rare Frankish coin: a denier of Pepin III (*c.* 755-768) (Faulkner et al., 2014, 126).

4.5 Dating the malting complex

The malting complex was initially dated by a ceramic 'signature': both the features and overlying plough-soil are heavily dominated by Ipswich ware (sparse sherds of later Anglo-

Saxon pottery are believed to be residual) (Faulkner, 2019). This gives a maximum date range of *c.* 725-850. In 2019, radiocarbon dating was carried out on three samples, each of three rye grains, from kilns 1, 2 and 3, respectively (**Table 4.1**) (McKerracher, 2022b). Dates were calibrated using IntCal20 (Reimer et al., 2020) and OxCal 4.4.2 (Bronk Ramsey, 2009), and modelled assuming the earliest (*c.* 725) and latest (*c.* 850) dates mandated by Ipswich ware in the trench.

Table 4.1 Results of radiocarbon dating on samples from the malting complex.

Kiln	Context / sample	Material	Age BP	Calibrated years AD	Modelled years AD (confidence)
1	17026	3 rye grains	1318 ± 18	657-703 @ 51.8%, 740-774 @ 43.7%	748-770 (68.3%)
2	19061	3 rye grains	1269 ± 18	672-777 @ 95.4%	734-775 (68.3%)
3	23372	3 rye grains	1225 ± 18	772-880 @ 83.7%	772-819 (68.3%)

The modelled dates suggest kilns 1 and 2 were broadly contemporaneous (cal. AD 748-770, and cal. AD 734-775, respectively), with kiln 3 (cal. AD 772-819) apparently in use a generation later, though all three kilns may have overlapped chronologically.[54] Significantly, the dates suggest Sedgeford's is the earliest malting complex in the early medieval British Isles. Other, similarly dated features include the single (though 'monumental') malting kiln at Higham Ferrers in Northamptonshire, and also the set of four pits, hypothesised to be drying kilns and found to contain germinated barley, at South Hook, Pembrokeshire (Wales), (see **Descriptive Catalogue**) (Hardy et al., 2007; Moffett, 2007, 163; McKerracher, 2014a;

[54] The sampled grains likely derive from the kilns' final firing and thus cannot be used to date their construction (Blakelock and Caroe, in prep.).

Carruthers, 2019, 164, 174–75; Crane and Murphy, 2019, 132–136). Sedgeford is unprecedented for its era in comprising a *complex* of several malting kilns along with associated germination floors and steeping tank.

4.6 Summary

This chapter has described in some detail archaeological findings to date from the malting complex at Sedgeford. The project features a thorough examination of an assemblage of charred plant material recovered from the malting complex. The subsequent chapter details the methods which were used to extract, assess and quantitively analyse this archaeobotanical material.

5 METHODS

5.1 Introduction

Principal methods employed in this research were as follows: 'primary' archaeobotanical analysis (extraction, identification and quantification of charred plant remains); germination assessment; crop processing analysis; stable isotope analysis; functional weed ecology (FWE) and seasonality analysis. Additionally, colleagues at the University of Oxford School of Archaeology used plant material extracted by the author from Sedgeford for two further sets of analyses: geometric morphometric analysis (GMM) was performed by T. Roushannafas, and scanning electron microscopy (SEM)-based analysis by Y. Zhou. In each case, the researcher generously agreed for their results to be shared as part of this study (see **Chapter 6**). Methods employed to generate all the results presented and evaluated in succeeding chapters are briefly described here. For each set of analyses, a theoretical background is provided in addition to description of the practical aspects involved.

The choice of analyses applied herein merits brief discussion: as noted (**section 1.2**), the study uniquely presents both qualitative research and the results of a set of quantitative analyses, with the aim of creating a 'three-dimensional' perspective on a site where malting is hypothesised. Since no model for thorough empirical surveying of potentially 'malted' ancient plant material exists, the use (by the author and colleagues) of three analytical methods for testing levels of germination in the malting complex was perforce exploratory, and intended either to compellingly support (if all results were complementary) or challenge (where results differed) the 'malting hypothesis' for Sedgeford. It is fairly 'standard' practice in any comprehensive body of archaeobotanical research to supplement insights gained through 'primary' archaeobotanical assessment with crop processing analysis (e.g., Stroud, 2016;

Diffey, 2018; McKerracher, 2019), whilst use of FWE, stable isotope analysis and seasonality analysis to investigate practices used to cultivate crops from the malting complex assemblage followed FeedSax protocol (e.g., Hamerow et al., 2020; McKerracher and Hamerow, 2022; Hamerow et al., in prep.).

5.2 Primary archaeobotanical analysis

5.2.1 Excavation

From 2013 until 2018, two strategies were employed in sampling for archaeobotanical material from Trench 23 at Sedgeford: judgment samples (M. Jones, 1991, 55) were extracted where rich (dark) organic remains were visible, or where charred plant remains might be expected, e.g., inside and surrounding the several kiln structures. Samples varied in volume from five up to 70 litres, depending on the size of the deposit.

From 2019, systematic recording of context information and collection of precise coordinate data for each context sampled was instituted. It was also specified from this time that, wherever possible, sediment samples should be of at least 20 litres. In 2019 the sampling strategy was based on 'judgement' sampling as in previous years, but, additionally, a grid-sampling system was implemented in a part of the trench comprising kiln 3 and surroundings and a further area, east of the kiln 3 feature, hypothesised at the time to be the clay 'germination floor' associated with kiln 3 (each then only partially excavated) (**section 4.3**). This was a form of 'interval' sampling, according to M. Jones' distinctions (ibid.). Members of the SHARP team excavated 65 samples, with each up to a total of 20 litres, from 66 1.0m x 1.0m squares in a 6 x 11 grid (the samples from squares G7 and H7 were mistakenly amalgamated). The kiln 3 gridded area is located in **Figure 5.1.**

As described in **section 4.3**, excavation in 2021 revealed a feature beneath what had been thought the 'kiln 3 germination floor' which, it is hypothesised, may represent a further (fourth) kiln. Samples included in this study excavated from the gridded area in 2019 were collected from the sediment layer above this feature (**Figure 4.10**), (the 'undefined feature'). Again, as described, 2021 excavation also revealed a clay floor to the north of kiln 3, precipitating further re-consideration of the nature of each feature – with this area to the north (beyond the grid, and not, as previously thought, to the east, within the grid) now believed to be the clay 'germination floor' associated with kiln 3.

In addition to those extracted from Trench 23, a total of 375 samples intended for archaeobotanical analysis were collected from the 'settlement' part of the site at Sedgeford between 2008 and 2016. Regretfully, detailed context information for these was not always retained (although the relevant trench numbers are recorded), and many of the 'settlement' area samples have yet to be attributed to phase.

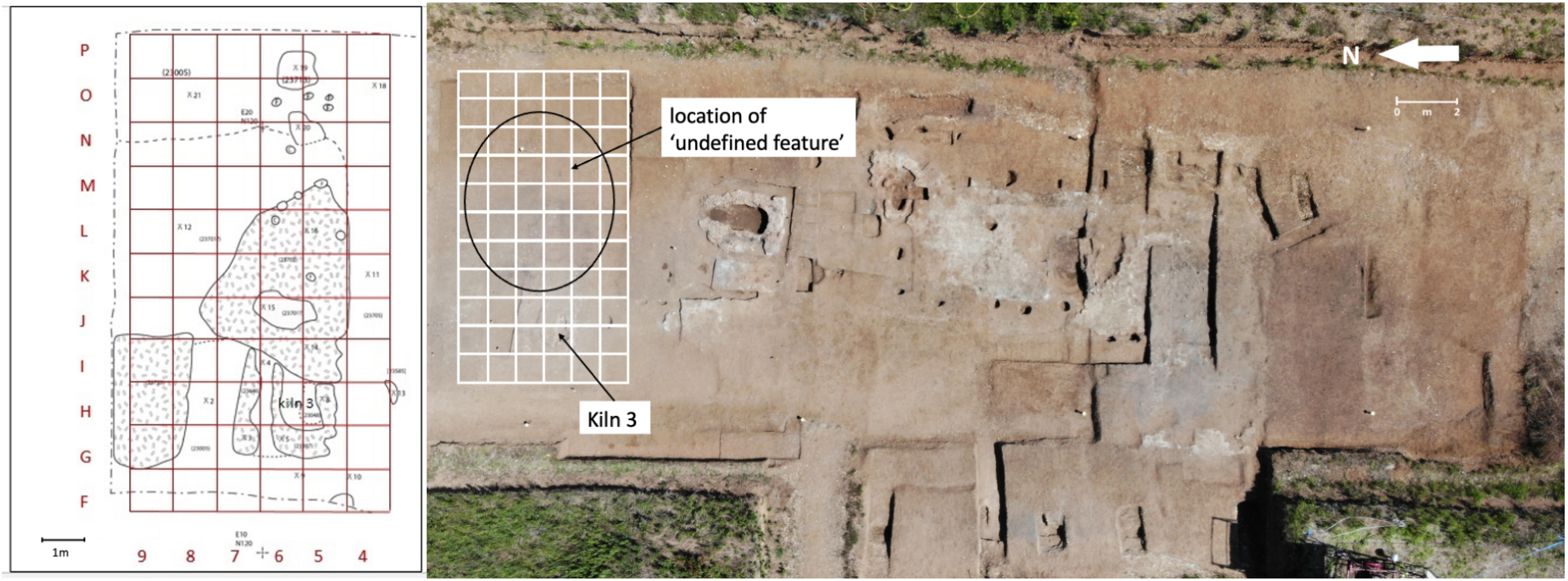


Figure 5.1 Kiln 3/undefined feature gridded area, superimposed on aerial photograph of Trench 23 (right) (Image: Ian Drummond/SHARP 2019) and on plan of north end of Trench 23, with features as at the 2019 season-end (left) (Image: Gary Rossin/SHARP 2019)

5.2.2 Flotation

Plant material was recovered from excavated samples using a flotation device (as depicted in **Figure 5.2**), modelled on French's 'Ankara type' design (1971). Heavy residue was collected in a mesh with an aperture of 1mm. The light residue (or flot, i.e., the floating portion from each sediment sample) was captured by a fine mesh (aperture < 0.3mm). 100% of the heavy residue for each sample was sorted by trained volunteers, and botanical material in the heavy residue set aside to be amalgamated with the respective flot for archaeobotanical analysis.

Figure 5.2 a) the floatation device used at Sedgeford b) the floatation device in use

5.2.3 Scanning

Up to the close of the 2021 season, a total of 602 samples from Sedgeford (including those from both the settlement area and Trench 23) have been processed using flotation. The author scanned the flot for each of the 227 samples from the malting complex using a stereoscopic light microscope, and scored each for estimated richness, into categories as follows: <30 plant items, 30-49, 50-99, 100-299, >300 plant items. Preservation was also briefly assessed. Samples from the settlement area were scanned by M. McKerracher.

A combination of estimated richness, diversity in plant taxa and quality of information about archaeological context was used to select samples to further analyse. Less rich samples from an assemblage may represent different activity types, and hence contain distinctive plant taxa. However, scanning suggested no significant difference in the spectra of taxa represented between rich and less rich samples. It was decided not to analyse samples estimated to contain fewer than 100 plant items. Van der Veen and Fieller (1982, 296) demonstrate that sub-samples of 100 or more represent the range and proportions of plant items in the wider population with reasonable robustness. However, since a high proportion of the malting complex samples (n = 100) passed this 'richness' criterion, and with time limitations, additional criteria were employed to narrow down the selected samples. Firstly, it was decided to further analyse only samples for which secure context information was available. Secondly, samples were selected for further consideration which had a broad distribution across Trench 23, and represented a range of context types, e.g., ditch-fill, kiln-fill, posthole-fill, floor (**Figure 5.3**). No grain-rich samples were taken from the clay layer hypothesised to be 'germination floor 1' (**Figure 4.6**), due to a lack of organic remains in this layer; sediment samples were collected from the 'new' kiln 3 floor (to the north of kiln 3) in 2021, however, these were similarly found to be grain-poor and unsuitable for further analysis. Further, the

five samples collected from the 'kiln 2 germination floor' are from postholes on the edge of this part of the trench and may only tentatively be classified as belonging to the 'floor'. The lack of archaeobotanical data (securely attributable as) from 'germination floor' areas of Trench 23 is a limitation of the present study.

Scanning of flots from the kiln 3/undefined feature gridded area revealed that samples from the outer part of the grid were conspicuously less rich, generally containing fewer than 100 plant items (**Figure 5.4**). Hence, these were excluded from comprehensive analysis. With the aim of balancing archaeobotanical analysis of samples from the gridded area with those from the remainder of the trench, only samples from alternate grid squares – in the centre of the gridded area – were fully analysed: 15 in total.

In a separate but associated study, 18 samples from the Mid Saxon settlement part of the site at Sedgeford (**section 4.2**) were analysed – despite the lack of specific context information and, in general, a small number of identifiable remains (McKerracher and Caroe, in prep.). Combining samples from the malting complex (55, of which 15 are from the gridded area) and those from the settlement area (18), a total of 73 archaeobotanical samples from Mid Saxon deposits at Sedgeford have been to date comprehensively analysed. This study focuses on the malting complex (Trench 23) assemblage; with, in places, samples from the settlement area supplying a helpful comparison. All Trench 23 samples have been hypothesised to derive from a single phase of occupation (**section 4.3**); if so (though radiocarbon dates do suggest some chronological separation between features, see **section 4.5**), the research falls well within Van der Veen and colleagues' (2013, 164) recommendation of 30-50 samples per phase for 'reliable analysis'.

In order to avoid the over-representation of a single 'behavioural event' G. Jones recommends (1991, 67) the amalgamation of samples where these have similar density and

composition and derive from a single context. Samples 23650A and 23650B are sourced from a single context to the west of kiln 3. The samples share a similar cereal grain composition (**Figure 6.9**); however, their 'weed seed' species profiles differ considerably (**Figure 6.18**). Hence, it was deemed justifiable to retain these as distinct analytical units.

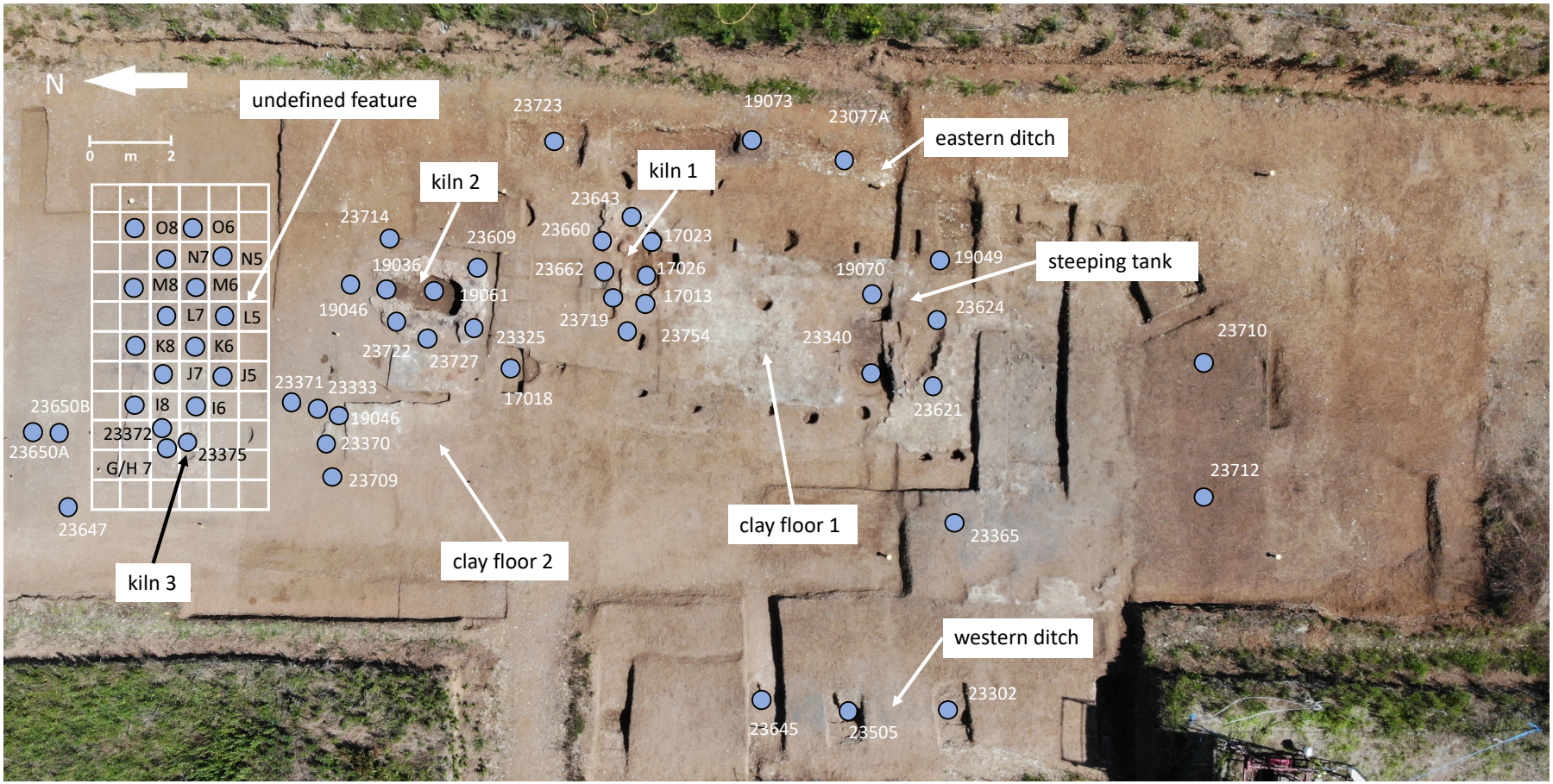


Figure 5.3 Trench 23, locating contexts from which samples analysed in this study derive. Context/samples numbers are shown. (Image: Ian Drummond/SHARP 2019)

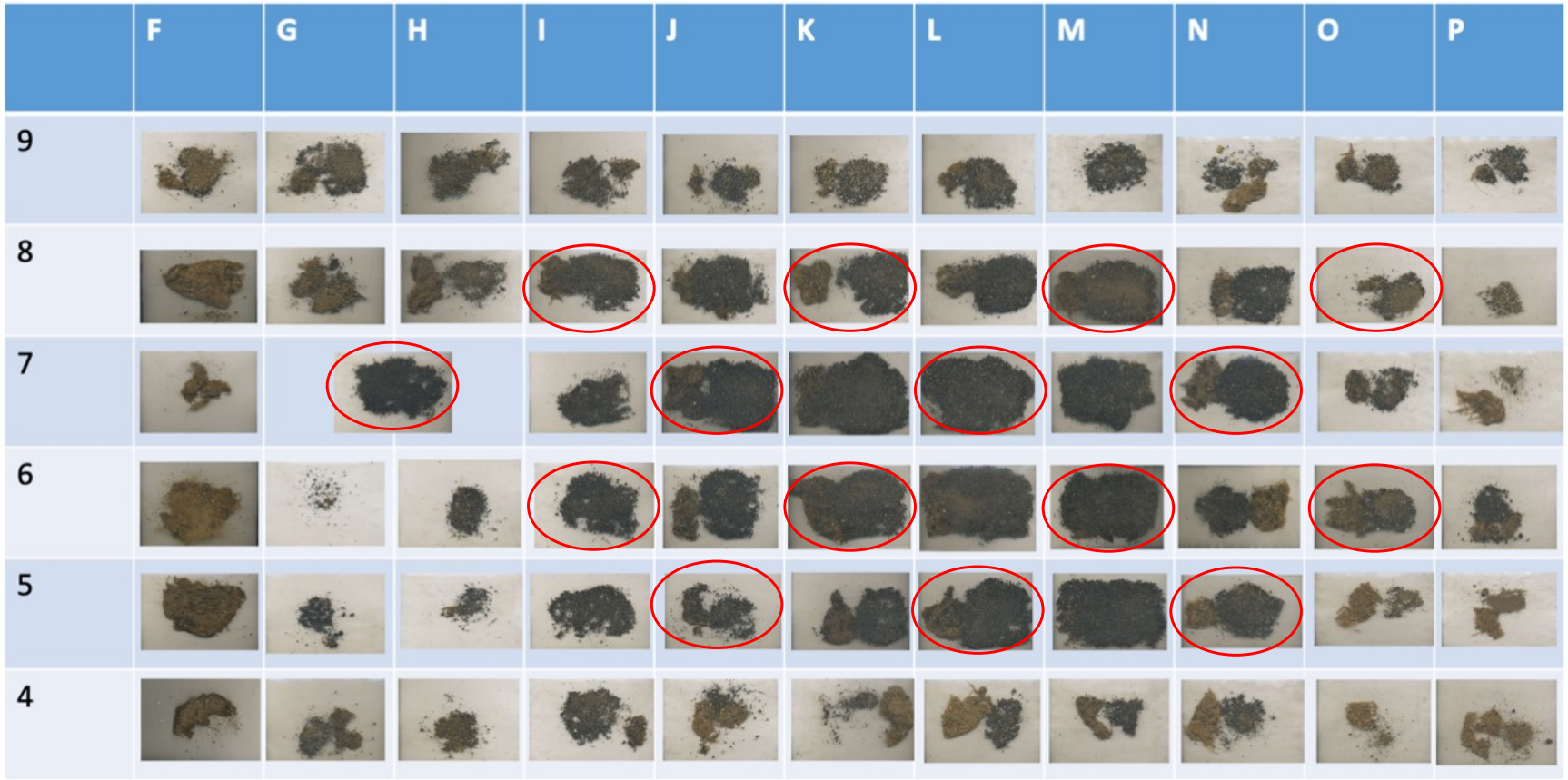


Figure 5.4 Matrix showing photographs of unsorted flots for each grid square from the kiln 3/undefined feature gridded area (flots for G7 and H7 were mistakenly amalgamated). Sample flots selected for analysis are highlighted.

5.2.4 Sub-sampling

Selected samples were sieved using stacked sieves of successive mesh-sizes 4mm, 2mm, 1mm and 0.3mm. To enable sorting within a manageable timeframe, the size-sorted-fractions of the richer samples were randomly split using a riffle box, in general to give sub-samples ½, ¼ or ⅛ of the whole, down to minima recommended (van der Veen and Fieller, 1982, 296).

5.2.5 Identification and sorting

Samples were sorted using a stereomicroscope in the Archaeobotany Laboratory in the School of Archaeology, University of Oxford, with plant material identified using both the lab's reference collection and relevant literature (Jacomet, 2006; Stace, 2010; Cappers et al., 2013). Latin nomenclature is after Stace (2010). All plant material in the samples is charred.[55]

Cereal grains and chaff were recorded by species, with grains showing morphology intermediate between two species types (for both grains and chaff items) recorded separately as an amalgamated category. Photographs showing 'model' grains from Sedgeford and from Mid Saxon Lyminge (with thanks to M. McKerracher for loaning the Lyminge specimens), as well as modern charred grains, were used for identification purposes.

[55] A single seed from the Boraginaceae family occurs in the assemblage; Boraginaceae seeds are classed as mineralised since their carbonate rich seedcoat prevents decay: it is not possible to tell whether these are archaeological or modern (Pustovoytov et al., 2004, 207).

5.2.6 Quantification

In order to avoid over-estimating abundance of plant items, the minimum number of individuals (MNI) was determined by counting specific diagnostic zones (see G. Jones, 1991, 65–66). For cereal grains and other large-seeded grasses, the frequency of both apical and embryo ends was counted, and the higher figure recorded. Additionally, the frequency of longitudinally split grains (where embryo and apical ends were both present) was counted, halved, and added to the apical/embryo end count.

Most of the species of weed seed occurred so infrequently in each sample that it was not necessary to quantify using diagnostic zones. However, several samples contained abundant weed seeds of one species (most frequently, black bindweed *Fallopia convolvulus* (L) Á. Löve), with both seed cores (achenes) and empty seed-coats common (**Figure 5.5**). In these cases, the frequency of both achenes and seedcoats was noted, and the higher count recorded. Where seedcoats were fragmented, MNI was estimated.

The seeds of corncockle (*Agrostemma githago* L.), also common in the Sedgeford assemblage, frequently occur fragmented into a separate achene and embryo (**Figure 5.6**). These were quantified by counting both achenes and embryos and recording the higher figure.

Detached sprouts occurred in the fine fractions of many samples, with varying frequency. These were counted only where the sprout included its 'base' – from the embryo end of the caryopsis (a practice shared by Smith (2011, 105–106), in her quantification of abundant detached sprouts at the Roman site of Northfleet, Kent). **Figure 5.7** shows sprouts from the Sedgeford assemblage, each complete with its respective 'base'.

The approximate volume of charcoal in both the 4mm and 2mm fractions was recorded for each sample using a graduated cylinder. Finally, here, after identification but

prior to statistical and other analyses, cereal grains and chaff items intermediate between two species were proportionately apportioned to the respective categories.

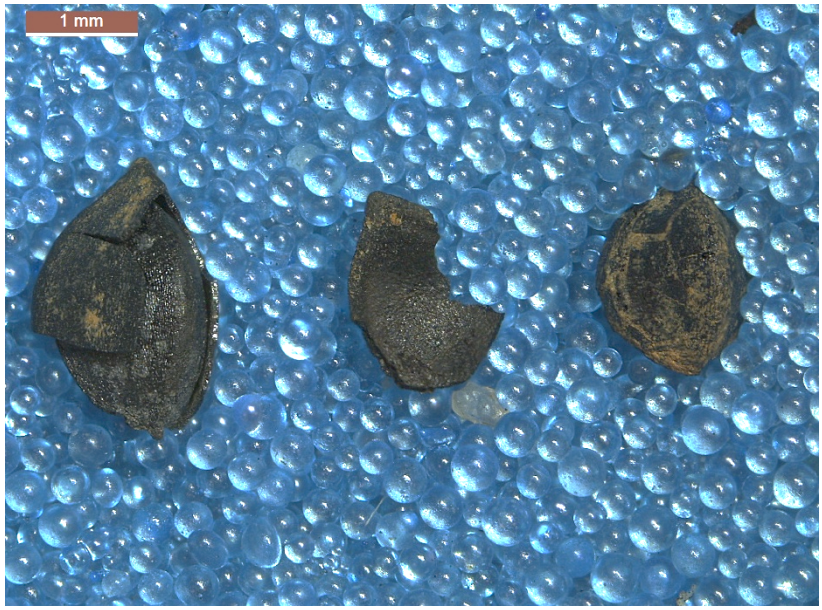


Figure 5.5 Fallopia convolvulus seeds from malting complex assemblage showing, from left to right, damaged seed coat and achene, fragmented seed coat and 'naked' achene

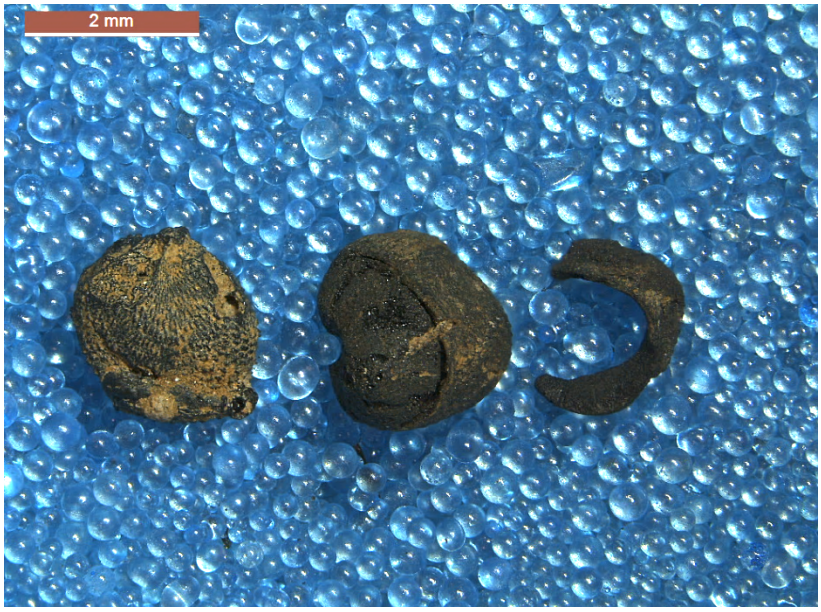


Figure 5.6 Agrostemma githago seeds from malting complex assemblage showing, from left to right, a complete seed, an achene with embryo 'wrapping' and a separated embryo 'wrapping"

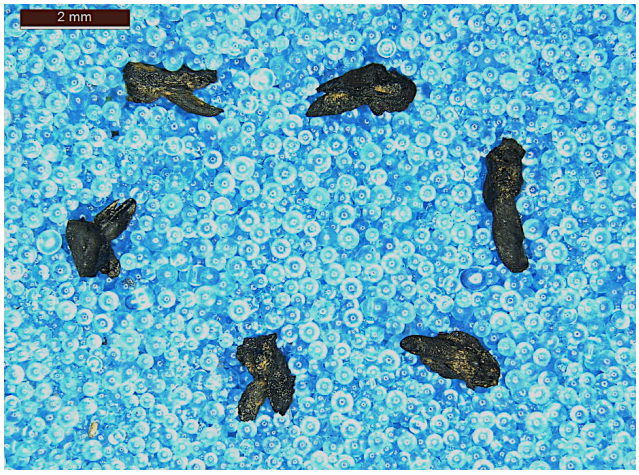


Figure 5.7 Detached sprouts from the malting complex assemblage, each complete with its 'base'

5.2.7 Multiplication of fractions

As is standard practice, the scores for each plant item were summed across sorted fractions for every sample, with fractions that had been sub-sampled first multiplied up to estimate overall abundance (for instance, generally, where 25% of a sample fraction had been sorted, this was multiplied by four). However, where any fraction would otherwise require multiplication by a factor larger than eight, counts for other fractions were divided down. For example, counts for a sample sub-sampled as follows – 100% >4mm fraction, 25% >2mm fraction, 25% >1mm fraction and 3.125% >0.3mm would be adjusted thus – >4mm fraction divided by four, >2mm fraction unchanged, >1mm fraction unchanged, >0.3mm multiplied by eight. Thus, the final estimated abundances would be those for 25% of the entire sample. The proportions of fully and partially sorted samples are summarised in **Table 5.1**.

Table 5.1 Summarising samples by proportion analysed

Proportion sorted	whole sample	1/2	1/4	1/8	TOTAL
Trench 23 ('malting complex')	25	16	6	8	55
Settlement area	18				18

5.2.8 Correspondence analysis

Correspondence analysis is an exploratory statistical approach commonly used in ecology and archaeology, designed to assess patterns in datasets comprising multiple variables per sample; it is a form of 'multivariate ordination' analysis. Much archaeobotanical research has relied on correspondence analysis to reveal trends in samples and among species (e.g., Bogaard, 2004b; Filipović, 2014; McKerracher, 2019; Diffey et al., 2020; Hamerow et al., in prep.).

Correspondence analysis takes a combined dataset and represents this as a scatterplot with up to three axes (all plots used in this project are displayed on two axes), which best display variation in the data, such that similarities and differences in (in this case) samples' plant taxa composition are rendered more clearly visible (e.g., G. Jones, 1991, 72–73). Associations between samples are shown by the direction and distance each diverges from the graph's origin (where the axes meet) with the origin representing 'average' (mean) values (e.g., McKerracher, 2019, 98; Diffey et al., 2020, 3). Thus, closely related samples will tend to cluster together, and those which diverge considerably will be distanced from one another. Additional helpful information can be provided by coding data by other pertinent variables, for instance, in this case, area of the site (e.g., Stroud, 2016, 156). Each correspondence analysis also generates a second scatterplot displaying the variables (in this case, taxa), where

the similarities and differences in divergence from the origin indicate levels of association between these.

Correspondence analyses were created using CANOCO version 5.0 (ter Braak and Smilauer, 2012). CANOCO generates for each analysis four axes, with axis 1 accounting for the greatest amount of variation in the data. In each of the plots shown in this study the horizontal (x) axis is axis 1, and the vertical (y), axis 2. Rare taxa, and samples with few items, tend to skew the analysis (G. Jones, 1991, 78): for this reason, the author included in the analyses used here only taxa occurring in over 10% of samples, and only samples containing 10 or more weed seeds (these criteria are applied recursively). For analyses examining only samples from the malting complex, 18 taxa and 54 samples are used. For those in which samples from the settlement area are also incorporated, a total of 63 samples are included (54 from the malting complex and 9 from the settlement area).[56] It is possible, using CANOCO, to perform transformations on the data e.g., 'log', 'square root', and others. Unless otherwise stated, all correspondence analyses conducted in this project use untransformed data. **Table 5.2** summarises the short names allotted to each taxon included in the correspondence analyses, as displayed in the scatterplots (**sections 6.5, 6.6** and **7.4**).

[56] The total number of taxa included in these correspondence analyses depends on whether 'occurring in 10% of samples' is understood to mean 10% of all 73 samples (in which case 19 are eligible) or 10% of each set of samples (i.e., a combination of those occurring in 10% of the 55 malting complex samples and those occurring in 10% of the 18 settlement area samples); where the latter guideline is applied, a total of 26 taxa are eligible. In this case, two analyses are run, one for each scenario, see **section 6.5**.

Table 5.2 Short names of taxa as used in correspondence analysis

Plant taxon / item	Short name
Secale cereale L.	S_cer
Secale cereale L. chaff	S_ch
Triticum L. (free-threshing)	T_ft
Triticum L. (free-threshing) chaff	T_ch
Triticum spelta L.	T_sp
Hordeum vulgare L.	H_vul
Hordeum vulgare L. chaff	H_ch
Avena L.	Avena
Avena L. chaff	A_ch
Indet. cereal chaff	I_ch
Agrostemma githago L.	A_gith
Anthemis cotula L.	A_cot
Atriplex hastata L. / *patula* L. / *prostrata* Boucher ex.	Atri_p
Brassicacaeae	Brass
Brassica L./ *Sinapis* L.	Bra_sin
Brassica rapa ssp *campestris* (L.) A.R. Clapham	Bra_rap
Bromus L.	Bro
Chenopodium album L.	C_alb
Chenopodiaceae	Cheno
Fallopia convolvulus (L.) Á.Löve	F_conv
Phleum L.	Phle
Phleum pratense L.	P_prat
Pisum sativum L.	P_sat
Plantago lanceolata L.	P_lanc
Poaceae <1mm	Poac_s
Poaceae >2mm	Poac_l
Poaceae chaff	P_ch
Polygonum aviculare L.	Pol_avic
Raphanus raphanistrum L.	R_raph
Rumex L.	Rum
Silene dioica (L.) Clairv.	Sil_di
Urtica urens L.	U_uren
Vicia faba L.	V_fab
Vicia hirsuta L. (Gray)/ *tetrasperma* (Screb.)	V_h_l
Vicia L. / *Lathyrus* L. (1-2mm)	Vic_lath
Vicia L. / *Lathyrus* L. / *Pisum* L. (>2mm)	Vi_la_pi

5.3 Germination assessment

As established, germination in cereal grains is fundamental to malting, and evidence for germination in assemblages has long been used to identify malting in the archaeological record. A comprehensive study of germination levels in grains from the Sedgeford malting complex is thus essential to this work.

The two most-cited indicators of germination are, firstly, morphological changes in grains *per se* (most commonly a visible sprout growing from the embryo-end, or a 'dorsal furrow' formed by a sprout which has since become detached), and, secondly, the presence of 'loose' detached sprouts (**section 2.4**). This study aims to reveal overall levels of germination, and spatial trends in germination, in charred grains across the malting complex (and a few samples from the 'settlement' area) by quantifying both forms of evidence, sample-by-sample.

Detached sprouts were identified and quantified in each sample, along with grains, chaff and weed seeds, as described above (**section 5.2**), with each sprout recorded only where it included a 'base', to avoid over-estimation of true frequency (**section 5.2.6**).

It has been argued (**section 2.4**) that there are particular difficulties in detecting germination in 'naked' grains, which are less likely to display the conventionally recognised morphological characteristics of germination (i.e., an attached sprout or dorsal furrow). Sedgeford's malting complex assemblage is dominated by two 'naked' grain cereal types: rye and free-threshing wheat (**section 6.3.1**). Although it is theoretically possible, using SEM, to identify germination in grains of any taxon from internal histological features, (as have, e.g., Cordes *et al.* (2021) using naked barley), use of SEM to comprehensively examine germination levels across the malting complex would be wholly impractical. It was therefore deemed

necessary to devise novel methods for identifying germination in naked grains, based on external morphology (as visible under light microscopy) alone. This necessitated conducting of a set of germination experiments, using modern grains, to facilitate recognition of signs of germination in malting complex grains.

5.3.1 Germination experiments

Modern accessions, equivalent to the four cereal species occurring in the assemblage from Mid Saxon Sedgeford, were experimentally germinated (in some cases, then dried) and charred (**Table 5.3**). In all cases, the crops from which these grains derived were cultivated organically in the UK and harvested in 2018.

Table 5.3 The four modern equivalents of cereal species occurring in the Mid Saxon malting complex, used in germination experiments

Crop type occurring in malting complex	Modern equivalent used experimentally	Variety of modern cereal grain
Rye (*Secale cereale* L.)	Rye (*Secale cereale* L.)	unknown
Free-threshing wheat (*Triticum* L.)	Bread wheat (*Triticum aestivum* L.)	'Maris widgeon'
Six rowed hulled barley (*Hordeum vulgare* L.)	Two-rowed hulled barley (*Hordeum vulgare subsp. distichum* L.)	'Plumage archer'
Oats (*Avena* L.)	Cultivated oats (*Avena sativa* L.)	'Mascari'

Two sets of experiments were conducted. These aimed to replicate conditions undergone by archaeological grains from Trench 23, where it is expected that some grains will have charred whilst still 'wet' and germinating on a germinating floor, whilst others became charred in the kilns during or after drying.

In both experiments, ~50 grains of each taxon were placed in a single layer of a Johnsons Microgreens Kitchen Seed Sprouter, respectively, with 50ml of water, measured using a graduated cylinder, poured onto each layer. The grains 'sat' in small amounts of water: time did not permit re-iteration of the experiment – however, if repetition were possible, the grains would instead be 'steeped' for a short time prior to being drained and permitted to germinate, arguably more closely replicating malting. After the following number of hours, successively, several grains of each taxon were removed from the seed sprouter: four hours, 24 hours, 48, 72 and 96 hours.

In the first experiment, grains from each taxon, for each germination period, were then charred in a Gallenkamp plus II industrial oven at 230°C for three hours – within the temperature and time range specified by Charles *et al.* (2015, 12) for 'optimum' charring. In each case, grains were wrapped in aluminium foil and positioned in the midst of a glass beaker full of sand, which was placed in the oven. The germinated and charred grains were photographed.

The second experiment included a 'drying' stage: wherein, after 'sitting' in water, the grains were dried, 'loose' in glass beakers, in the same oven at 50°C for 24 hours (to approximate the conditions of kilning). The germinated, dried grains were photographed both prior and subsequent to charring.

Study of each set of photographs, as well as careful observation of the (modern) germinated grains using light microscopy, informed the creation of the key for assessing germination in archaeological grains from Sedgeford.

5.3.2 Germination key

A key was created to discern whether each grain could be classified as 'germinated', 'ungerminated' or 'indeterminate', based on a set of morphological features identified as signifying germination by previous work or part of this study. It is important to consider whether any of these features could have alternative underlying causes, e.g., the process of charring itself. Braadbaart has experimented to investigate the effects on cereal grains of charring at different temperatures and with varied heating regimes; his work on wheat is referenced here (2008).

Features selected as indicators of germination were:

1. *A visible sprout* growing from the embryo end of the grain (**Figure 5.8**). This is an unambiguous indicator of germination, though rarely observed in naked grains, as their 'unprotected' sprouts readily detach, (**section 2.4**).

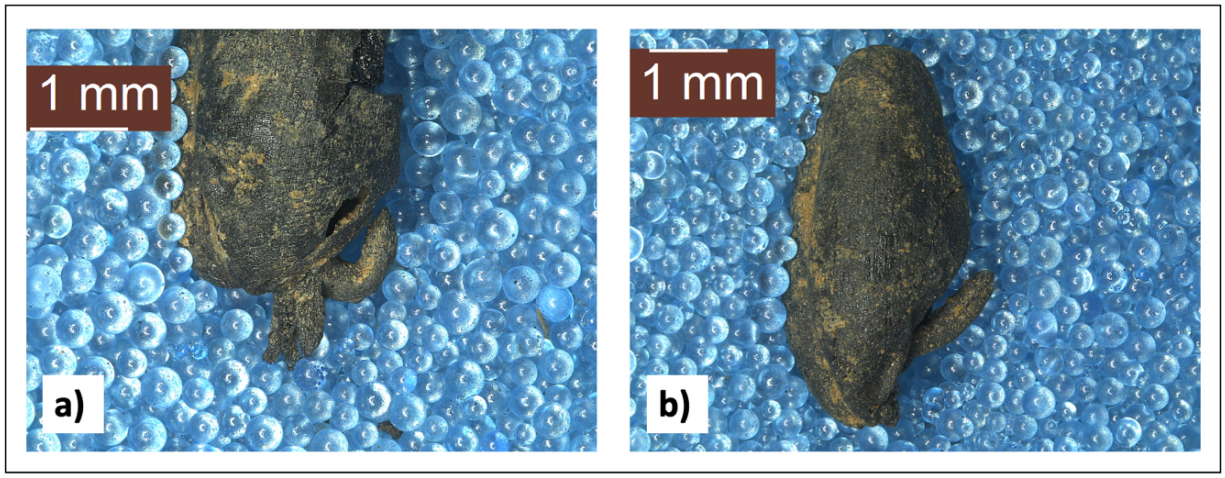


Figure 5.8 a) embryo end of a free-threshing Mid Saxon wheat grain b) a Mid Saxon rye grain, each from the malting complex, and complete with sprout (lateral view)

2. *A visibly 'collapsed' grain, with 'shrivelled' body*. This is caused by enzymatic activity degrading starches in the endosperm during germination (**section 2.3.1**), (**Figure 5.9**) (Moffett,

1994b, 405; Stika, 1996, 83; Helm and Carruthers, 2011, 363; Crane and Murphy, 2019, 174–175 R. Ballantyne, *pers. comm.*),[57] and not equivalent to the 'concave' sides observed in grains charred at high temperature (**Figure 5.10**) (Braadbaart, 2008, 163–164).

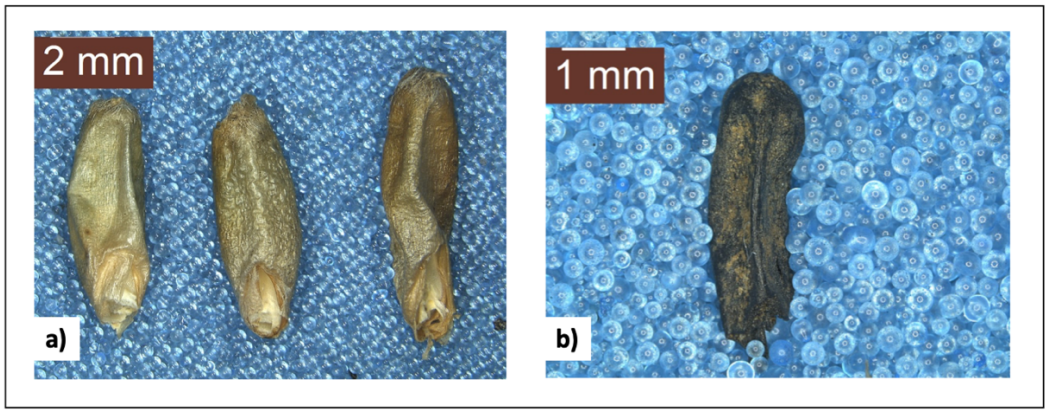


Figure 5.9 Rye grains with 'shrivelled' endosperm a) modern grains after 96 hrs germination, and drying b) grain from malting complex assemblage (all in the dorsal view)

Figure 5.10 Drawing of modern emmer wheat (Triticum dicoccum L.) grain, after charring at 310ºC for 60 minutes (after Braadbaart 2008, p.163, Figure 3), identified by Braadbaart as showing 'concave flanks' (dorsal view)

[57] 'Shrunken' grains are particularly associated with an extended period of germination; these are often considered 'over-germinated' for malting, as their store of useful starches is partially depleted (e.g., Carruthers, 2019, 174–175). Notably, Larsson (2018, 1967) suggests that 'shrivelling' of the endosperm due to germination may be partly counteracted by swelling or 'puffing' of the grain during charring.

3. *Missing embryo or embryo-end.* It is common for charred grains in archaeobotanical assemblages to have a missing embryo or embryo end. However, a preponderance of grains without embryos or an embryo end, relative to those lacking an apical end, may indicate germination (Stika, 1996, 109; Helm and Carruthers, 2011, 363; Smith, 2011, 109; Larsson et al., 2018, 1967; Carruthers, 2019, 164–165). Carruthers (2019, 164–165) relates experimental findings suggesting that this 'halfing' effect may be attributable to softening of the grain's embryo-end, where starch degradation commences, during early germination – such that this part of the grain is easily lost during charring or mechanical disturbance. At Iron Age Hochdorf, Stika (1996, 83) observed a particular, distinctive, form of embryo-loss in germinating grains (also observed in the Sedgeford assemblage): the creation of an 'inverted, V-shaped pit' at the grain's embryo-end (**Figure 5.11**).

Figure 5.11 Embryo-end of a free-threshing wheat grain from the Sedgeford malting complex, showing an 'inverted V-shaped pit', as observed by Stika, (1996, p.84) (dorsal view).

4. *A 'wrinkly collar' on the dorsal side of the grain*, surrounding the embryo end. This phenomenon has been observed by the author in experimentally germinated grains (**Figure 5.12**). It is likely attributable to 'wrinkling' or distortion of the epidermis caused

by the growth of a sprout from the embryo-end. There are no known parallel features in grains charred at high temperatures.

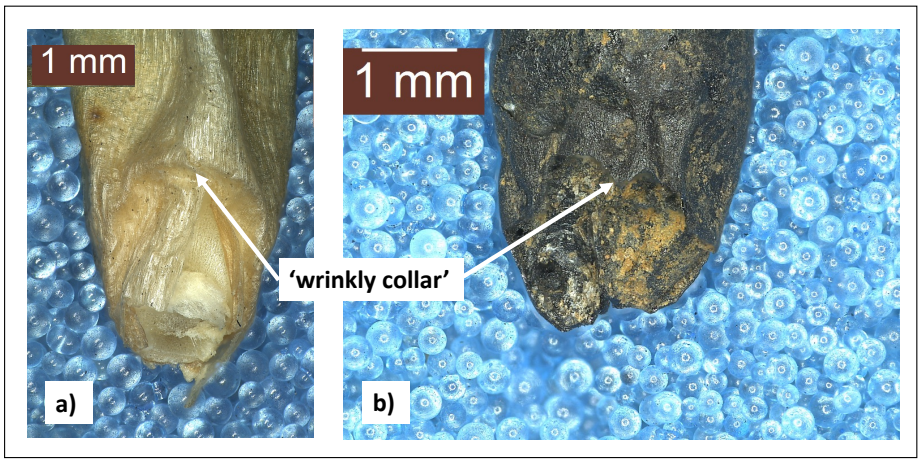


Figure 5.12 Grains exhibiting 'wrinkly collar' a) Embryo end of a modern rye grain following 72 hours germination and drying, b) Embryo end of archaeological free-threshing wheat grain from Sedgeford's malting complex (both in the dorsal view)

5. '*Protrusions' of material from the endosperm.* This has been observed by the author in germination experiments and may be caused by endosperm material losing its structural integrity due to enzymatic activity degrading cell wall starches (see **section 2.3.2**) (**Figure 5.13**). Braadbaart attests that protrusions are a relatively common feature of grains charred at 250°C and above, particularly when accompanied by a high rate of heating (Braadbaart, 2008, 159–160). Protrusions found by the author in germination experiments occurred in grains heated at <250°C (at 230°C), implying that these are different phenomena. Cordes *et al.* (2021, 5) also found evidence for experimentally germinated grains extruding some of their contents during charring. It is difficult to distinguish between protrusions caused by charring at high temperatures and by germination; this is considered in the key's structure.

Figure 5.13 'Protrusion' in an archaeological free-threshing wheat grain from Sedgeford's Mid Saxon malting complex (ventral view)

Informed by these considerations, the key is as follows:

Key for assessing germination in 'naked' grains, with justification

1. **a) sprout clearly growing from embryo end of grain ..... germinated**

b) no such sprout ..... go to 2

2. **a) embryo missing** (either inverted V-shaped germination 'pit' at embryo end, entire embryo end missing, or just embryo itself missing) ..... go to 3

b) embryo present ..... go to 4

3. **a) collapsed endosperm** ..... **germinated**

b) no collapsed endosperm ..... go to 5

4. **a) collapsed endosperm** ..... go to 5

b) no collapsed endosperm ..... **ungerminated**

5. **a) AT LEAST ONE OF wrinkly 'collar' or 'protrusion'**..... **germinated**

b) NEITHER wrinkly 'collar' nor 'protrusion'..... **indeterminate**

Priority is given here to features that are considered least ambiguous evidence of germination (an attached sprout, or a collapsed ('shrivelled') endosperm). Further, an 'inverted V' in the embryo area will clearly not be apparent if the embryo end of the caryopsis is

missing, and the embryo itself will always be missing where there is an 'inverted V' i.e., these categories are not mutually exclusive. Hence all scenarios with a missing embryo are grouped into one 'entry' in the key (point 2a).

Finally, the germination criteria a 'wrinkled collar' and 'surface protrusion' are not reported in the literature as evidence for germination – hence, these are judged to be rarer; further, these are insufficiently diagnostic of germination to classify a grain as germinated without additional diagnostic features – thus, only in combination with a collapsed endosperm or a missing embryo is one of these here sufficient to deem a grain germinated. This should reduce the chance of e.g., grains with protrusions being mistakenly identified as germinated, where these are simply due to charring at high temperatures.

Procedure for assessing germination

Once all samples had been sorted, with plant material identified and quantified as described (**section 5.2**), 10 grains of each of the four species occurring therein ('naked' rye and wheat, as well as hulled barley and oats) were selected from each sample fraction containing grains (i.e., commonly >4mm and >2mm fractions and occasionally >1mm) for germination assessment. Where the total complement of grains from a particular species in any fraction was less than 10, all grains were assessed. Care was taken to select grains randomly for assessment.[58] Time limitations precluded assessment of more than 10 grains per sample fraction.

[58] This involved in each case, first, agitating the petri dish in which the grains were contained and then, selecting the 10 'uppermost' grains – farthest from the microscope-user, for further assessment.

All samples from the malting complex were examined in this way, with the exception of three in which preservation was judged too poor to permit accurate germination assessment (23077, 23365 and 23505),[59] i.e., 52 samples in total. A further four samples from the settlement area (15158, 15187, 15355 and 15467(B)) were also thus examined, for comparative purposes.

This selection method partially favoured rarer species (barley and oats), with, in many cases, (where the total number in that fraction was 10 or fewer grains), 100% of grains from these species in a sample fraction assessed for germination – and a considerably smaller proportion of the more abundant species (for instance, only 10 out of 34 grains, or 29%). This limitation was considered not so serious as to render results of these assessments unreliable.

Rye and free-threshing wheat ('naked') grains were classified as germinated, ungerminated or indeterminate through application of the key. Barley and oats (hulled grains) were assessed using more standard methods i.e., discerning the presence or otherwise of an attached sprout or dorsal furrow (**Figure 5.14**.), with grains missing an embryo or embryo end classified as 'indeterminate'.

This novel methodology has potential significance for identifying germination in naked grains at settings other than Mid Saxon Sedgeford, including archaeobotanical assemblages distant either geographically or chronologically (see **Chapter 9**).

[59] Further, since poor preservation implies charring at high temperatures, there was more potential for conflation of signs of germination and of high temperature charring, the latter as revealed by Braadbaart, in these samples.

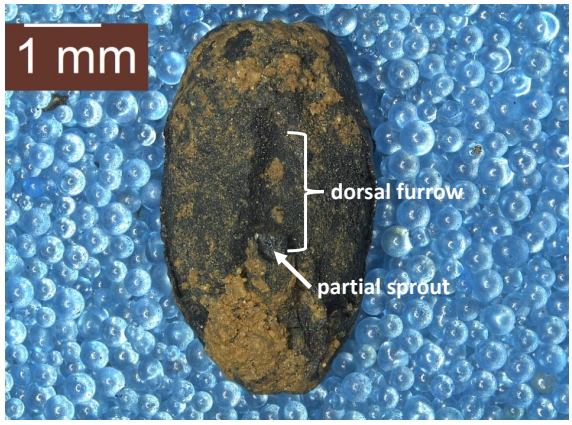


Figure 5.14 Partial sprout and dorsal furrow in archaeological barley grain from Sedgeford's malting complex, (dorsal view)

5.4 Crop processing analysis

A key factor influencing the composition of archaeobotanical material is the stage (or stages) of crop processing represented by each sample (e.g., Bogaard, 2004a, 64). Understanding crop processing is therefore critical for fully assessing an assemblage.

Once crops have been harvested, these require processing prior to consumption. For the purposes of archaeobotanical research, harvested material comprises three key components: grains, cereal chaff and the seeds of weeds growing with the crops. The relative proportions of these contained in a batch of harvested material change in largely predictable ways as this progresses through the various stages of crop processing. The processes involved are constrained by the nature of harvested plant material: hence it is reasonable to assume that methods used are conserved in places distanced in time and space (Hillman, 1981, 126–138; G. Jones, 1984, 46). Building on this assumption, G. Jones conducted ethnographic studies of crop processing in the 1980s, (1984; 1987; 1990) with the aim of facilitating recognition of the (by)products of distinct crop processing stages in archaeological plant material. She

established quantitative understanding of shifts in relative proportions of grains, chaff and weeds – and of the associations of particular weed types with given crop processing stages – which are widely applied to archaeobotanical material today. The stages of crop processing differ somewhat between free-threshing cereals and the glume wheats (such as spelt and emmer) (e.g., Hillman, 1981, 132–136; Hillman, 1984, 4–5). All the cereal grains found at Sedgeford are free-threshing varieties (**section 6.3.1**), hence the crop processing sequence for glume wheats is not considered here.

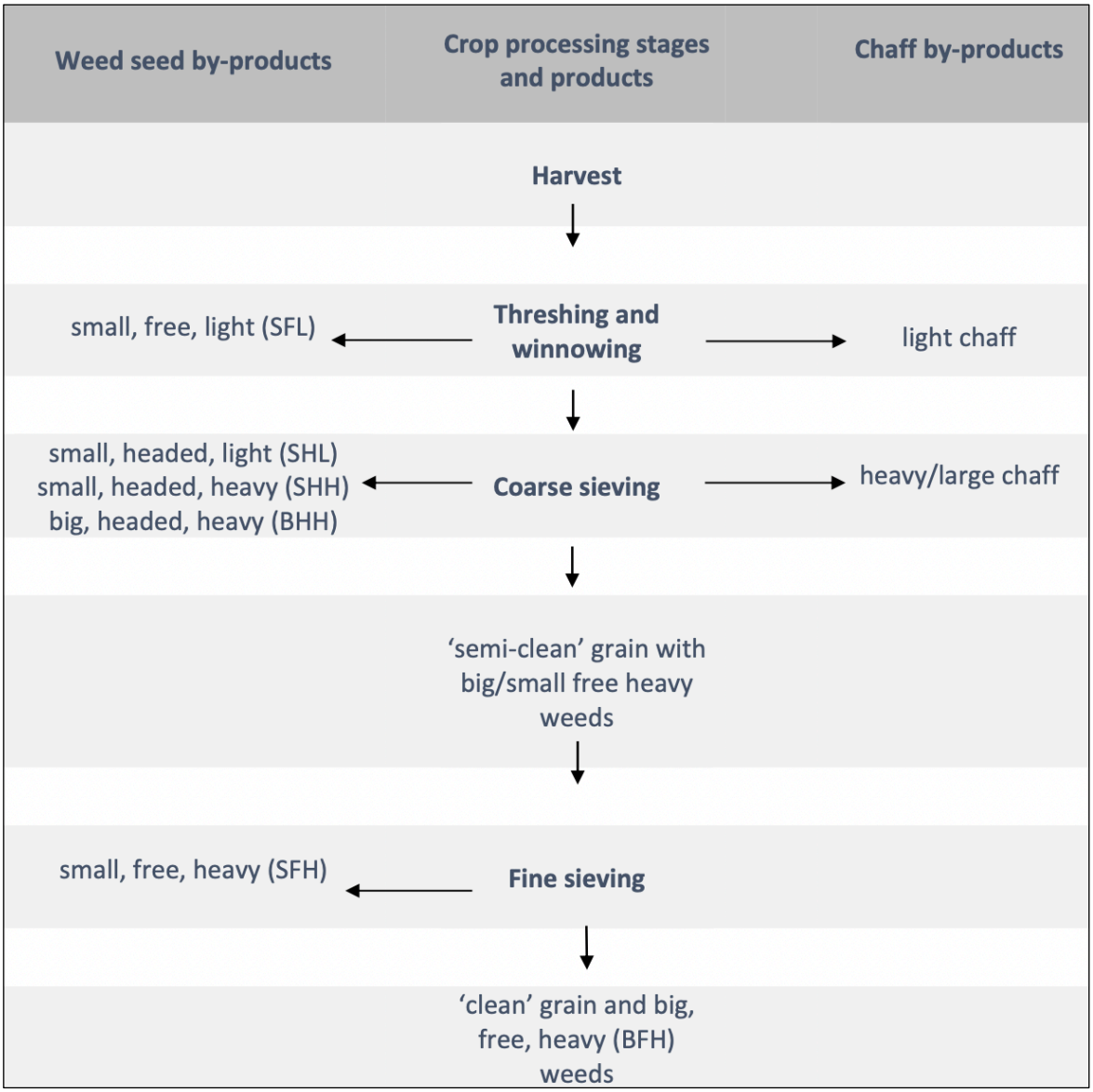
Significantly, a review of pertinent literature suggests that stages of crop processing for malting may diverge from the 'standard' free-threshing sequence. For clarity's sake, the standard sequence is described first here (and illustrated in **Table 5.4**), and a potential 'malting-specific' set of crop processing stages later presented.

Generally, the crop processing sequence for free-threshing cereals is as follows: after harvesting, grains are released from the cereal ear through threshing; next the threshed crop is winnowed i.e., cast into the air (for example using a winnowing fork) such that light chaff is blown away, with grains and heavier chaff falling directly to the ground. Subsequently, coarse sieving is used to separate grains, which pass through the sieve's mesh, from large pieces of straw, weed heads and any remaining unthreshed crop material, which are retained. A fine sieve is then used to segregate grains (this time retained in the mesh) from small weed seeds and any other fine non-grain material remaining. Finally – and sometimes at a later stage, e.g., just prior to cooking or grinding – hand-sorting may be used to remove any weed seeds of comparable size to the grains, which are not removed by either coarse or fine sieving (e.g., G. Jones, 1984, 45–46).

A final note: whilst barley is a free-threshing crop variety, and thus generally processed as described, where *hulled* barley is to be used to create food items for human consumption

e.g., through baking, a further stage of processing, termed 'pearling', is required to remove the grains' close-fitting 'hull', comprising lemma and palea (e.g. Hillman, 1981, 132–136). Where barley is to be malted and used for producing beer, such 'pearling' is not necessary; in fact , as noted, the barley grain hulls form an important 'filter bed' for the lautering stage (**section 2.3.3**).

Table 5.4 Simplified flowchart summarising the stages of crop processing for free-threshing grains, including the expected products and by-products, after (McKerracher, 2014 p.88 Table 3.7), and (G. Jones 1984, p.44 Figure 1)



5.4.1 'Basic components' analysis

G. Jones identified four main products and by-products for processing of free-threshing crops (**Table 5.4**): these are the by-products of winnowing, coarse-sieving and fine-

sieving, respectively, and fourthly, fine-sieving product. Each of these has a broadly predictable (and quantifiable) composition in terms of the ratio grains: chaff: weed seeds. Winnowing by-product and coarse sieve by-product are characterised by a high proportion (at least 50%) of chaff, whilst fine-sieve by-product is generally rich in the seeds of crop weeds; fine-sieve product will be dominated by (comprise over 80%) cereal grains (G. Jones, 1990, 92–93) (expected proportions of grain, chaff and weed seeds in each type of (by)product are specified in **Table 5.5**). Hence, where relative frequencies of grain, chaff and weed seeds are plotted on a tri-polar graph, specific areas of the chart are occupied by the respective products and by-products. Such a chart, adapted from McKerracher's work, (which in turn draws on G. Jones' research), is displayed in **Figure 5.15**) (McKerracher, 2014b, 90; McKerracher, 2019, 39). McKerracher identifies two additional categories, in addition to G. Jones' four types of crop processing products and by-products: namely, 'unsieved grain', i.e., material which has yet to be fine-sieved, and whose composition is thus intermediate between the product and by-product of fine-sieving, and 'mixed stages'.

Table 5.5 Expected proportions of grain, chaff and weed seeds in crop processing by(products), after (McKerracher 2019, p.38 Table 3.8; 2014, p.89 Table 5) and (G. Jones 1990, p.92-93)

(By)product	**% Grain**	**% Chaff**	**% Weed seed**
FSP (fine sieve product)	≥80	≤5	
USG (unsieved grain – FSBP and FSP prior to sieving)	<80	≤5	15-50
FSBP (fine sieve by-product)		≤5	≥50
C/WBP (coarse sieving / winnowing by-product)		>30	
MS (mixed stages)		6-30	

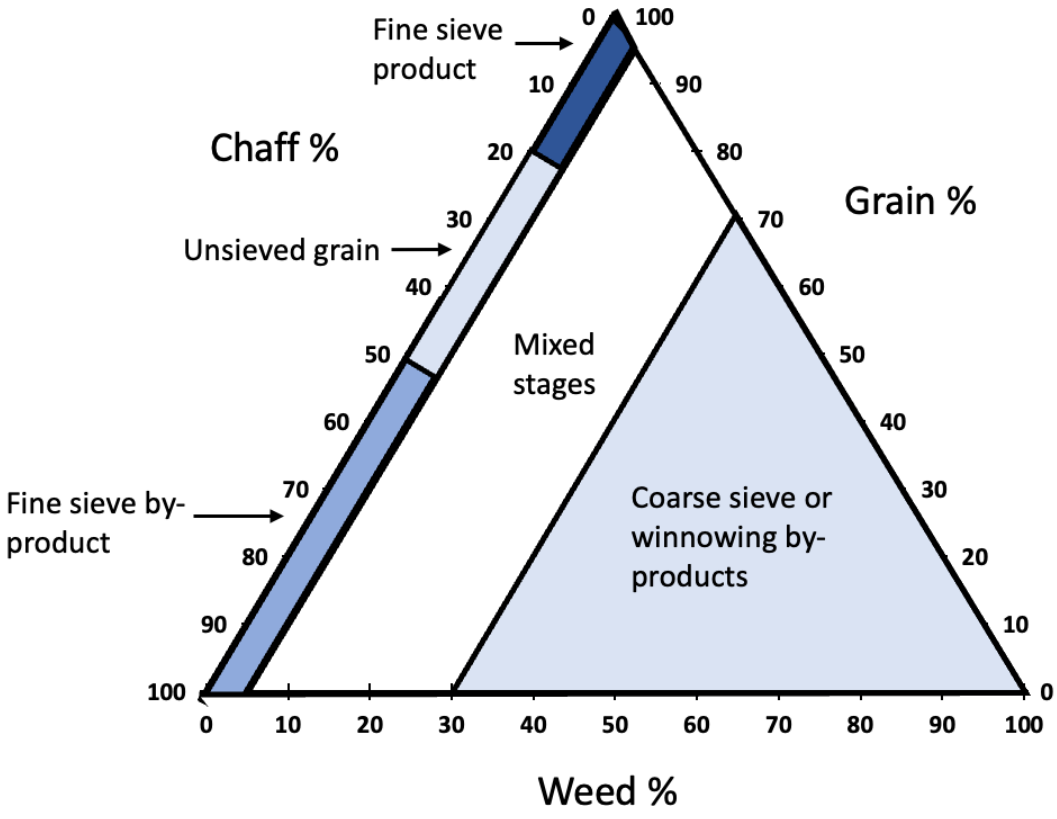


Figure 5.15 Model tri-polar graph showing expected distributions of (free-threshing) crop processing products and by-products, based on expected ratios of grain: chaff: weed seed, drawing on the research of G. Jones, after McKerracher (2014 p.90 Figure 3.7, 2019 p.39 Figure 6)

This form of analysis, founded on the relative proportions of grains, chaff and weed seeds in each sample, and here termed 'basic component analysis', has been widely applied in archaeobotanical research (e.g., Valamoti, 2004; Bogaard et al., 2011; McKerracher, 2014a; McKerracher, 2019; Stroud, 2016; Diffey, 2018), and is applied to Sedgeford's assemblage in this study. However, it is not without limitations: as G. Jones suggests, precise translation of archaeological onto ethnographic 'basic component' data may not be possible, for several reasons. Firstly, there will be variation in the 'weediness' of harvested material; secondly, the

thoroughness of threshing, winnowing and sieving will vary, and further, the three components typically do not preserve equally well during charring, with chaff frequently less well preserved than grains in charred archaeobotanical material (Boardman and G. Jones, 1990; G. Jones, 1990, 92–93). Finally, as noted, 'basic components analysis' cannot easily be applied to samples dominated by glume wheats.

5.4.2 Discriminant analysis for crop processing

Each of these concerns is overcome by the second method devised by G. Jones for discerning crop processing stages, founded on her observation that the weed seeds removed at each stage of processing share distinctive physical properties. According to G. Jones' system (1984; 1987), weed seeds fall into one of six categories, based on size (big or small), aerodynamism (heavy or light) and 'headedness' (headed or free). For example, small, free, light seeds tend to dominate the winnowing by-product, whilst fine-sieve product generally contains an abundance of large, free, heavy seeds. The expected weed types for each of G. Jones' four crop-processing (by)products are displayed in **Table 5.4**. The author is grateful to A. Bogaard for kindly granting access to a catalogue (compiled from the work of several researchers) allocating numerous weed taxa – including those occurring in the Sedgeford malting complex assemblage – to a G. Jones 'processing group'. **Table 5.6** lists the weed taxa encountered in this research (at Sedgeford's malting complex and settlement area), classified into G. Jones' crop processing groups.

Table 5.6 Weed seed classification, according to crop processing group

Taxon	**Seed classification**
Agrostemma githago L.	bfh
Bromus arvensis L. / *hordeaceus* L. / *secalinus* L.	bfh
Fallopia convolvulus (L.) Á. Löve	bfh
Large legume indet.	bfh
Large *Galium* L.	bfh
Poaceae indet. (large)	bfh
Polygonum aviculare L.	bfh
Veronica hederifolia L.	bfh
Vicia L./ *Lathyrus* L.	bfh
Vicia L. / *Lathyrus* L. / *Pisum* L. (>2mm)	bfh
Anthemis cotula L.	bhh
Raphanus raphanistrum L.	bhh
Atriplex L. / *Chenopodium* L.	sfh
Atriplex hastata L. / *patula* L./ *prostrata Boucher* ex. D.C.	sfh
Brassicaceae indet.	sfh
Brassica L.	sfh
Brassica L. / *Sinapis* L.	sfh
Brassica napus L.	sfh
Brassica rapa ssp *campestris* (L.) A.R. Clapham	sfh
Carex L.	sfh
Chenopodiaceae indet.	sfh
Chenopodium album L.	sfh
Cyperaceae	sfh
Galium verum L.	sfh
Hyoscyamus niger L.	sfh
Phleum L.	sfh
Phleum pratense L.	sfh
Poaceae (small)	sfh
Rumex L.	sfh
Trifolium L.	sfh
Urtica urens L.	sfh
Arenaria serpyllifolia L.	sfl
Juncus L.	sfl
Malva sylvestris L.	shh

Taxon	Seed classification
Plantago lanceolata L.	shh
Silene dioica (L.) Clairv.	shh
Silene L.	shh
Papaver argemone L.	shl
Papaver L.	shl
Papaver somniferum L.	shl

G. Jones' method (1984, 49–51; 1987) uses the statistical procedure discriminant analysis. This is used to classify cases of previously unknown membership into one of several known groups. In this case, 'unknown' cases correspond to archaeobotanical samples, and 'known' groups to samples from ethnographic research deriving from each of the four classes of (by)product i.e., winnowing by-product, fine sieve product etc. Allocations (of both known and unknown cases) are based on the relative frequency of weed seeds belonging to each of G. Jones' six categories. The procedure first creates discriminant functions which separate the 'known' groups with greatest efficiency. These same functions are then used to allocate each unknown case to one of the known groups. Results can be displayed graphically, with x and y axes representing the two discriminant functions which most effectively separate the groups of known cases; a 'centroid' may be displayed for each group.

In this study, IBM SPSS Statistics version 27 was used to conduct discriminant analyses comparing samples from Sedgeford's malting complex, i.e., 'unknown' cases, with 'known' groups based on G. Jones' ethnographic research (data shared with kind permission). For the malting complex assemblage, a single sample, 17018, which contained fewer than 10

weed seeds[60] was excluded from the analysis. A high proportion (83.8%) of original grouped cases were correctly classified using the discriminant functions selected by the program.

Where these concur, the application of both crop processing methods i.e., basic components analysis, and discriminant analysis based on weed seed processing groups, permits more robust conclusions to be drawn regarding the crop processing stage represented by a given sample; and further can lend confidence that plant material in a sample was processed together and may therefore originate from a single 'arable unit', or field (Bogaard, 2004b, 65). The crop processing (by)product classifications awarded by basic components and discriminant analysis were compared for each sample from the malting complex and settlement area assemblages, to ascertain where these coincided. **Table 5.7** summarises compatibilities between the slightly differing crop processing types identifiable through the two forms of analysis.

Table 5.7 Compatibility between (by)product types identifiable using discriminant and basic components analyses, after (McKerracher 2019 p.48 Table 8)

		Basic components analysis				
		CWBP (coarse sieve/winnowing by-product)	**FSBP**	**USG**	**FSP**	**MS**
Discriminant analysis	**WBP**	X				
	CSBP	X				
	FSBP		X	X		
	FSP			X	X	

[60] Weed seed frequency here is counted for samples after multiplying up – see **Section 5.2.7**.

5.4.3 Crop processing for malting – alternative methods?

Crop processing methods for free-threshing grains, as described above, have been adopted widely across time and space. However, it seems that the processing of harvested crops for malting may traditionally have used different methods. A novel model for crop processing for traditional malting is here developed.

Sources suggest that crop processing for malting often did not include the stages of winnowing, coarse and fine sieving directly following threshing, since there was an expectation that – whilst grains will sink in the water – weeds and remaining chaff could be 'skimmed', floating, from the surface of the steeping tank (**section 3.2.3**) (Tusser, 1710, 161; Tusser, 1812, 47; Muspratt, 1860, 275; Krzywinski and Soltvedt, 1988, 62; Hertrich, 2013, 133). As Krzywinski and Soltvedt observe (1988, 62), skimming material from the surface of a steeping vessel will alter the expected frequency of weed seed types – the physical property influencing removal of weed seeds in this case being buoyancy in water: and the by-product primarily composed of taxa that float. However, significantly, the authors also note that where harvested material is 'contained' during steeping, for instance suspended in sacking, 'skimming' will not be possible and associated alterations in weed seed frequency therefore not observed (ibid.).

It has further frequently been claimed that traditional malting involved a stage unnecessary in 'ordinary' processing of free-threshing crops: namely, the removal of 'rootlets' i.e., sprouts and root sheaths by 'de-culming' (**section 3.2.3**) (Smith, n.d., 7; Muspratt, 1860, 278; Krzywinski and Soltvedt, 1988, 62; Briggs, 1998, 8, 10; Brears, 2008, 93). Malt processing to this day involves the removal of rootlets following kilning (Neylon et al., 2020, 119). Bearing these factors in mind, **Table 5.8** presents a hypothesised model, developed from G.

Jones' 1984 scheme, summarising the stages of crop-processing the author posits were involved in traditional, including Mid Saxon, malting.

Table 5.8 Simplified model summarising the hypothesised stages of crop processing for malting free-threshing grains, including the expected products and by-products, after (McKerracher 2014 p.88 Table 3.7) and (G. Jones 1984, p.44 Figure 1)

Weed seed by-products	Crop processing stages and products	Chaff by-products
	Harvest	
	↓	
	Threshing	
	↓	
buoyant seeds ←	**Steeping**	→ all detached chaff
	↓	
	wet grain 'couched' onto germination floor	
	↓	
	Kilning	
	↓	
small unbuoyant seeds ←	**De-culming**	→ 'rootlets' (sprouts and root sheaths)
	↓	
	'clean' germinated grain without 'rootlets', and large and headed unbuoyant seeds	

To summarise: the expected products and by-products of the 'new malting model' are - (so-called) 'skim by-product (SBP)' comprising chaff and buoyant seeds; 'de-culming by-product (DBP)' comprising detached sprouts and small unbuoyant seeds, and 'de-culming product (DP)' comprising 'clean' grains and large and headed unbuoyant weed seeds.

Where it had been determined that an archaeobotanical assemblage had been subject to crop processing according to the new malting model, it would not be possible to assign samples to these crop processing (by)product types using either basic components or discriminant analysis without first conducting a large-scale project of either ethnographic or experimental archaeobotany (involving reconstructing traditional malting methods) to collect data approximating the dataset collated by G. Jones through her ethnographic research. Whilst this would be highly interesting, it lies far beyond the scope of the current study.

These two models: the 'conventional' crop processing model advocated by G. Jones and many since (**Table 5.4**), and the author's own malting model (**Table 5.8**), were, as far as possible, tested to discern which better describes trends observed in the Sedgeford malting complex assemblage. This necessitated some simple experimental archaeobotany to ascertain which, amongst the most common weed seed taxa occurring in the malting complex and settlement area assemblages, are buoyant in water. The results of this investigation are presented in **Table 5.9**. Weed seeds only identified to family e.g. as 'Brassicaceae' or to genus, e.g., as 'large Poaceae' were not included in analyses based on buoyancy, since these groups of taxa includes some species whose seeds float in water and others which do not. As shown in **Table 5.9**, all of the most common seed taxa found in the malting complex and settlement area are buoyant in water, with the exception of *Vicia* L. / *Lathyrus* L. / *Pisum* L. (>2mm), and of *Agrostemma githago* L., *Vicia* L. /*Lathyrus* L. and *Silene dioica* L. which sink when agitated.

Moving harvested material into and out of the steeping cistern plausibly involved considerable agitation.

Table 5.9 Buoyancy in water of weed taxa seeds occurring in the Sedgeford malting complex and settlement assemblages

Weed taxa	Floats in water	Sinks in water	Sinks in water when agitated
Agrostemma githago L.			X
Anthemis cotula L.	X		
Atriplex hastata L. / *patula* L./ *prostrata Boucher* ex. D.C.	X		
Brassica L./ *Sinapis* L.	X		
Bromus L.	X		
Chenopodium album L.	X		
Chenopodiaceae	X		
Fallopia convolvulus (L.) Á.Löve	X		
Plantago lanceolata L.	X		
Poaceae <1mm	X		
Polygonum aviculare L.	X		
Raphanus raphanistrum L. (pods)	X		
Rumex L.	X		
Silene dioica (L.) Clairv.			X
Vicia L. / *Lathyrus* L. (1-2mm)			X
Vicia L. / *Lathyrus* L. / *Pisum* L. (>2mm)		X	

5.5 Stable isotope analysis

Isotopes are alternative forms of chemical elements having in each atom the same number of protons and electrons, but different numbers of neutrons, and hence different weights. Archaeobotanists are increasingly utilising carbon and nitrogen stable isotopic ratios of charred grains to make inferences about aspects of past arable husbandry methods. The ratio of ^{12}C to ^{13}C (commonly denoted $\delta^{13}C$) has been used to infer levels of soil water

availability for crops, and thus, where these were cultivated in semi-arid to arid climatic zones, whether crops were irrigated, and to what degree (e.g., Flohr et al., 2011; Wallace et al., 2013; Styring, Rösch, et al., 2017; Stroud, 2022). The ratio of ^{14}N to ^{15}N ($\delta^{15}N$) in cereal grains, correctly interpreted, can be used to indicate whether, and to what extent, crops were manured (i.e., anthropogenic soil enrichment) (e.g., Bogaard et al., 2007; Fraser et al., 2011; Styring, Rösch, et al., 2017; Szpak and Chiou, 2020; Stroud, 2022). In each case, such inferences can reasonably be drawn because *fractionation* has occurred during phase transitions, either enhancing or depleting the relative proportion of the heavier stable isotope, such that the isotopic ratio deviates detectably.

Stable isotopic values are calculated as the ratio of the heavier to the lighter isotope, and expressed in parts per 1000, or 'per mil' (‰). The use of, first, carbon, and second, nitrogen stable isotope ratios as proxies for past crop cultivation methods is explored in greater detail below.

5.5.1 Carbon stable isotope analysis

Of the two stable isotopes of carbon, ^{12}C is considerably more abundant, with ^{13}C comprising only ~1.1% of all carbon atoms in atmospheric carbon dioxide (e.g., O'Leary, 1981, 553; Farquhar et al., 1989, 504). Carbon dioxide is vital for plant photosynthesis and enters leaves' intercellular space by diffusing through pores on leaf surfaces known as stomata (Schulze and Hall, 1982). Plants are commonly separated into three groups (C_3, C_4 and CAM), based on the type of photosynthetic pathway they employ. Wheats, barleys, rye and oats (the crops commonly cultivated in the UK, both historically and in the present day) are all C_3 type plants. For C_3 plants the first stage of the Calvin cycle (a vital set of processes in

photosynthesis) involves conversion of carbon dioxide and the compound ribulose 1,5 bisphosphate into 3-phosphoglycerate, catalysed by the enzyme ribulose-1,5-bisphosphate carboxylase-oxygenase (RuBisCo) (e.g., Benson, 1951; Wildman, 2002). Significantly, RuBisCo discriminates against carbon dioxide molecules with the heavier ^{13}C isotope, due to slight disparities in chemical and physical properties between ^{12}C and ^{13}C, attributable to weight differences (O'Leary, 1988, 328; Wallace et al., 2013). As a result, plant tissues are depleted in ^{13}C relative to atmospheric carbon dioxide.

Open stomata permit diffusion of carbon dioxide from the surrounding atmosphere into leaf intercellular space, and of oxygen (a product of photosynthesis) from plant tissues into the atmosphere; unavoidably, they also allow evaporation of water from plant tissues exposed to the intercellular space (Schulze and Hall, 1982). 90% of plant water loss occurs via transpiration through the stomata; this constitutes a significant disadvantage for plants growing in water-stressed environments (Pei et al., 1998, 287). Hence, when a plant is undergoing water scarcity, stomatal pores close, preventing further CO_2 diffusion. Stomatal closure eventually results in a dearth of carbon dioxide and consequently, (since these become proportionately more abundant), reduced discrimination against CO_2 molecules with the ^{13}C isotope by RuBisCo (e.g., Farquhar et al., 1989; O'Leary, 1993). With persistent water stress, a plant's tissues will thus become less depleted in ^{13}C: i.e., there is a relationship between a plant's carbon stable isotope ratio and its water status.

Extensive research involving both modern crops and archaeobotanical assemblages has been founded upon use of the carbon isotopic ratio in plant tissues as an effective proxy for water availability during plant growth (e.g., Araus et al., 1999; Ferrio et al., 2005; Ferrio et al., 2007; Flohr et al., 2011; Wallace et al., 2013; Bogaard, Hodgson, et al., 2016). This research has, perhaps unsurprisingly, focused on crop husbandry in semi-arid or arid climates where

plants are susceptible to water stress. However, measuring carbon isotopic ratios is not without value for understanding cultivation methods in more temperate climates, such as the UK's. For instance, and with relevance for the current project, Hamerow *et al.* (2020, 600). argue in their study of agriculture in medieval Stafford that consistency in carbon isotopic values across crop species in an archaeobotanical assemblage (or, more specifically, where crop taxa display expected offsets – see below) implies, significantly – where these are corroborated by comparable trends in nitrogen isotopic values – that these were exposed to similar soil conditions, with equivalent water availability – potentially indicative of crop rotation (**section 1.4.2**). Two alternative explanations for such a trend would be either that crops were grown together in the same field simultaneously, as a maslin, or that these were cultivated in neighbouring fields with similar water availability.

Extrapolation of water availability from measured ^{12}C:^{13}C in ancient plant material, using data from stable isotope analysis, is complicated by the fact that the $\delta^{13}C$ of atmospheric CO_2 has fluctuated over time. Hence, when comparing carbon isotopic data from different time periods, it is now common practice to convert plant $\delta^{13}C$ to $\Delta^{13}C$, where the latter represents the plant's carbon stable isotope ratio independent of atmospheric $\delta^{13}C$ values (Farquhar et al., 1982, 122; Farquhar et al., 1989, 507–508; Wallace et al., 2013, 390).

Research using modern crops has revealed that $\delta^{13}C$ values are not the same for all plant tissues, with grains typically having a higher $\delta^{13}C$ value than other plant parts. Such studies have further suggested that barley grains have a $\delta^{13}C$ value of c. 1-2‰ lower (with six-row barley grains c. 2‰ lower) than free-threshing wheat grains from plants cultivated with the same water availability (Anyia et al., 2007, e.g., 318; Wallace et al., 2013, 398). It should be noted however that Styring *et al.* (2017, 17084), researching archaeological grains from *c.* 4000

cal. BC, found a smaller average $\delta^{13}C$ offset of ~1‰ between wheat and six-row barley grains exposed to the same watering conditions.

Finally, and significantly, evidence suggests plant $\delta^{13}C$ values are influenced not only by water availability but also by additional factors including soil type, canopy cover, light, temperature, and topography. For instance, research indicates that cereals growing on steeply-sloping fields may have lower $\delta^{13}C$ values, (perhaps since these experience faster run-off and hence less access to water) (Heaton, 1999, 638; Bogaard, Hodgson, et al., 2016, 69; Diffey, 2018, 72).

5.5.2 Nitrogen stable isotope analysis

There are multiple nitrogen isotopes, however ^{14}N and ^{15}N are the only stable forms amongst these. The lighter ^{14}N comprises ~99.64% of all nitrogen on earth, with ^{15}N ~0.36% (Burlingame and Schnoes, 1969, 96; Hoefs, 2018, 66–67). The nitrogen cycle is complex, involving multiple phase transitions, with associated fractionation of ^{14}N:^{15}N (e.g., Dawson et al., 2002, 521); only those elements of the cycle essential to this discussion are described below.

Nitrogen is vital for plant growth, comprising a key constituent of, amongst other essential compounds, amino acids, nucleic acids and chlorophyll – the latter fundamental for photosynthesis. The great majority of earth's nitrogen occurs in the atmosphere, which is 78% N_2, however this is unreactive and hence inaccessible to most living organisms (e.g., Stein and Klotz, 2016, 94). There are multiple pathways by which nitrogen can be converted to forms in the soil accessible to plants; all of these involve, first, the fixation of N_2 into ammonia (NH_3). This 'nitrogen-fixation' is catalysed by the enzyme nitrogenase, generally within diazotroph

bacteria (e.g., Newton, 2007, 109; van Lis et al., 2011). Plants require nitrifying bacteria e.g., *Nitrosomonas* to cause soil ammonia and ammonium to further undergo 'nitrification' to form nitrites (NH_2^-) and nitrates (NH_3^-), before they can utilise the soil's nitrogen (e.g., Ferguson et al., 2007, 209). The main process by which nitrogen is removed from the soil is 'denitrification'; a set of anaerobic reactions facilitated by microorganisms in low-oxygen sediments (such as waterlogged soils), by which nitrates and nitrites are converted to gaseous forms: most commonly nitrous oxide (N_2O) and N_2 (van Spanning et al., 2007, 3).

A wide range of factors influence soil, and thus plant tissue, $\delta^{15}N$ values. These include climate, salinity, water-logging and, significantly here, the anthropogenic enhancement of soil nitrogen levels through crop manuring (Heaton, 1987; Handley et al., 1999; Bogaard et al., 2007; Senbayram et al., 2008; Fraser et al., 2011; Larsson et al., 2019). Ammonium in soil enriched with manure has a raised ^{15}N level, due to volatisation of some of the lighter ^{14}N isotope in the form of gaseous ammonia (NH_3); following nitrification, such soil ammonium is converted to nitrates and nitrites, with raised ^{15}N (Bogaard et al., 2007, 336). Plants which utilise these compounds themselves become enriched in ^{15}N (ibid., Bol et al., 2005, 3216). Where measured $\delta^{15}N$ signatures in preserved plant tissues are carefully interpreted, these can thus give an indication of the degree to which local crop husbandry regimes have relied upon manuring (Fraser et al., 2011). 'Careful interpretation' of $\delta^{15}N$ values rightly requires knowledge of the baseline $\delta^{15}N$ signature for plants growing on unenriched soil in the local environment (e.g., Stroud et al., 2021, 103014). This permits discernment of whether apparently elevated $\delta^{15}N$ values are attributable to manuring or, rather, to alternate factors such as salinity, aridity or other soil processes. Researchers have, in places where this is available, utilised the $\delta^{15}N$ values of archaeological wild herbivore bone collagen as an

indicator for 'natural' plant baseline δ^{15}N values in past environments, on the assumption that herbivores were foraging on wild (non-arable) plants. This necessitates subtracting the ~3-5‰ (mid-value: 4‰) associated with a single trophic shift between forage and herbivore (Hedges and Reynard, 2007, 1241; Bogaard et al., 2013, 12590; Styring et al., 2016, 5).

Modern studies indicate that manuring soil can raise the δ^{15}N values of plants by up to 10‰ (Fraser et al., 2011, 2799; Styring et al., 2016, 4). Plant ^{15}N enrichment depends on both the volume and frequency of manuring, as well as the type of fertiliser applied: e.g., animal manure or middening (with household waste material); further, manure from animals at higher trophic levels (such as seabirds) will have higher δ^{15}N values; Szpak *et al.* find application of seabird guano manure can raise plants' δ^{15}N values by up to ~20‰ (Szpak et al., 2014, 72). Bogaard *et al.* have assimilated data from a set of modern field surveys from temperate Europe to produce a model with three manuring 'bands' (**Figure 5.16**) (Bogaard et al., 2013, 12590). According to this scheme, grain δ^{15}N values below 3‰ indicate no manuring in the last three years; values between 3 and 6‰ signify moderate manuring, and any grains having δ^{15}N values exceeding 6‰ suggest a farming regime utilising frequent and intense manuring (~30+ tonnes manure/hectare) (ibid.). It should be noted, however, that use of the model is predicated upon the hypothesis that 'baseline' soil δ^{15}N values at the site in question were the same as those from the modern study sites from which data for the model were collected. This is not always a reasonable assumption, e.g., as noted, local soil salinity or waterlogging may affect past soil δ^{15}N values at an archaeological site.

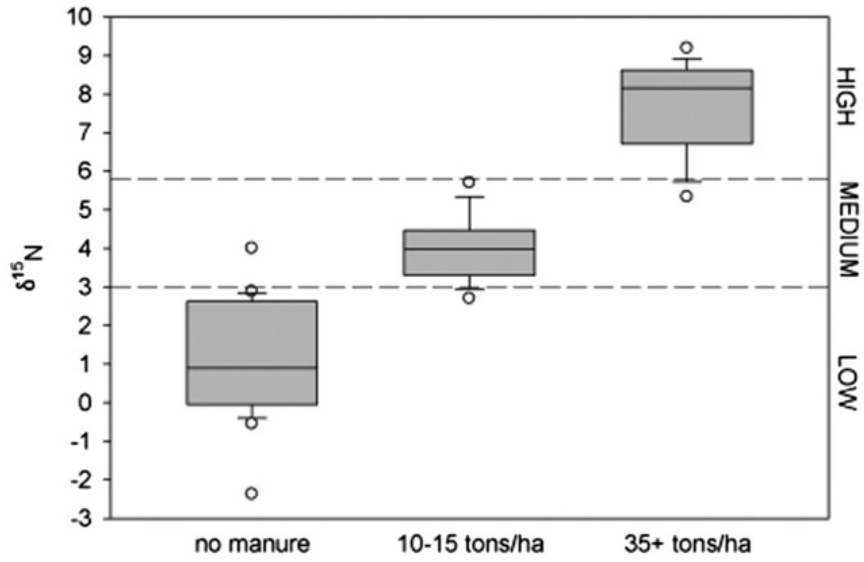


Figure 5.16 Graphical model summarising manuring bands against grain $\delta^{15}N$ levels, reproduced with kind permission from Bogaard et al. (2013 p.12590, Figure 1)

Finally, interpretations of grain $\delta^{15}N$ values are best reified through use of additional methods for revealing crop husbandry methods, for instance FWE (Bogaard, Hodgson, et al., 2016, 58; Stroud et al., 2021, 103010).

5.5.3 Stable isotope analysis of archaeological grains from Sedgeford

Stable isotopic analysis was conducted on charred grains from Sedgeford with the aim of answering the following questions, concerning, *inter alia,* the husbandry regime(s) used to cultivate crops malted at the site:

1. *Do $\delta^{15}N$ values suggest soil ^{15}N enrichment, potentially indicative of manuring?*
2. *In terms of potential manuring, is there evidence consistent with preferential treatment of one crop species over others?*
3. *Is there evidence of variation in $\delta^{13}C$ and $\delta^{15}N$ values between grains deriving from different areas of the malting complex i.e., kilns 1, 2, 3 and the steeping tank?*

4. *Is there evidence for change in crop $\delta^{13}C$ and $\delta^{15}N$ values over time?*
5. *Is evidence from stable isotopic analysis consistent with crops deriving from a single agricultural context?*
6. *Does stable isotopic analysis evidence support that from FWE and other archaeobotanical assessments of the malting complex assemblage?*
7. *Do results from stable isotopic analysis indicate, or are they consistent with, particular crop husbandry regimes?*

Sample selection

A sampling strategy was devised aiming to permit response to these questions. Samples of grains were selected from key 'features' (areas) within the malting complex i.e., kilns 1, 2, 3, and the steeping tank, to enable comparison between features. Further, samples of different grain species (namely rye, free-threshing wheat and hulled barley) were selected from each context, to permit comparison of stable isotope values across species. Oats were not included; it was deemed that the scarcity of oats in the malting complex assemblage means any stable isotope values obtained for these would not be statistically robust and, further, that their infrequency implies oats may be a 'weedy', rather than deliberately cultivated, variety at Sedgeford (**section 6.3.1**).

Isotopic studies of charred grains have to date tended to use 'bulk' samples, often combining 10 homogenised grains of a single taxon from a single context in one sample, as recommended by Kanstrup *et al.* and Nitsch *et al.* Both sets of authors reason that a 10-grain sample should adequately represent the mean isotope signature of the context (whilst not being overly destructive of material) (Kanstrup et al., 2012, 2539; Nitsch et al., 2015, 11). In

contrast, this study uses single grain samples, with the aim of selecting, where sufficient grains were available, five grains of each species per context (for each 'feature', samples from two contexts were analysed; i.e., a total of 10 grains of each species per feature) (Lightfoot and Stevens, 2012; Larsson et al., 2019; Stroud, 2022). Justification for this strategy using Sedgeford material includes plans to incorporate samples from the steeping tank in the analysis; these are likely to be mixed rather than 'in situ' deposits, deriving from several 'use episodes'. Were homogenised bulk samples to be used for these contexts, variability between grains would likely be unhelpfully 'averaged out'. Whilst other contexts to be sampled – namely, those associated with the kilns, are more likely to comprise 'in situ' deposits from a single use episode (in this case plausibly a single firing of the kiln), the use of bulk samples for these contexts and not others would be inadvisable; researchers' experience highlights difficulties in meaningfully comparing stable isotopic variability for bulk and single-grain samples from the same site (e.g., E. Stroud, *pers. comm.*). Thus, it was decided to use entirely single-grain samples for stable isotope analysis in the current research.

Single-grain sample selection was determined by the strategy outlined above, however three further criteria also informed selection strategy: namely, grain size, germination, and the likely effects of charring on stable isotope signatures. Firstly, in order to supply sufficient grain material for both carbon and nitrogen isotope analysis, as well as potential pre-treatment of each sample to remove any contaminants detected (see below), grains selected were as large as possible amongst those available (minimum mass 3.2 mg). Secondly, the effects of germination on grain $\delta^{13}C$ and $\delta^{15}N$ values, though currently the subject of research (Stroud

and Lodwick, in prep.), are, as yet, unknown.[61] To limit any confounding effects of germination on stable isotope values, grains showing clear evidence for germination (**section 5.3**) were not selected.[62]

Finally, heating grains above certain temperatures and for extended periods of time causes physical changes to grain structure and morphology (Charles et al., 2015). It has been shown that charring can also affect both δ^{13}C and δ^{15}N values (Fraser et al., 2013; Styring et al., 2013; Nitsch et al., 2015; Stroud, in press). Nitsch *et al.* conducted a set of isotopic studies on modern bread wheat and hulled barley grains, amongst other (modern) taxa (2015). In her recent study, Stroud (in press) has extended this research to include modern rye and oats, in addition to bread wheat and hulled barley (four crop species fairly commonly cultivated in temperate parts of Europe, including at Mid Saxon Sedgeford). Stroud's research suggests grains of these four species charred within a specified charring 'window' (215-300°C) should have offsets applied as follows: +0.33‰ for δ^{15}N values, and +0.12‰ for δ^{13}C values. (ibid.). The effect on grains of heating above 300°C was not tested; associated offsets for grains charred at these temperatures are thus unknown.

Hence the subset of grains initially selected was further 'filtered' according to level of preservation – indicative of charring conditions. Research suggests that grains' interior structure is a better indication of charring conditions than their external appearance (Vaiglova

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[61] L. Lodwick and E. Stroud (*pers. comm.*) note that isotopic offset between the grain and sprout has not yet been investigated; further, the point at which a germinating grain begins to photosynthesise (converting carbon from the atmosphere into structural proteins) is not yet known – photosynthesis may have significant effects on grain isotope values.

[62] For several contexts, the dominance of grains missing an embryo – potentially indicative of germination (see **section 2.4**) – meant these could not always be excluded, hence some germinated grains will have been unavoidably included amongst those selected.

et al., 2022; Stroud, in press). Thus, after gentle cleaning using a scalpel to remove adhering soil particles, grains were dissected (halved, to show a cross-section), the interior viewed under light microscopy, and compared with interiors of modern grains: rye, free-threshing wheat, and hulled barley respectively, experimentally charred at known temperatures and for prescribed periods of time (the author is grateful to E. Stroud for preparing and loaning these grains). Grains judged to fall outside Stroud's 'optimum charring window' were excluded from further analysis.

The numbers of grains of each species selected for carbon and nitrogen stable isotope analysis according to the criteria outlined above, and their associated contexts, are summarised in **Table 5.10**. This table also shows the 'isotope analysis code' assigned to each group of samples. It was decided, where possible, to analyse five grains (with an absolute minimum of three) for each species/context combination, to adequately represent variability within the context. Where sufficient grains fitting all criteria were not available in sorted fractions for a particular context (**section 5.2.4**), unsorted fractions of flot were revisited and additional grains selected. No hulled barley grains were analysed for context 23719, as it was not possible to identify three grains passing each of the criteria identified. A combined total of 112 single-grain samples was analysed.

Table 5.10 Summarising frequency of single-grain samples selected for stable isotope analysis, per species, context and feature type, with allocated isotope analysis code

Feature	Context number	Species	Number of samples	Isotope analysis code
Kiln 1	23719	rye	5	SED01
		FT wheat	4	SED02
		hulled barley	0	
	23754	rye	4	SED04
		FT wheat	5	SED05
		hulled barley	5	SED06
Kiln 2	23722	rye	5	SED07
		FT wheat	5	SED08
		hulled barley	5	SED09
	19061	rye	5	SED10
		FT wheat	5	SED11
		hulled barley	5	SED12
Kiln 3	23375	rye	5	SED16
		FT wheat	5	SED17
		hulled barley	5	SED18
	23646 G/H7	rye	5	SED19
		FT wheat	5	SED20
		hulled barley	4	SED21
Steeping tank	19049	rye	5	SED28
		FT wheat	5	SED29
		hulled barley	5	SED30
	23621	rye	5	SED31
		FT wheat	5	SED32
		hulled barley	5	SED33
TOTAL	112			

FTIR and pre-treatment

It is widely recognised that grains can become contaminated with compounds from the soil during deposition and extended periods of burial. Amongst these, certain compounds, primarily carbonates, nitrates and humic acids, are known to affect grain stable isotopic values (e.g., Schnitzer and Khan, 1975; Vaiglova et al., 2014). Pre-treatment methods can be used to

remove contamination from grains, however, as Vaiglova *et al.* (2014, 2497) identify, some of these methods themselves affect grains' stable isotopic ratios. These authors recommend first the use of Fourier Transform Infrared Spectroscopy (FTIR) as a means of discerning evidence for contamination, and thus determining any need for pre-treatment. FTIR generates spectra based on the reflective or absorptive nature of compounds occurring within a sample of powdered grain. Vaiglova *et al.* artificially contaminated grains using carbonates, nitrates and humic acids respectively, and used an FTIR with an Attenuate Total Reflectance (ATR) attachment to generate a set of spectra displaying distinctive peaks associated with each type of contamination. Spectra from archaeological grains analysed using FTIR-ATR can be usefully compared with these (ibid., Figure 4a, 5a and 6a).

More than 10% of the single-grain samples (a total of 15 grains) selected for stable isotope analysis were subjected to FTIR assessment to identify any possible contamination, aiming to avoid unnecessary pre-treatment. The samples were first crushed using a pestle and mortar, then analysed using FTIR-ATR. The 'background' spectrum[63] was deducted from initial spectra, and these were then subjected to baseline correction, using the programme Agilent Resolution Pro. **Figures 5.17**, **5.18** and **5.19** show spectra for carbonate, nitrate and humic contamination, respectively, for samples selected from kiln 1; in each case these are compared with those for artificially contaminated samples produced by Vaiglova *et al.* (2014). No evidence of contamination with carbonates, nitrates or humic acids was found in any of the selected subset of samples, thus it was deemed unnecessary to pre-treat any samples prior to stable isotope analysis.

[63] The background spectrum here referred to is that of the 'ambient' range of substances occurring in the atmosphere of the room where FTIR was performed.

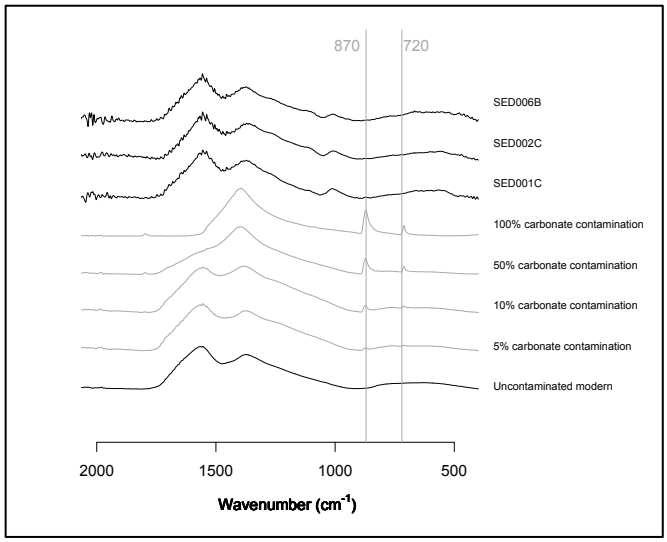


Figure 5.17 FTIR spectra comparing modern grains artificially contaminated with carbonates, (Vaiglova et al. 2014) (lower spectra), with archaeological grains from Sedgeford's kiln 1 (top three spectra)

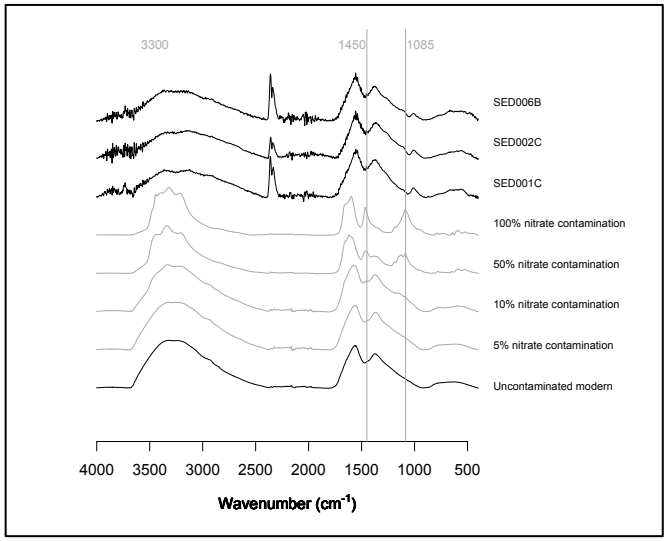


Figure 5.18 FTIR spectra comparing modern grains artificially contaminated with nitrates, (Vaiglova et al. 2014) (lower spectra) with archaeological grains from Sedgeford's kiln 1(top three spectra)

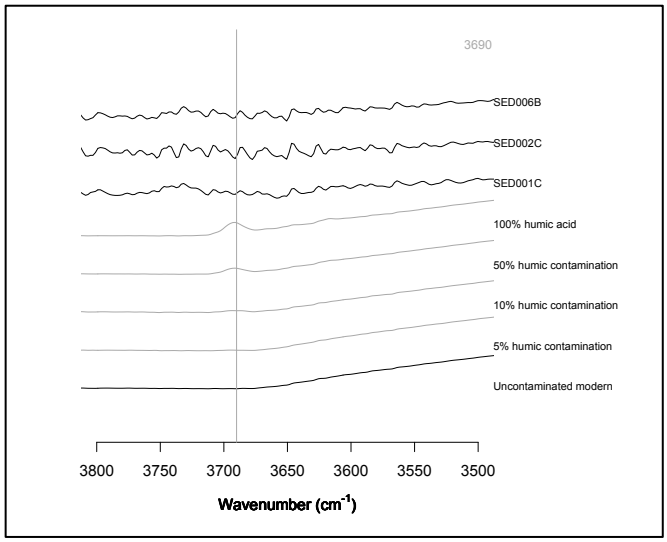


Figure 5.19 FTIR spectra comparing modern grains artificially contaminated with humic acids (Vaiglova et al. 2014) (lower spectra) with archaeological grains from Sedgeford's kiln 1 (top three spectra).

Measuring stable carbon and nitrogen isotope values

Each single-grain sample was crushed using a pestle and mortar and weighed into a tin foil capsule. The samples were analysed using a Sercon 20-22 EA-GSL isotope mass spectrometer at the University of Oxford Research Laboratory for Archaeology and the History of Art. Given the abundance of nitrogen in the samples, it was possible to measure carbon and nitrogen isotope values together in each run. Stable isotope values are calculated relative to an internationally determined scale: VPDB (Vienna Pee Dee Belemnite) for carbon and AIR for nitrogen (Hoefs, 2018, 34).

The in-house standards Cow, Seal (each a form of collagen) and Alanine were used to calibrate the data according to VPDB and AIR, i.e., three-point calibration was employed. Leucine (also an in-house standard) and EMA-P2 were used in the runs as check standards to ascertain the mass spectrometer's accuracy: a measure of the extent to which it is measuring

the 'true' isotope values for each sample. The machine's precision: an indication of its measurement consistency over time, was assessed by introducing a duplicate for every 10th sample in the run, i.e., a repeat of material from the same sample, and by noting any variation in repeated measurements of the several calibration and check standards in each run.

Standards comprised at least 10% of each isotopic run, as recommended by Szpak *et al.* (2017, 615). All standards used have well-characterised isotopic compositions; their means and standard deviations are listed in **Table 5.11**.

Table 5.11 Means and standard deviations for calibration and check standards used in mass spectrometer runs for samples from Sedgeford

Standard	Type	$\delta^{13}C$ ‰		$\delta^{15}N$ ‰	
		Mean	Standard deviation	Mean	Standard deviation
Alanine	Calibration	-26.91	±0.11	-1.57	±0.13
Cow	Calibration	-24.28	±0.12	7.86	±0.18
Seal	Calibration	-12.54	±0.15	16.14	±0.24
EMA-P2	Check	-28.19	±0.16	-1.57	±0.29
Leucine	Check	-28.24	±0.21	6.29	±0.24

Employing the formulae devised by Szpak *et al.*, the accuracy (u(bias)) of the carbon runs was calculated as ±0.305‰, and the precision (u(Rw)) as ±0.423‰. Combined total analytical uncertainty for $\delta^{13}C$ values was ±0.522‰. For nitrogen, accuracy was ±0.404‰ and precision ±0.195‰. Overall uncertainty for $\delta^{15}N$ values was calculated as ±0.448‰ (Szpak et al., 2017). The data were normalised using the statistical programme R (version 4.1.2), and accuracy, precision and uncertainty calculated using Excel, version 16.58.

Samples with low nitrogen yield are known sometimes to give spurious measurements: an approximate 'bench-mark' suggests nitrogen yield should exceed 50μg (E. Stroud, *pers.*

comm.). Calculation of accuracy, precision, and uncertainty according to Szpak *et al.* (2017) is based partially upon consistency in normalised values between duplicate samples. These calculations were re-run for nitrogen isotope values excluding duplicates from grains with <50μg nitrogen (SED08A and SED09A), giving a combined uncertainty of ±0.445‰ (precision ±0.186‰ and accuracy ±0.404‰). In other words, low nitrogen yield has a limited effect on normalised values. Hence, the nine samples having <50μg nitrogen were not excluded from subsequent analysis.

Prior to further analysis, following Stroud (in press) as described above, 'charring' offsets were applied to the normalised values: +0.33‰ for δ^{15}N values, and +0.12‰ for δ^{13}C values. Duplicate values (pairs from the same sample) were averaged. Following FeedSax practice (e.g., Stroud, 2022), it was deemed unnecessary to convert normalised δ^{13}C values to Δ^{13}C, since, in this project, δ^{13}C values for archaeological grains are not compared with those for modern grains (see e.g., Farquhar et al., 1989).

Assessing reliability of the isotopic data

It is important to be able to discern whether the δ^{13}C and δ^{15}N values of archaeological grains have been altered by post-depositional processes, for example bacterial activity (see Hartman et al., 2020, 105129). This can be assessed through FTIR and also by comparing grains' C:N ratios with those for modern grains (Fraser et al., 2013). C:N is here calculated as: (%C/%N) x (14/12).

C:N ratios for Sedgeford's grains (rye, free-threshing wheat, and hulled barley) were compared with those for modern grains of the same taxa, experimentally charred by Stroud (in prep.). Specifically, Sedgeford grains were compared with grains charred for either four or

eight hours, at temperatures ranging from 215°C to 260°C. However, it should be noted that the ratios compared are not wholly 'like-for-like'; the archaeological samples are single-grain, whilst the Stroud (in press) measurements are based on bulk samples of 10 grains. Equivalent data for single-grain samples of rye, wheat and barley are not yet available.

C:N ratios for Sedgeford's single grains ranged from 8.95 to 31.65., and for modern bulk samples from 19.90 to 41.15. C:N ratios for the archaeological and modern grains are significantly different (Mann Whitney *U* test, $U = 228$, $p = <0.001$).[64] This is likely due to several archaeological grains of each taxon having a low C:N ratio, owing to high %N (average archaeological %N is 3.1, compared with 2.3) (**Figure 5.20**). One plausible explanation for higher %N in the Sedgeford grains is the relationship between yield and nitrogen utilisation in cereal plants. Triboi *et al.* (2006) have established experimentally a strong negative correlation between grain yield and %N. Certainly, grains from Sedgeford likely had a significantly lower yield than modern varieties, due to both genetic and environmental factors (see Diffey, 2018, 112).[65] If so, high %N is 'intrinsic' to the grains and not a result of post-depositional processes. Further, there is no significant correlation between %N and δ^{15}N values for Sedgeford grains (Pearson's correlation co-efficient, $p = 0.08$). Hence, it seems high %N in some grains did not have a distorting effect on δ^{15}N values.

Additionally, Szpak and Chiou (2020, 533) suggest that post-burial alteration of isotopic values may be signalled where there is strong positive correlation between C:N ratios and δ^{15}N values for archaeological grains. **Figure 5.21** and statistical testing suggests no evidence of correlation for rye ($p = 0.21$) and free-threshing wheat ($p = 0.76$); correlation for

[64] The data did not pass the assumption of homogeneity of variances, as tested using Levene's test, hence a non-parametric Mann-Whitney U test was used.
[65] Grain weight is one component of total yield. Anecdotally, Sedgeford grains are small.

hulled barley grains (p=<0.001) is negative rather than positive. This indicates δ^{15}N values for all three taxa are free of alteration post-burial.

These statistical analyses, combined with FTIR results (**Figures 5.17** to **5.19**) suggest no particular cause for concern regarding possible effects of post-depositional processes on isotopic values. Isotopic values generated for all the Sedgeford grain samples are therefore considered sufficiently reliable to be included in subsequent analyses.

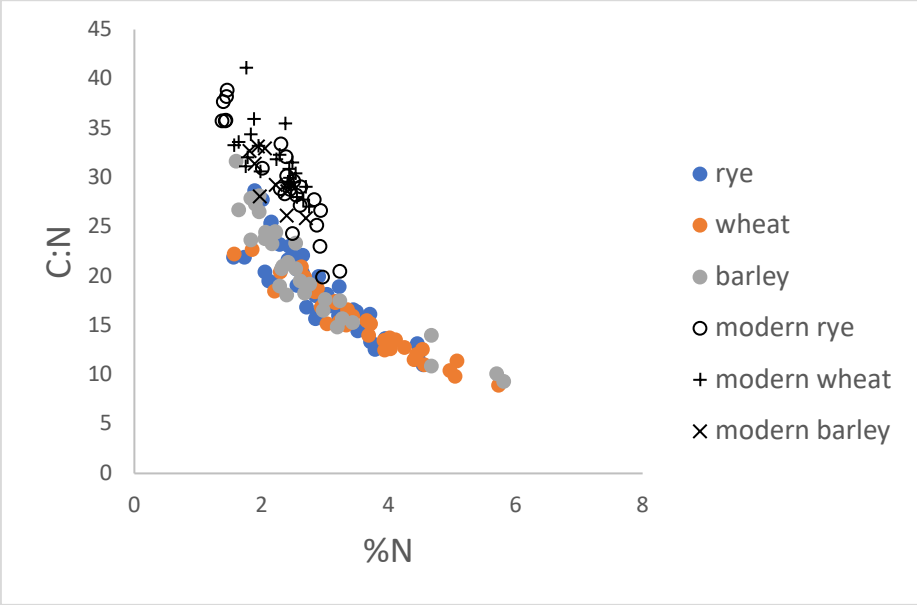
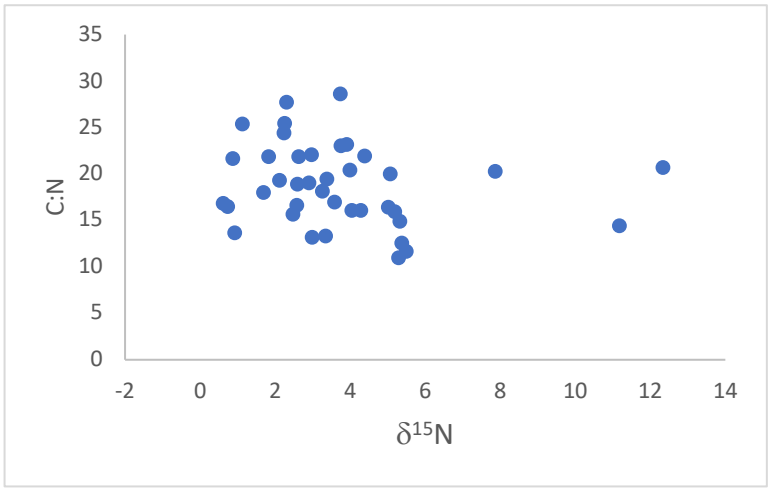
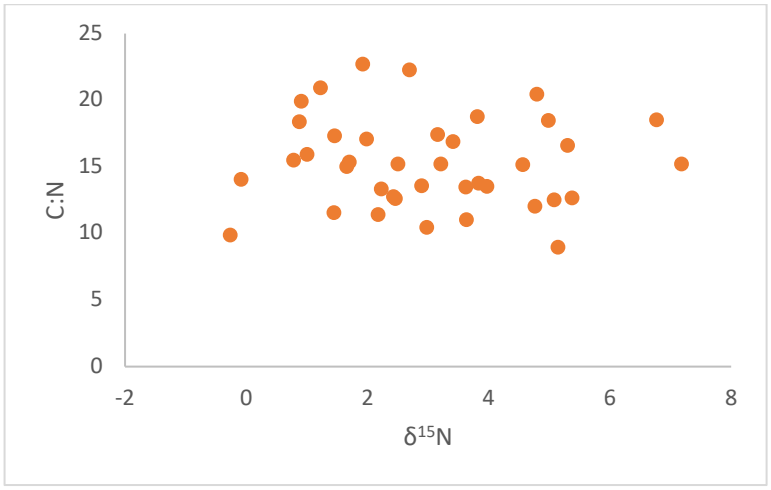


Figure 5.20 C:N values plotted against %N for grains from Sedgeford and for modern grains, experimentally charred by Stroud (in prep.)

a)


35
30
25
20
15
10
5
0
C:N
-2
0
2
4
6
8
10
12
14
δ15N

b)


25
20
15
10
5
0
C:N
-2
0
2
4
6
8
δ15N

c)

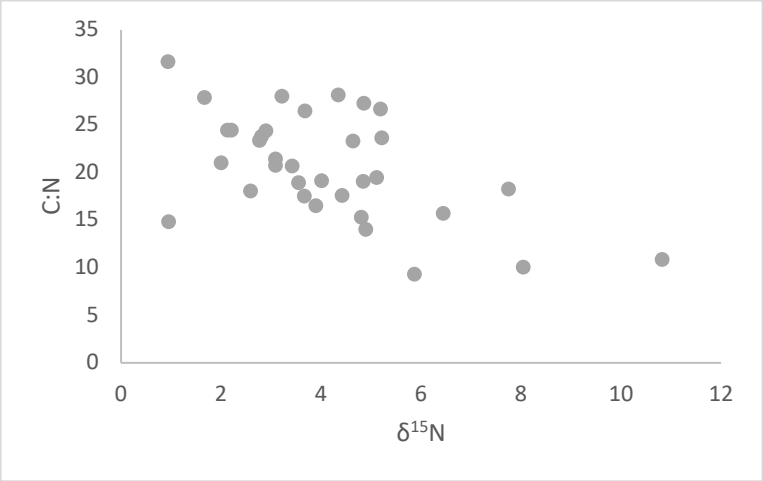


Figure 5.21 C:N values plotted against normalised $\delta^{15}N$ for grains from Sedgeford a) rye, b) wheat c) barley

5.6 Functional weed ecology

Perhaps unexpectedly, the ecological characteristics of weed species whose seeds occur alongside cereal grains in archaeobotanical samples can reveal much about the ways in which these crops were husbanded. Since arable weeds, as all plant species, have particular ecological tolerances and preferences, the collection of weed species growing in a particular field will reflect the farming methods there used. For instance, certain taxa will occur more abundantly in fields where the soil is enriched by manuring or middening (Glauninger and Holzner, 1982, 151–152; Bogaard, 2004b, 5). Archaeobotanists have long exploited this phenomenon – traditionally most often using either so-called phytosociological methods or, alternatively, techniques based on 'Ellenberg numbers'. These methodologies are elsewhere described in some detail (e.g., Bogaard, 2004b, 5–7). Here, the key features of a more recently

developed (and, arguably, somewhat more helpful) method, namely, 'functional weed ecology' (FWE), are delineated. The current work uses this method to elucidate some of the characteristics of crop husbandry regimes used to grow the crops malted at mid Anglo-Saxon Sedgeford.

FWE approaches (focusing here particularly on that originally developed at the University of Sheffield and initially known as Functional Interpretation of Botanical Surveys, or FIBS) are founded on the measuring of particular 'functional attributes' or traits in modern plant analogues of weed taxa whose seeds occur in archaeobotanical assemblages. These attributes include canopy height, leaf surface area, stomatal density, flowering period, and others. Research has demonstrated that certain plant functional attributes correlate (positively or negatively) with particular growing conditions, including moisture levels, sowing times, and root disturbance (Charles et al., 1997; Bogaard et al., 1999; G. Jones et al., 2000; Bogaard et al., 2001; G. Jones, 2002). For example, maximum canopy height, mean specific leaf area, and leaf thickness relate to plant growth rate and thus to soil fertility (G. Jones et al., 2000; Bogaard et al., 2001; Charles et al., 2002). An extensive database of recorded functional trait values for arable weed species has been developed at the University of Sheffield (e.g., Hodgson, 1991; Hodgson et al., 1999).

This method has been tested using present-day field surveys (Bogaard et al., 2001; Charles et al., 2002; Fraser et al., 2011; Bogaard, Hodgson, et al., 2016; Bogaard, Styring, et al., 2016; Bogaard et al., 2022). FWE has been shown to successfully identify particular cultivation regimes. For example, weed functional trait data were able to distinguish between farming with high labour inputs in Asturias, Spain ('intensive' cultivation, with high fertility indicating heavy manuring, and much disturbance caused by weeding and tillage), and agricultural

methods using low labour inputs ('extensive' farming with little manuring, weeding or tillage) in Haute Provence, France (Charles et al., 2002; Bogaard, Hodgson, et al., 2016).

Weed functional ecological data (specifically, the length of the flowering period and – for perennial plants – capacity for vegetative regeneration from pieces of rhizome, root or stolon) have also been used to successfully distinguish between farming regimes with differing levels of mechanical disturbance (from hand-weeding and tillage) *alone* (Hamerow et al., 2020, 598; Bogaard et al., 2022). In this case, a discriminant analysis model was created contrasting areas of unploughed grassland, not treated with herbicides (but occasionally grazed and annually cut) – so-called 'sykes', part of the open-field farming system still in use at Laxton, Nottinghamshire – with ploughed arable areas (at field edges, so not treated with herbicide) and additionally fallow fields, (in the third year of the rotation pattern and thus not recently sprayed), also at Laxton. The results of modern field surveys of regularly ploughed fields at the Highgrove Home Farm in Gloucestershire were also added to the model.

FWE methods can readily be applied to data from archaeobotanical assemblages: knowledge of the functional trait values for present-day weed species can be 'translated' onto the same species occurring as seeds in preserved archaeological plant material. Discriminant analysis may then be used to quantitatively compare functional trait values for the set of weeds in each archaeobotanical sample with modern 'models' – for instance with values from field surveys in Haute Provence in France, typifying extensive farming, and those from Asturias typifying intensive farming – such that samples can, in this case, be positioned on a 'high-intensity low-intensity' spectrum (**Figure 5.22**) (e.g., Styring, Rösch, et al., 2017, 371 Figure 6; Diffey et al., 2020, 1216 Figure 8; Hamerow et al., 2020, 12 Figure 7). In the case of the 'disturbance model' functional traits for modern analogues of species in archaeobotanical assemblages are compared with equivalent values from the Laxton sykes, typifying low levels

of disturbance, and the Laxton ploughed and fallow fields, along with ploughed fields at Highgrove, typifying high levels of disturbance – such that samples are placed on a 'high disturbance low disturbance' spectrum (Hamerow et al., 2020, 599 Figure.8; Bogaard et al., 2022 Figure 13) (**Figure 5.23**).

Notably, in contrast with other methods, FWE is concerned not with the assemblage of weed species in any given sample *per se*, but rather with the plants' functional attributes – since it is these, specifically, which are associated with a particular husbandry regime (e.g., Stroud, 2016, 92–93; Diffey, 2018, 79). This permits the recognised correlation between one set of species and a given environment in the present-day to be translated onto a distinct set, in similar ecological conditions, but occurring elsewhere in time and location – for which there may be no modern analogue (Charles et al., 1997, 1151; G. Jones, 2002, 189). Finally, and significantly, FWE permits disentangling of precisely which ecological conditions determine a plant's occurrence in a given environment, and can thus, potentially, facilitate the recognition of 'new' farming regimes from the past with combinations of practices unknown in the present (Charles et al., 1997, 1151; G. Jones, 2002, 190).

5.6.1 Use of FWE to analyse archaeobotanical samples from Sedgeford

A form of FWE was used to investigate both the 'intensity' (i.e., labour input level) and 'disturbance' (i.e., level of hand-weeding and tillage) of the Mid Saxon agricultural regime used to cultivate cereal grains recovered from Sedgeford's malting complex. The methods used in this study were first developed at the Unit of Comparative Plant Ecology at the University of Sheffield (e.g., Hodgson, 1991; Hodgson et al., 1999) and further refined by the 'Agricultural Origins of Urban Civilisation' (AGRICURB) research project at the University of Oxford (Bogaard, Hodgson, et al., 2016; Bogaard, Styring, et al., 2016).

FWE as used here depends on much previous research including the amassing of a sizeable database of functional traits for arable weeds (the original Sheffield FIBS database, augmented through subsequent fieldwork as part of the AGRICURB project) and, further, botanical field surveys in modern fields employing disparate (traditional) cultivation methods; these survey locations also represent a range of climatic conditions. Such surveys have been conducted in Asturias, northern Spain; Haute Provence, southern France; Evvia, Greece; and parts of Germany, Morocco and the U.K., (Bogaard et al., 2001; Charles et al., 2002; Bogaard, Hodgson, et al., 2016; Bogaard, Styring, et al., 2016; Hamerow et al., 2020; Bogaard et al., 2022) (the results from Provence, Asturias and the U.K. concern us most here). Surveys were conducted, with weed species identified, in several fields in each region.

These data have been used to create discriminant analysis models, ultimately permitting archaeobotanical samples of 'unknown' origin to be compared with, and classified against, modern sets of weed species from 'known' agricultural regimes. For each field survey, relevant functional trait values (i.e., canopy height, canopy diameter, specific leaf area and leaf area per node – or leaf thickness - for the 'intensity' model; and flowering duration and capacity for vegetative regeneration for the 'disturbance' model) for all species identified were elicited from the FIBS database, and the presence or absence of each species per field noted. The discriminant analysis procedure has been applied to all data, with functional traits operating as 'discriminating variables'. A 'discriminant function', which most efficiently distinguishes between the two groups, is in each case extracted from all the data provided. The success of the analysis is determined by the accuracy with which each field unit is allocated to its respective group. **Figure 5.22** shows initial discriminant analysis results for the 'intensity' model, with each symbol representing a single field, plotted relative to the extracted discriminant function. Fields with a 'high-input' regime (from Asturias), coloured black, are

contrasted with fields where cultivation is 'low-input' (from Provence), in white. The larger symbols represent a weighted average 'centroid' for each regime. **Figure 5.23** shows initial results for the 'disturbance' model, with each symbol representing a single field or arable area, plotted relative to the extracted discriminant function. Fields with a 'low-disturbance' regime (from the Laxton sykes), in open squares, are contrasted with fields where cultivation is 'high disturbance' (from other fields at Laxton, and Highgrove), represented by other symbols. Again, the larger symbols represent a weighted average 'centroid' for each regime.

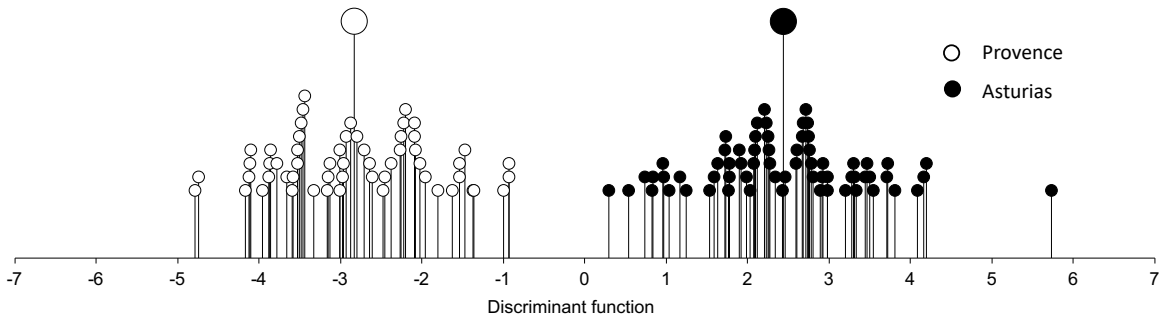
Archaeobotanical samples can then be introduced to the model(s). Following sorting, identification and quantification of preserved plant remains in all 55 samples from the malting complex (**section 5.2**), these were reviewed to select those suitable for FWE analysis. It was decided to use 'behavioural episodes' as the unit of analysis, necessitating sets of neighbouring samples with similar composition (in terms of relative frequencies of both cereal grains and weed seed taxa) to be grouped, respectively, into a single unit (**section 6.3.1**, **Figure 6.16** and **Figure 6.41**). Samples without similar neighbours remained ungrouped, with each treated as representing a single-sample 'episode'.

Only samples /sample groups with (in total, after multiplying up) at least 10 weed seeds identified to species level were selected (on this basis, a single sample – 17018 – was excluded). Exceptions were made for seeds identified only to genus level where the potential candidate species all possess identical functional trait values e.g., candidate species for blunt-ended seeds of the genus *Bromus*, (near-ubiquitous in Sedgeford's samples) in the UK are *Bromus secalinus, Bromus hordeaceus* and *Bromus arvensis*. These three species share the same functional trait values and hence it was deemed valid to include *Bromus* seeds in the assessment. A total of 12 sets of grouped samples, and 14 ungrouped samples (a combined total of 26 'units') were selected for analysis.

Functional trait values for all weed seeds occurring in the selected units were elicited from the FIBS database,[66] and, to permit viable comparison with modern field survey data, seed frequencies per unit converted to presence/absence values (i.e., semi-quantitative data). In each case, the discriminant analysis method then allocated each archaeobotanical unit to one of the pre-determined groups (from the modern field surveys), thus indicating (using the 'intensity' model) the level of labour input and (using the 'disturbance' model) the level of mechanical disturbance, respectively, in the husbandry regime used to grow crops malted at Mid Saxon Sedgeford.

In each case, discriminant analysis was performed using IBM SPSS version 27 (using 'leave-one-out' classification for greater robusticity), and data plotted using Microsoft Excel, version 16.5.

a)



[66] The author is grateful to the Unit of Comparative Plant Ecology at the University of Sheffield for access to these data.

b)

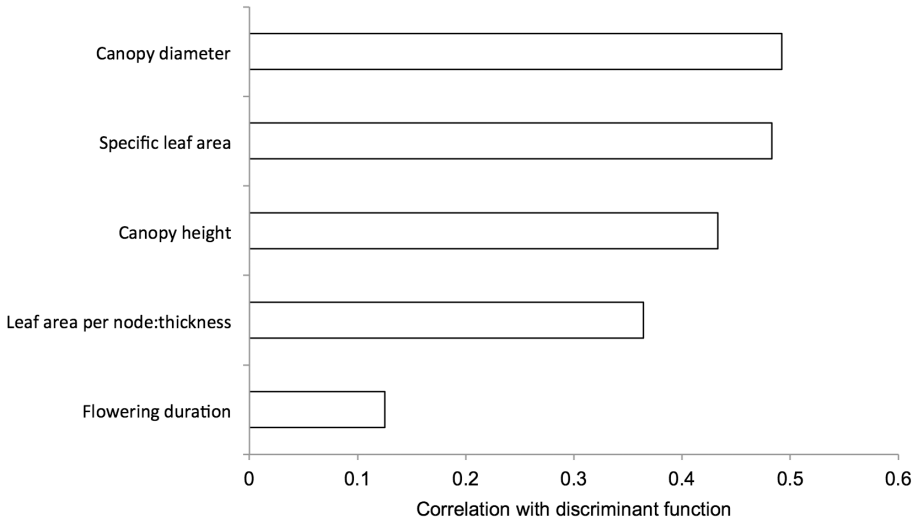
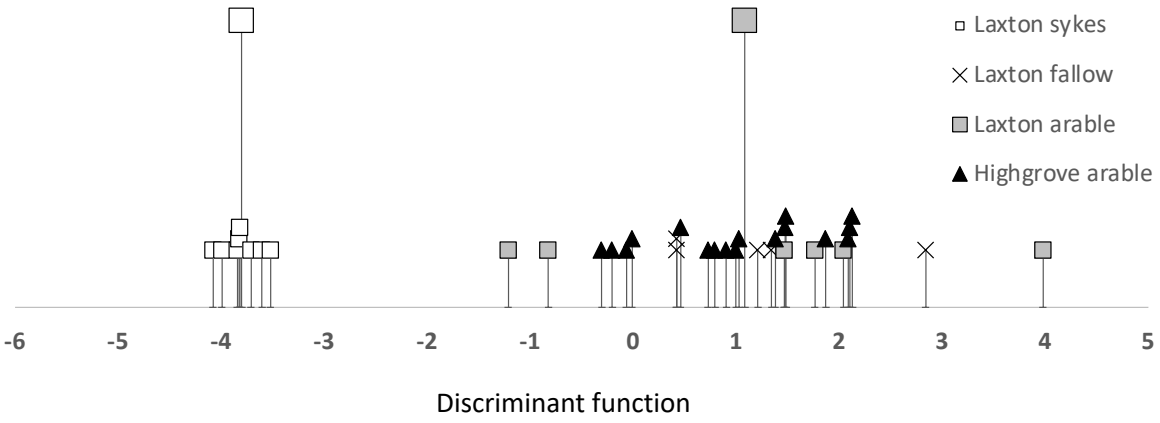


Figure 5.22 a) Data from modern field surveys distributed according to the 'intensity' discriminant function which best separates low (white) and high (black) intensity crop cultivation regimes. Larger symbols indicate group centroids. b) Correlations between functional trait scores used as variables to discriminate between groups, and the discriminant function. Both plots are reproduced with kind permission from Bogaard et al. (2016, p.66, Figures 6b and 7b)

a)



b)

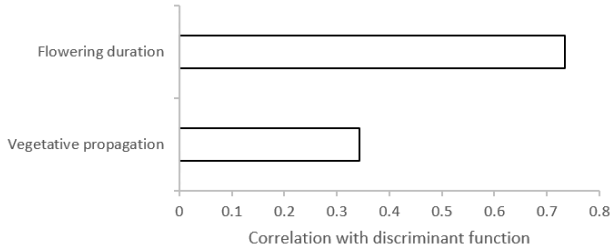


Figure 5.23 a) Data from modern field surveys distributed according to the 'disturbance' discriminant function which best separates low (open squares) and high (other symbols) disturbance crop cultivation regimes. Larger symbols indicate group centroids. b) Correlations between functional trait scores used as variables to discriminate between groups, and the discriminant function. Both plots are reproduced with kind permission from Hamerow et al. (2020, p.599, Figure 8a and 8f)

5.7 Seasonality

To gain a more complete understanding of husbandry methods used to cultivate the crops malted at Mid Saxon Sedgeford, it is helpful to deduce when (in which season: spring or autumn) the cereal species encountered in the archaeobotanical assemblage were sown; in particular with reference to potential crop rotation (see **section 1.4.2**). Once again, the specific spectrum of weed species in each sample can be used to help reveal this (Bogaard et al., 2001).

An ecological analysis conducted by Bogaard *et al.* (2001) on weed flora in harvested material of known origins from modern fields in Germany, demonstrated that the weed ecological traits which can best reveal crop seasonality are flowering duration and the timing of flowering onset. Essentially, annual weed species whose flowering time is either late in the year or of long duration, and perennials which can regenerate from root/rhizome fragments (both thus setting seed after ploughing for spring sowing), are at a competitive advantage among fields of spring sown crops. Species which flower early or for a short period of time, unless weeded out, flourish (being undisturbed) among autumn-sown fields (**Table 5.12**) (Bogaard et al., 2001, 1173; McKerracher, 2019, 97).

A recent study has demonstrated that use of correspondence analysis (rather than the discriminant analysis employed by Bogaard *et al.* (2001)), classifying weed species using the same functional traits, permits detection of subtle seasonality trends in an archaeobotanical assemblage (McKerracher, 2019, 96–124). Correspondence analyses (**section 5.2.8**) are used in this study to infer crop seasonality based on associations with weeds whose ecological traits (as described) render them more likely to co-occur with either spring or autumn-sown cereals.

Table 5.12 Annual weed species types based on flowering onset and duration, with the associated crop sowing regime in which each is favoured, after (Bogaard et al. 2001, p.1175, Table 3) and (McKerracher, 2019, p.97, Table 27)

Type	Flowering onset	Flowering duration	Competitive advantage in…
Early/short	Jan.-Jun.	1-3 months	Autumn-sown fields
Late	Jul.-Dec.	1-5 months	Spring-sown fields
Long	Jan.-Jun.	>5 months	Spring-sown fields
Intermediate	Apr.-Jun.	4-5 months	Autumn and spring-sown fields

5.7.1 Use of seasonality-based correspondence analysis to analyse samples from the Sedgeford assemblage

The principles underlying correspondence analysis are described in **section 5.2.8.** For the analyses in question, samples with fewer than 10 weed seeds were excluded (only sample 17018 required exclusion on this basis), as were weed species occurring in fewer than 10% of samples. This reduces bias attributable to weed-poor samples whose weed spectra are not representative of the cultivated field from which they originated, and to rare species which are more likely to be chance contaminants (**section 5.2.8**). Further, weed taxa identified only to the family or genus level were excluded since broader taxonomic groupings can comprise species of differing seasonality classes (however, where a weed seed was confidently identified to either two or three species whose 'seasonality' class coincided e.g., *Bromus arvensis* / *Bromus hordeaceus* / *Bromus secalinus*, these were incorporated). Eligible weed seeds from the Sedgeford assemblage included two perennials: *Plantago lanceolata* and *Phleum pratense*. Each of these

regularly regenerates by seed (as well as through vegetative propagation) hence, following Bogaard *et al.* (2001, 1173) these were treated as annuals.

Crop processing can bias results – creating spurious associations between weed species whose co-occurrence with one another and with associated grains post-dates crop cultivation (McKerracher, 2019, 98). However, all samples from the malting complex assemblage classify as either FSP or USG in terms of crop processing i.e., as grain-rich products (**sections 5.4** and **6.6.2**); this type of sample is less likely to be affected by crop-processing-bias (ibid.), hence no samples were thereby excluded.

Considering these restrictions, a total of 53 samples, and 12 weed species (as well as the four cereal taxa) were included in the correspondence analysis. The 'seasonality' designation for each weed species used by any researcher depends somewhat on the reference material consulted; hence it is important to specify explicitly the seasonality category awarded to each species (**Table 5.13**).

Table 5.13 Weed species from Sedgeford's malting complex assemblage included in 'seasonality' correspondence analysis, with flowering onset/duration 'class' and associated seasonality

Species	Class	Resultant seasonality
Agrostemma githago L.	early/short	autumn seed
Anthemis cotula L.	late	spring seed
Atriplex hastata L. / patula L. / prostrata Boucher ex. D.C.	intermediate	n/a
Bromus arvensis L. / *Bromus hordeaceus* L. / *Bromus secalinus* L.	early/short	autumn seed
Chenopodium album L.	late	spring seed
Fallopia convolvulus (L.) Á.Löve	late	spring seed
Phleum pratense L.	early/short	autumn seed
Plantago lanceolata L.	long	spring seed
Raphanus raphanistrum L.	intermediate	n/a
Urtica urens L.	intermediate	n/a
Vicia hirsuta L. (Gray) / *tetrasperma* L. (Schreb.)[67]	intermediate	n/a

5.8 Geometric Morphometric analysis

Morphometrics is a form of analysis which uses statistical methods to describe forms (including biological entities) according to their size and shape, in a way which compares to numerical analysis. Morphometrics traditionally relies on a set of measured distances (Rohlf and Marcus, 1993). Geometric Morphometrics (GMM) is a relatively new field which, using multivariate statistics, permits analysis of the overall shape of an organism. In archaeobotany, GMM has been successfully applied to distinguishing between cereal grains belonging to different species and landraces (e.g., Bonhomme et al., 2017; Wallace et al., 2018; Roushannafas et al., 2022).

[67] It was surmised that the most likely candidate species for the taxa classified as *Vicia* L./*Lathyrus* L. are *Vicia hirsuta* L. (Gray) / *tetrasperma* L. (Schreb.) (A. Bogaard, *pers. comm.*)

5.8.1 Using GMM to analyse grains from Sedgeford

T. Roushannafas (in prep, 110–148), in association with the FeedSax project, has investigated whether it is possible using GMM to distinguish between the various taxa of free-threshing wheat believed to be present in Anglo-Saxon England: namely bread, club, durum and rivet, by comparing archaeological grains from across the country with sets of charred modern grains belonging to each of these taxa (**section 1.4.4**).

Only well-preserved and undistorted archaeological grains were analysed (ibid.). A total of 81 modern grains of each (sub-)species were analysed (324 in total). Both modern (charred) and archaeological grains were photographed (in dorsal, lateral and polar views) and their outlines digitally traced. Grain embryos were excluded from the outlines, as these are often damaged or missing, and may not be consistently developed in all grains. A technique known as Elliptic Fourier Analysis (Giardina and Kuhl, 1977) was applied in 'R' (3.6.2) using GMM packages 'geomorph' and 'momocs' (Roushannafas, in prep, 122). Linear discriminant analysis was then used to ascertain how accurately modern charred grains could be classified according to their shape; generating a score for each specimen according to the group centroid it most closely approximated. For charred modern grains, the 're-classification' rate (proportion of grains correctly classified) was 89.3% (ibid., 123).

A total of 463 archaeological wheat grains of unknown classification were then introduced to the linear discriminant analysis model. This included 40 wheat grains from the Sedgeford malting complex, deriving from contexts surrounding kiln 1: these were well-preserved grains that were not obviously germinated according to the methods described in **section 5.3.2**. A further preliminary investigation involved analysing using GMM 24 experimentally germinated, dried and charred modern bread wheat grains, (from the second

'germination experiment' described in **section 5.3.1**) and adding these data to the linear discriminant analysis model. Full description of methods used is provided in Roushannafas (in prep, 117–125).

5.9 Scanning Electron Microscopy

It is suggested in **section 2.4** that germination-induced changes in the internal histology of cereal grains can be detected under SEM. Y. Zhou has recently conducted a set of analyses using SEM to compare experimentally germinated, dried and charred rye grains with archaeological rye grains: both from the Sedgeford malting complex assemblage and from the Mid Saxon site of Lyminge, in Kent (the latter a 'control', since these are not expected to be germinated) (Zhou, 2022). This is the first time that use of SEM to investigate signs of germination in the internal microstructure of archaeological rye grains has been trialled.

5.9.1 Using SEM to analyse grains from Sedgeford

All samples were of rye. Archaeological samples prepared were as follows: 10 archaeological grains from Lyminge, sourced from the FeedSax project archive; and nine from the Sedgeford malting complex, comprising three judged to be 'germinated, three 'ungerminated' and three 'indeterminate', according to the gross morphology assessment methods presented in **section 5.3** (of the nine, four were from context/sample 23723, two from 23660 and one from each of 23333, 23719 and 23701 J7). All archaeological grains selected were judged to be well-preserved, as per Charles (2015). Archaeological grains were compared with modern germinated and dried grains (both charred and uncharred) from the second 'germination experiment' described in **section 5.3.1** (Zhou, 2022, 21, 25).

Archaeological grains were freeze-dried, and then cut using a scalpel near the embryo-end, where the effects of germination are expected to be more pronounced (Heiss et al., 2020, 6). Cross-sections were mounted on stubs prior to carbon coating using a BIO-RAD SEM Coating System. SEM images were generated using a JEOL JSM-5510, with an accelerating voltage of 9kv. Each sample was examined at several magnifications between x37 and x5000, and at spot sizes 5, 15 and 25 (Zhou, 2022, 22). Methods used are fully detailed in Zhou (2022).

5.10 Summary

The current chapter having detailed methods used in this project to extract, assess, and quantitatively analyse archaeobotanical material from Sedgeford's malting complex, the next two chapters turn to presenting results obtained from analyses conducted using these methods.

6 CHARACTERISING THE ARCHAEOBOTANICAL ASSEMBLAGE

6.1 Introduction

This chapter summarises characteristics of the Sedgeford assemblage by describing findings from identifying and quantifying the charred plant material. 'Identifying' here includes assessing the frequency of germination among grains in the samples (with analyses used by fellow archaeobotanists Tina Roushannafas and Yu Zhou to assess germination levels presented at the chapter's close). Correspondence analysis is used to reveal compositional trends in the data. The chapter includes an examination of crop processing stages represented by samples in the assemblage; specifically, two models for crop processing – the 'conventional' model as established by G. Jones (1984; 1987) and a new model developed by the author specifically to describe traditional methods of preparing crops for brewing, are here tested against archaeobotanical data from Sedgeford. The complete set of archaeobotanical data from both Sedgeford assemblages (the malting complex and settlement area) can be found in **Appendix C**.

6.2 Locating sample contexts

Where indicated below, the 55 samples from the Sedgeford malting complex have been grouped according to the feature, or area of the trench, from which they derive (**Table 6.1**). These groupings are shown in **Figure 6.1**.

Table 6.1 Grouping of samples by feature in Trench 23

Feature	Number of samples
Kiln 1	8
Kiln 2	7
Clay floor 2	5
Kiln 3	5
Undefined feature	14
Steeping tank	5
Western ditch	3
Eastern ditch	3
Other	5

Figure 6.1 Aerial photograph of the malting complex mapping contexts for each sample (numbered). Contexts are grouped by feature/area of the trench. Photograph taken 4 July 2019 (Image: Ian Drummond/SHARP)

6.3 Compositional analysis

All plant items in the Sedgeford malting complex assemblage are preserved through charring. The assemblage is remarkably rich, with an average density of 228 charred plant items per litre of sediment. Three samples, all from the vicinity of kiln 2 (19036, 23722 and 23727) have more than 1000 plant items per litre (sample 23727 has 1,825).

The stacked bar charts in **Figure 6.2** and **Figure 6.3** show the relative composition of charred plant material (in terms of cereal grains, chaff, detached sprouts and weed seeds) in samples from across the malting complex, firstly ungrouped, and secondly grouped by feature. **Figure 6.4** displays these data both averaged over all samples from Trench 23, and feature by feature.

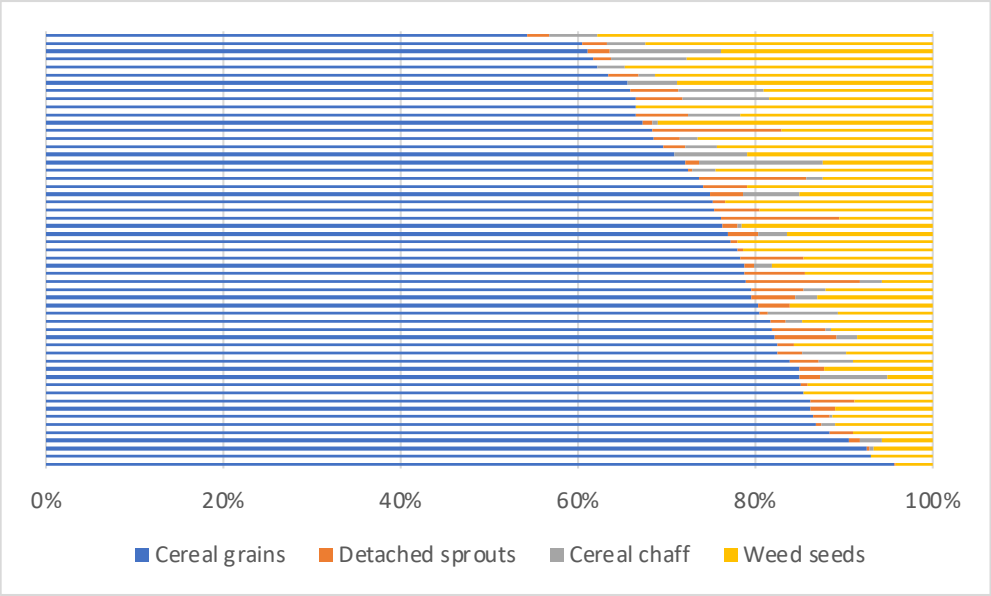


Figure 6.2 Composition of all malting complex samples, ordered by descending proportion of grain

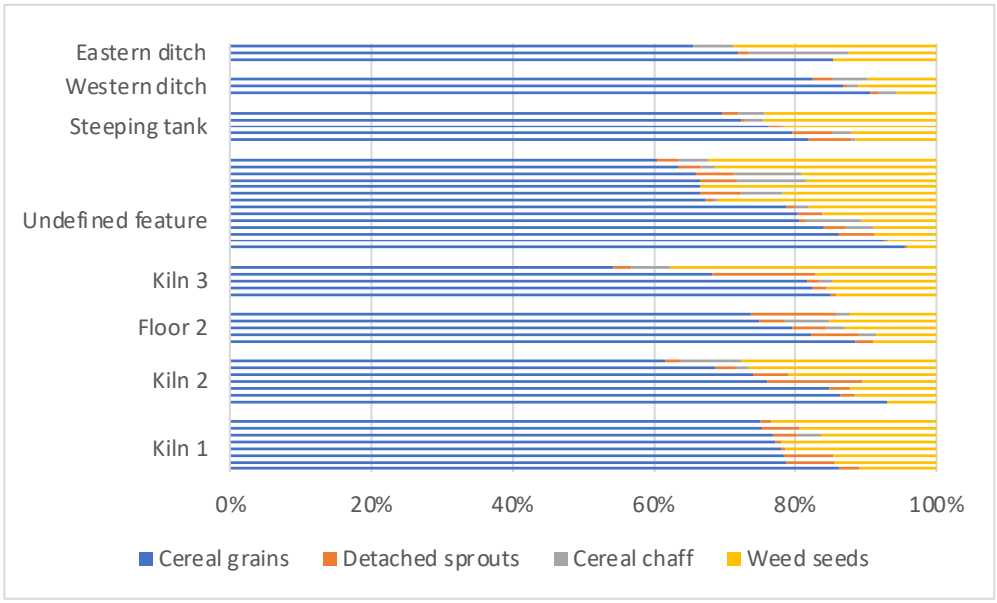


Figure 6.3 Composition of samples from the malting complex grouped by feature/area of the trench, in order of descending proportion of grain

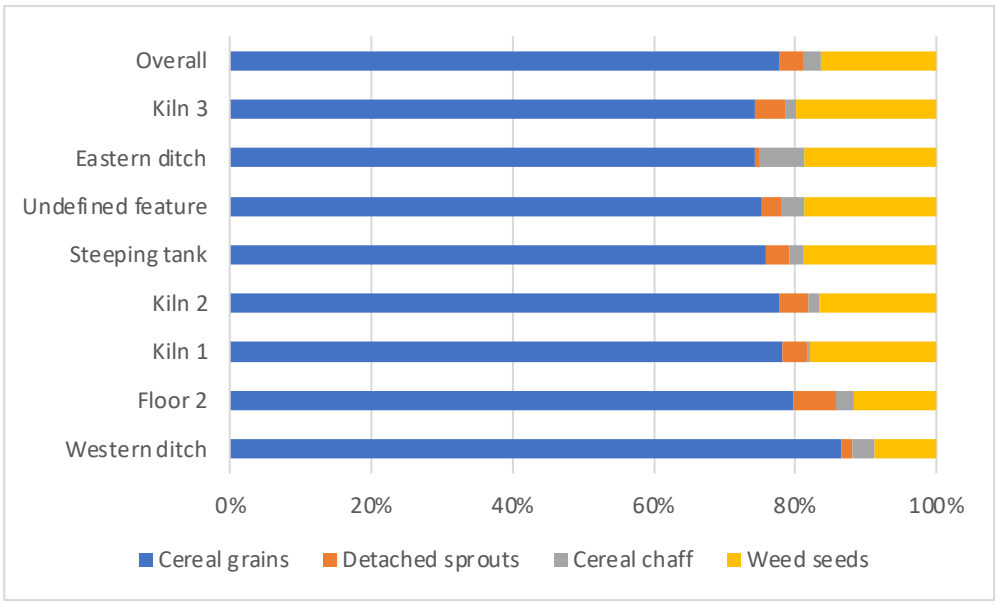


Figure 6.4 Average composition of samples from the malting complex overall, and from each feature/area of the trench, ordered by descending proportion of grain

These charts show that the Trench 23 assemblage is very grain-rich: all samples from the malting complex comprise over 50% cereal grain, and 34 of 55 samples (61.8%) have over three-quarters grain. The mean proportion of cereal grains across all malting complex samples is 76.9%. The non-grain component of all but four samples (17018, 23077A, 23325, and 23647) consists primarily of weed seeds – 16.7% on average.

In terms of broad categories of charred plant material, the average composition of samples when separated by feature is very consistent (**Figure 6.4**), with, for instance, on average, aggregated samples comprising 78.2%, 77.9% and 74.4% grains in kilns 1, 2 and 3, respectively. One distinctive feature is the particularly low frequency of chaff in samples from kiln 1 – only one sample of eight here contains any chaff. The average proportion of chaff across all malting complex samples is remarkably low – only 2.4% (n = 25); indeed, 20 samples from Trench 23 (36.4%) are entirely without chaff.

Notably, on average, the Trench 23 samples contain 4.0% (n = 41) detached sprouts; this is a conservative estimate of their true frequency, due to the way these were quantified – (**section 5.2.6**). The maximum percentage of detached sprouts per sample is 14.5% in sample 23375 (n = 248), from a context adjacent to kiln 3. Significantly, detached sprouts occur across Trench 23, in 49 of 55 samples (**Figure 6.5**), with the proportion averaged across samples from each kiln consistently ~4% of plant items (**Figure 6.4**) (3.5%, 4.0% and 4.3% respectively, in kilns 1, 2 and 3). Where samples are averaged across features, the highest mean proportion of detached sprouts (6.1%) occurs on floor 2, while the lowest proportions occur in the ditches (2.0%, averaging across all ditch samples).

Understanding the relative importance of a plant item (e.g., detached sprouts) in samples from an excavated area is not wholly straightforward; abundance will be affected both by sample density and by the stage of crop processing achieved by respective samples

(**section 5.4**). The sequence of bubble charts (**Figures 6.5**, **6.17**, **6.21-6.23**, **6.45**) which follow plot abundance relative to grain frequency, as a means of overcoming the first of these difficulties, however, the likelihood that samples represent different crop processing stages, potentially biasing results, is an unavoidable limitation of thus displaying data. Frequencies of plant items relative to grain frequency are expressed rounded to three decimal places.

Figure 6.5 Frequency of detached sprouts relative to grain frequency in samples from the malting complex (right) (Image: Ian Drummond/SHARP 2019) and the gridded area (left) (Image: Gary Rossin/SHARP 2019). Bubble size corresponds to detached sprouts/grains.

6.3.1 Crops

Four cereal taxa were identified in the Sedgeford malting complex assemblage: rye, free-threshing wheat, hulled barley and oat (**Figure 6.6**). All of these are free-threshing cereal varieties (with associated connotations for the ways in which the grains are processed, see **section 5.4**). As shown in **Table 6.2** and **Figure 6.7,** approximately two-thirds (64.9%, n= 21,935) of all grains identified in the Sedgeford malting complex are *Secale cereale* (rye).

More than one quarter (27.2%, n = 9,209) of grains recovered from Trench 23 are free-threshing wheat. As noted in **section 1.4.4**, both hexaploid bread wheat (*Triticum aestivum*) and tetraploid rivet wheat (*Triticum turgidum*) are known to have been cultivated in Anglo-Saxon England, with *Triticum aestivum* occurring far more frequently (glume wheats, including spelt, are very sparse by the Mid Saxon era). Free-threshing wheats can be readily distinguished only by the morphology of their accompanying chaff (Hillman, 2001, 34–36; Jacomet, 2006, 33). All wheat chaff (n = 124 items) identified from the Sedgeford malting complex to date derives from *Triticum aestivum* (**Table 6.2**); i.e., at least some of the free-threshing wheat grains from the malting complex must belong to this species group (**section 1.4.4**). Both rye and free-threshing wheat are 'naked' cereals: hence, ~92% of all charred grains in the malting complex assemblage are without a hull – with, as discussed, important implications for discerning evidence for germination (**section 2.4**).

Significantly, in their forthcoming assessment of plant remains from the 'settlement' part of the site at Sedgeford, McKerracher and Caroe (in prep.) tentatively identified a small number of grains (n = 10) as (the glume wheat) spelt (**section 1.4.4**).

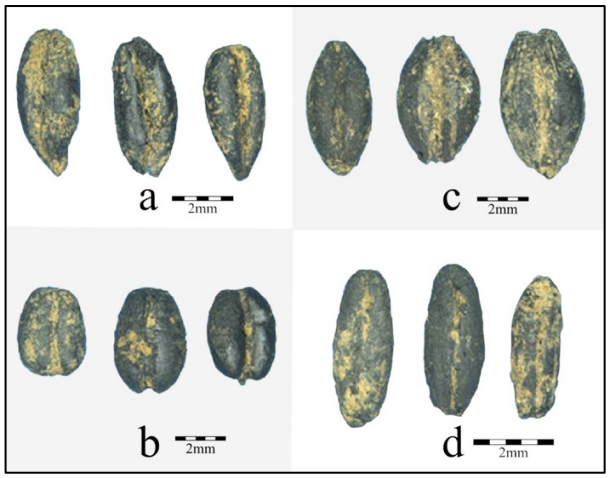


Figure 6.6 Cereal taxa from the Sedgeford assemblage: a) rye, b) free-threshing wheat, c) hulled barley, d) oat (all in ventral view)

Table 6.2 Summarising ubiquity and abundance of crop and weed remains in all 55 samples from the malting complex

Plant item	Samples where present		Max. items per sample	Sum of items
	No.	%		
Cereal grains				
Rye total	55	100	1,391	21,935
Free-threshing wheat total	55	100	997	9,209
Hulled barley total[68]	53	96.4	267	2,357
Straight hulled barley	48	87.3	72	538
Twisted hulled barley	50	90.1	150	1,213
Indet. hulled barley	39	70.9	74	514
Oat total	25	45.5	40	301
Chaff				
Rye rachis total	22	40	125	724
Bread wheat (T. aestivum) rachis total	12	21.8	32	124
Hulled barley rachis total	15	27.3	48	195
6-row hulled barley rachis	12	21.8	48	171
Indet hulled barley rachis	3	5.5	8	24
Oat floret base total	2	3.6	8	12
Weedy oat floret base	2	3.6	8	12
Weed seeds				
Weed total	55	100	544	9,446

[68] The total figure for hulled barley is larger than the combined total for straight/twisted/indet. barley grains since it includes proportionately allocated grains from amalgamated categories e.g., barley/wheat.

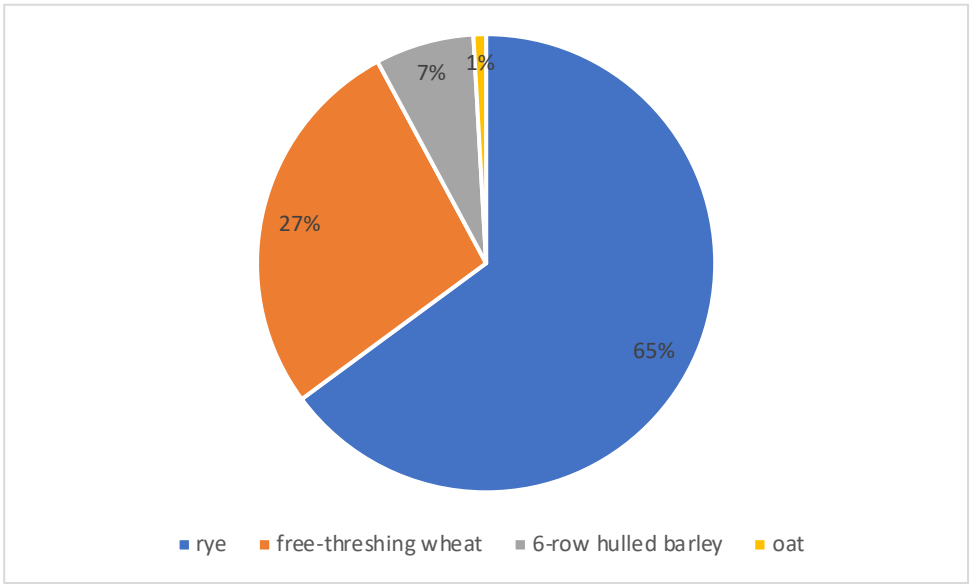


Figure 6.7 Total proportions of cereal taxa from the Sedgeford malting complex (n = 33, 802)

Seven per cent (7.0%, n = 2,357) of grains from the malting complex are *Hordeum* (barley). A well-recognised means of distinguishing between two and six-row barley taxa involves quantifying proportions of 'straight' and 'twisted' grains (e.g., Jacomet, 2006, 37). Barley caryopses from the trench fall approximately into a ratio 2:1 for twisted: straight varieties (**Table 6.2**), indicating that, as at most Anglo-Saxon sites, at least the great majority of barley at Sedgeford is *Hordeum vulgare* subsp. *vulgare* (six-row hulled variety) (see Moffett, 2011, 251). Barley types can further be identified by chaff morphology (Charles, 1984, 28, Figure 5; Jacomet, 2006, 42): most *Hordeum* chaff in the malting complex is clearly six-row variety (n = 171), though a few rachis segments (n = 24) are indeterminate. Two-row barley is not believed to have been introduced to England until considerably later in the medieval period (Hornsey, 2003, 244); hence the indeterminate rachis from Sedgeford is unlikely to be from this form.

Avena (oat) grains are rare in the malting complex (0.9%, n = 301). Cultivated oat (*Avena sativa*) is easily distinguishable from wild varieties (in the UK, *Avena fatua* and *Avena*

sterilis), only by chaff morphology (**section 1.4.4**) (Ruas and Pradat, 2001, 71–72). Only two oat florets have been recovered in the malting complex assemblage: each of these is from the wild species *A. fatua*, suggesting that oats in this part of the site may be a crop contaminant. **Section 3.2.2** suggests weedy oats may have been deliberately retained with crops intended for brewing in the Mid Saxon era because of the additional flavour they are believed to contribute. In contrast, *Avena* constitute the largest proportion of grains (40.9%, n=2,064) identified in the 18 samples from the settlement part of the site (**Figure 6.8**) (McKerracher and Caroe, in prep.). Oats here recovered clearly cannot be dismissed as a weedy contaminant.

The proportions of cereal taxa from the settlement area differ in other ways from those in the malting complex assemblage, with rye grains comprising less than one fifth (18.0%) of the total (n=908), and the most common taxa being instead oat and free-threshing wheat (29.6%, n=1,495) (**Figure 6.8**).

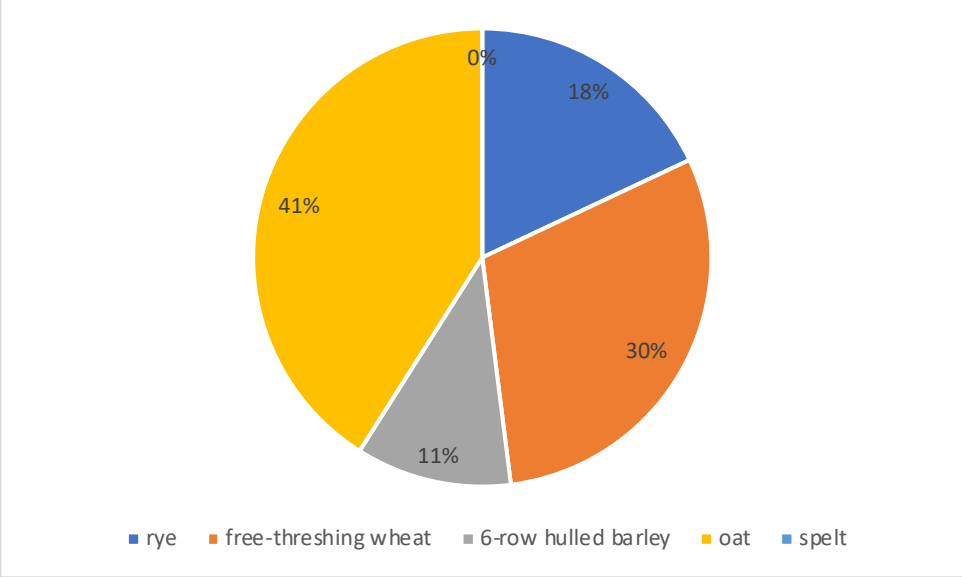


Figure 6.8 Total proportions of cereal taxa from the Sedgeford settlement area (n = 5,049)

When the proportions of different cereals are disaggregated and shown sample by sample, mapped onto an aerial photograph of the entire malting complex, and a plan of the

kiln 3 area (**Figure 6.9**),[69] a number of trends are apparent (**Figures 6.10, 6.11** and **6.12** are also useful for comparative purposes). **Figure 6.10** shows that 40 of 55 samples (72.7%) from the malting complex contain at least 50% rye, and 18 of 55 samples (32.7%) are clearly dominated (>75%) by rye. Only four of the eight samples from the area of hypothesised malting kiln 1 contain over 50% rye, compared with each of the eight samples from around kiln 2 and 13 of the 19 samples (68.4%) from the combined kiln 3 /undefined feature area. Wheat grains are disproportionately abundant around kiln 1 – as shown in **Figures 6.9, 6.12,** and **6.13**, with all samples containing at least 43%, and two (17013 and 23754), over 62% wheat. On average, samples from kiln 1 contain 53.5% wheat, compared with 10.8% and 18.6% for kilns 2 and 3, respectively (**Figure 6.12** and **6.13**). The western ditch contains a significantly higher proportion of free-threshing wheat (47.7%) than the eastern (29.8%).

Figure 6.9 shows an east-west transition in samples from the gridded area – surrounding kiln 3 and the undefined feature – with samples from contexts closest to kiln 3 in the west (from rows G to K, with the exception of I6) containing between 14.0% and 25.3% barley, and all those to the east (rows L to O) with over 80% rye, and a maximum of 8.6% barley – thereby mirroring samples from the western side of kiln 2 (e.g., 23722, 23727, 23325), which lies immediately to the south of the gridded area. When cereal proportions are aggregated by feature (**Figure 6.13**), there is a notable similarity between kiln 3 and the undefined feature. Trends in cereal proportions across the malting complex are discussed in **section 8.1.2**.

[69] It is, as yet, not possible to similarly display results for samples from the settlement area, due to a lack of accurate context information.

Figure 6.9 Relative proportions of cereal taxa in each sample shown on an aerial photograph of Trench 23 (right) (Image: Ian Drummond/SHARP 2019) and a plan of the gridded area (left) (Image: Gary Rossin/SHARP 2019)

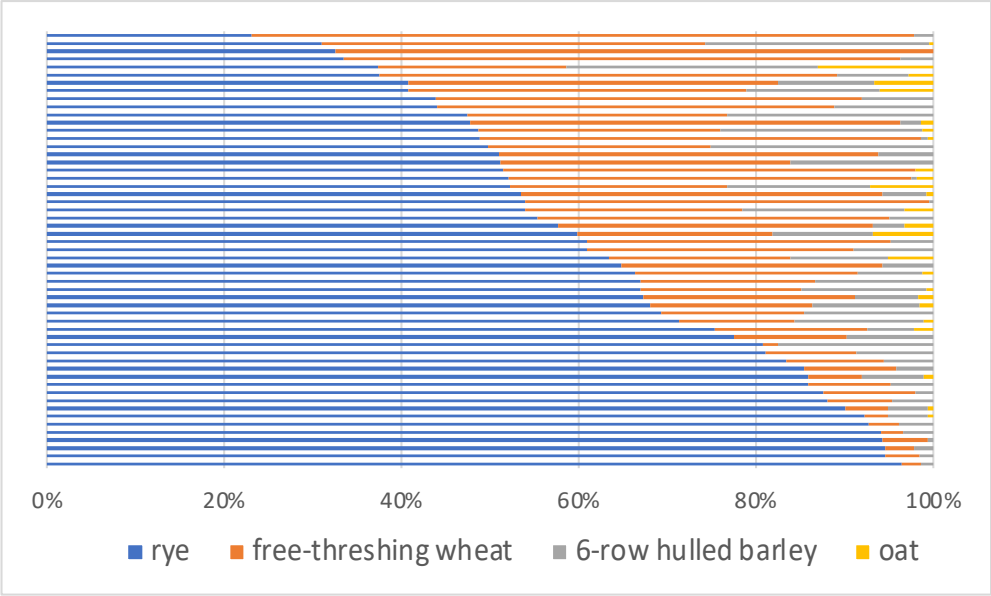


Figure 6.10 Proportions of cereal taxa for all samples from the malting complex, ordered by descending proportion of rye

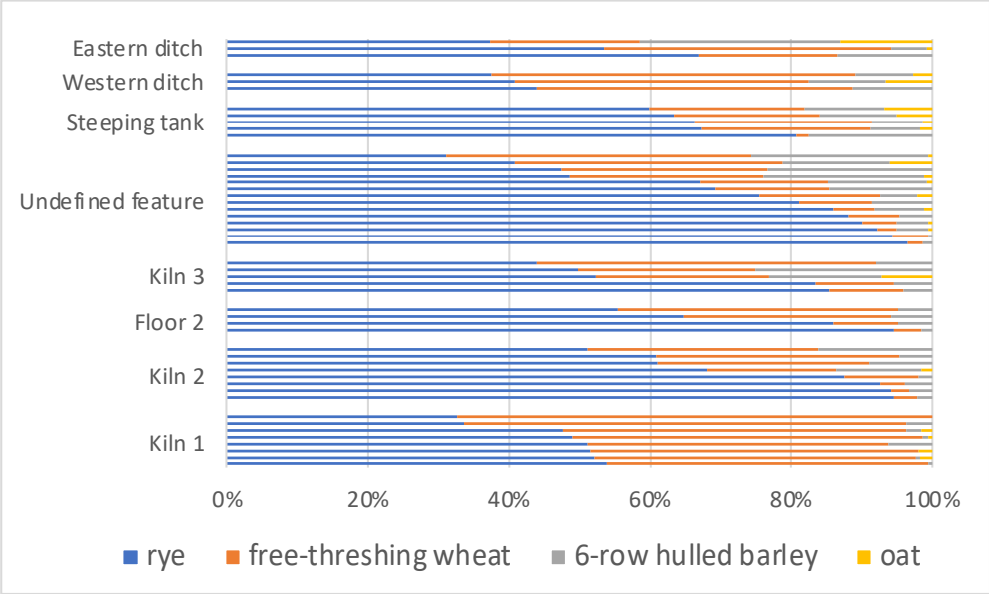


Figure 6.11 Proportions of cereal taxa for all samples from the malting complex, grouped by feature / area of trench and ordered by descending proportion of rye

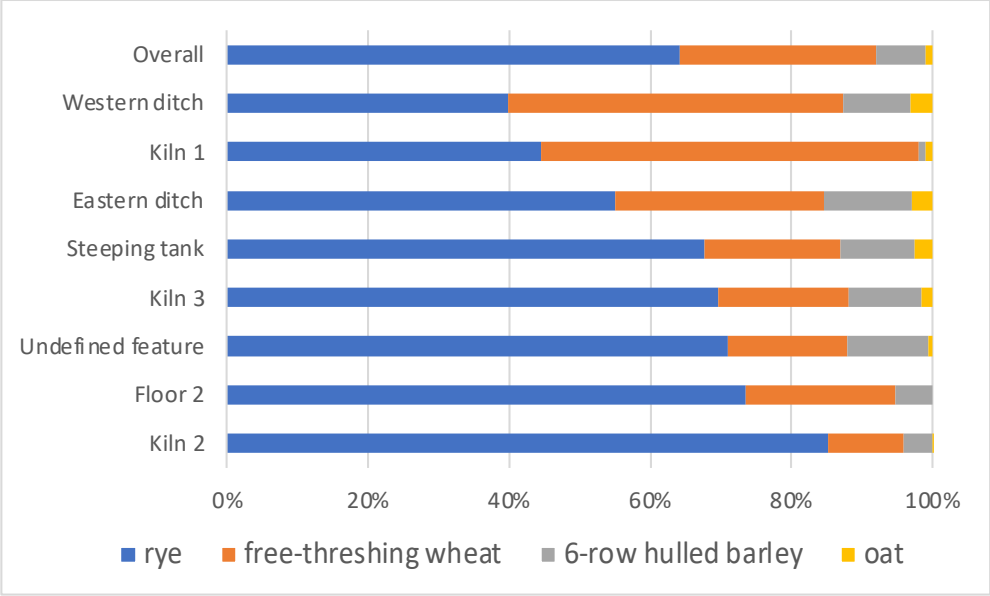


Figure 6.12 Average proportions of cereal taxa for all malting complex samples, and by feature, ordered by descending proportion of rye

Figure 6.13 Trench 23, showing average proportions of cereal taxa for each feature/ area of trench (Image: Ian Drummond/ SHARP 2019)

Trends in the density of grains per litre sediment, as displayed graphically in **Figure 6.14** and **Figure 6.15**, enable further understanding of each kiln's use. Samples with densest grain concentrations are clearly clustered around each of the three known malting kilns: however, the average grain density in samples from kiln 2 contexts (593 grains/litre) is 5.5 times greater than the equivalent figure for kiln 1 (107 grains/litre). Further, the densest sample from kiln 2 (23727, with 1549 grains/litre), is 6.5 times denser than the densest sample from kiln 1 (23754) with 238 grains per litre. The density of grains from samples surrounding kiln 3/the undefined feature, including all from the gridded area, is comparable to kiln 1, at 166 grains/litre. However, this lower density may be partly attributable to the distinctive sampling method employed in the gridded area, with samples taken consistently from each quadrat irrespective of apparent 'richness' of organic material (unlike in other parts of the malting complex – see **section 5.2.1**). The strikingly grain-rich sample from context M6 in the gridded area (599 grains/litre) (**Figure 6.14** and **6.15**) shows cereal proportions (**Figure 6.9**) consistent with those to the north and west of kiln 2.

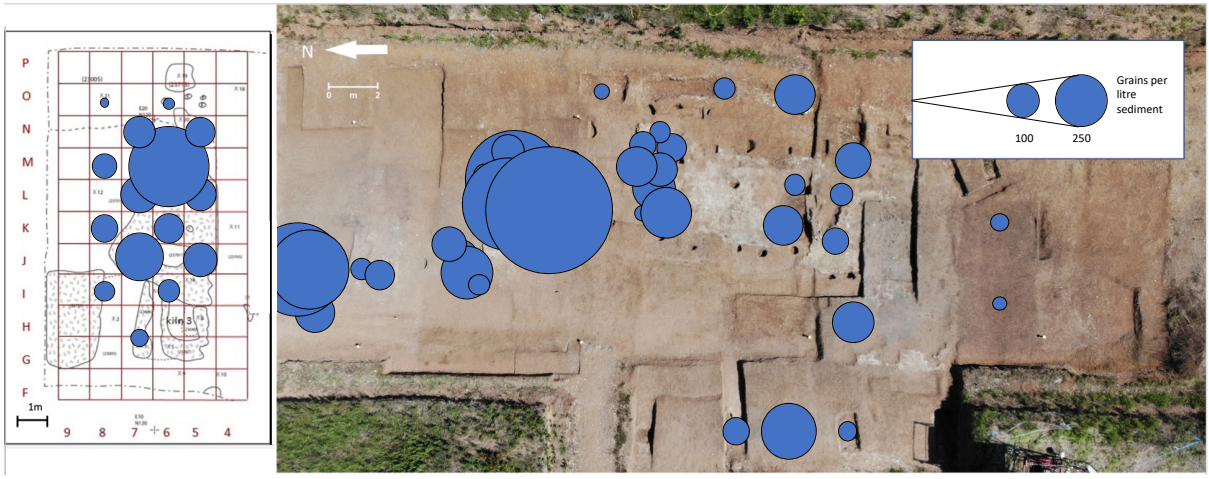


Figure 6.14 Density of cereal grains in samples across the malting complex (right) (Image: Ian Drummond/SHARP 2019) and in the gridded area (left) (Image: Gary Rossin/SHARP 2019). Bubble size corresponds to grains per litre sediment.

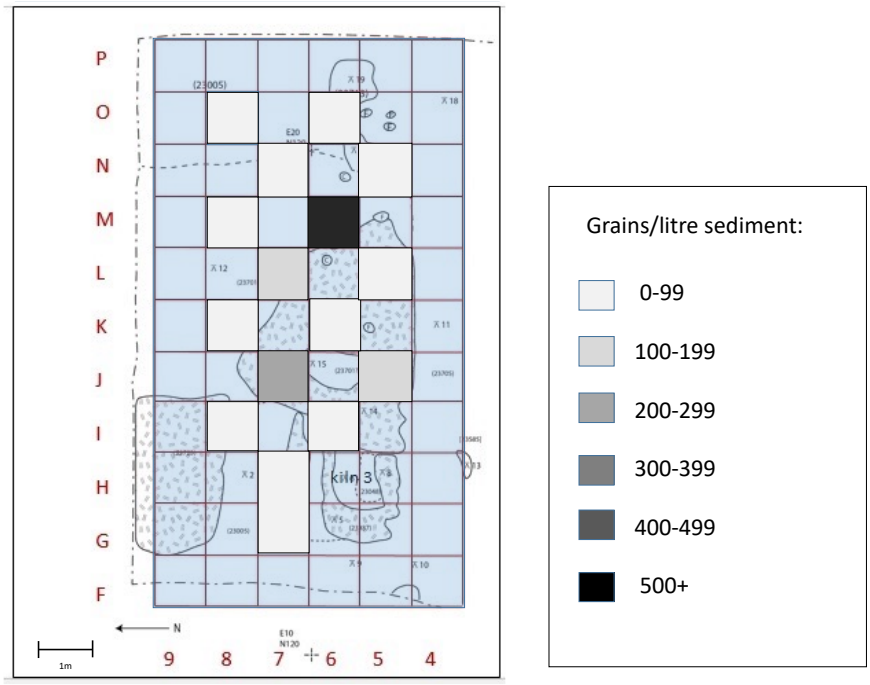


Figure 6.15 Density of grains per litre sediment in samples from the gridded area (Image: Gary Rossin/SHARP 2019)

Where samples from adjacent, stratigraphically equivalent contexts in an excavated area have similar composition, it is reasonable to assume that these derive from a single human activity or 'behavioural episode' – such as a single storage context (e.g., G. Jones et al., 1986, 100–101; Twiss et al., 2009, 886–888). **Figure 6.16** identifies 'clusters' of neighbouring samples from Sedgeford's malting complex, each of which, it is hypothesised, represents a single behavioural episode. For example, the six samples from kiln 1 having approximately equal proportions of *Triticum aestivum* and *Secale cereale* have been tentatively grouped into one 'episode' (number 5) – as have three samples from the western part of kiln 2, with neighbouring sample 23370, all of which comprise over 92% *S. cereale* (episode 3). Samples grouped into episode 5 (six of eight samples from in and around this feature) may derive from the final firing of kiln 1; the picture for kiln 2 is somewhat less clear.

Figure 6.16 Charts showing relative proportions of crop species in each sample analysed, with hypothesised 'behavioural episodes' highlighted, in aerial photograph of Trench 23 (right) and plan of gridded area (left) (both photo and plan, credit: SHARP 2019)

6.3.2 Weeds

Table 6.3 shows ubiquity and summed frequencies for all weed seed taxa occurring in at least 10% of samples from the malting complex. **Figure 6.17** (a bubble chart) represents the relative abundance of all weed seeds, proportional to grain richness, in samples across Trench 23, and in the gridded area. Pie charts in **Figures 6.18** and **6.19** show proportions of the 12 most ubiquitous weed seed taxa in samples, again in these two areas. There is a notably close resemblance in relative (aggregated) weed proportions between kiln 3 and the undefined feature, as shown in **Figure 6.19**. The three most abundant weed seed taxa in samples from the Sedgeford malting complex are members of the *Bromus* sub-family of grasses (brome), and the species *Agrostemma githago* (corncockle) and *Fallopia convolvulus* (black bindweed) respectively (**Table 6.3** and **Figure 6.20**). Notably, the seeds of each of *Bromus* grasses (of the type occurring at Sedgeford), *Fallopia convolvulus* and *Agrostemma githago* are all what G. Jones (1984, 55) would term 'big, free, heavy' seeds, which mimic cereal grains and can be separated from these only by hand-sorting (**Table 5.4**). Distributions of these taxa across Trench 23 are briefly examined here.

Table 6.3 Summarising ubiquity and frequencies of the most common weed seed taxa (occurring in over 10% of samples) across the malting complex

Weed taxon	Samples where present		Max. items per sample	Sum of items
	No.	%		
Agrostemma githago L.	42	76.4	120	1,183
Anthemis cotula L.	9	16.4	16	68
Brassica L. / *Sinapis* L.	22	40.0	64	284
Brassicaceae	8	14.6	16	58
Bromus arvensis L. / *Bromus hordeaceus* L. / *Bromus secalinus* L.	54	98.2	237	2,766
Chenopodiaceae	33	60.0	344	1178
Chenopodium album L.	8	14.6	8	44
Fallopia convolvulus (L.) Á.Löve	36	65.5	480	1,791
Phleum L.	21	38.2	24	234
Phleum pratense L.	24	43.6	72	380
Plantago lanceolata L.	7	12.7	8	44
Poaceae <1mm	13	23.6	24	164
Raphanus raphanistrum L.	10	18.2	8	42
Vicia L. / Lathyrus L. (1-2mm)	12	21.8	16	80

Figure 6.17 Frequency of weed seeds relative to grain frequency in samples from the malting complex (right) (Image: Ian Drummond/SHARP 2019) and the gridded area (left) (Image: Gary Rossin/SHARP 2019). Bubble size corresponds to weed seeds/grains.

Notably, *Bromus* seeds occur in all but one sample (98.2%), and, combined, are the most abundant weed seed in the assemblage. *Fallopia convolvulus* occurs in 36 out of the 55 malting kiln samples (65.5%). However, as shown in **Figures 6.18, 6.19** and **6.21** this seed is heavily concentrated around kiln 1. The ratio grain: *Fallopia convolvulus* seeds is highest for sample 17026 (from a bottom fill of the kiln) – at 1:0.232. The mean grain: *Fallopia convolvulus* ratio for samples from kiln 1 is 1:0.145, compared with 1:0.015 for samples from kiln 2 and 1:0.006 for kiln 3 samples. *Fallopia convolvulus* seeds are yet more infrequent in the 18 analysed samples from the settlement part of the site, with an average grain: *Fallopia convolvulus* ratio of 1:0.001 (McKerracher and Caroe, in prep.).

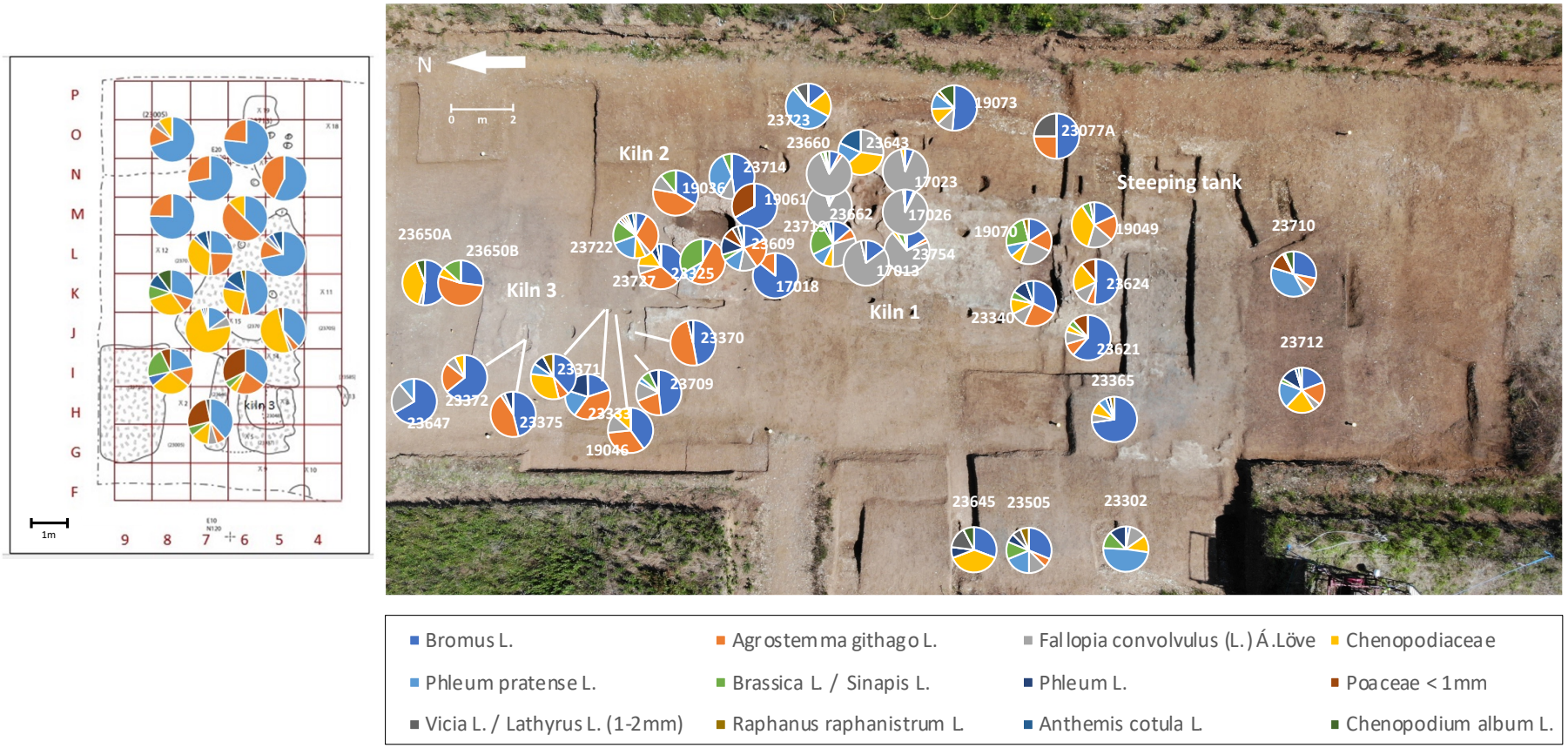


Figure 6.18 Relative proportions of 12 most common weed seed taxa in each sample, as shown on aerial photograph of the malting complex (right) (Image: Ian Drummond/SHARP 2019) and plan of the gridded area (left) (Image: Gary Rossin/SHARP 2019).

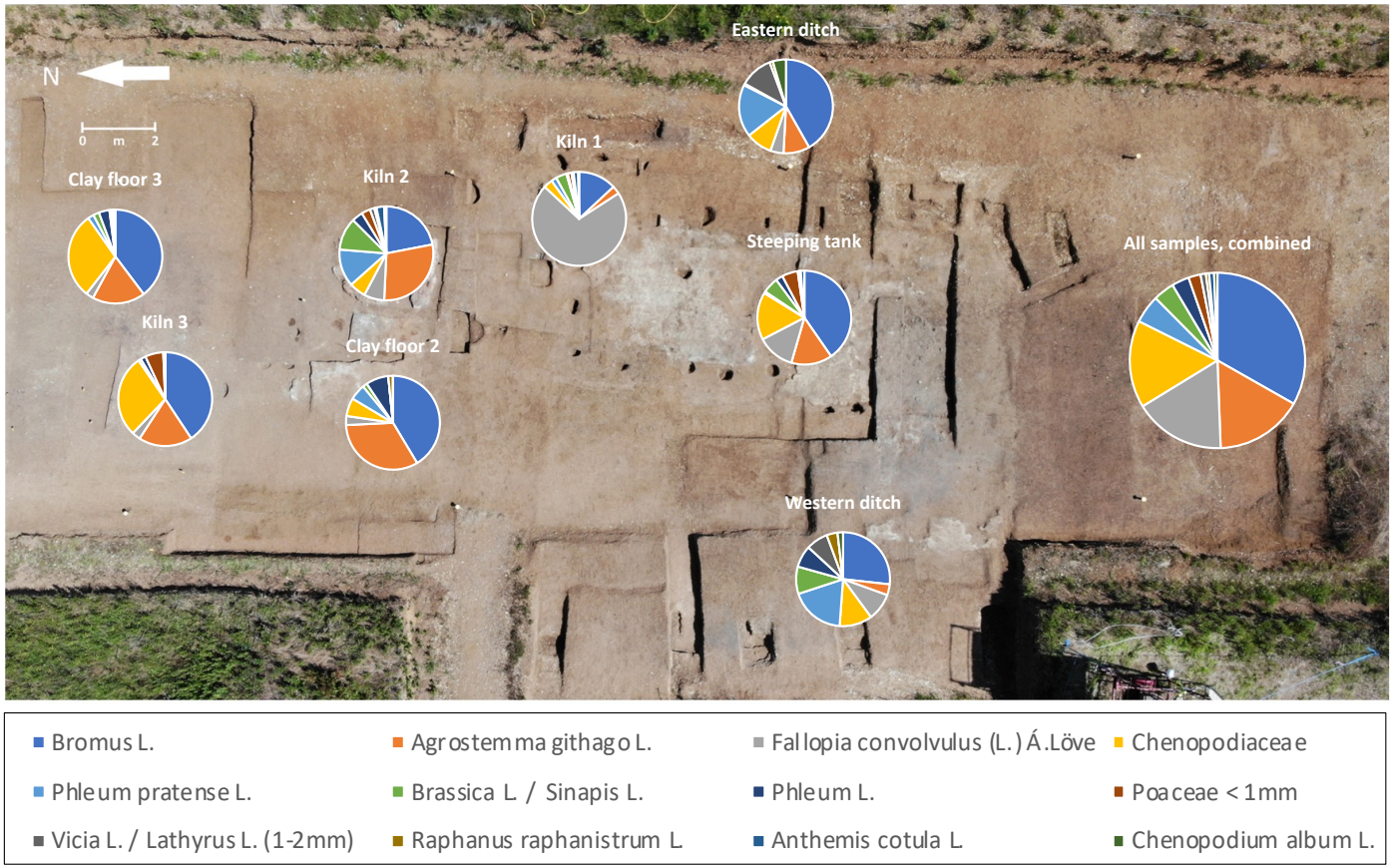


Figure 6.19 Average proportions of 12 most common weed seed taxa for each feature/ area of trench, as shown in aerial photograph of Trench 23 (Image: Ian Drummond/ SHARP 2019)

Figure 6.20 The most common weed seed taxa from the malting complex a) Brome grasses, Bromus b) Corncockle, Agrostemma githago c) Black bindweed, Fallopia convolvulus

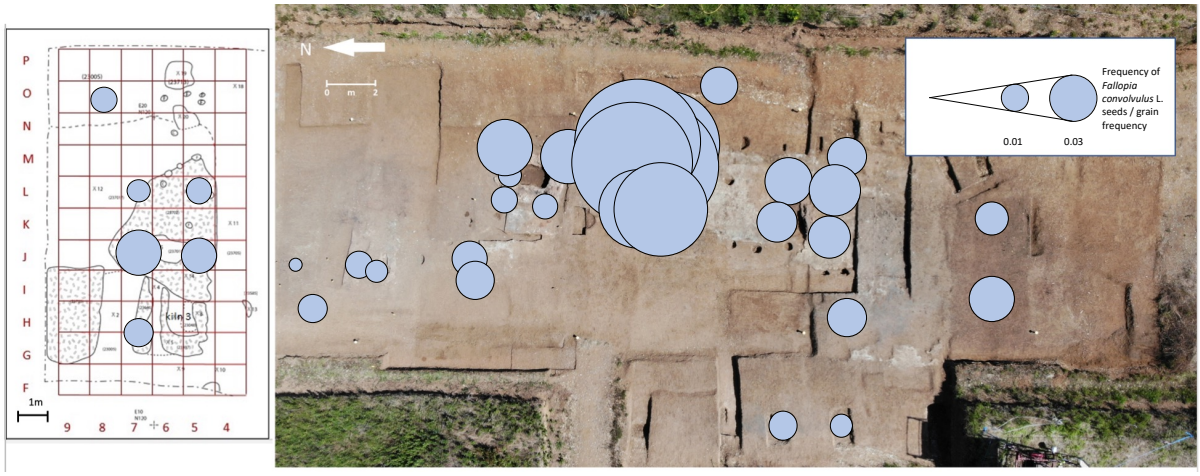


Figure 6.21 Frequency of Fallopia convolvulus seeds relative to grain frequency in samples from the malting complex (right) (Image: Ian Drummond/SHARP 2019) and in the gridded area (left) (Image: Gary Rossin/SHARP 2019). Bubble size corresponds to (Fallopia convolvulus seeds/grain).

Agrostemma githago (corncockle) occurs in over three quarters (76.4%) of all samples from the malting complex, and as shown in **Figure 6.18** and **Figure 6.22**, has a broad distribution across the trench, though occurring proportionately slightly more frequently in the kiln 2 and kiln 3 areas (with grain: seed ratios of 1:0.039 and 1:0.042 respectively, as

opposed to a combined average for all samples of 1:0.026). Six of the seven samples with highest proportions of corncockle (grain: corncockle ratio of 1:0.05 or greater) comprise over 88% rye.

Finally, here, *Anthemis cotula* L. (stinking chamomile) seeds occur in 16.4% of samples from the malting complex (**Table 6.3**), and 27.8% of samples from the settlement area assemblage (McKerracher and Caroe, in prep.). These have also (see G. Jones) been categorised as 'big, headed, heavy' (**section 5.4**) (e.g., McKerracher, 2013, 10; McKerracher, 2019, 142). Stinking chamomile is conventionally regarded as an indicator for heavy clay soils; implications of its relative abundance at Sedgeford are considered in **section 8.1.4** (e.g., Kay, 1971, 625; Stevens, in Hey, 2004, 362).

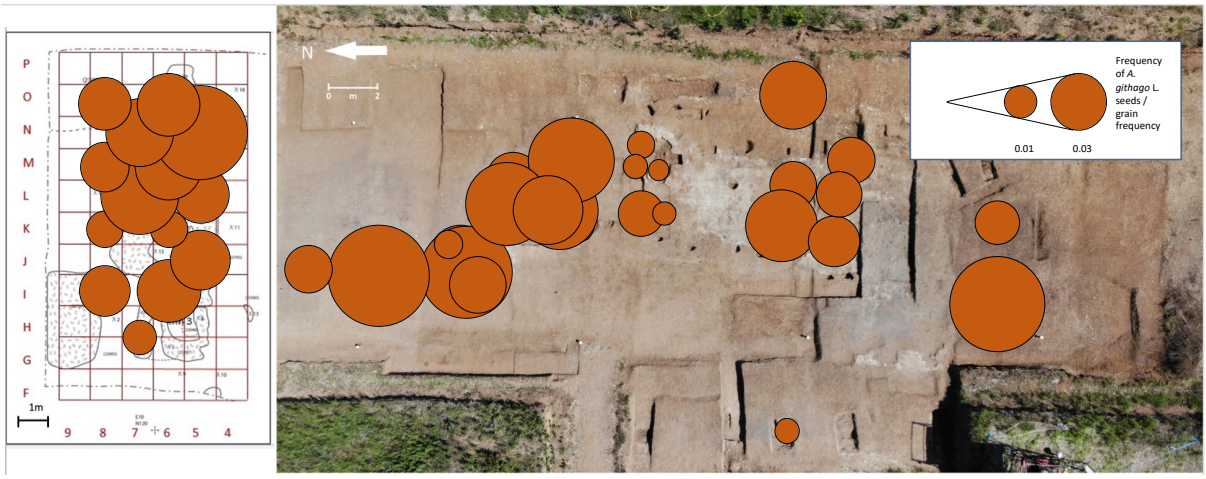


Figure 6.22 Frequency of Agrostemma githago seeds relative to grain frequency in samples from the malting complex (right) (Image: Ian Drummond/SHARP 2019) and the gridded area (left) (Image: Gary Rossin/SHARP 2019). Bubble size corresponds to Agrostemma githago seeds/grain.

6.3.3 Charcoal

The relative abundance of wood charcoal (in millilitres charcoal/total grain frequency) in samples from across the malting complex, and from the gridded area more specifically, is shown in **Figure 6.23.** Charcoal is relatively evenly distributed across the trench, with two notably charcoal-rich samples from contexts G/H7 (immediately to the north of kiln 3) and O6, each from the gridded area. Each of these samples is six times richer in charcoal than the average across the malting complex. Sample 23325, from the south wall of kiln 2, and sample 23643, on the perimeter southeast of kiln 1, are noteworthy since many large pieces of charcoal (of at least several cm in length) were recovered from these contexts and not included in the archaeobotanical analysis.

Figure 6.23 Volume of charcoal relative to grain frequency in samples across the malting complex (right) (Image: Ian Drummond/SHARP 2019) and in the gridded area (left) (Image Gay Rossin/SHARP 2019). Bubble size corresponds to millilitres of charcoal/grain.

6.4 Levels of germination: Gross-morphology based assessment

The results of three sets of analyses aimed at determining the level of germination in grains from the malting complex assemblage are presented in this chapter: the author's own 'gross-morphology based' analysis – with results described here – and the results of geometric morphometric analysis (GMM) and scanning electron microscopy (SEM), respectively, each conducted by a colleague, described in **section 6.7**.

Figures here are created with data collected using the new methods for discerning germination (including in naked grains: here, rye and free-threshing wheat) described in **section 5.3** (see **section 5.3.2** for photographs of germinated grains from the malting complex). **Figure 6.24** summarises the total proportion of germinated grains (of all four taxa) in samples across the malting complex. Overall, the total proportion of clearly germinated grains is 17% (this increases to 46% when grains of indeterminate germination status are proportionately reassigned). In total, 98% (51/52) of samples from the malting complex include germinated grains. Amongst the four samples from the settlement part of the site (where malting is not believed to have taken place), which were assessed for comparative purposes, no grains showed clear evidence for germination, 44% were indeterminate, and 56% ungerminated. However, a combined total of 40 detached sprouts (evidence for germination in grains – see **section 2.4**) were identified in the 18 samples from this part of the site analysed by McKerracher and Caroe (in prep.).[70] These represent, on average, 0.4% of the

[70] Only detached embryos incorporating a 'base' are included in this figure (i.e., standard methods for quantifying detached embryos were used for both malting complex and 'settlement area' samples; **section 5.2.6**).

total plant items in this assemblage, compared with 4.0% for the malting complex samples (**Figure 6.4**), i.e., detached sprouts are 10 times more common in the malting complex assemblage, and cannot here easily be accounted for in terms of 'accidental germination'.

Figure 6.25 shows, for samples from the malting complex, the overall proportions of germinated grains by cereal taxon. Although there is some variation in germination levels between the taxa, it is notable that over 11% of rye, wheat and barley grains are germinated (increasing to over 36% when indeterminate grains are proportionately reassigned).

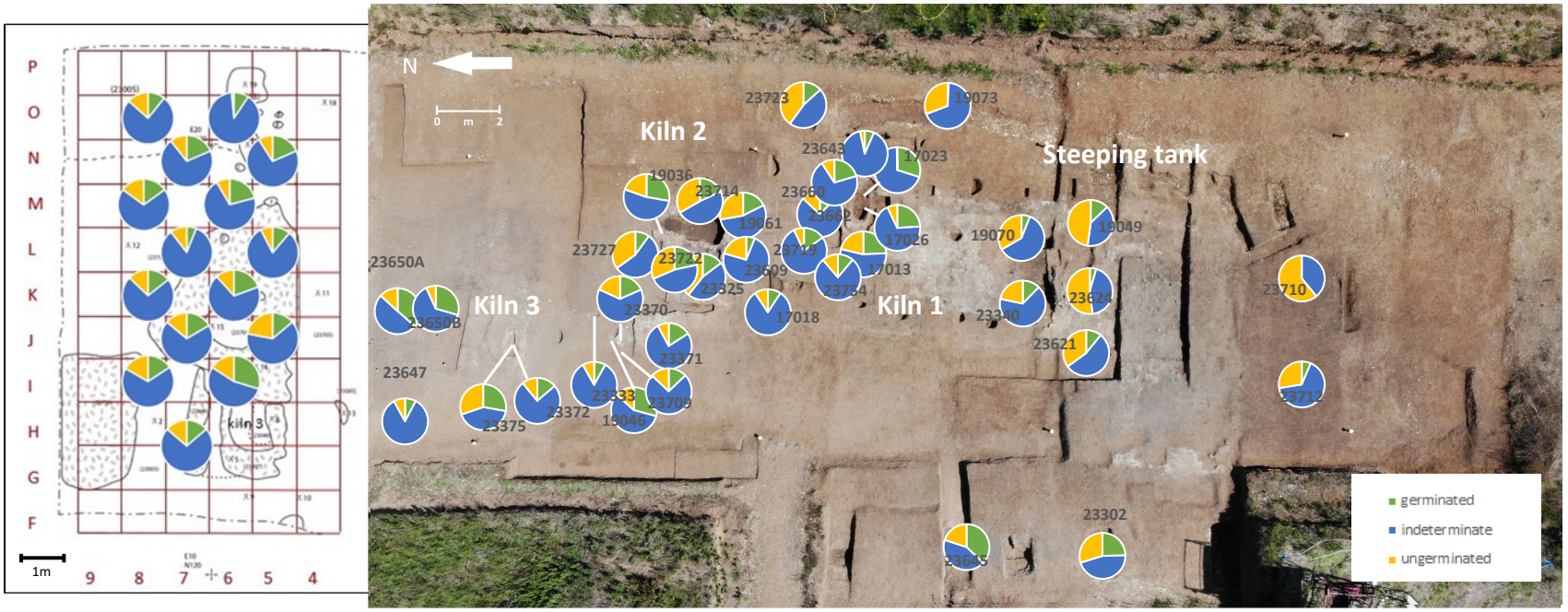


Figure 6.24 Proportions of germinated, ungerminated and indeterminate grains in each sample, as shown in aerial photograph of malting complex (right) (Image: Ian Drummond/SHARP 2019) and plan of gridded area (left) (Image: Gary Rossin/SHARP 2019)

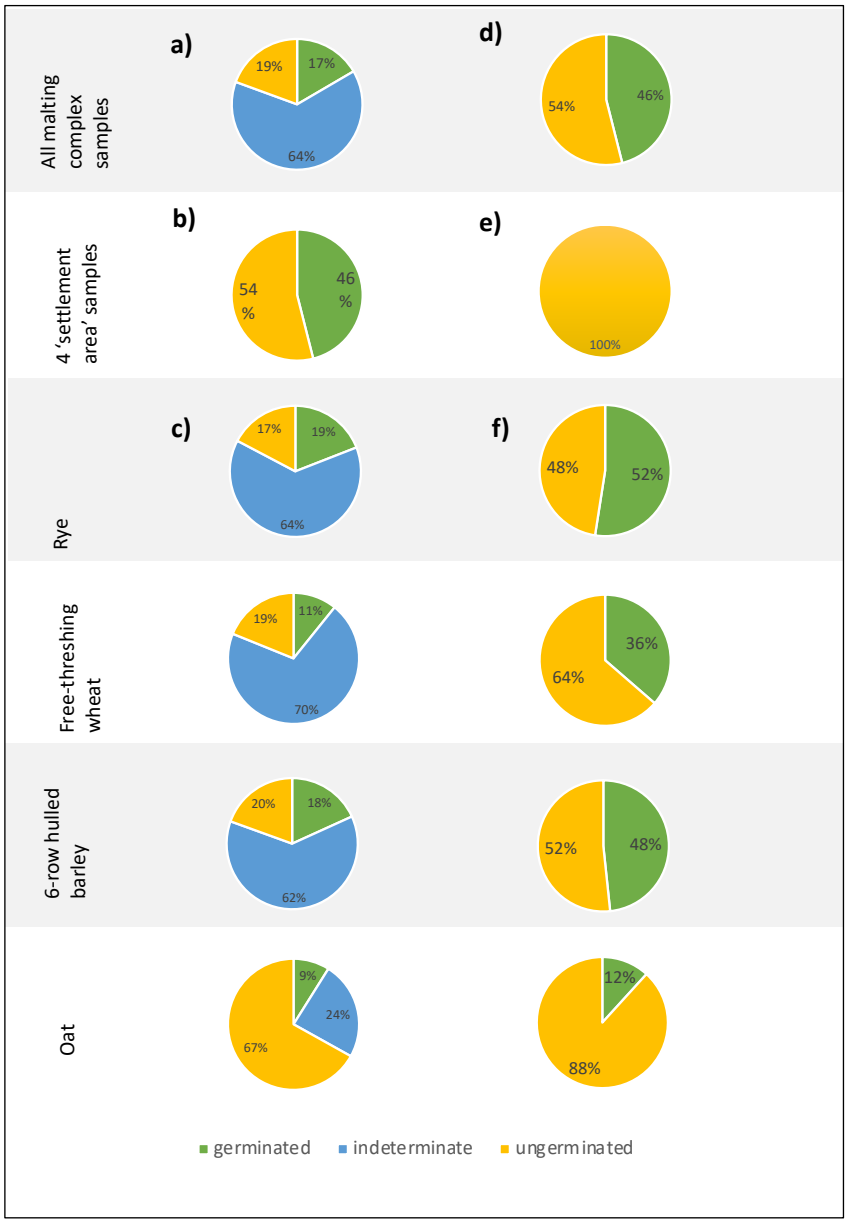


Figure 6.25 Total proportions of germinated, ungerminated and indeterminate cereal grain in samples a) from the malting complex (52 in total), b) from the 'settlement area' (four samples in total) and in c) each of the four cereal taxa, for samples from the malting complex. Charts d), e) and f) represent the same samples but here 'indeterminate' grains have been proportionately apportioned between 'germinated' and 'ungerminated'

Figures 6.26 and **6.27** display proportions of germinated and ungerminated grains (following reassignment of indeterminate grains), averaged across samples from features

within the malting complex. The highest proportion of germinated grains (almost two thirds of the total – 64.9%) occurs in samples from kiln 1. Samples from four further features also comprise over 50% germinated grains: kiln 3 – 51.5%, clay floor 2 – 55.2%, the western ditch – 55.2% and the undefined feature – 60.8%. The lowest proportion of germinated grains (13.8%) and the lowest proportion of detached sprouts (0.5%) each occur in samples from the eastern ditch. Notably, on average, samples from the hypothesised steeping tank contain only 21.0% germinated grains (although the average percentage of detached sprouts in these samples is not particularly low – at 3.3%).

Further, clay floor 2 has a significantly higher proportion of germinated grains (55.2%) than kiln 2 (35.2%). Samples from floor 2 also contain the highest percentage of detached sprouts (6.1%), compared with 4.0% in those from kiln 2 and an overall average of 3.2%. If clay floor 2 is indeed associated with kiln 2, evidence for a higher level of germination on the clay germination floor than in the kiln would be consistent with the kiln's also, at times, being used to dry ungerminated grain (i.e., as corn-dryer). The lack of samples from clay floor 1 and (likely) clay floor 3 precludes further testing of this hypothesis for the other kilns. Regarding the 'undefined' feature, grains originating here display a considerably higher level of germination (60.8%) than those from the neighbouring kiln 3 (51.5%). These trends are further considered in **section 8.2**.

Figure 6.28 displays the percentage of germinated grains (following reassignment of indeterminate grains) in samples from the gridded area. In each of the samples from column 6 (in line with the stoking end of kiln 3), and from row N, over 60% of grains are germinated. Notably, the highest proportion of germinated grains (85.7%) occur in the sample from grid square O6, approximately six metres east of kiln 3.

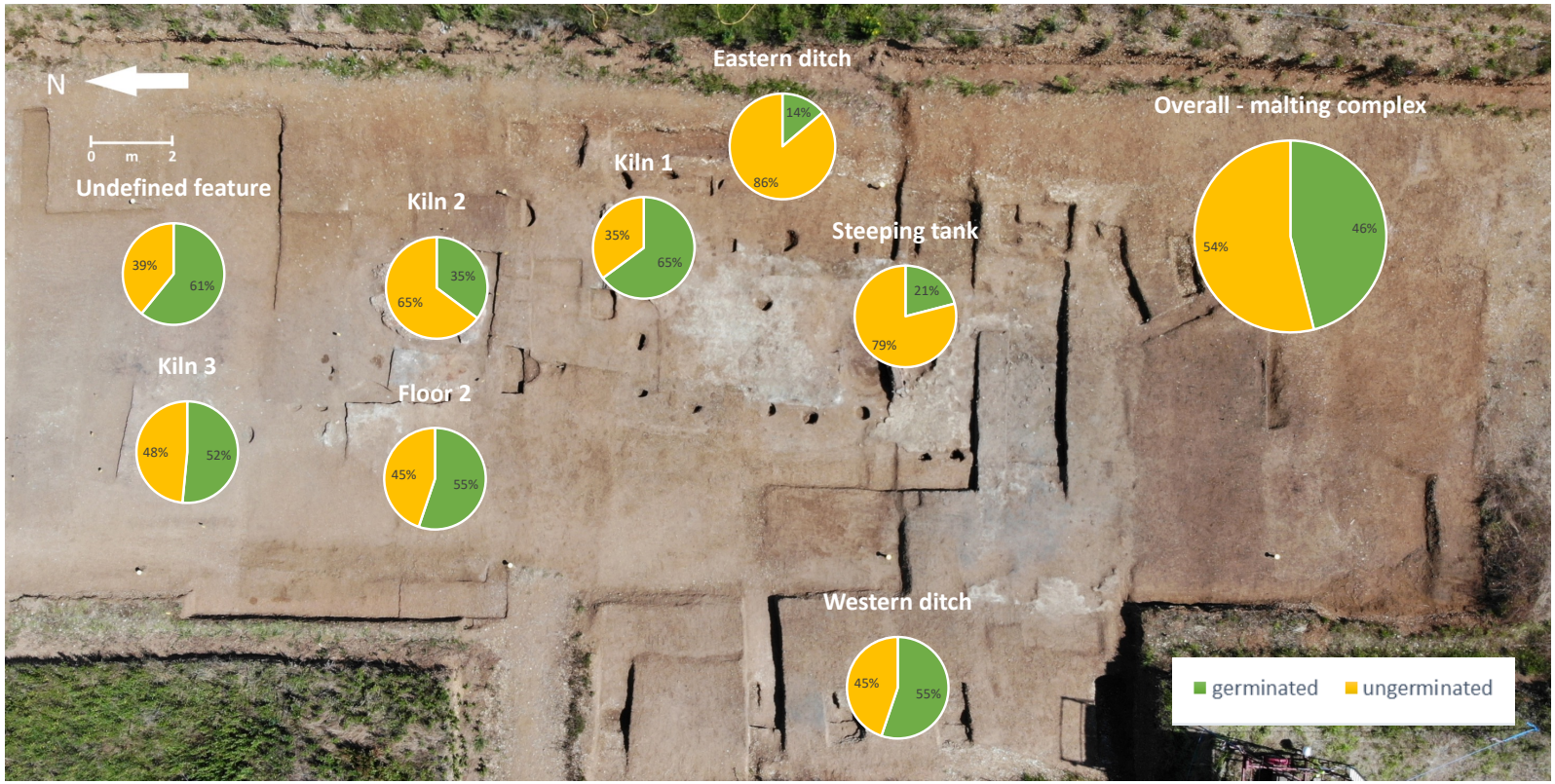


Figure 6.26 Average proportions of germinated and ungerminated grains for each feature/area of trench as shown in aerial photograph of Trench 23, (Image: Ian Drummond/SHARP 2019)

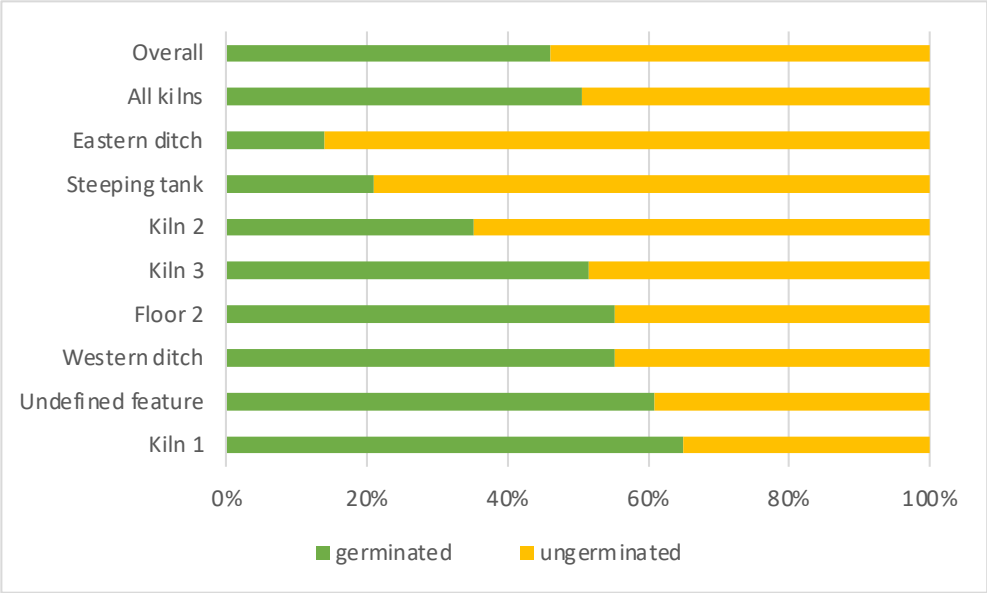


Figure 6.27 Average proportions of germinated and ungerminated cereal grains for the malting complex overall, for all kilns combined, and by feature/ area of trench, ordered by descending proportion of germinated grains

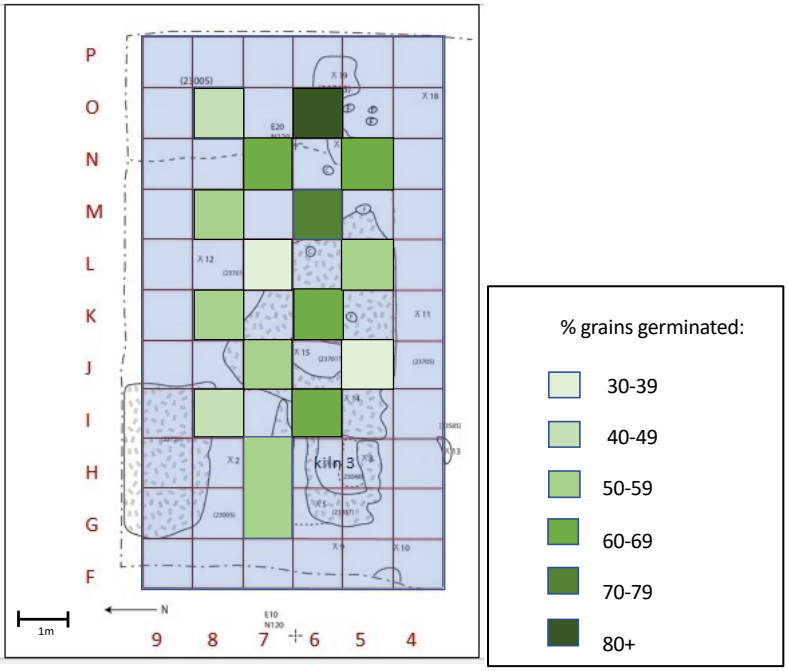


Figure 6.28 Proportions of germinated grains in samples from the gridded area (Plan image: Gary Rossin/ SHARP 2019)

6.5 Correspondence analyses

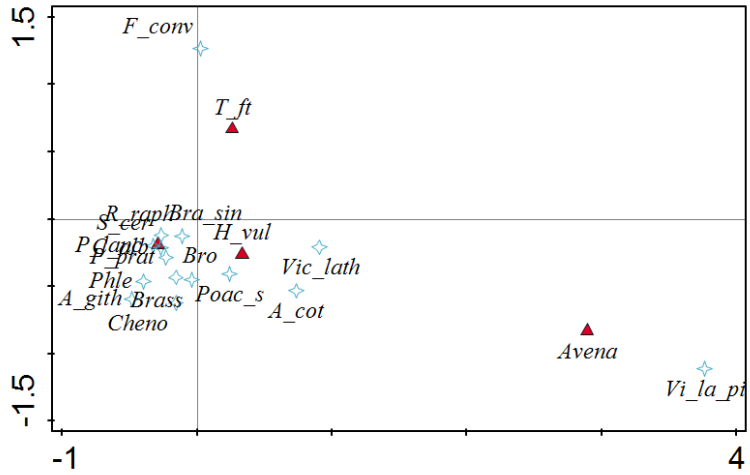
The results of a set of correspondence analyses conducted on the archaeobotanical data from Sedgeford (examining both the malting complex and settlement area assemblages but focusing on the malting complex) are here presented and described. **Figure 6.29** displays two correspondence analysis plots including all samples with over 10 weed seeds: 54 samples from the malting complex and eight from the settlement area (62 samples altogether) are distributed according to composition in terms of the 19 most common taxa (both cereals and weed taxa). The 19 taxa selected occur in over 10% of the combined total of 73 samples (55 from the malting complex and 18 from the settlement area, where samples with fewer than 10 weed seeds are included). One taxon (*Vicia* L./*Lathyrus* L./*Pisum* L. (>2mm)) occurred sufficiently frequently in the 18 settlement samples that it qualified for inclusion in the category of taxa occurring in over 10% of all 73 samples, despite occurring rarely in the malting complex assemblage.

The plots show that all samples from the settlement area occur at the positive end of axis 1, with all data points but one falling further to the right than all those from the malting complex; six samples form a distinct cluster. This is attributable to the relative abundance of both *Avena* (oat) and *Vicia* L./*Lathyrus* L./*Pisum* L. (>2mm) in these samples, with each of these taxa occurring towards the extreme positive end of axis 1 in plot A (which shows the distribution of taxa). The single sample from the settlement assemblage (15262) which is positioned within the cluster of malting complex samples contains a relative abundance of Chenopodiaceae and *Agrostemma githago* seeds, each of which is more common in the malting complex assemblage, accounting for its location here.

The correspondence analysis in **Figure 6.29** excludes several weed seed taxa (also one cereal taxon and two other taxa which were potentially cultivated as crops) that occur in over 10% of the 18 settlement area samples but not in over 10% of all 73 samples, where malting complex samples are included. Hence, it arguably discounts much of the distinctiveness of the settlement area samples. This analysis was rerun incorporating these taxa (seven altogether: *Triticum spelta*, *Pisum sativum* L., Poaceae >2mm, *Polygonum aviculare* L., *Rumex* L., *Silene* L., and *Vicia faba* L.), as shown in **Figure 6.30** (crop taxa among these being *Triticum spelta* and, potentially, *Pisum sativum* and *Vicia faba*). In this case, nine samples from the settlement area qualified as containing over 10 weed seeds from the included taxa.

As displayed in **Figure 6.30 plot A**, six of the seven 'new' taxa (along with *Vicia* L./*Lathyrus* L./*Pisum* L. (>2mm) and *Avena*) are clustered at some distance from the remaining taxa, at the positive end of axis 1 and the negative end of axis 2. *Polygonum aviculare* is the only 'new' taxon occurring within the cluster which contains most taxa, to the negative end of axis 1. The distribution of samples from the settlement area does not differ markedly between **Figure 6.29** and **Figure 6.30***,* with, again, all data points but one occurring to the right (more positive on axis 1) of all malting complex samples, and six of these forming a distinct cluster. The single remaining sample is again 15262, likely owing to its abundance of Chenopodiaceae, *Agrostemma githago* and *Polygonum aviculare* seeds. In other words, there is a clear (and unsurprising) association between samples from the settlement area and those taxa occurring chiefly in the settlement area assemblage; more pertinently, these samples are, by-and-large, clearly distinct from those in the malting complex.

a)



b)

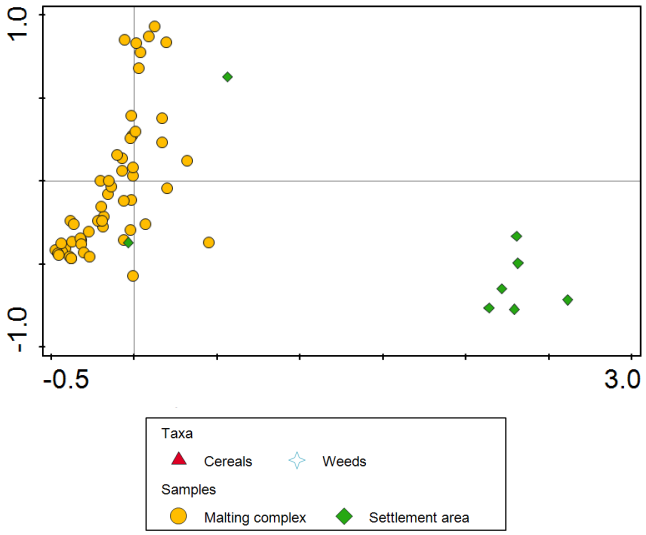


Figure 6.29 Correspondence analysis plots showing 62 samples distributed according to composition in terms of four cereal and 15 commonest weed taxa, coded by area of site

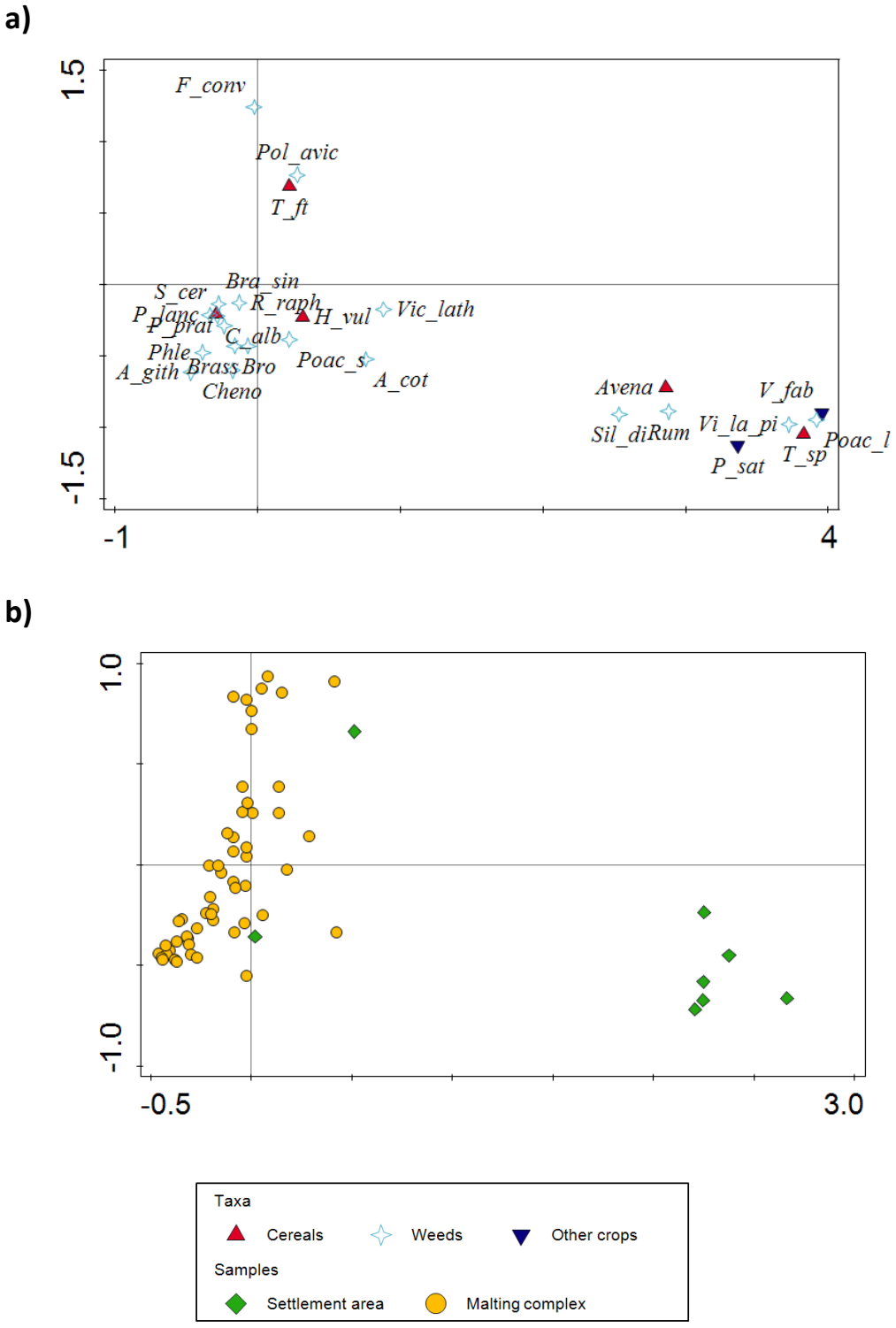


Figure 6.30 Correspondence analysis plots showing 63 samples distributed according to composition in terms of five cereal, two other crop and 19 weed taxa, coded by area of site

Further analyses focus on samples from the malting complex alone, more specifically to explore patterns in this assemblage. **Figure 6.31** shows 54 samples from the malting complex distributed according to composition in terms of all plant taxa occurring in over 10% of samples (four cereals and 14 weed taxa), coded by area within the malting complex, whilst **Figure 6.32** displays the same samples distributed according to composition in terms of the 14 commonest weed taxa only.

The clearest trend in each pair of plots is the distinctiveness of the eight samples from kiln 1. In both figures, these all occur at the positive end of axis 1. In **Figure 6.32**, the kiln 1 samples all occur more to the positive end of axis 1 than any other samples from the malting complex. This trend can be attributed to the relative abundance of both free-threshing wheat grains (*Triticum*) and black bindweed (*Fallopia convolvulus*) in samples from this feature, since (as shown in **Figure 6.31**) free-threshing wheat and (as displayed in both figures) black bindweed occur to the positive end of axis 1, with black bindweed being particularly distinct from the other taxa.

In **Figure 6.31** the three samples from the western ditch all co-occur to the upper right of the plot, towards the positive end of both axes, and the steeping tank samples all fall to the left (negative) end of axis 1. Excepting these two further groupings, samples from all other areas of the malting complex show considerable overlap and dispersal in each set of plots, with samples from kiln 2, kiln 3 and the undefined feature largely overlapping (it is worth noting that samples from kiln 3 and the undefined feature are not spatially distinct from one another in these plots).

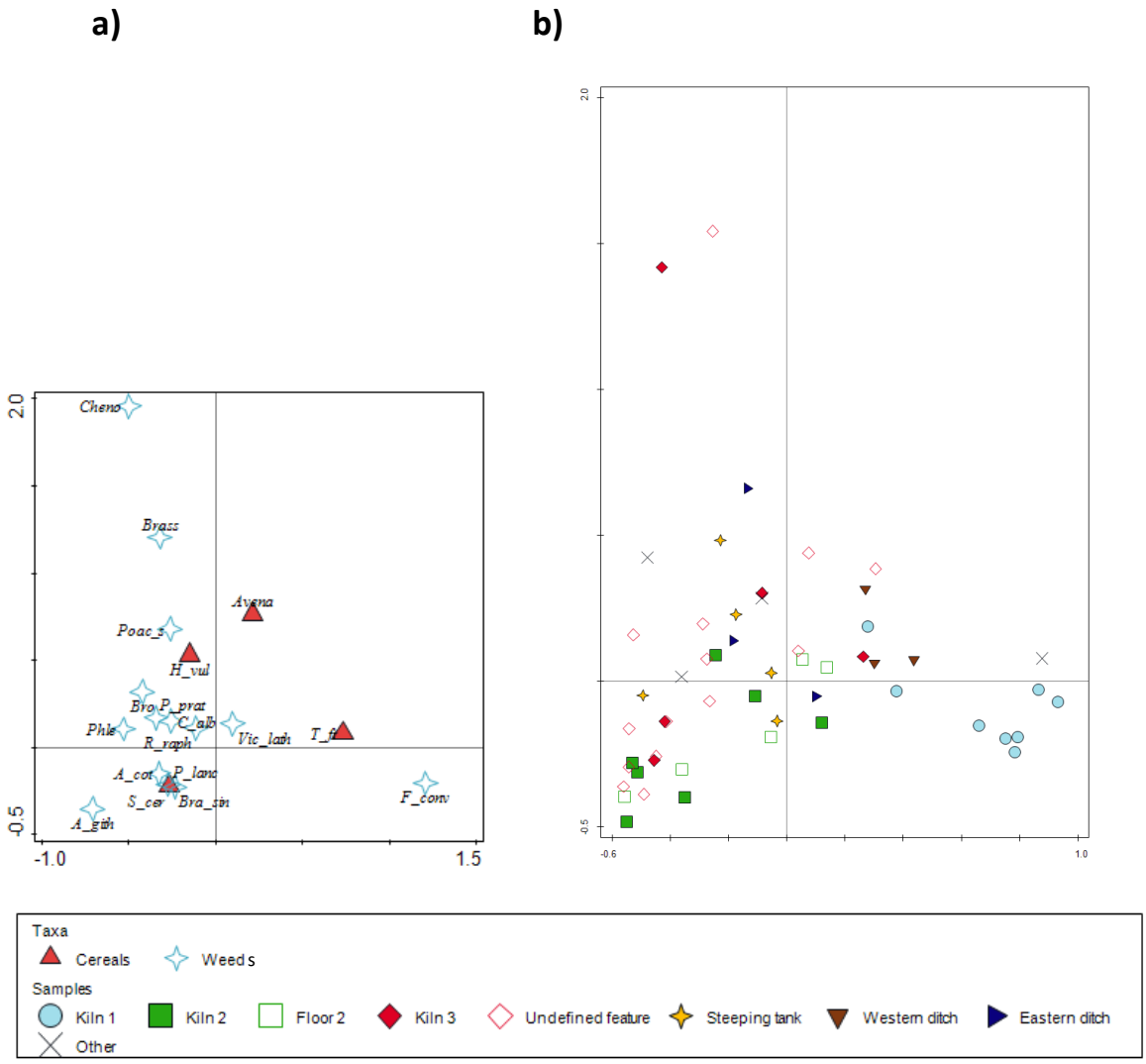
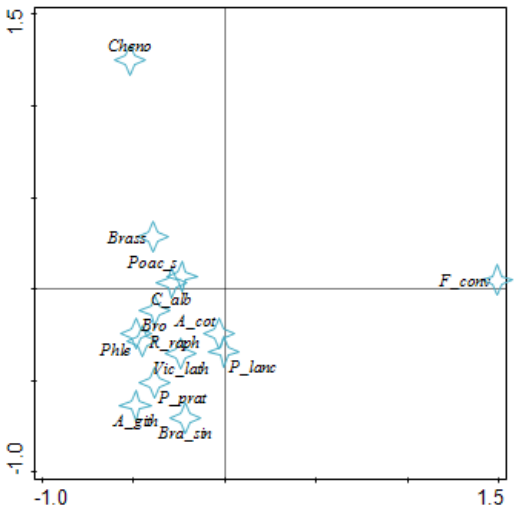
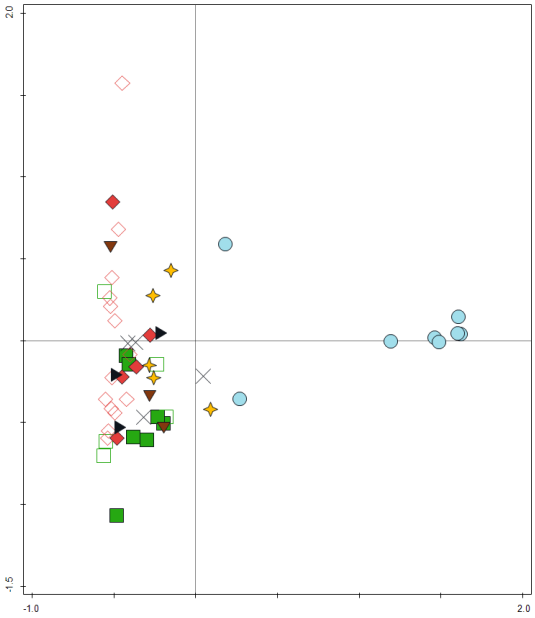


Figure 6.31 Correspondence analysis plots showing 54 malting complex samples distributed by composition in terms of four cereal and 14 commonest weed taxa, coded by feature/trench area

a)



b)



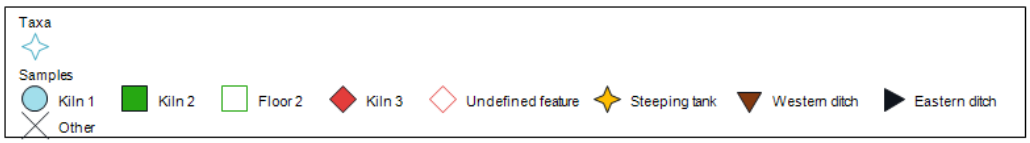
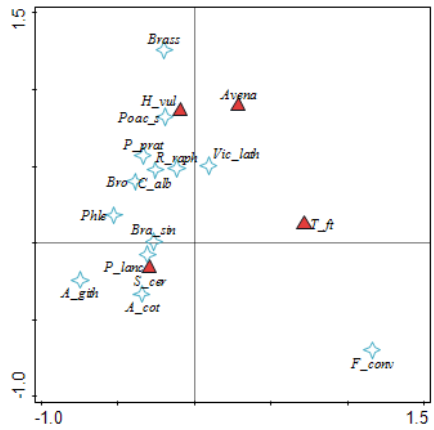


Figure 6.32 Correspondence analysis plots showing 54 malting complex samples distributed by composition in terms of 14 commonest weed taxa, coded by feature/area of trench

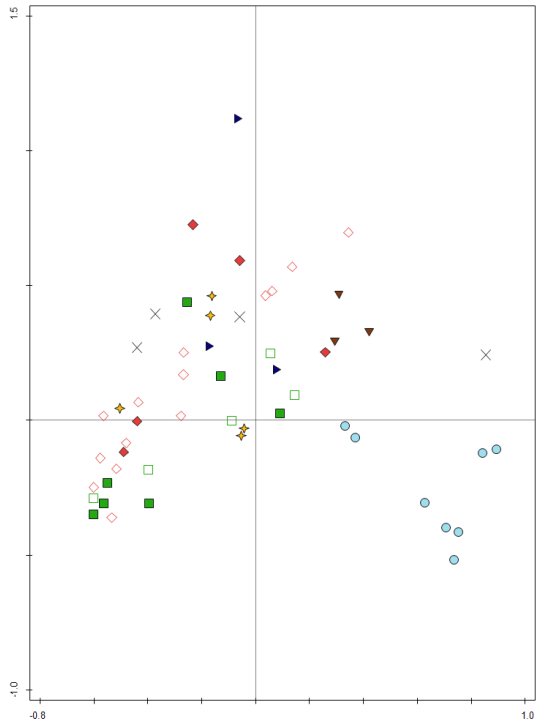
It is apparent in both sets of plots that the taxon 'Chenopodiaceae' is distinct from the remaining taxa, occurring towards the top (positive) end of axis 2. Each set of analyses was rerun excluding 'Chenopodiaceae' (as shown in **Figures 6.33** and **6.34**), with the aim of discovering the extent to which this taxon may be 'skewing' patterns in the data.

The distinctiveness of kiln 1 samples is particularly notable in **Figure 6.33**, in which all eight samples from this feature (and no other samples) occur in the lower right part of the plot. Otherwise, **Figure 6.33** is not significantly different from **Figure 6.31**, and **Figure 6.34** not notably different from **Figure 6.32**. In other words, despite its clear status as a spatial 'outlier' as seen in **Figures 6.31** and **6.32**, omitting the 'Chenopodiaceae' taxon does not seem to markedly alter the distribution of either other taxa or of samples.

a)



b)



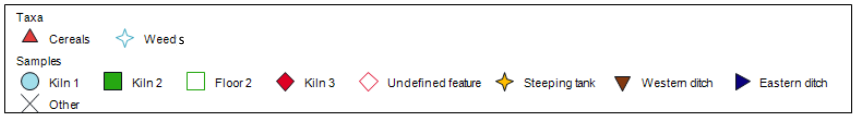
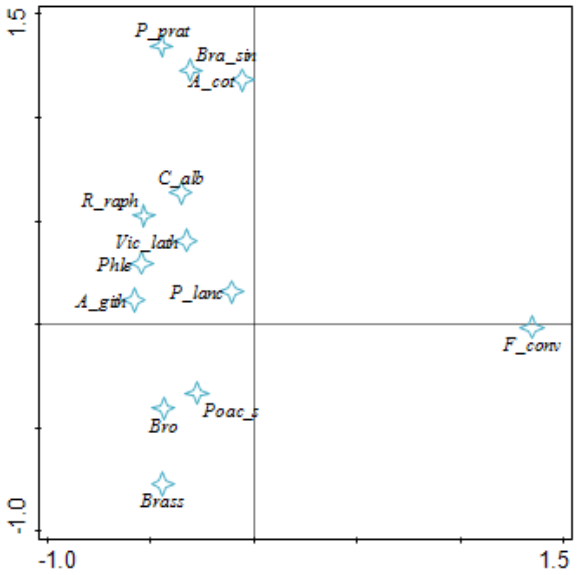


Figure 6.33 Correspondence analysis plots showing 54 malting complex samples distributed by composition in terms of four cereal and 13 commonest weed taxa (omitting Chenopodiaceae), coded by feature/area of trench

a)



b)

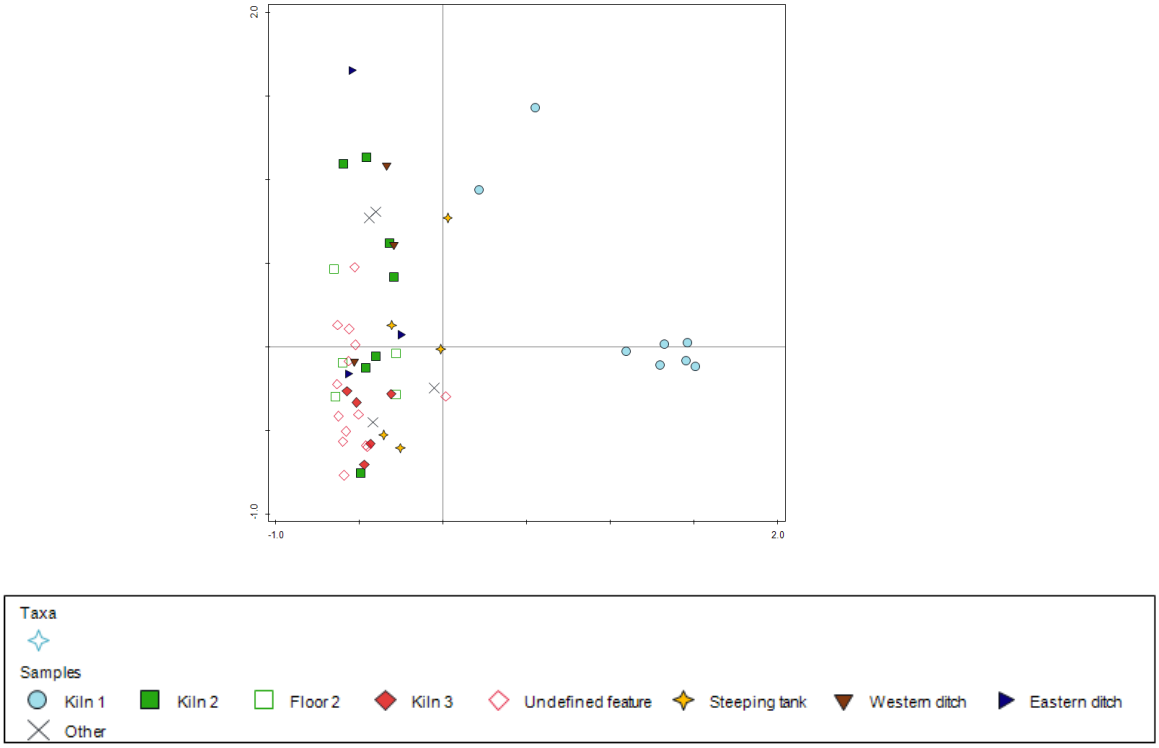


Figure 6.34 Correspondence analysis plots showing 54 malting complex samples distributed by composition in terms of 13 commonest weed taxa (omitting Chenopodiaceae), coded by feature/area of trench

The final correspondence analysis presented here (**Figure 6.35**), with malting complex samples distributed according to composition in terms of four cereal and 14 weed taxa, is similar to **Figure 6.31**; however, in this case, taxa are coded by 'behavioural episode', and samples not grouped into such an episode are excluded from the analysis (**Figure 6.16** maps the samples grouped as 'behavioural episodes').

The plots show a level of spatial association or grouping for each of the sets of samples i.e., for each 'behavioural episode'. For example, the samples for behavioural episode 3 occur in a tight cluster in the bottom left-hand part of the plot, with those for episode 6 co-occurring in the bottom right and those from episode 12 all positioned at the left (negative) end of axis 1. These associations suggest that grouping of the samples into 'episodes' based on relative cereal proportions, as described in **section 6.3.1**, is largely justified; the samples within each group also share similar weed taxa frequencies, and it is thus reasonable to assume that each group represents a single 'behavioural episode'.

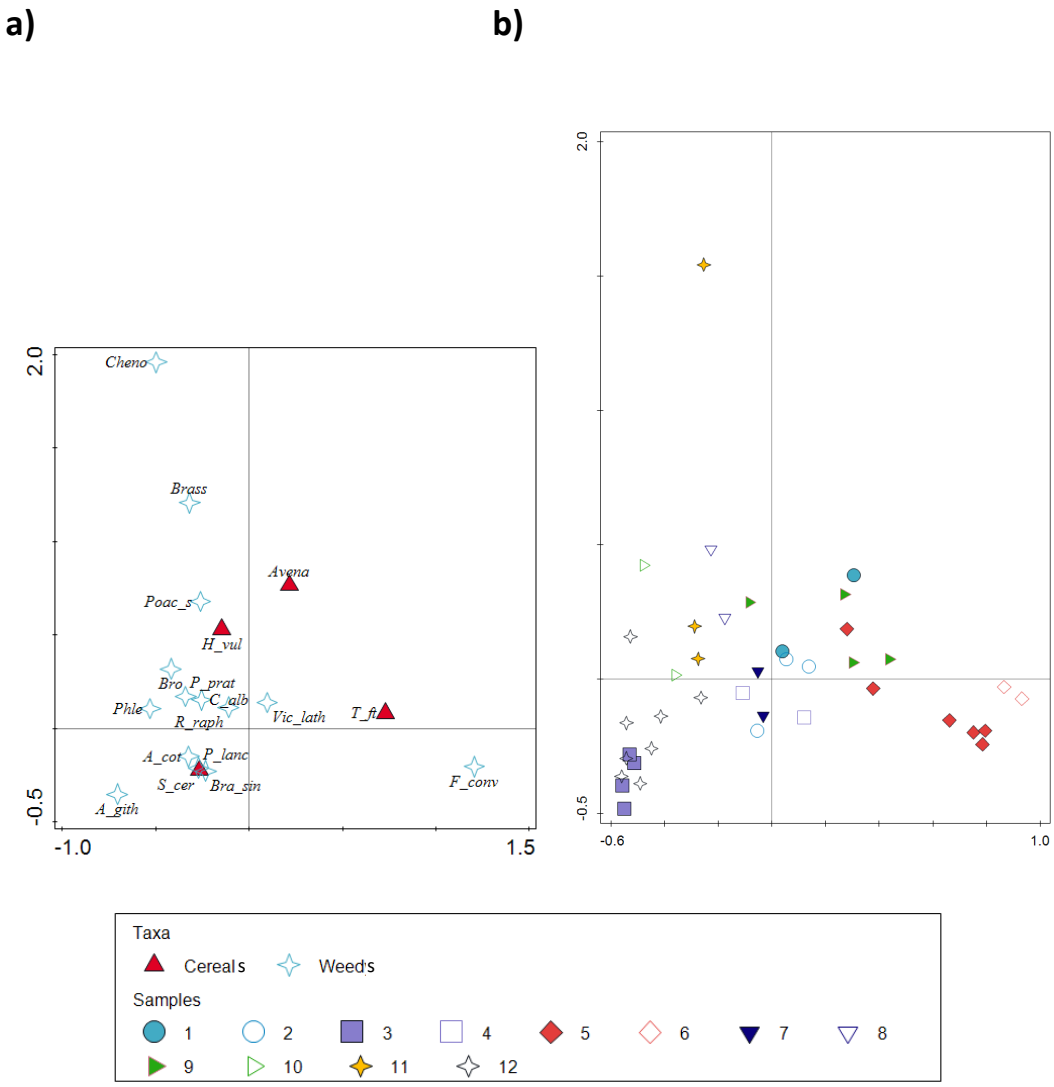


Figure 6.35 Correspondence analysis plots showing 40 malting complex samples arranged in terms of distribution of four cereals and 14 commonest weed taxa, coded according to numbered hypothesised 'behavioural episodes'; samples not belonging to an 'episode' are omitted.

6.6 Crop processing

As described in **section 5.4**, a study of the way(s) in which past peoples processed crops whose remains are recovered at an archaeological site is imperative to any thorough

assessment of an archaeobotanical assemblage, since crop processing can have profound effects on sample composition. In Sedgeford's case, understanding crop processing can augment developing appreciation of methods used by maltsters at the site. **Section 5.4** presents two possible crop processing models: a 'conventional' model (as developed by G. Jones (1984; 1987) and since widely applied), and a new model (developed by the author) which relates specifically to crop processing for 'traditional' malting. These models are here tested against archaeobotanical data from Sedgeford's malting complex, to determine which best accounts for patterns therein revealed. This is facilitated through comparison with plant material from the settlement part of the site: a 'control' dataset, since there is no structural or archaeobotanical evidence (without any germinated grains in samples from this area, see **section 6.4**) that malting was here taking place.

6.6.1 Crop processing models

This discussion refers to the two crop processing models initially presented in **section 5.4** (**Tables 5.4** and **5.8**). **Table 6.4**, based on the model in **Table 5.4**, summarises the types of products and by-products which are expected where crops are processed according to G. Jones' conventional model. **Table 6.5**, based on the model in **Table 5.8**, summarises types of (by)products expected where crops are processed according to the author's new malting model. (By)products are described in terms of proportions of grain, chaff and weed, and in terms of weed seed type. **Table 6.5** also specifies the proportion of detached sprouts expected in each product/by-product. G. Jones' (1990, 93–96) detailed ethnographic research permits quantitative definition of the expected proportions of grains, chaff and weeds (as percentage ranges) for crop processing (by)products in the model she developed, as shown in

Table 5.5. However, for ease of comparison, proportions for both models are here expressed semi-quantitively (as low, high etc.).

As established in **section 5.4.2**, the conventional model classifies weeds in terms of size (big or small), headedness (headed or free) and aerodynamism (heavy or light), since these are the properties which influence the stage of crop processing at which the weed seeds are removed from crop material. The model recognises six categories of weed, as follows: BFH ('big, free, heavy'), BHH ('big, headed, heavy'), SFH ('small, free, heavy'), SHH ('small, headed, heavy'), SHL ('small, headed, light') and SFL ('small, free, light'). The new malting model classifies weed seeds by buoyancy in water and by size, as either F ('floating'), SS ('sinking, small') or SB ('sinking, big'), since, according to this model, buoyancy in water and size are the properties which determine the stage at which weed seeds are removed. These categories do not map exactly onto those of G. Jones. For example, whilst it might be expected that weed seeds classified as 'small, free, light' according to G. Jones' model would be buoyant in water, this is not always the case e.g., *Euphrasia* L./*Odontites vernus* (Bellardi) Dumort., widely categorised as SFL, in fact sink in water, so would be classed as 'sinking, small' (SS) according to the new model.

Table 6.4 Products and by-products generated according to conventional crop processing model, with expected characteristics (G. Jones, 1984, 55; 1990, 93-96; McKerracher, 2019, 89, Table 5). 'Unsieved grain' and 'mixed stages' are McKerracher's interpolations from G. Jones' research.

Product / by product	**Proportions of plant items**			**Weed seed type**
	Grain	**Chaff**	**Weed seeds**	
Winnowing by-product (WBP)	Very low	Very high	Medium to high	SFL
Coarse sieve by-product (CSBP)	Very low	High	Medium to high	SHL, SHH, BHH
Unsieved grain (USG) i.e., FSP and FSBP prior to sieving	High	Very low	Medium to high	SFH, BFH
Fine sieve by-product (FSBP)	Low	Very low	High	SFH
Fine sieve product (FSP)	Very high	Very low	Low	BFH
Mixed stages (MS)	Low to high	Low to high	Low to high	n/a

Table 6.5 Products and by-products generated according to new malting model for crop processing, with expected characteristics

Product/ by-product	**Proportions of plant items**				**Weed seed type**
	Grain	**Chaff**	**Weed seeds**	**Detached sprouts**	
Skim by-product (SBP)	Very low	Very high	High	None	F
De-culming by-product (DBP)	Very low	Low	Low to medium	High	SS
De-culming product (DP)	Very high	Very low	Low to medium	Very low	SB

Examining these tables reveals subtle differences in terms of trends each model would predict to find in an archaeobotanical assemblage, and these differences can be used to test the models against plant data from the malting complex. It is not possible to distinguish which model holds based on proportions of grain: chaff: weed seeds alone, since the models'

expectations here coincide. For instance, were a sample to contain a high proportion of chaff and little grain, this would qualify as either winnowing by-product (WBP) or coarse sieve by-product (CSBP) according to the conventional model, or as skimming by-product (SBP) according to the new model. Conversely, a sample containing much grain and very little chaff could be classed as fine sieve product (FSP) according to the conventional model or de-culming product (DP) according to the new. Testing the models requires examination of the *type of weed seed* occurring in each sample.

One way of discriminating between the models is to discern whether, as the new model would predict, buoyant seeds occur predominantly in chaff-rich samples (as skim by-product, SBP). A further key distinction is that according to the conventional model, fine-sieve product (FSP) should be characterised by a preponderance of 'big, free, heavy' (BFH) weeds. In contrast, the malting model predicts weeds occurring in de-culming product (DP) samples should generally have 'sinking, big' (SB) seeds; significantly, this model specifies that any large buoyant weeds seeds should *not* occur in samples with a high grain component. **Table 6.6** identifies several weed taxa occurring at Sedgeford classified as both BFH (according to the conventional model) and as F (or 'floating', according to the new model): namely, *Bromus*, *Fallopia convolvulus* and *Polygonum aviculare*. *Bromus* and *Fallopia convolvulus* are amongst the most frequently occurring weed seed taxa in the assemblage (see **section 6.3.2**). A high frequency of these weeds in grain-rich samples would favour the conventional model.

Table 6.6 Common weed seed taxa from the malting complex and settlement area assemblages, classified according to the two proposed crop processing models

Taxon	Weed seed classification	
	Conventional model	New malting model
Bromus L.	BFH	F
Fallopia convolvulus (L.) Á. Löve	BFH	F
Poaceae indet. (large)	BFH	N/A
Polygonum aviculare L.	BFH	F
Vicia L./ *Lathyrus* L.	BFH	SB
Vicia L. / *Lathyrus* L. / *Pisum* L. (>2mm)	BFH	SB
Anthemis cotula L.	BHH	F
Raphanus raphanistrum L.	BHH	F
Brassicaceae indet.	SFH	N/A
Brassica L. / *Sinapis* L.	SFH	F
Chenopodiaceae indet.	SFH	F
Chenopodium album L.	SFH	F
Phleum L.	SFH	F
Phleum pratense L.	SFH	F
Poaceae indet. (small)	SFH	F
Rumex L.	SFH	F
Plantago lanceolata L.	SHH	F
Silene dioica (L.) Clairv.	SHH	SS

Crop processing stages represented by the Sedgeford malting complex and settlement assemblages are here examined using two methods: firstly, 'basic components analysis', based on relative proportions of grains, chaff and weed seeds in each sample (G. Jones, 1990) and secondly using a form of discriminant analysis founded on the type of weeds occurring in the samples (G. Jones, 1984; 1987). The methodological background for these analyses is outlined in **sections 5.4.1** and **5.4.2** respectively. Each method was developed by G. Jones, founded on extensive ethnographic research, and assumes that crops were processed as per her conventional model.

As established in **section 5.4.2**, more robust conclusions can be drawn about the crop processing (by)product type represented by each sample, and there can be greater certainty that all plant material in a sample originates from the same arable 'unit', where the results of basic component and discriminant analysis concur, than from results of either analysis alone. Hence here, for each sample, the (by)product classifications of the two analyses are compared to determine compatibility between these (according to **Table 5.7**). Correspondence analyses are then conducted on data from both the malting complex and settlement assemblages to further test which model best describes crop processing methods used in the malting complex.

6.6.2 The malting complex

All 55 samples from the malting complex were included in a basic components analysis. 54 of 55 samples were deemed eligible for discriminant analysis (with sample 17018 excluded). The tripolar graphs in **Figures 6.36** and **6.37** summarise results of basic components analysis conducted on the malting complex assemblage, displaying the relative proportions of grain, chaff and weed seeds in each sample. In **Figure 6.37** samples are classified by G. Jones' product and by-product type, according to the expected percentages of the three components in each, as specified in **Table 5.5** (and in the 'idealised' tripolar chart in **Figure 5.15**).

Figure 6.36, **6.37** and **Table 6.7** confirm that, as established in **section 6.3**, samples from Sedgeford are grain rich, with very little chaff and somewhat variable proportions of weed seeds**. Figure 6.37** and **Table 6.7** show that, according to basic components analysis, nearly half of all 55 malting complex samples (26 samples) classify as fine sieve product (FSP).

Of the remaining samples, 19 are classified as unsieved grain (USG), and 10 as mixed stages (MS).[71]

The abundance of grain-rich, chaff-poor samples in the malting complex is further discussed in **section 8.1**. It is worth noting here that sample selection during excavation may have introduced bias towards grain-rich samples, with visible charred grain deposits being preferentially sampled for floatation and analysis (**section 5.2**). Notably, samples from the gridded area, where an 'interval' rather than 'judgement' sample selection method was used (and hence visibly grain-rich contexts were not deliberately sampled) (**section 5.2.1**), have amongst the highest proportions of chaff, samples 23701 L5 and 23701 L7 each containing over 10% chaff, compared with an average across the malting complex of 2.86% (**Figure 6.38**).[72]

[71] The exact proportions of grain, chaff and weeds seeds in each sample as listed in **Table 6.7** and plotted in **Figures 6.42** and **6.43** differ slightly from those specified in **Section 6.3** since, for the purposes of basic components analysis, detached sprouts are not included.
[72] All figures in this chapter are for proportions calculated where the total number of plant items excludes detached sprouts.

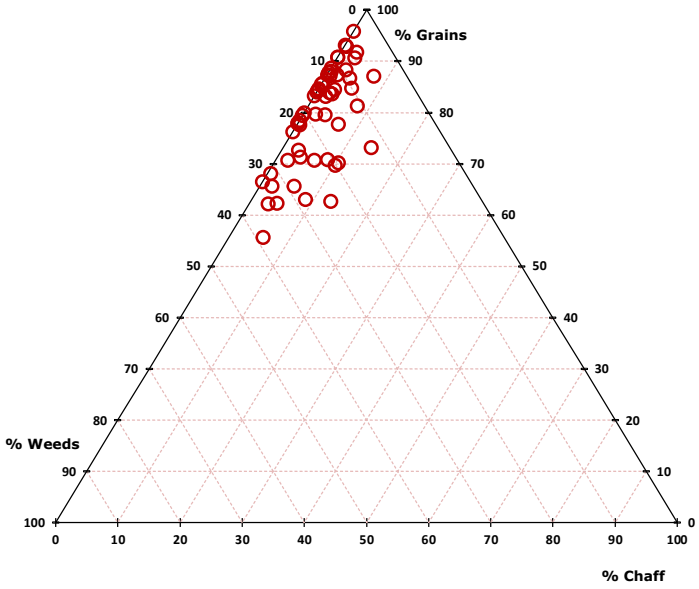


Figure 6.36 Tripolar plot showing percentages of cereal grains, cereal chaff and weed seeds in 55 samples from the malting complex

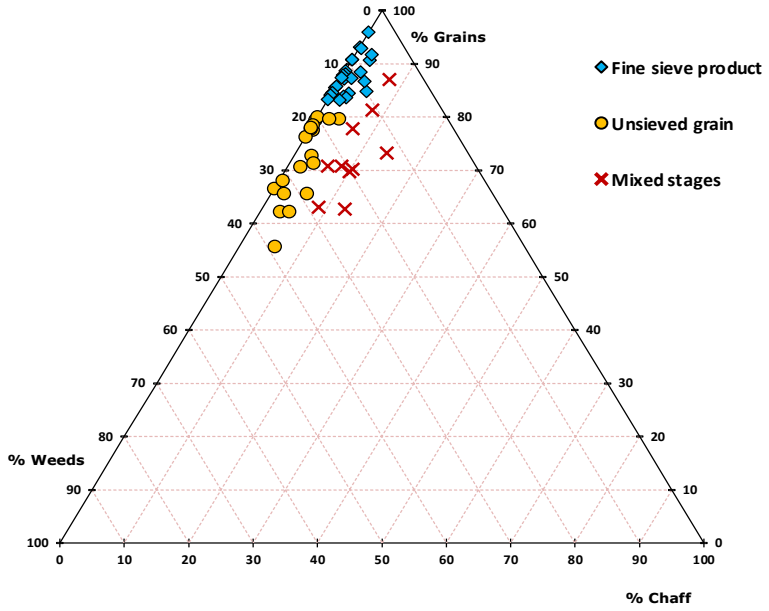


Figure 6.37 Tripolar plot with 55 samples coded by crop-processing (by)product type, according to basic components analysis

Table 6.7 Percentages of cereal grains, cereal chaff and weed seeds in 55 samples from the Sedgeford malting complex, and the crop processing (by) product type to which each has accordingly been allocated, based on basic components analysis

Context / sample number	% Cereal grains	% Cereal chaff	% Weed seed	Basic components interpretation
17013	88.70	0.00	11.30	FSP
17018	90.65	2.80	6.54	FSP
17023	84.34	0.00	15.66	FSP
17026	79.40	0.00	20.60	USG
19036	88.10	0.31	11.59	FSP
19046	77.78	6.54	15.69	MS
19049	87.18	0.60	12.22	FSP
19061	93.08	0.00	6.92	FSP
19070	84.48	2.66	12.86	FSP
19073	85.48	0.00	14.52	FSP
23077A	73.20	14.19	12.61	MS
23302	91.76	2.49	5.75	FSP
23325	87.83	0.00	12.17	FSP
23333 slot 1	88.38	2.49	9.13	FSP
23340	77.60	0.43	21.97	USG
23365	62.69	12.87	24.45	MS
23370	83.87	2.12	14.02	FSP
23371	90.77	0.00	9.23	FSP
23372	85.77	0.00	14.23	FSP
23375	79.98	0.00	20.02	USG
23505	84.81	5.22	9.97	FSP
23609	70.65	1.99	27.36	USG
23621	72.71	2.73	24.56	USG
23624	71.36	3.72	24.92	USG
23643	79.61	3.47	16.92	USG
23645	87.31	1.64	11.05	FSP
23647	87.07	7.66	5.27	MS
23650A	92.91	0.36	6.72	FSP
23650B	95.86	0.00	4.14	FSP
23660	77.82	0.00	22.18	USG

Context / sample number	% Cereal grains	% Cereal chaff	% Weed seed	Basic components interpretation
23662	78.48	0.00	21.52	USG
23709	83.67	2.58	13.75	FSP
23710	70.80	8.34	20.86	MS
23712	62.21	3.10	34.69	USG
23714	63.02	8.70	28.28	MS
23719	76.28	0.00	23.72	USG
23722	77.97	0.00	22.03	USG
23723	65.63	5.56	28.82	USG
23727	87.37	0.00	12.63	FSP
23754	84.59	0.00	15.41	FSP
23646 G/H7	83.18	1.82	15.00	FSP
23337 I6	84.06	0.00	15.94	FSP
23005 I8	62.26	4.44	33.30	USG
23701 J5	55.64	5.56	38.79	USG
23701 J7	65.64	1.94	32.43	USG
23701 K6	70.73	6.21	23.06	MS
23701 K8	81.26	7.89	10.85	MS
23701 L5	70.16	10.43	19.41	MS
23701 L7	69.67	10.11	20.22	MS
23701 M6	90.77	0.00	9.23	FSP
23701 M8	86.73	3.96	9.32	FSP
23701 N5	79.70	1.91	18.38	USG
23701 N7	83.26	0.00	16.74	FSP
23701 O6	66.55	0.00	33.45	USG
23713 O8	68.05	0.59	31.36	USG

The discriminant analysis performed using SPSS classified 40 samples from the malting complex as fine sieve product, and 14 as fine sieve by-product. **Figure 6.38** displays these results graphically. **Table 6.8** lists for each sample the crop processing (by)product type allocated by discriminant analysis and the probability of the sample belonging to its assigned group. 35 of 54 samples have been assigned to a (by)product group with a probability greater than 0.9 (>90% certainty).

Tables 6.9 and **6.10** show that classifications generated by the two forms of analysis were compatible for 39 out of 54 samples. Of these, approximately half (20 samples – 51.3%) are categorised as fine sieve product and half (19 samples – 48.7%) as unsieved grain. The high degree of concurrence between the results of each analysis suggests that the model on which both are founded – the conventional crop processing model – describes well the methods used to prepare crops malted at Sedgeford. Further, it has been suggested that the alternative (malting) model predicts samples with high grain content to contain few buoyant weed seeds. In fact, of the samples ranked as FSP by basic component analysis (i.e., with >80% grain content), on average, 80.59% of weed seeds are buoyant. Moreover, the malting model predicts co-occurrence of buoyant weed seeds and chaff (in 'skim by-product', or SBP) (**Table 6.5**); yet of the 34 samples from the malting complex assemblage whose weed component is composed of 80% or more buoyant seeds, 10 are entirely without chaff. For example, as noted in **section 6.3.2**, *Fallopia convolvulus* weed seeds, which float in water, are abundant in samples from kiln 1, however, as shown in **Figure 6.39** and described in **section 6.3**, only one sample of the eight from this feature contains any chaff.

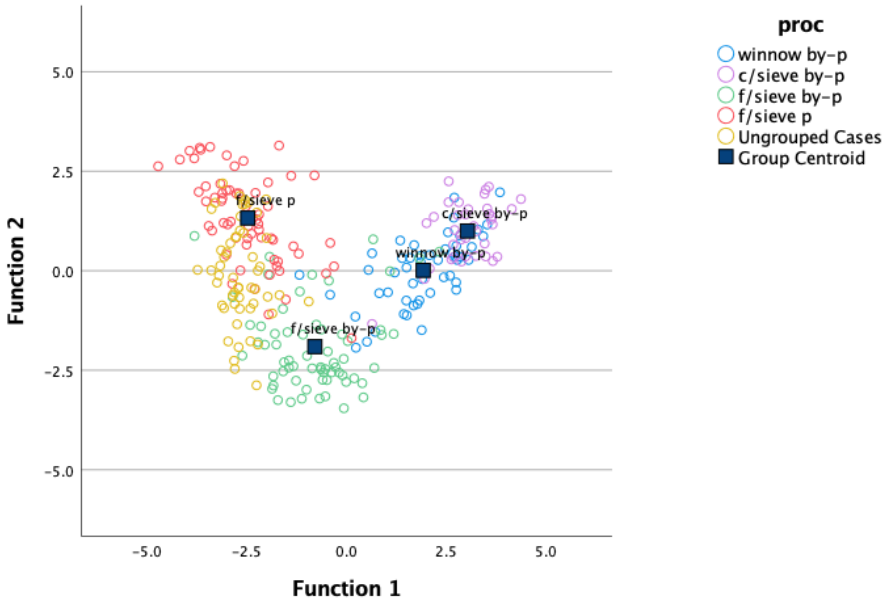


Figure 6.38 Results from a discriminant analysis performed on 54 samples from the Sedgeford malting complex (shown here as 'ungrouped cases'). Proportions of weed seeds from G. Jones' six types in each sample are statistically compared with the same data from 216 samples from G. Jones' ethnographic research, of known crop-processing categories (winnowing by-product, coarse sieve by-product, fine sieve by-product and fine sieve product), and the 'ungrouped cases' allocated to one of the four categories accordingly. The first two discriminant functions extracted in the analysis are plotted against one another, with centroids for each group of pre-determined samples shown.

Table 6.8 Crop processing (by)product type allocated by discriminant analysis for each sample, and probability of that sample belonging to its assigned group

Context / sample number	Discriminant analysis interpretation	Probability (max = 1.00)
17013	FSP	1.00
17023	FSP	1.00
17026	FSP	1.00

Context / sample number	Discriminant analysis interpretation	Probability (max = 1.00)
19036	FSP	0.99
19046	FSP	1.00
19049	FSP	0.99
19061	FSBP	0.88
19070	FSP	0.74
19073	FSP	1.00
23077A	FSP	1.00
23302	FSBP	0.59
23325	FSP	0.55
23333 slot 1	FSBP	0.82
23340	FSP	0.97
23365	FSP	1.00
23370	FSP	0.58
23371	FSBP	0.98
23372	FSP	1.00
23375	FSP	0.99
23505	FSP	0.97
23609	FSP	0.94
23621	FSP	1.00
23624	FSP	0.87
23643	FSBP	0.99
23645	FSBP	1.00
23647	FSP	0.76
23650A	FSP	0.93
23650B	FSP	1.00
23660	FSP	1.00
23662	FSP	1.00
23709	FSP	0.78
23710	FSBP	0.91
23712	FSBP	0.68
23714	FSP	0.71
23719	FSP	0.57
23722	FSBP	0.98
23723	FSBP	1.00
23727	FSP	0.99

Context / sample number	Discriminant analysis interpretation	Probability (max = 1.00)
23754	FSP	0.80
23646 G/H7	FSP	0.60
23337 I6	FSP	0.99
23005 I8	FSBP	0.83
23701 J5	FSP	0.96
23701 J7	FSBP	0.89
23701 K6	FSBP	0.96
23701 K8	FSBP	0.99
23701 L5	FSP	0.68
23701 L7	FSP	1.00
23701 M6	FSP	1.00
23701 M8	FSP	1.00
23701 N5	FSP	1.00
23701 N7	FSP	0.56
23701 O6	FSP	0.97
23713 O8	FSP	0.89

Table 6.9 Allocations of 55 samples from the malting complex to 'crop processing (by)product type' according to basic components analysis and to discriminant analysis (see above), and an overall interpretation for each sample based on compatibility between these

Context / sample number	Basic components interpretation	Discriminant Analysis interpretation	Overall interpretation
17013	FSP	FSP	FSP
17018	FSP	n/a	n/a
17023	FSP	FSP	FSP
17026	USG	FSP	USG
19036	FSP	FSP	FSP
19046	MS	FSP	n/a
19049	FSP	FSP	FSP
19061	FSP	FSBP	n/a
19070	FSP	FSP	FSP
19073	FSP	FSP	FSP

Context / sample number	Basic components interpretation	Discriminant Analysis interpretation	Overall interpretation
23077A	MS	FSP	n/a
23302	FSP	FSBP	n/a
23325	FSP	FSP	FSP
23333 slot 1	FSP	FSBP	n/a
23340	USG	FSP	USG
23365	MS	FSP	n/a
23370	FSP	FSP	FSP
23371	FSP	FSBP	n/a
23372	FSP	FSP	FSP
23375	USG	FSP	USG
23505	FSP	FSP	FSP
23609	USG	FSP	USG
23621	USG	FSP	USG
23624	USG	FSP	USG
23643	USG	FSBP	USG
23645	FSP	FSBP	n/a
23647	MS	FSP	n/a
23650A	FSP	FSP	FSP
23650B	FSP	FSP	FSP
23660	USG	FSP	USG
23662	USG	FSP	USG
23709	FSP	FSP	FSP
23710	MS	FSBP	n/a
23712	USG	FSBP	USG
23714	MS	FSP	n/a
23719	USG	FSP	USG
23722	USG	FSBP	USG
23723	USG	FSBP	USG
23727	FSP	FSP	FSP
23754	FSP	FSP	FSP
23646 G/H7	FSP	FSP	FSP
23337 I6	FSP	FSP	FSP
23005 I8	USG	FSBP	USG
23701 J5	USG	FSP	USG
23701 J7	USG	FSBP	USG
23701 K6	MS	FSBP	n/a

Context / sample number	Basic components interpretation	Discriminant Analysis interpretation	Overall interpretation
23701 K8	MS	FSBP	n/a
23701 L5	MS	FSP	n/a
23701 L7	MS	FSP	n/a
23701 M6	FSP	FSP	FSP
23701 M8	FSP	FSP	FSP
23701 N5	USG	FSP	USG
23701 N7	FSP	FSP	FSP
23701 O6	USG	FSP	USG
23713 O8	USG	FSP	USG

Table 6.10 Compatibility between results of basic components analysis and discriminant analysis for malting complex samples. Compatible categories are highlighted. After (McKerracher 2014 p.206 Table 6.5)

		Basic components analysis				
		CWBP (coarse sieve/winnowing by-product)	**FSBP**	**USG**	**FSP**	**MS**
Discriminant analysis	**WBP**					
	CSBP					
	FSBP			6	5	3
	FSP			13	20	7

Figure 6.39 displays the relative proportions of chaff in samples across the malting complex. The two samples with the highest proportions of chaff occur in the eastern ditch (sample 23077A with 14.19% chaff) and in a layer from a slightly sloping area immediately to the west of the steeping tank (sample 23365, 12.87% chaff), respectively. Deposition of crop processing by-product (or 'waste'), either deliberately or accidentally, in a ditch would be unsurprising. The SHARP team have tentatively hypothesised (here assuming use of conventional crop processing methods) that the gently sloping area west of the steeping tank may be a Mid Saxon 'threshing floor' (**Figure 4.6**). Relative abundance of both chaff and

weed seeds (24.5% weeds, compared with an average of 17.7%) in sample 23665 seemingly supports this notion, based on the (not necessarily reasonable) assumption that charred plant material recovered from this stratigraphic layer was burned in situ. However, equally, if maltsters were skimming chaff and buoyant weed seeds from the water's surface during steeping, one might easily imagine this 'skim by-product' being deliberately deposited close to the tank, forming the sample 23655 context. All seeds occurring in this sample are buoyant in water (but represent a mixture of G. Jones' weed categories), implying that sample 23655 may comprise largely 'skim by-product'. In contrast to the assessment so far, this evidence is seemingly supportive of Sedgeford's maltsters' processing crops according to the new model.

Some further support is leant to the new malting model by the correspondence analysis in **Figure 6.40**. This shows a degree of patterning in the distribution of plant items where cereal taxa, chaff and the 13 most commonly occurring weed taxa[73] are all coded by whether these float in water. In plot A, all 'floating' taxa except for *Fallopia convolvulus* occur at the negative end of axis 1. In plot B, samples in the upper left-hand part of the plot mostly contain over 25% 'floating' taxa. However, taxa with small seeds are evidently more likely to be buoyant in water; a plot of the same plant items with weed taxa coded by G. Jones' seed types (**Figure 6.41**) shows a concentration of 'small, free, heavy' (SFH) taxa in the upper left-hand of the plot. These small weeds may account in part for the trends observed in **Figure 6.40**, but in fact be clustered due to their co-occurrence in 'unsieved grain' (USG) samples generated by crop processing according to the conventional model (**Table 5.4**).

[73] Brassicaceae were excluded from this analysis, see **section 5.4.3.**

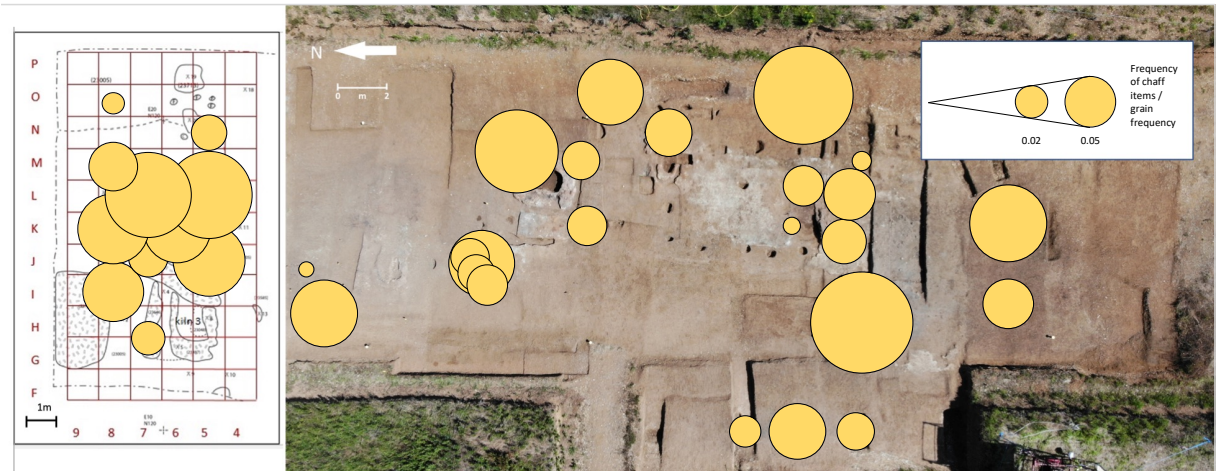


Figure 6.39 Chart showing the frequency of cereal chaff relative to grain frequency (chaff items/grain) in samples from across the malting complex (right) and in the gridded area (left) (photo and plan credit: SHARP 2019)

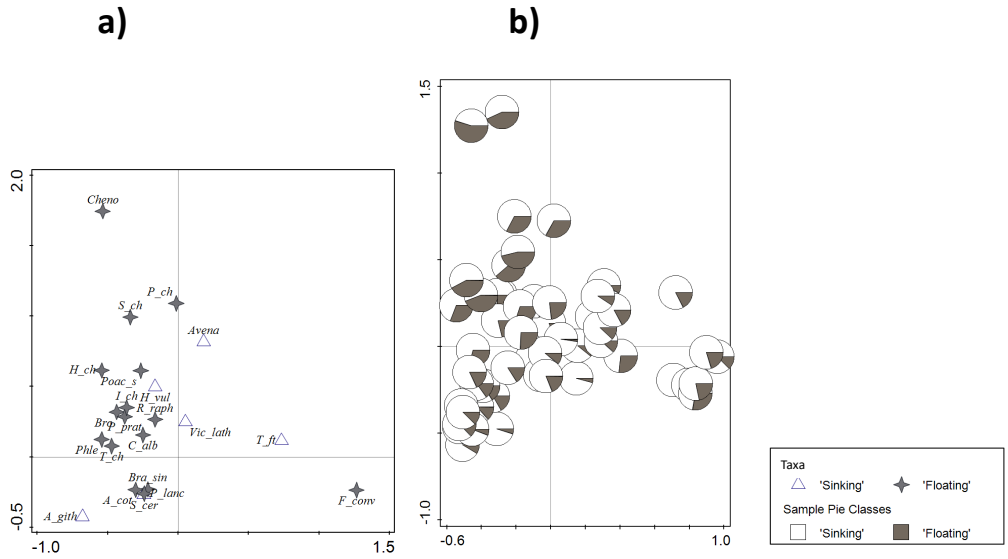


Figure 6.40 'Buoyancy' correspondence analysis showing 54 samples from the malting complex distributed according to composition in terms of four cereal taxa, five types of chaff and 13 weed taxa. In plot (a), all types of plant item are coded by buoyancy in water. In plot (b) sample pie charts have wedges corresponding to the proportion of 'sinking' and 'floating' plant items in each.

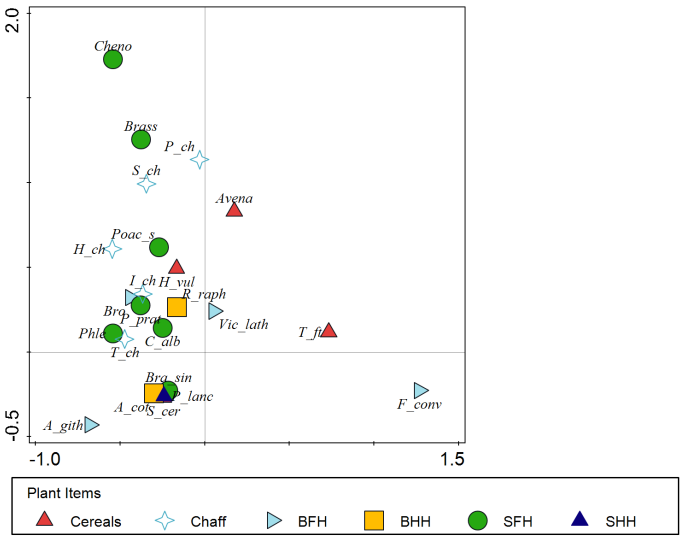


Figure 6.41 'Crop-processing group' correspondence analysis showing four cereal taxa, five types of chaff and 13 weed taxa distributed according to associations in 54 samples from the malting complex. Weed taxa are coded according to G. Jones' crop-processing group. Sample plot is not shown.

Irrespective of whether Mid Saxon peoples at Sedgeford were skimming buoyant by-product from the surface of water in the steeping tank, there is strong evidence that malting was taking plaice at this part of the site, necessarily involving germination ('sprouting') of cereal grains. It is consistently reported that, even to this day, sprouts are removed from malted grains using rubbing and sieving following kilning (de-culming) (**Table 3.2**) (Smith, n.d., 7; Muspratt, 1860, 278; Krzywinski and Soltvedt, 1988, 62; Brears, 2008, 93). Even if all prior preparation of crops followed the conventional model, we can expect that, post-kilning, sprouts were removed in this way. However, as noted in **section 2.4** sprouts detach readily from germinated grains. The broad distribution of detached sprouts across the malting complex (**Figure 6.5**) suggests that the majority of these may have been accidentally removed through pre- or post-depositional agitation and deposited *in situ* (perhaps as a result of the one or more conflagrations which burned the crop material before this final stage of crop

processing had been conducted), rather than as part of a planned stage of crop processing. Alternatively, detached sprouts may be widely distributed across Trench 23 since these were used as fuel for the kilns (**section 3.2.3**). However, contexts with particularly rich deposits of sprouts – for example as seen in sample 23375 (the grain: sprout ratio here being the highest of all samples – 1:0.212, with a mean ratio of 1:0.045), may include some 'de-culming by-product' (DBP) from the final stage of crop processing as suggested in **Table 5.8**.

6.6.3 The settlement area

It is helpful to compare the correspondence analysis in **Figure 6.40** with an equivalent analysis conducted on samples from the settlement area at Sedgeford: closely associated with that from the malting complex both spatially and chronologically. Thus, archaeobotanical material from the settlement area, where there is no evidence to suggest crops were being processed for malting, represents the best available 'control' against which to compare the malting complex samples (and test the two crop processing models). A disadvantage of the settlement assemblage is its small size – 18 samples have been analysed to date, and of these, only nine contained more than 10 weed seeds and hence were deemed eligible for correspondence analysis. Further, due to this small assemblage size, all weeds featured by definition occurred in more than 10% of samples; it was decided in this case to include only weed taxa found in at least two samples. A degree of caution is thus necessary for interpreting the results of these analyses.

The correspondence analysis in **Figure 6.42** shows samples from the settlement area plotted according to composition in terms of cereal taxa, chaff and weed taxa, with all plant items coded by buoyancy in water. In contrast with **Figure 6.40**, there are (arguably

unsurprisingly) no apparent spatial trends in the data. As shown in **Figure 6.43**, there is some slight suggestion of associations between weed taxa where these are coded by G. Jones' six weed types, as would arguably be expected if crop processing here followed the conventional model; with both weed taxa occurring at the positive end of the x-axis being 'BFH'. A seeming lack of very clear trends favouring either model in these data may be attributable simply to the small number of samples in this assemblage.

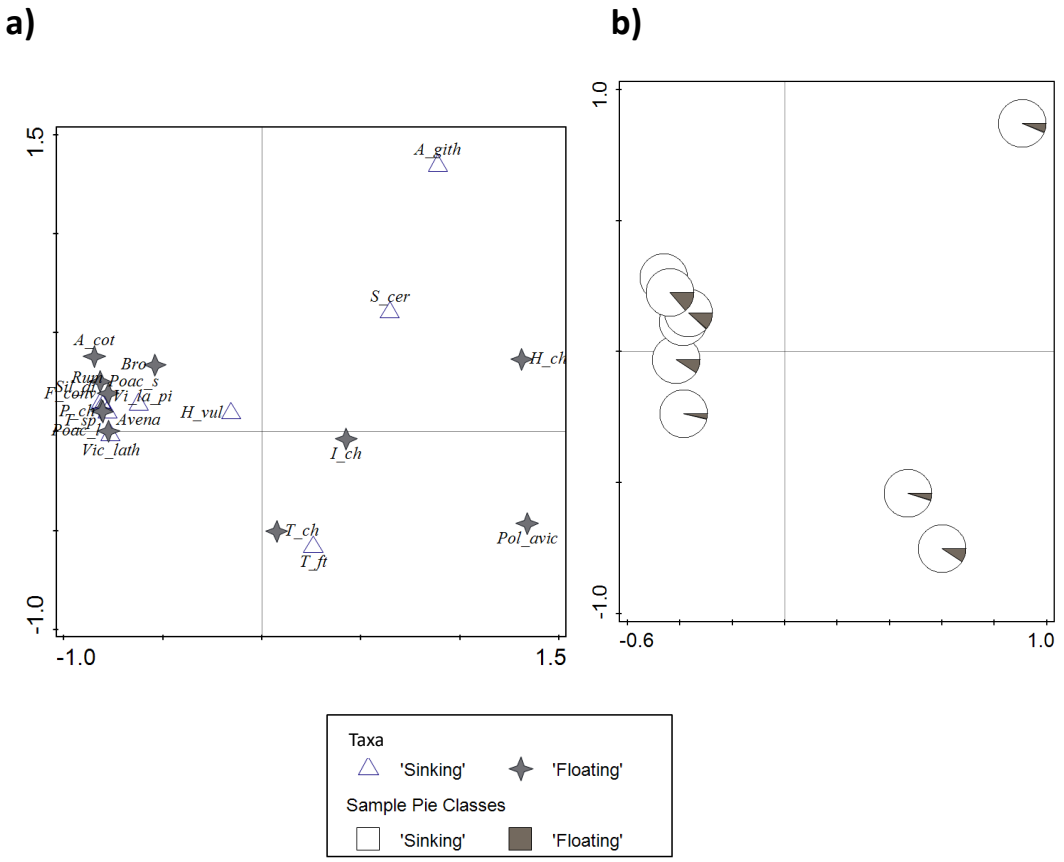


Figure 6.42 'Buoyancy' correspondence analysis showing nine samples from the Sedgeford settlement area distributed according to composition in terms of five cereal taxa, four types of chaff and 11 weed taxa. In plot (a), all types of plant item are coded according to buoyancy in water. In plot (b), sample pie charts have wedges corresponding to proportion of 'sinking' and 'floating' plant items in each sample.

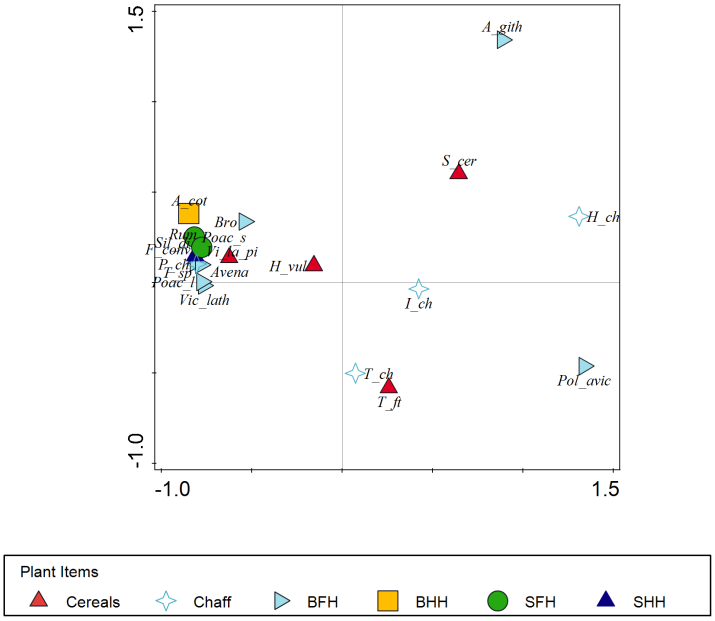


Figure 6.43 'Crop processing type' correspondence analysis showing associations between five cereal taxa, four types of chaff and 11 weed taxa for nine samples from the Sedgeford settlement area (sample plot not shown). Weed seeds are coded according to G. Jones' types.

6.6.4 Crop processing conclusion

It is not possible at this stage to rule out the possibility that crops were being prepared for brewing at Sedgeford as per the newly proposed malting model. However, a convincing body of evidence – particularly pertaining to the distribution of buoyant seeds across samples in the assemblage – favours instead the hypothesis that crop processing was taking place as described in G. Jones' conventional model. Implications of this finding, and other aspects of crop processing, are further considered in **Chapter 8** (**section 8.4.2**).

6.7 Levels of germination: other assessment methods

In this section, the results of additional analyses conducted by colleagues to test for evidence of germination amongst grains from the malting complex assemblage are presented.

6.7.1 Geometric morphometric analysis

The methods used by T. Roushannafas to compare archaeological free-threshing wheat grains from Sedgeford with modern charred grains of known (sub-)species, including experimentally germinated bread wheat, have been described in **section 5.8.1**. The results of a linear discriminant analysis, statistically comparing these categories of wheat grain are displayed graphically in **Figure 6.44**.

According to the analysis, 14 of the 40 grains from Sedgeford (35%) classify as durum wheat (Roushannafas, in prep, 130). This is not supported by 'standard' archaeobotanical identification methods, which suggest all wheat rachis in the assemblage is hexaploid-type (**section 6.3.1**).

Significantly, the analysis identified 24 (60%) of the Sedgeford grains as 'germinated' (ibid.). Grain embryos were excluded from the traced outlines of both modern and archaeological grains (**section 5.8.1**); hence this finding cannot be attributable to germination-induced changes in the embryo. It should be noted that these results are preliminary: only 24 modern germinated grains were used in the analysis, compared with 81 grains for each of the other four groups of modern grains. However, as Roushannafas notes, the results imply that the malting process at Sedgeford affected the grains' morphology, in a way that can be detected using GMM (ibid.), even when grains show no signs of germination to the 'archaeobotanist's eye'. Implications of these results are discussed in **section 8.2.**

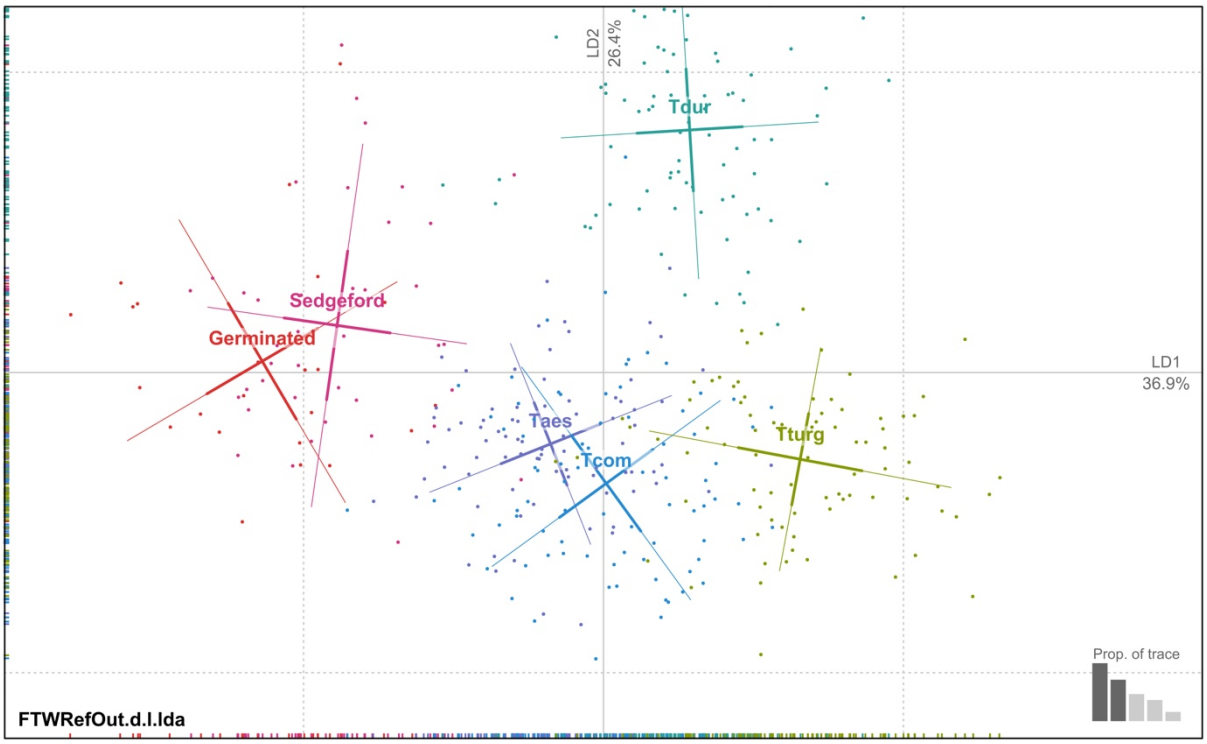


Figure 6.44 Linear discriminant analysis of free-threshing wheat grains from Sedgeford compared with a reference dataset comprisimg modern wheat grains of four varieties, and modern germinated grains. 'Taes' = bread wheat , 'Tcom'=club wheat, 'Tturg' = rivet wheat, 'Tdur'= durum 'Germinated'= experimentally germinated bread wheat. Reproduced with kind permission from T. Roushannafas (in prep., 131 Figure 8)

6.7.2 Scanning electron microscopy (SEM)

Methods employed by Y. Zhou to examine rye grains from Sedgeford using SEM and compare these with both 'control' rye from Mid Saxon Lyminge and experimentally germinated rye grains, are described in **section 5.9**. **Figures 6.45** to **6.49** are SEM images from this research. Zhou found three sets of histological changes in modern germinated rye grains compared with ungerminated equivalents: in the aleurone layer, the structure of the

grains' endosperm and in starch granules, respectively. Two of these modifications (in the aleurone layer and starch granules) were also apparent, or partially apparent, in germinated grains from Sedgeford.

Figure 6.45 displays an unaltered aleurone layer in an ungerminated, uncharred rye grain. **Section 2.3.2** describes the key role of the aleurone layer in germination: a protein-rich source of the lytic enzymes utilised for starch degradation in the endosperm. Zhou did not detect signs of aleurone cell-wall thinning, hypothesised by Heiss *et al.* (2020, 25) to evidence germination (**section 2.4**).[74] Rather, in both modern germinated grains (including those germinated for only 24 hours) and grains from Sedgeford, (including those judged 'indeterminate' according to the gross morphology method), large spaces (*lacunae*) between the aleurone layer cell walls and cell contents were apparent – these were not found in ungerminated modern grains (**Figures 6.46** and **6.47**) (Zhou, 2022, 34–35).

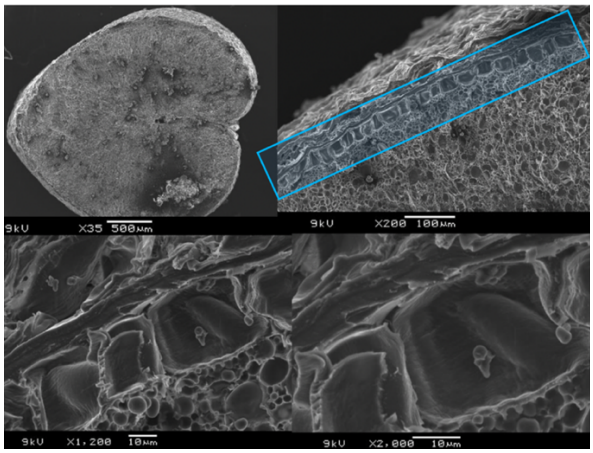


Figure 6.45 SEM image showing an ungerminated, uncharred modern rye grain, with aleurone layer highlighted (above), and aleurone layer cell contents shown (below) (reproduced, with kind permission, from Zhou, in prep., 34 Figure 17)

[74] Time did not permit quantification of results from this analysis: e.g., through measurement of aleurone cell walls or starch 'pits', and subsequent statistical analysis, as per Heiss *et al.* (2020) or Cordes *et al.* (2021). This is a possible avenue for future research (Zhou, 2022, 47).

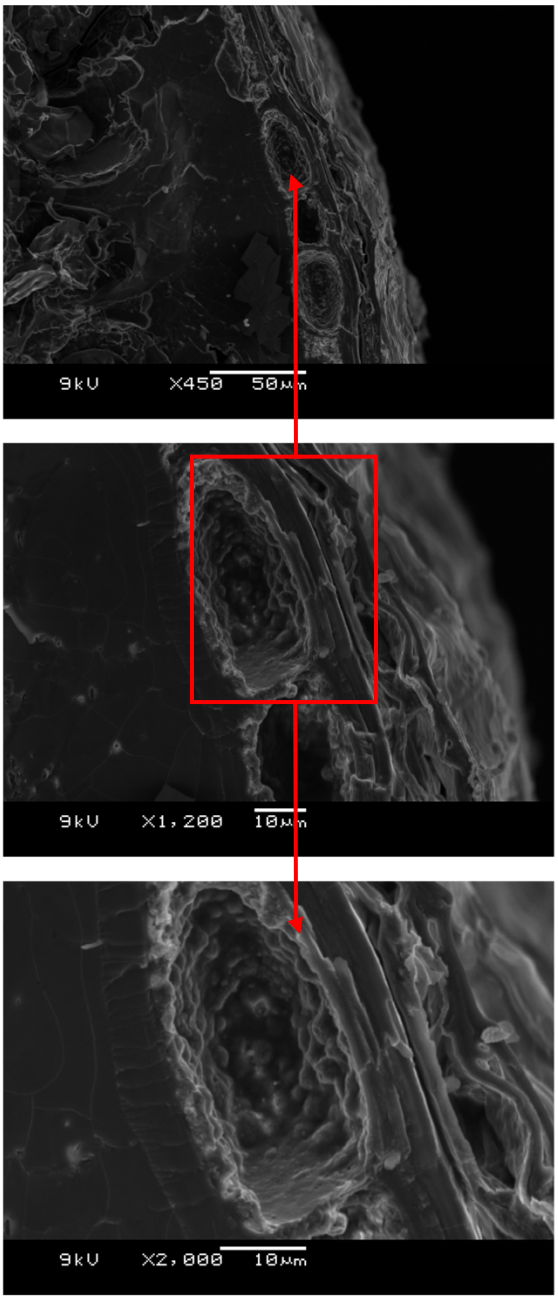


Figure 6.46 SEM image showing aleurone layer from a charred modern rye, having germinated for 24 hours, highlighting a within-cell lacuna (reproduced, with kind permission, from Zhou, in prep., 35 Table 2)

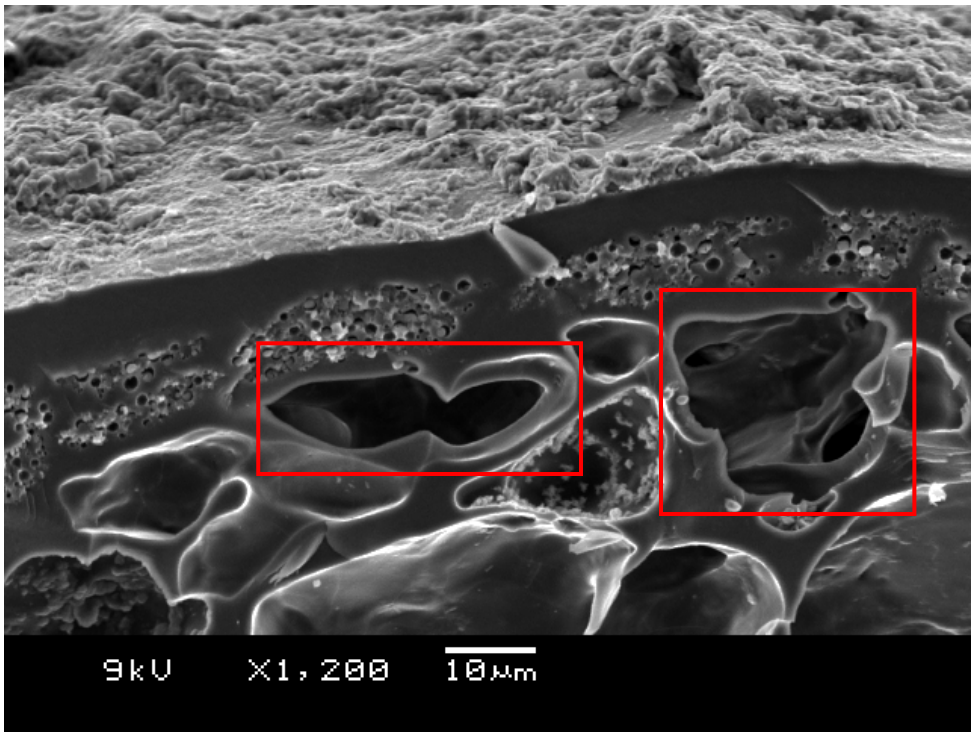


Figure 6.47 SEM image showing aleurone layer from a Sedgeford rye grain, judged 'indeterminate' using gross morphology methods, with lacunae highlighted (reproduced, with kind permission, from Zhou, in prep., p.36 Table 3)

Zhou's images of the interioir of modern grains indicate that the structure of endosperm cells is quickly degraded during germination (due to the activity of lytic enzymes, **section 2.3.2**), with clear loss of structural integrity after 24 hours of germination – before germination is discernible from external gross morphology (2022, 39–40). Similar degradation was not readily apparent in grains from either Sedgeford or Lyminge (ibid., 40).

Finally, clear evidence for amylolytic pitting in endosperm starch granules was visible in all experimentally germinated grains, from after only 24 hours of germination (**Figure 6.48**); this was not apparent in modern ungerminated grains (see **section 2.4**) (see Cordes et al., 2021, 4). Zhou found tentative evidence for similar pitting in rye grains from Sedgeford classified as 'germinated' according to the 'gross morphology' methods (**Figure 6.49**), and

also in one grain from Lyminge (2022, 41, 44–45). She suggests that some among the Lyminge grains may be 'unintentionally germinated' (Zhou, 2022, 29–30).

These preliminary results suggest that signs of germination are clearly recognisable in the internal microstructure of experimentally germinated rye grains (including only slightly germinated grains, in which no changes in gross morphology are identifiable), and that these can, at least to a degree, also be discerned and used as an indicator of germination, in archaeological grains of this taxon. Zhou's findings provide further evidence of germination amongst (at least some) grains from the Sedgeford assemblage.

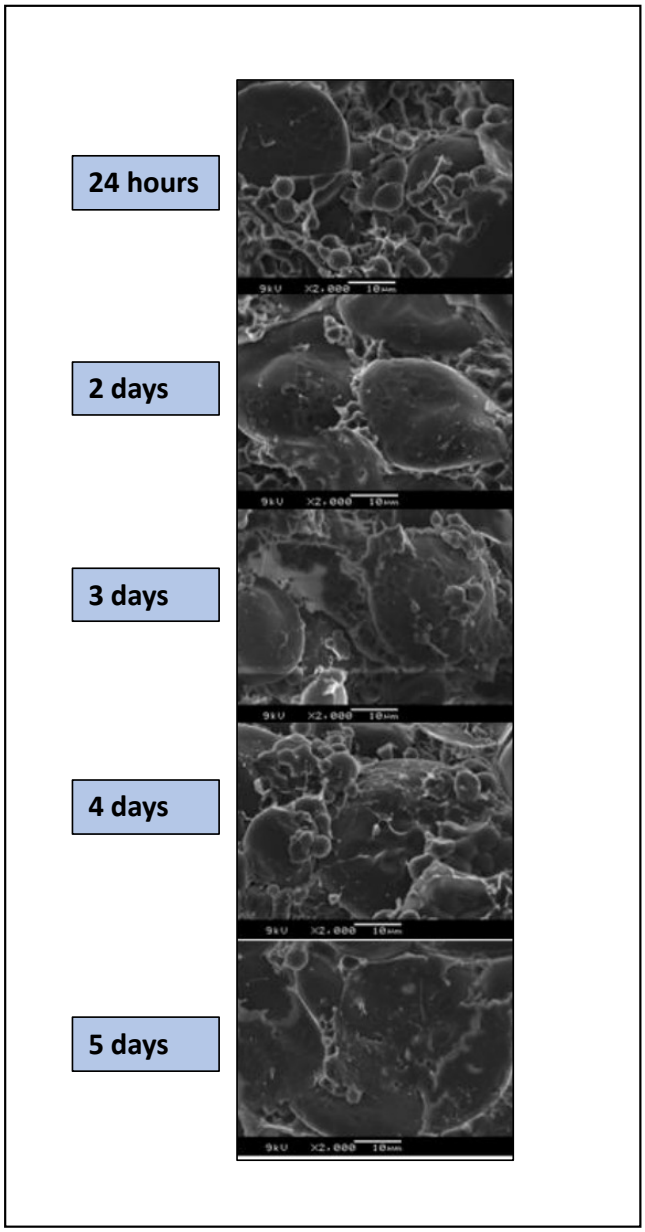


Figure 6.48 SEM images showing endosperm with starch granules in modern charred rye, after specified periods of germination(Adapted, with kind permission, from Zhou, in prep., p.42, Table 4). All images are x2,000.

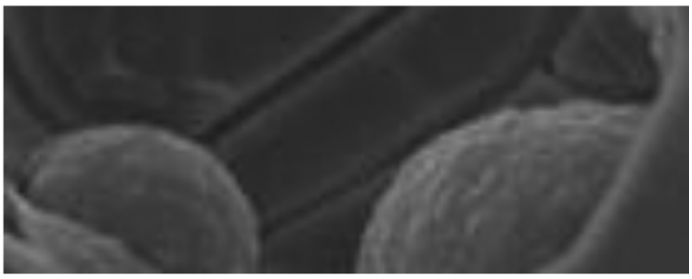


Figure 6.49 'Zoomed in' view of SEM image showing possible starch granules exhibiting surface amylolytic pitting, in rye grain from Sedgeford judged 'germinated' according to gross morphology assessment. (Reproduced with kind permission from Zhou, in prep., 45 Figure 23. Scale not supplied)

As revealed in **section 6.4**, the author's novel gross-morphology methods for discerning levels of germination provide persuasive evidence for widespread germination in grains from across the malting complex. The results of others' analyses (GMM and SEM), here presented (**section 6.7**), support these findings.

6.8 Summary

This chapter has identified several significant trends in archaeobotanical data from the malting complex: the abundance of rye, and high frequency of germinated grains, across the complex, along with the distinctiveness of plant material from kiln 1, being arguably chief amongst these. Analyses conducted to ascertain the type of crop processing used by Sedgeford's maltsters reveal, overall, no strong evidence in favour of a newly proposed model of crop processing for malting.

The next chapter turns to what can be discerned about the ways crops malted at Sedgeford were cultivated, examining the archaeobotanical assemblage using detailed analyses combined with statistical methods. What is Sedgeford's place in the story (described in **Chapter 1**) of changing agricultural practices in Mid-Saxon England?

7 CROP HUSBANDRY

7.1 Introduction

The results of key sets of analyses, namely stable isotope analysis and FWE, along with some correspondence analysis – and associated statistical methods – presented in this chapter, help to address the question of Sedgeford's place in the story of changing agricultural practices in Mid-Saxon England, as described in **Chapter 1**.. Results from carbon and nitrogen stable isotope analysis are presented first, followed by those from FWE and a shorter section using correspondence analysis to examine evidence for seasonality (sowing seasons) in crops recovered from the malting complex. The chapter's final section combines these three differing but complementary perspectives, comparing and integrating results from each to give an overview of the methods used to husband crops malted at Sedgeford.

7.2 Stable isotope analysis

Methods of selection and isotopic analysis of single-grain samples from the Sedgeford malting complex are set out in **section 5.5**. Normalised $\delta^{13}C$ and $\delta^{15}N$ values for each sample analysed are presented, (along with associated %C, %N values and C:N ratios), in **Appendix D**. $\delta^{13}C$ and $\delta^{15}N$ values are here compared first between taxa across all samples, and then both within (intra-) and between (inter-) features within the malting complex. Stable isotope values (after Szpak et al., 2017), and *p*- and *F*-values, are here rounded to two decimal points (*p*-values <0.01 to three d.p.).

7.2.1 Carbon stable isotope values

Figure 7.1 displays normalised $\delta^{13}C$ values for all 112 grains analysed, grouped according to the three major cereal taxa (rye, free-threshing wheat and hulled six-row barley). The most notable trend shown is the markedly lower $\delta^{13}C$ values for barley than for rye or wheat. This relationship is also clear in **Figure 7.2**, which presents graphically the mean $\delta^{13}C$ value and associated standard deviation for each taxon-group; the mean $\delta^{13}C$ value for barley (n=34) of -22.90±1.07‰ is approximately 2‰ lower than that for both rye (n=39), -21.09±0.98‰, and wheat (n=39), -21.05±0.84‰ (**Table 7.1**). Statistical comparison of mean $\delta^{13}C$ values for rye, wheat and barley grains using ANOVA reveals a significant difference when all taxa are compared (F (2, 109) = 44.73, p= <0.001). Use of Tukey post-hoc testing indicates, specifically, that there is no significant difference between rye and wheat (p-value = 0.98), but a highly significant difference (in each case significant at the 0.001 level) between both barley and rye, and barley and wheat (**Table 7.2**). In **section 6.3.1** it is argued that barley grains at Sedgeford are (at least) mostly of the six-row hulled variety. It has been suggested in **section 5.5.1** that, cultivated under the same water availability conditions, six-row hulled barley shows an expected offset of $\delta^{13}C$ values 2‰ lower than those of other cereal taxa (Anyia et al., 2007; Wallace et al., 2013, 398). Indeed, when an ANOVA is re-run to compare means for each taxon, with 2‰ added to the $\delta^{13}C$ value for each barley grain to compensate for the expected offset, the new test reveals no significant difference between means at the 0.05 level (F (2, 109) = 0.25, p =0.78) (**Table 7.2**). Mean $\delta^{13}C$ values for barley (all grains across all features) after compensating for the offset are also shown in **Figure 7.2**.

Evidently, values for rye and wheat have similarly sized ranges (3.68‰ for rye, 3.44‰ for wheat) (**Figure 7.1**). The considerably larger range for barley (5.61‰) is attributable solely

to a single outlier: a grain from SED12 i.e., context 19061 from kiln 2 (**Table 5.10**), with a value of -18.96‰. This is the highest $\delta^{13}C$ value for any grain analysed here; excluding this datapoint, the range in $\delta^{13}C$ values for barley is only 2.86‰. Outliers are further discussed in **section 7.2.3**.

Recent research by Stroud (in prep.) into stable isotope values for single grain samples of wheat cultivated at Highgrove Home Farm, Gloucestershire, suggests a maximum standard deviation for $\delta^{13}C$ values from grains originating in a single field (and, by implication, a single water condition), of ±0.33‰, with an associated maximum range of 1.24‰.

Standard deviations for the three cereal taxa, combined across all samples are: rye ±0.98‰; wheat ±0.84‰; barley ±1.07%. These values exceed the Stroud (±0.33‰) 'single-field threshold', and thus suggest variability consistent with each of rye, wheat and barley crops, when combined across all features, deriving from a range of water availabilities. However, it is important to recall that heterogeneity in other environmental conditions, including soil type, canopy cover, light and topography, may have contributed to the observed variability in $\delta^{13}C$ values (**section 5.5.1**).

Figure 7.1 Normalised δ13C values for all single-grain samples from the malting complex, by cereal taxon

Figure 7.2 Mean normalised $\delta^{13}C$ values with associated standard deviations for all single grain samples by cereal taxon. The mean value for barley after compensating for expected 2‰ offset is also shown.

Intra-feature comparisons

Statistical comparison of means for rye, wheat and barley *within* each feature reveal, in each case, no significant difference between rye and wheat, but differences significant at (at

least) the 0.05 level (in fact, all are <0.003) between both rye and barley, and wheat and barley. For grains from each feature, this difference disappears when 2‰ is added to the δ^{13}C value for each barley grain to compensate for the expected offset (**Table 7.2**).

All standard deviations for grains of each cereal type within each feature exceed the Stroud (±0.33‰) threshold, indicating that grains *within* each feature are consistent with cultivation in more than one condition of water availability (Nitsch et al., 2015, 11; Stroud, in prep.). The lowest level of variability (with standard deviation ±0.49‰) occurs among free-threshing wheat grains in kiln 1.

Inter-feature comparisons

Figure 7.3 replicates **Figure 7.1** but additionally displays data points coded by feature within the malting complex (kiln 1, kiln 2, kiln 3 and the steeping tank). It is notable that there are no clear trends in the distribution of samples by feature type; values for all four features occur throughout all three taxon groupings. The same trend is evident in **Table 7.1** and **Figure 7.4**, which show very little difference in mean δ^{13}C values between the features (where all three taxa are combined), with less than 0.5‰ between the highest and lowest mean values. The means are: kiln 1 (n=23) -21.50‰; kiln 2 (n=30) -21.39‰; kiln 3 (n=29) -21.87‰, and for the steeping tank, (n=30) -21.73‰.[75] This trend is statistically confirmed using ANOVA,

[75] Single-grain samples from kiln 1 include only five barley grains, compared with nine for kiln 3 and 10 for kiln 2 and the steeping tank. Considering the barley offset, it is to be expected that the mean δ^{13}C for kiln 1 is higher than that for the other features. However, statistical testing using ANOVA confirms that there is no significant difference between the mean δ^{13}C values for each feature either with or without compensation for the expected barley offset. With barley values unchanged, results are (F (3, 108) = 0.89, p = 0.45), and with compensation for the offset, the results are: (F (3, 108) = 1.67, p=0.18). The mean values quoted in the text are those without compensation for an expected offset.

which indicates that there are no significant difference in means between grains from each feature (F (3, 108) = 0.89, p = 0.45) (**Table 7.3**). After compensating for the expected barley offset, standard deviations for each feature are as follows: kiln 1 ±0.69‰; kiln 2 ±1.08‰; kiln 3 ±1.00‰ and the steeping tank, ±0.93‰. Each of these values exceeds the Stroud (in prep.) (±0.33‰) maximum threshold, i.e., the data are consistent with grains *between* the four features having been cultivated under more than one condition of water availability.

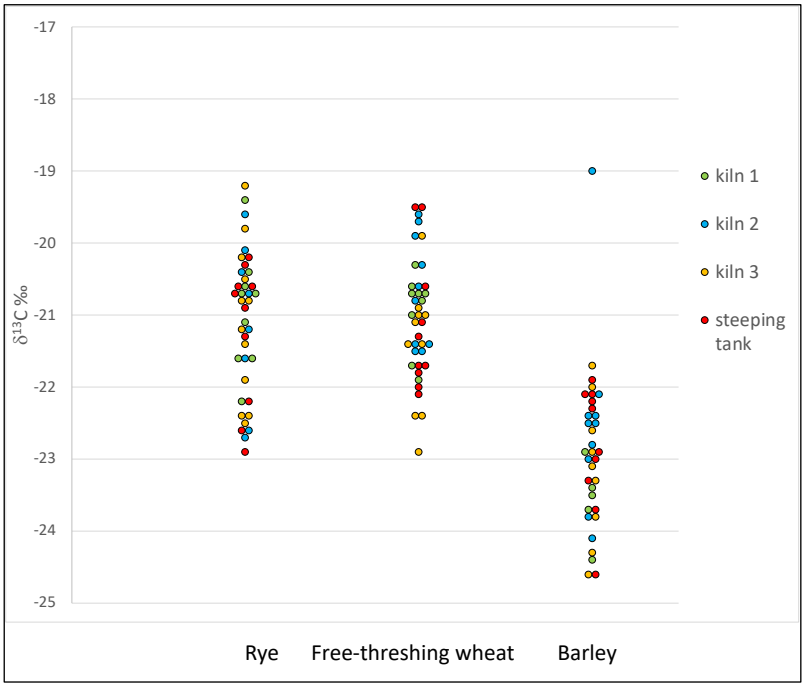


Figure 7.3 Normalised $\delta^{13}C$ values for all single-grain samples, grouped by cereal taxon and coded by feature within the malting complex

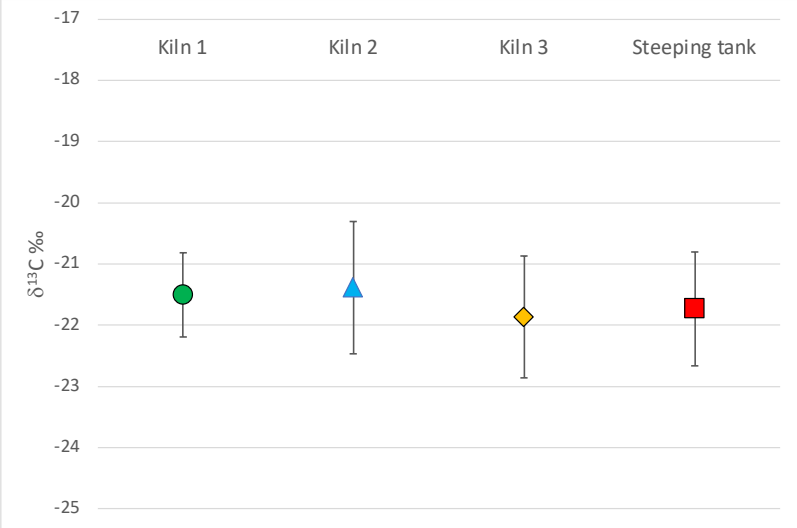


Figure 7.4 Mean normalised $\delta^{13}C$ values with associated standard deviations for all single grain samples by feature within the malting complex, standard deviations are calculated after compensating 2‰ for the barley offset

Table 7.1 Number of single grain samples, and mean normalised $\delta^{13}C$ values with associated standard deviation for each cereal taxon analysed across all features, for all grains within each feature, and for each taxon by feature within the malting complex.

Feature	Taxon	Number of (single grain) samples	Mean (‰)	Standard deviation (‰)
All	Rye	39	-21.09	0.98
	Free-threshing wheat	39	-21.05	0.84
	Barley	34	-22.90	1.07
Kiln 1[76]	All	23	-21.50	0.69
Kiln 2		30	-21.39	1.08
Kiln 3		29	-21.87	1.00
Steeping tank		30	-21.73	0.93
Kiln 1	Rye	9	-20.92	0.78
	Free-threshing wheat	9	-20.94	0.49
	Barley	5	-23.56	0.56
Kiln 2	Rye	10	-21.03	0.95
	Free-threshing wheat	10	-20.68	0.74
	Barley	10	-22.46	1.32
Kiln 3	Rye	10	-21.17	1.18
	Free-threshing wheat	10	-21.44	0.90
	Barley	9	-23.13	1.01
Steeping tank	Rye	10	-21.24	0.99
	Free-threshing wheat	10	-21.15	0.98
	Barley	10	-22.80	0.85

[76] See previous footnote (no.75).

Table 7.2 Results of ANOVA and Tukey post-hoc tests for differences in mean normalised $\delta^{13}C$ values between cereal taxa, across all features and within features from the malting complex. All tests were performed first without and secondly with compensation for the expected 2‰ barley offset. P-values indicating significant differences at the 0.05 level are marked in bold.

Feature	Barley offset	ANOVA			Tukey post-hoc test
		F-ratio	Degrees of freedom	P-value	
All	No offset	44.729	2, 109	**<0.001**	rye-wheat. 0.98
					wheat-barley **<0.001**
					rye-barley **<0.001**
	2‰ offset	0.253	2, 109	0.78	
Kiln 1	No offset	30.56	2, 20	**<0.001**	rye-wheat 0.10
					wheat-barley **<0.001**
					rye-barley **<0.001**
	2‰ offset	1.77	2, 20	0.20	
Kiln 2	No offset	7.49	2, 27	**0.03**	rye-wheat 0.75
					wheat-barley **0.003**
					rye-barley **0.02**
	2‰ offset	0.704	2, 27	0.50	
Kiln 3	No offset	10.107	2, 26	**<0.001**	rye-wheat 0.84
					wheat-barley **0.003**
					rye-barley. **<0.001**
	2‰ offset	0.237	2, 26	0.79	
Steeping tank	No offset	11.313	2, 27	**<0.001**	rye-wheat. 0.98
					wheat-barley **<0.001**
					rye-barley **0.001**
	2‰ offset	0.284	2, 27	0.76	

Table 7.3 Results of ANOVA statistical tests for differences in mean normalised $\delta^{13}C$ values between features within the malting complex for all taxa and for each cereal taxon, respectively

Taxon	ANOVA		
	F-ratio	Degrees of freedom	P-value
All	0.89	3, 108	0.45
Rye	0.19	3, 35	0.90
Wheat	1.50	3, 35	0.23
Barley	1.41	3, 30	0.26

7.2.2 Nitrogen stable isotope values

Figure 7.5 displays normalised $\delta^{15}N$ values for all 112 grains analysed, grouped according to the three major cereal taxa occurring in the malting complex (rye, free-threshing wheat and hulled six-row barley). The data seemingly exhibit considerable variability, with $\delta^{15}N$ values between 0.06 and 12.67‰ (i.e., a range of 12.61‰); the standard deviation for rye is ±2.46‰, for wheat, ±1.79‰, and for barley, ±2.04‰.

Modern crop studies using single grain samples suggest, for grains from a single arable experimental plot receiving up to 25 tonnes of manure per hectare, a maximum expected range in $\delta^{15}N$ values of ~5.40‰, and maximum standard deviation of ~±1.64‰ (Larsson et al., 2019, 7, Table 2). A comparable, unmanured plot exhibited less variability, with a maximum expected range of ~2.10‰, and maximum standard deviation of ~±0.56‰ (ibid.). Research conducted in a 'real' modern arable setting: the organically-cultivated fields at Highgrove in Gloucestershire, receiving low-level manuring, suggests a maximum range in $\delta^{15}N$ values within a single field of ~3.57‰, and a standard deviation of ~±0.90‰ (Stroud, in prep.). The Highgrove results, for a field receiving small amounts of manure, perhaps unsurprisingly suggest a level of variability intermediate between those for heavily manured

and for unmanured fields in the Larsson experiments. Significantly, results from Sedgeford demonstrate variability in normalised δ^{15}N values significantly greater than that expected for a single arable source according to both sets of research using modern fields. In other words, the data suggest, for each cereal taxon considered, grains recovered from the malting complex were cultivated in more than one setting. Significantly, whilst variability in δ^{15}N values is consistent with cultivation in a range of manuring conditions, the same trend may alternatively, or additionally, be explained by heterogeneity in the environmental conditions e.g., soil type, soil moisture level, and depth of the water table - in which crops were grown (Hamerow et al., in prep.).

Section 5.5.2 has discussed the manuring 'bands' devised by Bogaard *et al.* (2013, 12590) based on modern experimental data, and the proviso that these figures are complemented by a local 'wild herbivore baseline' (from which δ^{15}N value of unmanured plants in the locality can be inferred) has been noted (ibid.). Nitrogen stable isotope values are available for collagen from two wild herbivores from East Anglia (each a type of deer, and both originating in Suffolk), dated to the Anglo-Saxon era (**Table 7.4**) (Leggett, 2021, 93 Table 5.2). In order to compare the 'wild herbivore baseline' δ^{15}N values with those for cereal grains, these were adjusted to compensate for the trophic shift between vegetation and herbivore (by subtracting 4‰, see **section 5.5.2**) and for the expected offset between grains (and seeds/fruits) and rachis (and leaves/stems; the plant parts most likely consumed by foraging herbivores), by adding 2.40‰ (Fraser et al., 2011, 2799; Bogaard et al., 2013, 12590). The expected δ^{15}N values for unmanured cereal grains calculated in this way (based on respective wild herbivore collagen samples) are 4.1‰ and 4.5‰ (mean: 4.3‰). It is important to acknowledge associated caveats: these samples derive from sites over 34 miles from

Sedgeford. The potential confounding effect of soil moisture levels on δ^{15}N values has been noted; however, each site has, according to recent measurements, a low soil moisture level (<30%), approximately comparable with Sedgeford's (21%).[77] Nonetheless, these 'wild herbivore-baseline'- derived δ^{15}N values for unmanured grains in Anglo-Saxon East Anglia should be applied with caution.

Table 7.4 Characterising two 'wild herbivore' individuals from Anglo-Saxon East Anglia for which nitrogen stable isotope values are available

Descriptive category	**Wild herbivore 1**	**Wild herbivore 2**
Reference	(Leggett, Rose, et al., 2021)	(Purcell, 2012)
Location	Stanton, W. Suffolk	Lakenheath, Suffolk
Distance from Sedgeford	41.9 miles	34.6 miles
Soil moisture	22%	30%
Date	5th to 9th centuries	5th to 7th centuries
Species	Red Deer	'deer' (species not recorded)
Bone type	Astralgus	Tibia
δ^{15}N value	6.1‰	5.7‰
δ^{15}N value after compensating for offsets (expected value for unmanured grains)	4.5‰	4.1‰
Mean expected δ^{15}N value for unmanured grains	4.3‰	

[77] Countryside Survey topsoil moisture (%) data for Sedgeford, Stanton and Lakenheath were consulted using the UK Soil Observatory map available at URL: https://mapapps2.bgs.ac.uk/ukso/home.html?layers=CEHTSSoilMoisture&extent=57735,6963010,64615,6966498&basemap=topo& . Map data are from Esri UK, Esri, HERE, Garmin, GeoTechnologies Inc., USGS, METI/NASA |None. [Accessed 20.7.22, 15.11.22].

Returning to the Bogaard *et al.* (2013) research; notably, this is based on *bulk* samples from modern agricultural experiments; research using single-grain samples can be expected to show greater variability in δ^{15}N values. Thus, the Bogaard *et al.* (ibid.) manuring 'bands' superimposed on **Figure 7.5** must also be interpreted with care.

However, irrespective of caveats concerning wild herbivore baseline data, and the use of single-grain samples in this case, it is clear from the plot that most single grains from the malting complex analysed have notably low δ^{15}N values when compared to both the 'wild herbivore baseline' figure calculated above and the Bogaard *et al.* manuring bands (2013, 12590). 64% of all datapoints (72 samples) have δ^{15}N values *below* the expected herbivore-baseline figure for unmanured grains. 91% of all datapoints (102 samples) fall in the Bogaard *et al.* 'low to medium' manuring range (<6‰) and 36% (40 samples) classify as 'low' manuring (<3‰) (the latter implying no manuring, or residual manuring only – from former land use (ibid.). Only 10 datapoints (9% of the total) have δ^{15}N values exceeding 6‰ (indicative of 'high' manuring). Outlier datapoints are further discussed in **section 7.2.3**. As discussed, a further potential factor influencing δ^{15}N values in the Sedgeford samples is the local soils, which are free-draining with a low moisture content (21.07%). Heavy, water-retaining soils having been found to be associated with increased δ^{15}N values at other early medieval sites, likely due to attendant microbial activity (Hamerow et al., in prep.).[78]

Figures 7.5 and **7.6** each show broad overlap in the δ^{15}N values for samples of the three taxa, with free-threshing wheat grains from Sedgeford seeming to have slightly lower δ^{15}N values and slightly less variability overall. This is further suggested by the means and

[78] See footnote 74.

standard deviations for each crop (**Table 7.5**), which are as follows: rye (n=39) 4.06±2.46‰, wheat (n=39) 3.34±1.79‰ and barley (n=34) 4.44±2.04‰. Use of ANOVA to compare all grains of each taxon (**Table 7.6**) suggests, however, that differences in mean δ^{15}N values between crops are not statistically significant (F (2, 109) = 2.56, p= 0.08). It is notable that mean values for each taxon are *less* than the 'wild herbivore baseline'-expected figure for unmanured grains of 4.3‰.

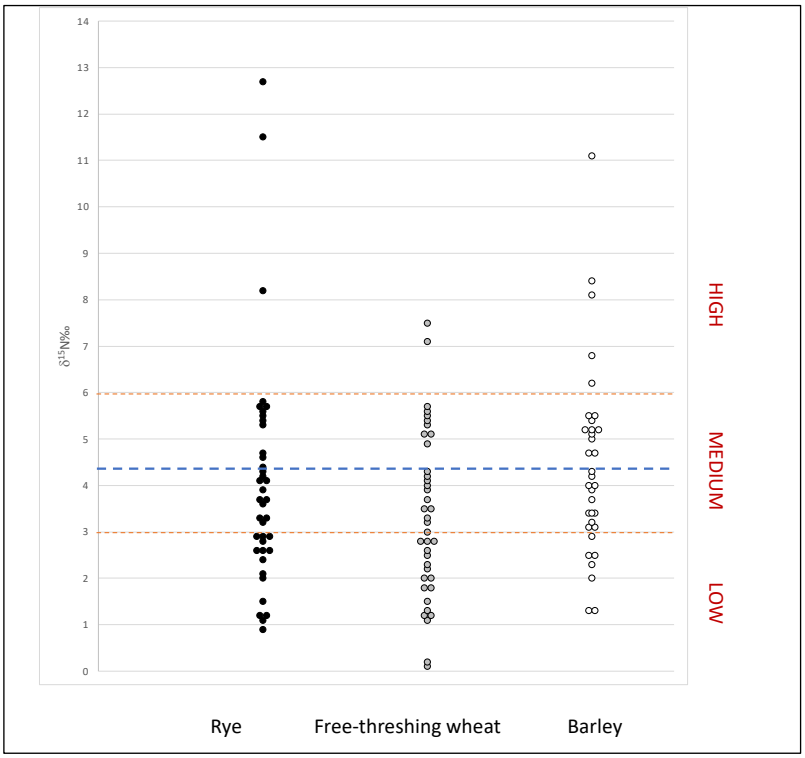


Figure 7.5 Normalised δ^{15}N values for all single-grain samples from the malting complex, by cereal taxon. Bogaard et al. (2013) manuring 'bands' (in red) and expected value for unmanured grains derived from 'East Anglian wild herbivore-baseline' (in blue) are shown.

Figure 7.6 Mean normalised δ^{15}N values with associated standard deviation for all single grain samples by cereal taxon. Bogaard et al. (2013) manuring 'bands' are shown in red, and the wild herbivore baseline-derived figure in blue.

Intra-feature comparisons

These findings are replicated when mean δ^{15}N values for rye, wheat and barley *within* each feature are statistically compared; in each case, no statistically significant difference is found between the three crops (**Table 7.6**). **Table 7.5** displays standard deviations for each taxon within each feature. Rye grains from kilns 1 and 2 have a standard deviation of less than ±1.64‰ (the calculated variability threshold for heavily manured fields); the same is true for both wheat and barley from kiln 3 and for barley from the steeping tank (Larsson et al., 2019, 7). Grains from all other taxa in each feature (at least one taxon from each feature) have standard deviations exceeding this threshold value. Standard deviations for *all* taxa from each feature equal or exceed ±0.90‰,[79] the calculated variability threshold for single grain samples

[79] Barley grains from the steeping tank have δ^{15}N values with a standard deviation of ±0.90‰.

of wheat cultivated in the same field treated with a *low* level of manure (Stroud, in prep.). These results are consistent with most, if not all, sets of grain taxa *within* each feature originating in more than one 'condition of manuring' (Larsson et al., 2019, 7, Table 2).

Significantly, and perhaps contrary to expectations, standard deviations for each grain taxon *within* each feature (mean value for these being ±1.98‰, n=12), suggest almost as much variability in grain δ^{15}N values as equivalent standard deviations for each crop *across* all features (mean of these standard deviations being ±2.10‰, n=3) (**Table 7.5**). As discussed, (**section 4.5**), radiocarbon dating evidences a likely chronological separation of kiln 3 (later) from kilns 1 and 2. Grains from different features were likely distinct not only in date but also in location of origin (i.e. were cultivated in different fields). Evidence for comparable variability within and between features implies significant heterogeneity in cultivation conditions *within* each field which ultimately supplied the kilns/steeping tank (assuming all grains of each taxon within each feature respectively, originated from a single field).

Inter-feature comparisons

Figure 7.7 replicates **Figure 7.5** but additionally displays datapoints coded by feature within the malting complex (kiln 1, kiln 2, kiln 3 and the steeping tank, respectively). It is notable that there are no clear trends in the distribution of samples by feature type; values for all four features occur throughout all three taxon groupings. The same trend is evident in **Table 7.5** and **Figure 7.8**, which show only slight differences in mean δ^{15}N values between the features, with 1.49‰ between the highest and lowest mean values. The means are: kiln 1 (n=23) 3.09 ±1.78‰; kiln 2, (n=30), 4.16±2.08‰; kiln 3, (n=29) 4.58 ±2.13‰, and for the steeping tank, (n=30), 3.68 ±2.33‰. This trend is statistically confirmed using ANOVA,

which indicates no significant difference in means between grains from each feature (F (3,108) =2.415, p = 0.07) (**Table 7.7**). However, Vaiglova *et al.* (2022, 8) suggest that statistical analyses which generate p-values close to 0.05 (such as the 0.07 here) should not be automatically disregarded; in fact, Tukey's post-hoc testing gives a p-value for the difference in mean δ^{15}N values between kiln 1 and kiln 3 of only 0.06 (Tukey's p-values for comparison of means between other features are higher).

Standard deviations for samples (of all taxa) grouped by feature all exceed (mostly by a small margin) the ±1.64‰ upper limit for grains deriving from a single source; and, by a larger margin, the ±0.90‰ limit for grains from a field with low-level manuring (**Table 7.5**) (Larsson et al., 2019, 7, Table 2; Stroud, in prep.). Again, this inter-feature variation suggests that grains recovered from *across* the various features in the malting complex plausibly derive from more than one 'condition of manuring'.

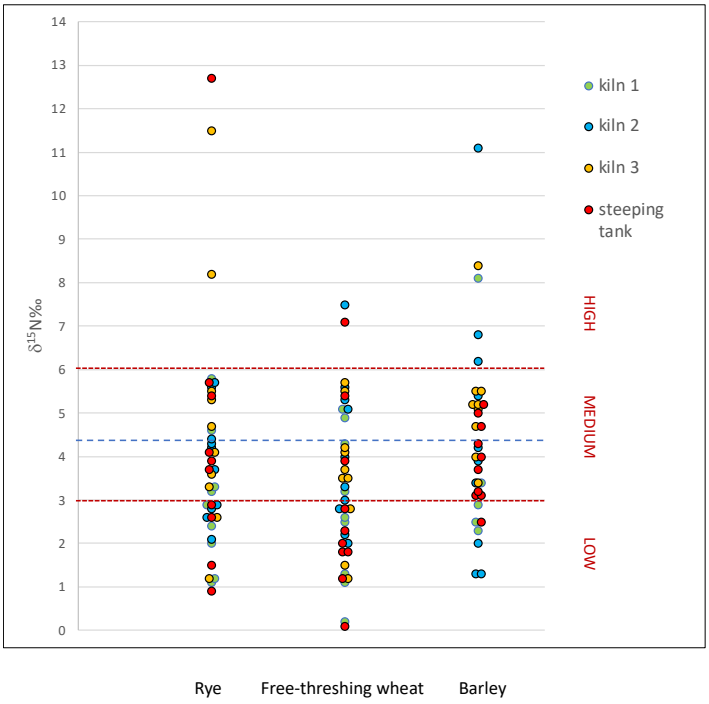


Figure 7.7 Normalised $\delta^{15}N$ values for all single-grain samples, grouped by cereal taxon and coded by feature within the malting complex. Bogaard et al., (2013) manuring 'bands' are show in red, and the wild herbivore baseline figure is marked in blue.

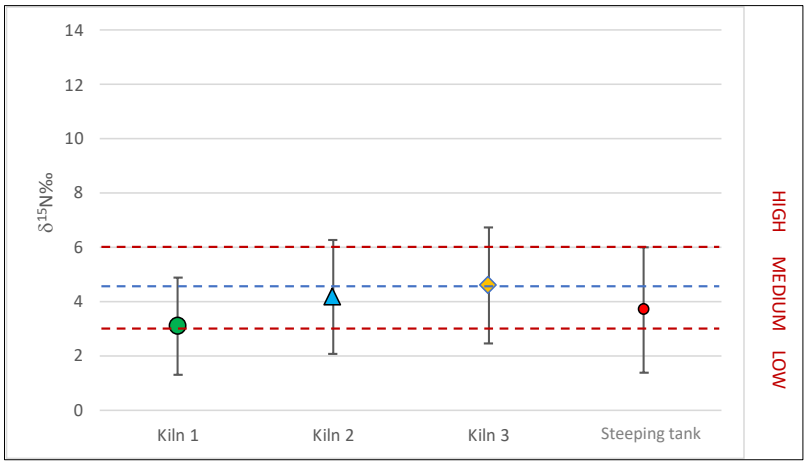


Figure 7.8 Mean normalised $\delta^{15}N$ values with associated standard deviation for all single grain samples by feature within the malting complex. Bogaard et al. (2013) manuring 'bands' are shown (in red) and the wild herbivore baseline figure marked (in blue).

Table 7.5 Number of single grain samples, and mean normalised $\delta^{15}N$ values with associated standard deviation, for each cereal taxon analysed across all features, for all grains within each feature, and for each taxon by feature within the malting complex.

Feature	Taxon	Number of (single grain) samples	Mean (‰)	Standard deviation (‰)
All	Rye	39	4.06	2.46
	Free-threshing wheat	39	3.34	1.79
	Barley	34	4.44	2.04
Kiln 1	All	23	3.09	1.78
Kiln 2		30	4.16	2.08
Kiln 3		29	4.58	2.13
Steeping tank		30	3.68	2.33
Kiln 1	Rye	9	2.96	1.53
	Free-threshing wheat	9	2.80	1.72
	Barley	5	3.84	2.41
Kiln 2	Rye	10	3.84	1.23
	Free-threshing wheat	10	4.09	1.76
	Barley	10	4.56	3.01
Kiln 3	Rye	10	5.00	2.96
	Free-threshing wheat	10	3.58	1.45
	Barley	9	5.23	1.36
Steeping tank	Rye	10	4.32	3.30
	Free-threshing wheat	10	2.83	2.10
	Barley	10	3.90	0.90

Table 7.6 Results of ANOVA statistical analyses for differences in mean normalised $\delta^{15}N$ values between cereal taxa, across all features and within features from the malting complex.

Feature	ANOVA		
	F-ratio	Degrees of freedom	P-value
All	2.56	2, 109	0.08
Kiln 1	0.56	2, 20	0.58
Kiln 2	0.29	2, 27	0.74
Kiln 3	1.8	2, 26	0.19
Steeping tank	1.10	2, 27	0.35

Table 7.7 Results of ANOVA statistical tests for differences in mean normalised $\delta^{15}N$ values between features, across all taxa and for each cereal taxon

Taxon	ANOVA		
	F-ratio	Degrees of freedom	P-value
All	2.41	3, 108	0.07
Rye	1.17	3, 35	0.33
Wheat	1.20	3, 35	0.32
Barley	0.83	3, 30	0.49

7.2.3 Comparing stable carbon and nitrogen isotope values

Figures 7.9 and **7.10** display $\delta^{15}N$ values plotted against $\delta^{13}C$ values for all grains, coded by grain taxon and by both taxon and area of the malting complex, respectively. The datapoints of each type evidently show considerable overlap. Statistical testing confirms that there is no significant relationship between $\delta^{15}N$ and $\delta^{13}C$ values (Pearson's product-moment correlation co-efficient = 0.12, *p*-value =0.23). However, two trends are evident: firstly, as discussed, barley grains have notably lower $\delta^{13}C$ values, falling to the more negative end of the x-axis. Secondly, five clear outlier datapoints (including grains of all three taxa, and from three of the four sampled features within the malting complex) have elevated values for both $\delta^{13}C$

(>-21‰) and δ^{15}N (>7‰). These results do not seem to arise from measurement or machine error, nor from post-depositional contamination (**section 5.5.3**).

Conceivably, combined high δ^{13}C and δ^{15}N values in this small proportion (4.46%) of the grains is attributable to the effect of salinity on growing conditions (Sedgeford being ~6km from the coast). Some research suggests salinity elevates δ^{15}N values in affected plants; salty conditions mimic aridity and thus also cause raised δ^{13}C values (Heaton, 1987; Yousfi et al., 2010). However, were one of the agricultural 'source areas' for Sedgeford's crops on the coast, it seems surprising that so small a proportion of grains in the assemblage should be correspondingly affected by salinity. Not all high δ^{15}N value grains can be thus accounted for; five additional datapoints which classify as 'high manuring' (>6‰) have 'mid-range' δ^{13}C values.

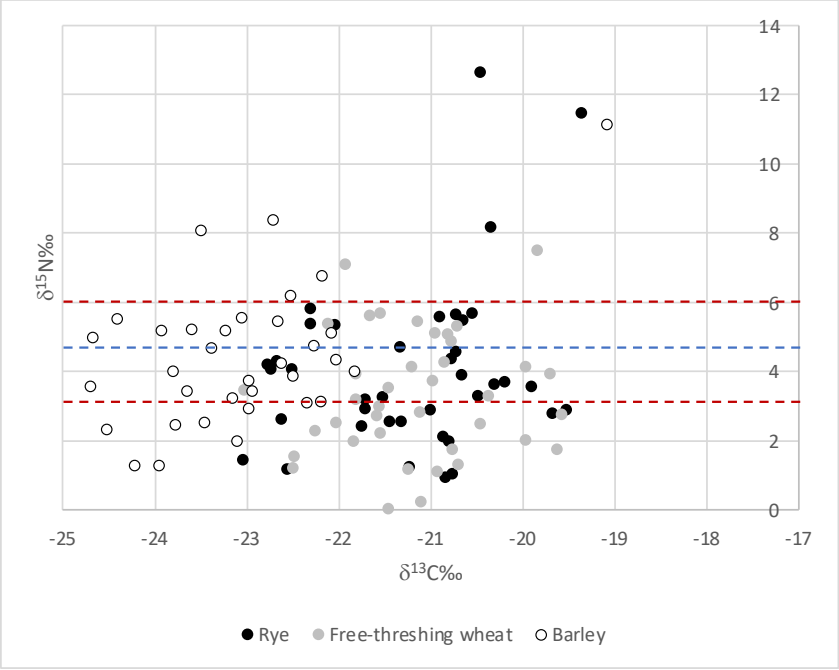


Figure 7.9 δ^{15}N values plotted against δ^{13}C values for all grains, coded by cereal taxon. Bogaard et al. (2013) manuring 'bands' are shown (in red) and the wild herbivore baseline figure marked in blue.

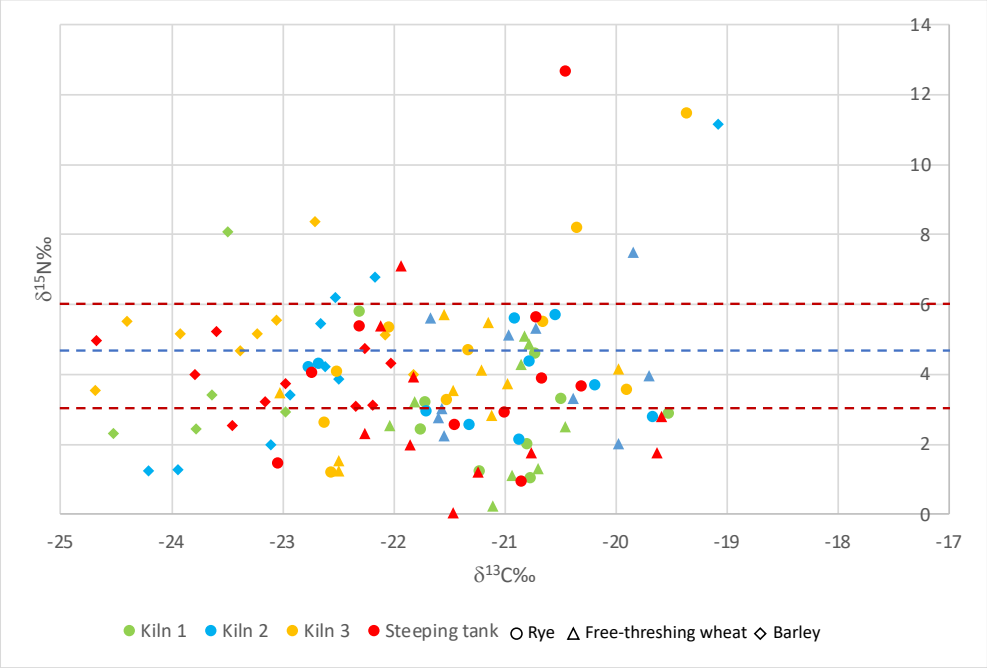


Figure 7.10 $\delta^{15}N$ values plotted against $\delta^{13}C$ values for all grains, coded by cereal taxon and by feature within the malting complex. Bogaard et al. (2013) manuring 'bands' are show (in red), and the wild herbivore baseline marked (in blue).

7.2.4 Stable isotope analysis conclusions

To conclude, it is helpful to revisit the questions outlined in **section 5.5.3**. These are listed, with responses, below.

1. Do $\delta^{15}N$ values suggest soil ^{15}N enrichment, potentially indicative of manuring?

Nearly 65% of samples analysed from the Sedgeford malting complex have $\delta^{15}N$ values *lower* than the expected value for unmanured grains inferred from a wild herbivore baseline; indicative of very limited, if any, manuring. Further, over 90% of all samples have $\delta^{15}N$ values consistent with either no manuring, or with moderate inputs equivalent to up to ~10-15 tonnes of manure per hectare ('low to medium' manuring according to the Bogaard *et*

al. bands (2013, 12590)). Of the ~9% of samples (n=10) having δ^{15}N values consistent with 'high' levels of manuring (>30 t/ha), high values in five samples may be attributable to other factors, as discussed. Low soil moisture conditions in the Sedgeford environ (more specifically, low levels of waterlogging-associated microbial activity) may partially account for the low δ^{15}N values here, compared with other sites (see Hamerow et al., 2020, 603). Overall, however, results are certainly consistent with crops malted at Sedgeford deriving from an agricultural regime(s) without, or with moderate, manuring input.

2. *In terms of potential manuring, is there evidence consistent with preferential treatment of one crop species over others?*

Statistical testing reveals no significant difference between the mean δ^{15}N values for rye, wheat and barley, both when comparing all samples *across* all features and when comparing mean values for taxa *within* features. In other words, for the three major crops occurring in the malting complex, there is no evidence suggesting preferential manuring of one crop over others.

3. *Is there evidence of variation in $\delta^{13}C$ and $\delta^{15}N$ values between grains deriving from different areas of the malting complex i.e., kilns 1, 2, 3 and the steeping tank?*

For both δ^{13}C and δ^{15}N values, statistical testing reveals no significant differences in mean values between any of the malting complex features from which samples derive (the greatest difference in mean δ^{15}N values is between kiln 1 and kiln 3, but this is not significant at the 0.05 level). Thus, there is no evidence of significant variation in δ^{13}C and δ^{15}N values between different areas of the malting complex.

4. *Is there evidence for change in crop $\delta^{13}C$ and $\delta^{15}N$ values over time?*

Section 4.5 (**Table 4.1**) describes the results of radiocarbon dating on grains from the three malting complex kilns at Sedgeford, suggesting that kiln 3 is likely approximately a generation later in date. However, (as noted), ANOVA testing for mean $\delta^{13}C$ and $\delta^{15}N$ values suggests no significant difference between samples from each of the kilns. In other words, results are consistent with crop $\delta^{13}C$ and $\delta^{15}N$ values being relatively consistent (conserved) over time.

5. *Is evidence from stable isotope analysis consistent with crops deriving from a single agricultural context?*

$\delta^{13}C$ values for grains from the malting complex have a high level of variability. Calculated standard deviations (for each crop taxon across all features; (mostly) for crop taxa *within* each feature; and for all taxa combined *between* features) suggest that the grains sampled were cultivated under more than one condition of water availability. Significantly, the samples also have highly variable $\delta^{15}N$ values, with standard deviations (for each taxon *across* all features; (mostly) for taxa *within* features; and for all grains combined *between* features) consistent with the crop plants from which grains derive being cultivated in more than one 'condition of manuring'. These two sets of findings corroborating one another provides strong evidence that crops in the malting complex were cultivated in a range of conditions – with variation (human-induced or naturally-occurring) either within or between fields, and/or over time.

The remaining questions from **section 5.5.3** will be addressed in **section 7.5.**

7.3 Functional weed ecology

In this section, results are presented for two sets of discriminant analyses based on functional ecological traits of arable weed species. For each analysis, functional trait data for weed taxa from the Sedgeford assemblage are statistically compared with a model set of results which contrasts different modern arable cultivation regimes; the first model pertains to 'intensity' of cultivation (extent of manuring and disturbance), and the second to the level of 'disturbance' alone (weeding and tilling or ploughing). **Section 5.6** sets out the methodological background to FWE, and methods used to create the weed ecology models used here, including discriminant analysis. Discriminant function scores and probabilities (expressing the certainty that a datapoint belongs to its assigned group) are here rounded to two decimal places.

7.3.1 Intensity of cultivation

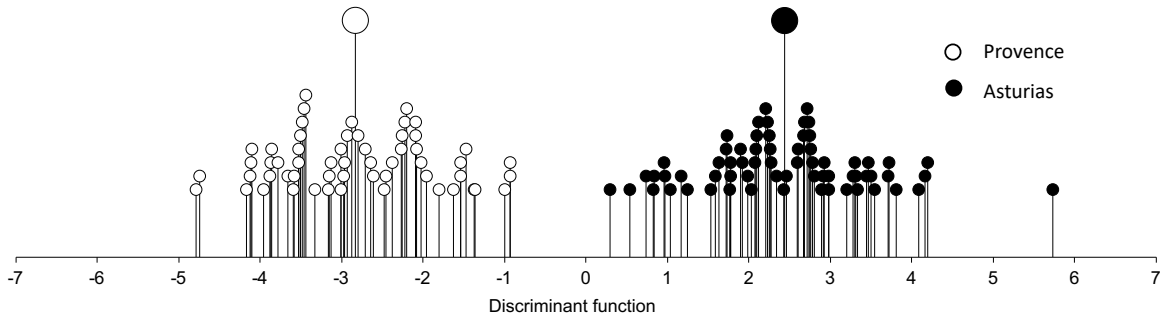
Figure 7.11(a) (replicating **Figure 5.22(a)**) displays weed ecology functional trait data on which the 'intensity' model here used is founded; each (smaller) symbol represents a single surveyed modern field, coded according to the two featured agricultural regimes, and plotted relative to the extracted discriminant function which distinguishes between these. Larger symbols represent the group centroids.

Figure 7.11(b) plots functional trait data from the 26 Sedgeford 'behavioural episodes' analysed, relative to the same discriminant function. All the episodes are clustered at the negative end of the discriminant function 'axis' and each is classed as 'low intensity' according to discriminant analysis, with a probability of 1.00 for all but one episode. The remaining episode (classified with probability 0.999) is that with the least negative

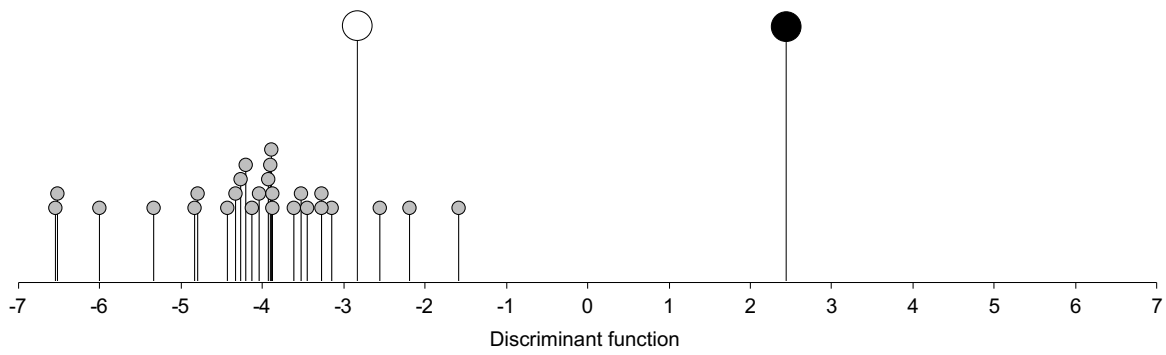
discriminant score – of -1.59. These results convincingly attest that the agricultural regime(s) from which the Sedgeford assemblage originates was characterised by decidedly low labour inputs.

Figure 7.11(c) shows no apparent trend when the datapoints are coded by the feature within the malting complex from which the 'episode' is sourced (kiln 1, kiln 2, kiln 3 and the steeping tank, respectively). Similarly, there does not seem to be any relationship between the date of the episodes (**section 4.5**, **Table 4.1**) and the discriminant function when datapoints are coded by approximate date range, i.e., these results provide no evidence for change in level of labour input over time (**Figure 7.11(d)**).

a)



b)



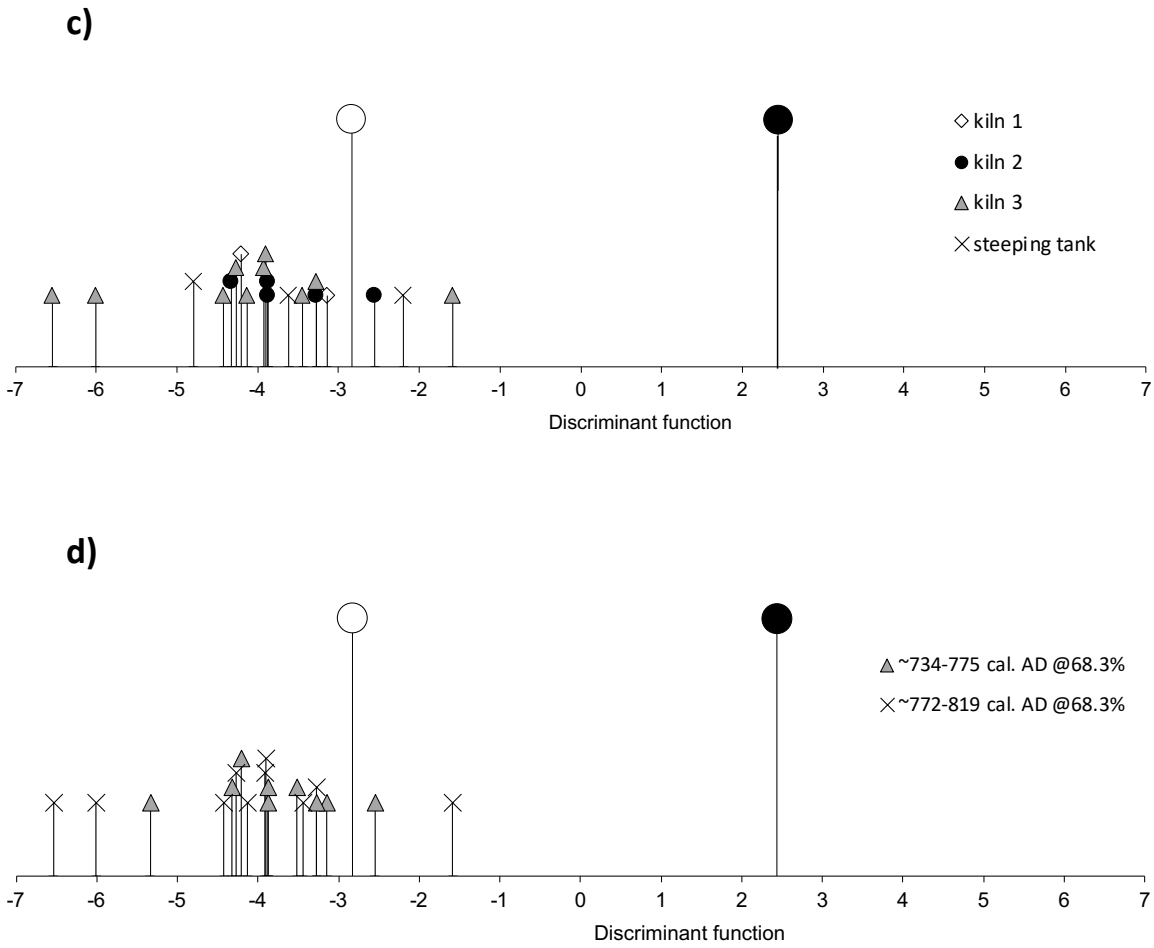


Figure 7.11 'Intensity' discriminant analysis plots (a) Relationship of Haute Provence fields (white circles) and fields from Asturias (black circles) with the discriminant function used to differentiate these. Larger circles represent group centroids. (b) Relationship between episodes from the Sedgeford assemblage and the discriminant function used to distinguish fields from Haute Provence (high input) and Asturias (low input). Larger circles indicate centroids for Haute Provence and Asturias groups. (c) Replica of plot b) with episodes coded by feature within the malting complex. (d) Replica of plot b) with episodes coded by approximate date range.

7.3.2 'Disturbance' levels

Figure 7.12(a) (replicating **Figure 5.23(a)**) displays the discriminant analysis model on which the 'disturbance' model is based. Each (smaller) symbol represents a single modern arable area, coded according to the type of agricultural regime it represents and plotted relative to the extracted discriminant function which distinguishes between the two groups of 'high-' and 'low-disturbance' farming systems. Larger symbols represent the group centroids.

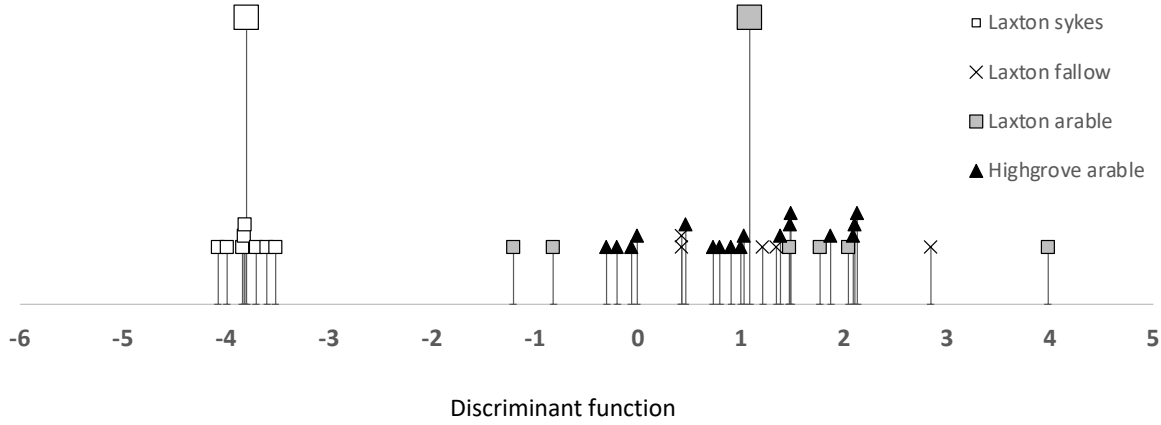
Figure 7.12(b) introduces data for the Sedgeford episodes to this model, using the same discriminant function and group centroids as displayed in **7.12(a)**. In this case, datapoints are clustered at the positive end of the discriminant function 'axis', with discriminant analysis classifying all episodes as 'high disturbance'. Each is allocated to this group with a probability of greater than 0.90, except for a single episode, that with the most negative discriminant score of -1.32, which is classified with probability 0.55.

It is helpful to compare the (functional trait-based) datapoints generated by this discriminant analysis with equivalent data from an experimental field study conducted at the Lauresham Open-Air Laboratory for Experimental Archaeology in Lorsch, Germany, where a reconstructed oxen-drawn mouldboard plough has in recent years been used to reconstruct ridge and furrow fields managed as part of a three-field rotation system (Kropp, 2022). Datapoints from Lorsch (**Figure 7.12(c)**) fall within the discriminant function score range of episodes from the Sedgeford malting complex. Overall, these results attest with some certainty that archaeobotanical material from the malting complex originates in an agricultural regime(s) with 'high disturbance', consistent with local use of mouldboard ploughing at the time.

According to **Figure 7.12(d)**, archaeobotanical episodes from the steeping tank exhibit the broadest range of discriminant function 'disturbance' scores; however, there is little other

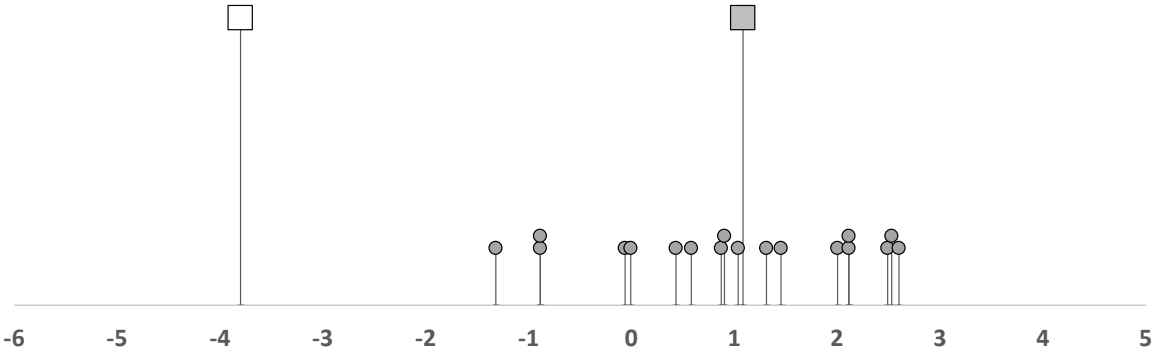
indication of a relationship between disturbance and the area of the malting complex from which episodes derive. There is, however, some suggestion (**Figure 7.12(e)**) of a shift from a more to less disturbed agricultural regime over time at Sedgeford, with episodes (from kiln 3) dated to *c.* 772-819 cal. AD at 68.3%, falling somewhat to the left, signalling a lower level of disturbance, of those (from kilns 1 and 2) which radiocarbon dating suggests may be a generation older (**section 4.5**). However, this apparent trend can be asserted only tentatively owing to the small number of episodes (two) with the later date.

a)



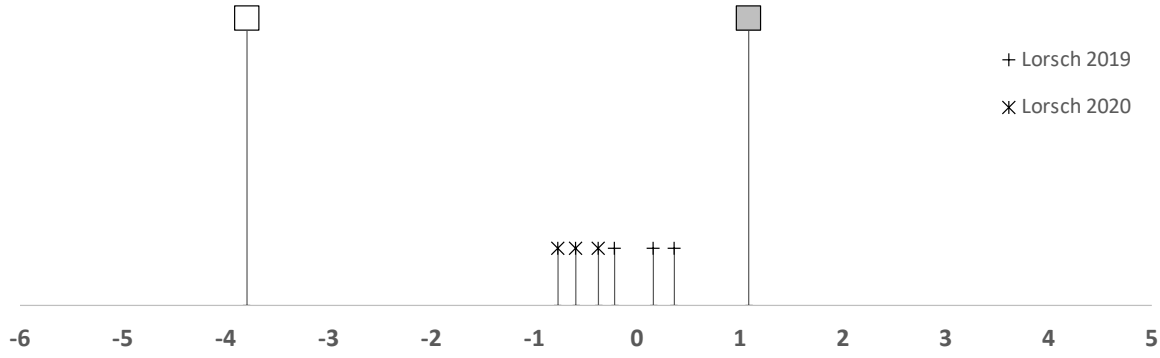
Discriminant function

b)



Discriminant function

c)



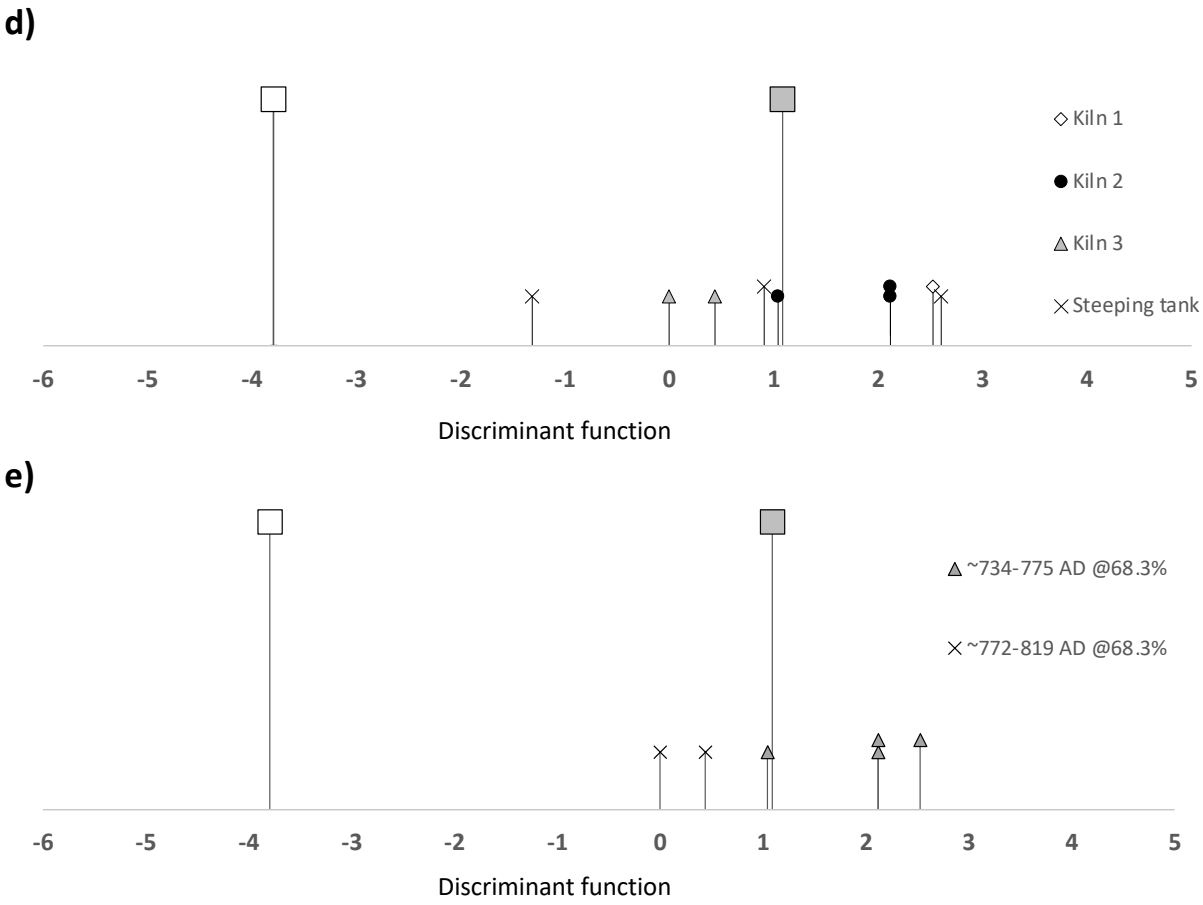


Figure 7.12 'Disturbance' discriminant analysis plots (a) Relationship of Laxton 'sykes' (white squares) and of fallow and arable fields from Laxton and arable fields from Highgrove (other symbols) with the discriminant function extracted to differentiate these. Larger circles indicate group centroids. (b) Relationship between episodes from the Sedgeford assemblage and the discriminant function extracted to distinguish Laxton sykes (low disturbance) from fallow and arable fields (high disturbance). Larger circles indicate centroids for the sykes and 'fallow and arable field' groups. (c) Relationship of experimental mouldboard-ploughed fields from Lorsch with the extracted discriminant function, with larger circles indicating centroids for the Laxton syke and fallow and arable field groups. (d) Replica of plot b) with episodes coded by feature within malting complex. (e) Replica of plot b) with episodes coded by approximate date range.

7.4 Seasonality

This section presents the results of correspondence analyses aimed at discerning any trends relating to seasonality (specifically, sowing season) in the Sedgeford plant data. The principles underlying correspondence analysis are outlined in **section 5.2.8**, while the methodology employed in this study to use correspondence analysis specifically to investigate seasonality in crop taxa are described in **section 5.7**.

'Seasonality' scatterplots – the output of correspondence analysis – including both cereal taxa and weed species (those judged eligible according to the criteria outlined in **section 5.7**) are displayed in **Figure 7.13** and **Figure 7.14.** In each case, weed species are coded by seasonality-association. **Figure 7.13** presents output of an analysis without any transformation of the data, whilst **Figure 7.14** further explores patterning in the assemblage by showing the same data following a square root transformation.

Clustering of taxon datapoints in such plots reflects their co-occurrence in samples from the assemblage (**section 5.2.8**). Where weed species associated with, for instance, spring-sowing, cluster spatially in a correspondence analysis plot with a particular cereal taxon (or cereal taxa), and distinct from, in this example, autumn-associated weed species, this is compatible with that cereal taxon (those taxa) having been regularly sown in the spring over the period in which the assemblage was formed (Hamerow et al., in prep.).

As shown in the scatterplots, in the Sedgeford plant data, only seven weed species (out of the 11 eligible for inclusion in the correspondence analysis) are clearly associated with a particular sowing season. This small number of species arguably renders any discernible trends in the scatterplots less compelling. Of the seven frequently occurring 'season-associated' species, four are spring-associated and three autumn-associated.

In both plots, there is some evidence for separation of weed seeds by seasonality-association; spring-associated seeds are widely dispersed across the plots, but, notably, all three autumn-associated seeds occur to the negative end of the x-axis, in a loose cluster with rye. In **Figure 7.14**, this cluster also includes barley. This group of datapoints, in both plots, also certainly includes (spring-associated) *Plantago lanceolata. Chenopodium album* and *Anthemis cotula* (both also spring-associated) are loosely associated with this cluster. Wheat falls to the positive end of the x-axis; the only seasonality-associated weed also occurring in this half of the plot is (spring-associated) *Fallopia convolvulus*

Before further interpreting these results, it is worth considering some provisos. Firstly, particularly considering the small number of species, even if no clear seasonality trend were evident in the plotted data, this would not definitively imply that particular seasonality regimes, such as systematic crop rotation, were not being employed in the arable areas which 'fed' the Sedgeford malting complex. As Hamerow *et al.* (in prep.) note, for such analyses, positive evidence for seasonality is more convincing than negative evidence. Secondly, it is worth noting that spring-associated weeds also occur amongst autumn-sown crops (but that the reverse is not true) (Bogaard et al., 2001, 1173).

Thirdly, it is plausible that, if three-field crop rotation were being employed in the fields from which the malting complex's cereal grains derive, a so-called 'autumn-blurring' effect may have spuriously inflated the number of frequently-occurring spring-associated weeds in the assemblage (Hamerow et al., in prep.). The fact that spring-associated weeds can do well among autumn-sown crops (and the reverse is not true) means that, in a three-year three-field rotation system (including a spring or summer ploughing of the fallow field), spring-associated weeds can grow in all three years, and have a competitive advantage in two

years, whilst autumn-associated weeds can flourish in only one year. The effect of this trend over repeated cycles will be to raise the proportion of spring-associated weeds (although the most competitive autumn-associated species such as brome grasses and corncockle will likely persist, as in the data presented here), in a field, and thus in the corresponding archaeobotanical assemblage (ibid.).

The final proviso relates to the distorting effects of crop processing on seasonality-association trends in weed taxa from an assemblage (here assuming 'classical' crop processing methods – **section 6.6**). In archaeobotanical assemblages dominated by fine-sieve *by*-products, crop processing biases plant data towards spring-associated weeds (Bogaard et al., 2005, 507). However, the Sedgeford assemblage is dominated by fine-sieve *products* and hence should be, if anything, biased towards more autumn-associated weeds.

Considering these factors, how might the trends in **Figure 7.13** and **Figure 7.14** be interpreted? Firstly, the lack of dominance, among species eligible for correspondence analysis, of either spring- or autumn-associated weeds (with weed seeds approximately equally divided between these) means there is little evidence for bias caused by either autumn blurring or crop processing (though it is conceivable that both are at play). Arguably the most unambiguous trend in the scatterplots is the co-occurrence of wheat with (spring-associated) *Fallopia convolvulus*. This trend is indubitably mostly attributable to the predominance of both wheat and *Fallopia convolvulus* in samples recovered from kiln 1 (**sections 6.3** and **6.5**); however, this relationship between the two taxa may be an artefact of wheat's having been consistently spring-sown in the fields supplying grain for the malting complex. No firm conclusion can be drawn, however, based on association between a cereal and a single seasonality-associated weed species.

It is conceivable that the occurrence in both plots of the datapoint for (spring-associated) *Plantago lanceolata* (and to a lesser extent, the two spring-associated species *Anthemis cotula* and *Chenopodium album*) close to that of (obligatory autumn-sown) rye, in a cluster with all three autumn-associated species at the negative end of the x-axis, is attributable to the noted potential for spring-associated species to persist among autumn-sown crops. If so, it can be posited that the scatterplots suggest that rye, certainly, and perhaps barley (loosely clustered in both plots) were autumn-sown, potentially even as a mixed crop, in a three-field crop rotation regime with spring-sown wheat. Alternatively, a two-field system may have predominantly been in place, with autumn-associated weeds favoured in the autumn-sown field (likely sown with rye, the dominant crop at Sedgeford) and spring-associated in the fallow – accounting for the co-occurrence of spring- and autumn-associated weeds across much of the plot, including with obligatory autumn-sown rye. As noted, the lack of clear evidence for seasonality in the malting complex assemblage does not necessarily imply a lack of underlying seasonality patterns in crop-sowing times. To summarise: datapoint distribution in **Figure 7.13** and **7.14** implies that rye, clustered with all the autumn-associated weed taxa, was the most consistently autumn-sown crop; wheat may have been spring-sown. Although trends are somewhat ambiguous, these results do not rule out potential two- or three-field crop rotation in the fields that 'fed' the malting complex.

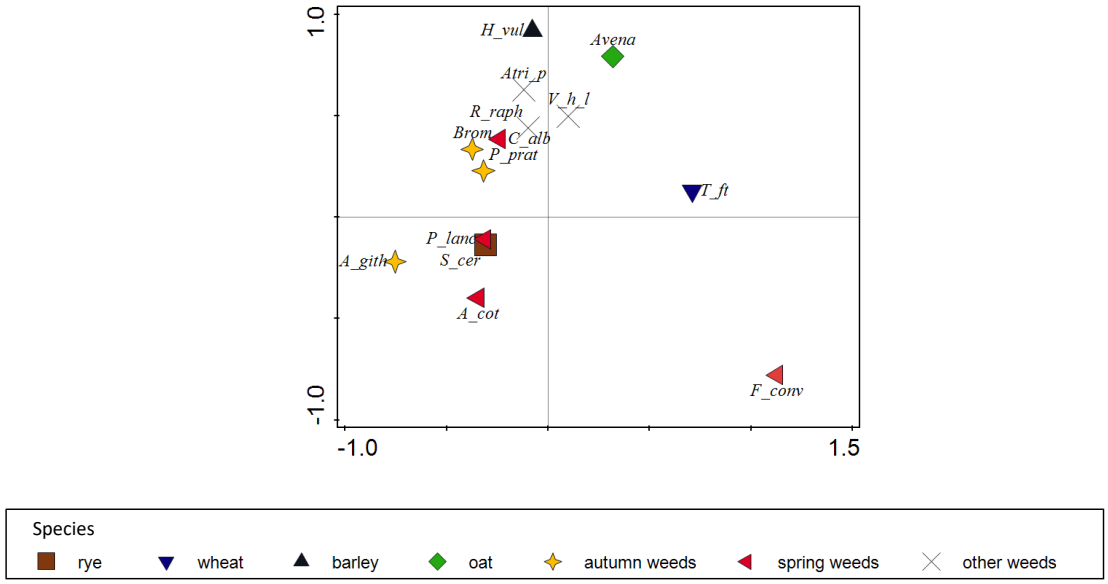


Figure 7.13 'Seasonality' malting complex correspondence analysis plot showing four cereal taxa and 11 weed species distributed according to associations in 54 samples from the malting complex. Weed species are coded according to seasonality class. Sample plot is not shown.

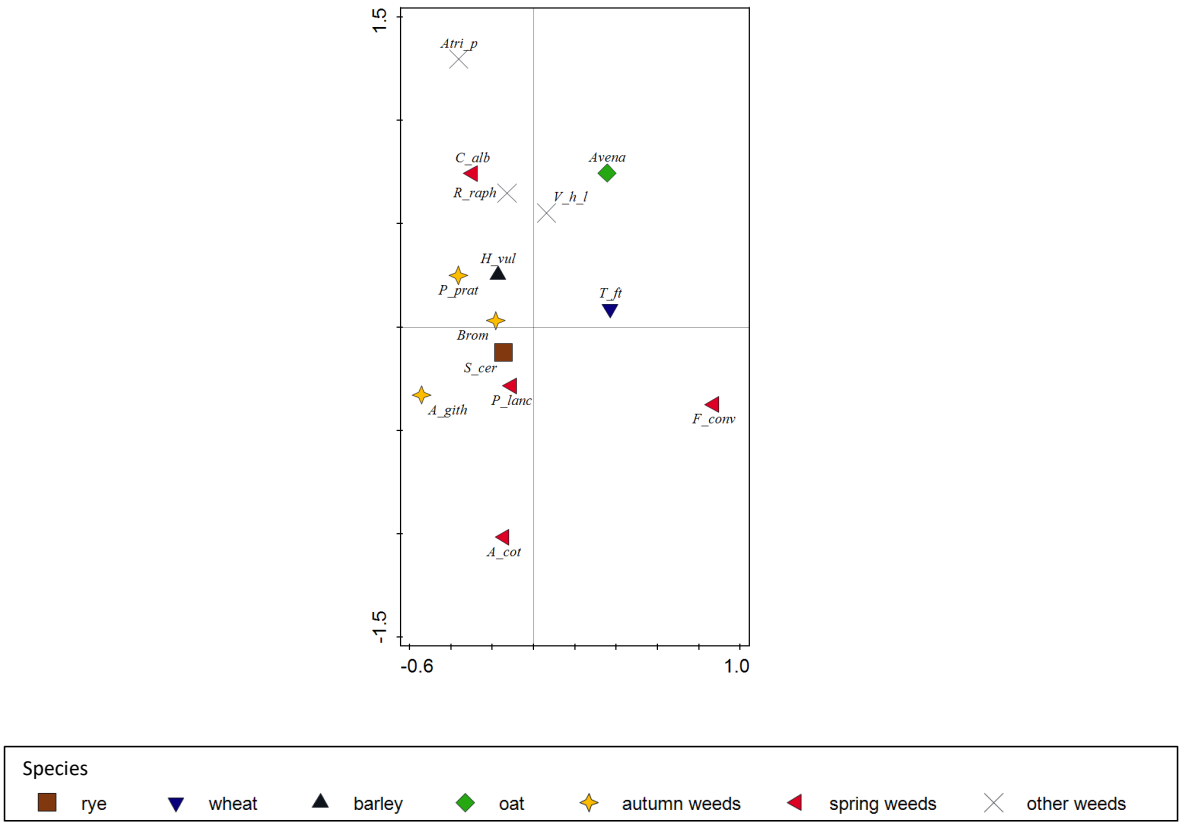


Figure 7.14 'Seasonality' correspondence analysis with square root transformation applied to the data, showing four cereal taxa and 11 weed species distributed according to associations in 54 samples from the Sedgeford malting complex. Weed species are coded according to seasonality class. Sample plot is not shown.

7.5 Combining perspectives on crop husbandry at Sedgeford

In this section complementary perspectives from the three analyses here employed (stable isotope analysis, FWE and seasonality-focused correspondence analysis) are combined to give a more complete 'picture' of crop cultivation methods. To so do, it is helpful to revisit (adapting as needed) the final two questions relating to stable isotope analysis, outlined in **section 5.6.3** (see **section 7.2.4** in this chapter).

Question 6:

Does stable isotope analysis evidence support that from FWE and other archaeobotanical assessments of the malting complex assemblage?

The results of stable isotope analysis, presented in **section 7.2**, are broadly compatible with those from FWE (**section 7.3**). δ^{15}N values suggest that crops from the malting complex derive from low-moderate manuring regimes, though low soil moisture levels in the region's free-draining soils may further contribute to the grains' low δ^{15}N values (with moist soils conversely associated with high δ^{15}N values) (Hamerow et al., in prep.). This is consistent with the results of the 'intensity' FWE discriminant analysis, which indicates that arable land supplying the malting complex was cultivated extensively, with low labour inputs including little manuring. The 'intensity' model assesses levels of both fertility and disturbance in the farming regime in question but is dominated in this case by functional traits relating to soil fertility. The 'disturbance' model presented here isolates disturbance as a separate variable and suggests high levels of disturbance. Intensive mouldboard ploughing of the soil around Sedgeford (bringing nutrients for plant growth to the surface) may have been a strategy used by local farmers in partial compensation for the soil's low fertility.

Question 7:

Do results from stable isotope analysis indicate, or are they consistent with, particular crop husbandry regimes?

This is here adapted:

Do results from crop husbandry analyses indicate, or are they consistent with, particular crop husbandry regimes?

Hamerow *et al.* (in prep.) have outlined a set of criteria, discernible through various analyses, for distinguishing between samples wherein crops were cultivated separately, together as a mixed crop (such as a maslin), or in rotation, respectively (with differing criteria specified for two and three-course rotation systems). A table summarising these criteria as related to the analyses presented in this chapter is reproduced below (**Table 7.8**).

Table 7.8 Criteria for discerning whether remains of different crops in archaeobotanical samples were cultivated as a mixed crop, in rotation or separately, after (Hamerow et al. in prep.)

Category	Mixed crop	2-course rotation	3-course rotation	Separate cultivation
Crop carbon and nitrogen stable isotope values	Compatible	Compatible	Compatible	Incompatible
Disturbance levels	Unclear	High	High	Unclear
Crop sowing times	Compatible	Compatible or contrasting	Contrasting	Compatible or contrasting

Each category listed in **Table 7.8** (relating to a particular set of analyses) is here addressed in turn. Firstly, results reveal that crops malted at Sedgeford have compatible carbon and nitrogen stable isotope values (with similar mean values for carbon, and, separately, for nitrogen, both within and across all features) (**section 7.2**); this is consistent with mixed cropping, two-course or three-course crop rotation, but not with separate cultivation. Secondly, disturbance levels for Sedgeford's crops are high (**section 7.3.2**); again, this is consistent with mixed cropping, two- or three-course rotation (but not separate cultivation). Finally, evidence for crop sowing times is somewhat ambiguous; seasonality evidence presented here could be viably interpreted as either 'compatible' (crops sown in the

same season) or 'contrasting' (crops sown in different seasons) (**section 7.4**); this is consistent with each of the agricultural regimes specified in **Table 7.8**. In other words, a preliminary assessment of the results of crop husbandry analyses presented here suggests that the Sedgeford material is consistent with a predominant farming regime either of cultivation as a mixed crop or with two- or three-course crop rotation, but not with separate cultivation of crops, in the fields that supplied the malting complex. These trends are explored more fully in **Chapter 8** (**section 8.3.2**). Further, as has been suggested in **sections 7.2.2** and **7.2.4** δ^{15}N values for samples analysed show variability consistent with grains originating from more than one set of agricultural conditions; implications thereof for Sedgeford's place in the local socio-economic context are also explored in **Chapter 8** (**section 8.6**).

7.6 Summary

Chapters 6 and **7** have together presented the findings of a comprehensive examination and analysis of the archaeobotanical assemblage from Sedgeford's Mid Saxon malting complex, culminating (this chapter) in sets of analyses aimed at revealing methods used to cultivate crops malted at Sedgeford. The next chapter turns to marshalling these understandings – together with those gleaned from chapters 1-4 – (reviews of Anglo-Saxon society, key concepts in beer making, the history of beer production and consumption, and the story of discoveries at Sedgeford to date) – with the aim of responding to the research questions presented in **Chapter 1.**

8 DISCUSSION AND SYNTHESIS

Understandings of malting, brewing and beer at Mid Saxon Sedgeford and beyond, developed in each of the foregoing chapters, are here synthesised and deployed to address each of the following research questions, first presented in **section 1.3**:

1. ***What is the nature of the archaeobotanical assemblage at Sedgeford?***
2. ***What evidence is there for malting and brewing at Sedgeford and beyond?***
3. ***How were the cereal plants from which beer was malted and brewed at Sedgeford and beyond likely cultivated?***
4. ***What can be discerned about how beer was malted and brewed at Sedgeford and beyond?***
5. ***How may the beer malted and brewed at Sedgeford and beyond have been consumed?***
6. ***What was the role of Mid Saxon Sedgeford and its malt in the wider socio-economic context?***

8.1 What is the nature of the archaeobotanical assemblage at Sedgeford?

8.1.1 Density and distribution of preserved plant material

Sedgeford's malting complex assemblage is entirely preserved by charring and is exceptionally rich (**section 6.3**). Three samples, containing more than 1000 plant items per litre (one having >1,800 items), compare with the densest samples encountered in

McKerracher's comprehensive review of Early and Mid Saxon assemblages in East Anglia and the Thames Valley (2018, 90–92). In the Anglo-Saxon period entire[80] the first 'high density' sets of charred plant remains[81] are dated to the 8th and 9th centuries (ibid.). Rich assemblages such as Sedgeford's are, arguably, amongst several archaeologically detectable signs of increased agricultural productivity in the Mid Saxon era (**section 1.4.2**).

It is worth considering how plant material from the malting complex came to be charred. Plant remains are (in the area excavated to date) concentrated around the three securely identified malting kilns (**Figure 6.14**, see also **Table 2.1**). Corn-dryers required 'scrupulous' raking and cleaning after each firing, to reduce the risk of accidental conflagration (Kelly, 1997, 242; Fosberry and Moan, 2018, 25). It is thus proposed that, when accidental fire occurs, very little *in situ* plant material will remain in a corn-dryer, other than from its final firing (however, 'rakings' – including fuel – charred from previous firings, may be deposited nearby) (Monk and Kelleher, 2005, 107; Rickett, 2021, 18–19). Final firing deposits may well not be representative of a kiln's lifetime use (van der Veen, 1989, 306).

The scale and distribution of charred plant material across the malting complex, combined with archaeological evidence for *in situ* burning (**section 4.3**), attest to at least one such large-scale conflagration's occurrence here. Only such an event, causing the kilns' drying floors to collapse (likely, in at least one kiln, during firing), could account for such dense deposits of charred material (Rickett, 2021, 18–19). Excavators have used distributions of (often wattle-marked) daub to understand the way in which each kiln's wattle and daub superstructure collapsed. For instance, fragmentary daub at the north end of kiln 2 likely

[80] Exceptions to this trend are a select number of 5th and 6th century sites where Romano-British cultivation methods seem to have persisted (McKerracher, 2018, 90–92).
[81] 'High density' is here defined as having more than 30 plant items per litre (McKerracher 2018, 89, 92).

indicates fire-caused collapse of the stoking arch; the drying floor probably also collapsed such that its contents spilled to the north (towards the 'undefined feature'), potentially accounting for cereal spectra resemblances between samples immediately north of this kiln and to the east of kiln 3 (episodes 3 and 12 in **Figure 6.16**; 12 being part of the 'undefined feature') (Blakelock and Caroe, in prep.).

An alternative explanation for trends in the gridded area samples is suggested by the strikingly similar profiles for both crops and weeds (**Figure 6.13** and **Figure 6.19**) between kiln 3 and the 'undefined feature' (**Figure 5.1**). Samples nominally from the 'undefined feature' area were extracted from a layer above the feature; these trends suggest that material being kilned on the kiln 3 drying floor may have spilled onto this layer to the east, during a conflagration.

Dense concentrations of grains being processed in the set of malting kilns at their time of burning are the likely source for almost all charred grains in the malting complex, with a combination of human and natural processes accounting for redistribution of some grains around the trench, after the kilns had burnt down, creating secondary (re-located) deposits including the sparser samples in the eastern and western ditches (see Charles et al., 2015, 2). Since much grain in the kilns (which were used at the last stage of the malting process) would likely have germinated, this is evidenced by the broad distribution of germinated grains and detached sprouts across the trench (**Figure 6.24** and **6.5**; as discussed in **section 8.2**). The hypothesised germination floors were largely barren of charred remains; any part-germinated grains here burnt in an accidental fire would have been easily 'swept away' by maltsters or precipitation run-off – a possible additional, lesser source of germinated grains across the trench.

Radiocarbon dating implies kilns 1 and 2 are a generation older than kiln 3 (**section 4.5**). Both dating and archaeological evidence (**Chapter 4**) suggest that, as in the complex of corn dryers at Hoddom (**section 1.4.5**), there was at Sedgeford an iterated sequence of destruction by fire and re-building (Holden, 2006a, 154; Faulkner, 2022, 173). One or more kilns burned down, in a large-scale complex-wide fire, and their charred contents partly deposited *in situ* and part-redistributed over time; new, later kilns were built (likely in a slightly different location) and these ultimately consumed by fire, and so on. In other words, the assemblage likely represents a palimpsest, resulting from repeated charring and deposition events over the complex's lifetime.

A final potential source of charred material is deliberate burning (then likely 'dumping' as refuse by maltsters) of contaminated crops – possibly including those with a high proportion of noxious corncockle (*Agrostemma githago*) seeds in the malting complex. Murphy (1985a, 102). suggests as much for a corncockle-rich sample from Saxon West Stow in the Suffolk Breckland. Weed seeds in the assemblage are further discussed in **section 8.1.4**.

8.1.2 Cereals

Cereal grains from all samples at Sedgeford are mostly unfragmented (whole). Where fragmentation has occurred, the exposed interior surface is generally rough, indicating breakage *after* charring. In other words, these grains likely represent 'whole grain malt' (as also found in later medieval deposits at Alms Lane, Norwich, and Redcastle Furze, near Thetford) (Murphy, 1985b; Murphy, 1995, 134). In contrast, 11th century samples from the Ipswich Buttermarket comprising abundant sprouts and mostly fragmented grains (whose broken

surfaces are predominantly convex or rounded, indicating breakage *before* charring) are hypothesised to represent malted grains following milling to 'grist' (Murphy, 1991, 7).

Grains in the malting complex assemblage are 65% rye, 27% free-threshing wheat, 7% hulled barley (likely the six-rowed variety) and trace amounts of oat – probably a weedy contaminant (**Figure 6.7**).[82] Each is a free-threshing cereal: typical for Mid Saxon assemblages (Stevens, 2011, 98).

The abundance of rye in the malting complex merits discussion. It has been noted in **section 1.4.4** that, although rye cultivation increased over time in Anglo-Saxon England, it never rivalled the cereal's position in northern continental Europe, as chief bread crop. However, there are, for example in samples from Brandon and Lackford Bridge Quarry (**Figure 8.1**), indications of geographic foci for rye cultivation in the Breckland (on the Norfolk/Suffolk border) – similarly on the Suffolk coast – in the 7th to 9th centuries: both regions of well-draining (dry) and sandy soils, to which rye is well adapted (Monk, 1977, 292; Murphy, 1985a, 103–104; Ballantyne, 2010, 315; Murphy and Fryer, 2014, 325; Rippon et al., 2015, 172; McKerracher, 2018, 105).[83]

In addition to macro-fossil (grain) evidence, consulting the palynological (pollen) record can helpfully inform this 'picture' of spatial trends in rye cultivation in the era. As the sole wind-pollinated cereal plant (**section 1.4.4**) (wind-pollinated taxa generally producing more pollen, which then is released and disperses more readily), if, as claimed, rye was locally commonly cultivated, rye pollen should be present in palynological cores in the region

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[82] Markham suggests (as described in **section 3.2.2**) that wild oats, if found with the harvested grain, should be tolerated (*TEH,* VII, 4).

[83] Based on archaeobotanical assemblages, Smith *et al* suggest rye, though always a 'minor crop' was disproportionately common (present at ~20-30% of sites) in the Breckland (and, interestingly, the East Anglian fens) in the Romano-British era (2016, 400).

(Vuorela, 1973, 12; Broström et al., 2008, 474; Forster and Charles, 2022, 79). Further, where rye pollen is present, this is (by comparison with pollen from other cereal taxa) morphologically distinct and thus usually clearly identifiable (Forster and Charles, 2022, 69).[84] Pollen preserves well in acidic, waterlogged conditions. As noted (**section 4.2**), Sedgeford and locality are characterised by dry, sandy soils and (alkaline) chalk bedrock: inimical to pollen preservation.[85] Forster and Charles have conducted a comprehensive review of all pollen records in England which are well-dated to any period within the 4th to 15th centuries, and in which a minimum of 300 (land) pollen grains have been counted (ibid., 67), noting the presence/absence of crops and other key species. Of the 49 sites identified as eligible, five are in East Anglia. These are between ~37 and ~50 miles from Sedgeford (and cannot be taken to indicate pollen frequencies in Sedgeford's immediate vicinity). A total of 12 sites (dispersed widely across the country), out of 49, evidence rye pollen grains dated to the 7th to 9th centuries; of these, two – Redmere and Brandon - are in East Anglia, specifically in the Breckland area (Wiltshire, 1990, 16; Waller, 1994, 126–133; Charles and Forster, in prep.). These trends imply broader rye cultivation across England than is suggested by the archaeobotanical evidence. I aver that pollen records' indicating unexpectedly broad rye cultivation across the country should be interpreted with some caution, owing (as noted) to the disproportionate abundance of rye pollen relative to that of other cereal taxa. However, the results of this meta-analysis are certainly not inconsistent with 7th to 9th century rye cultivation in the Breckland.

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[84] It should be noted that, for some among the 49 sets of pollen cores included in this review, rye pollen may have been grouped within the broader category 'cereals' (Forster and Charles, 2022, 69 fn. 3)

[85] Pollen cores extracted from the bed of the 'Reedam', a marshy area adjoining the river Heacham at Sedgeford, were found not to contain sufficient well-preserved pollen to make analysis worthwhile (Forster, *pers. comm.).*

Rye's abundance at Sedgeford seemingly evidences the localised cultivation practices in Breckland and the Suffolk coast extending to the valleys of northwest Norfolk – also characterised by free-draining, sandy soils (McKerracher and Caroe, in prep.). However, the lack of rich, well-dated pollen records from Sedgeford's immediate locality mean the possibility that rye was being transported to the site from, perhaps, the Breckland, cannot be ruled out. However, there is no convincing evidence to counter the proposition that rye was indeed cultivated in the fields surrounding Sedgeford. Agrarian adaptation to local conditions has been viewed as intrinsic to a trend of farmers becoming increasingly 'rooted' in the land – invested in their immediate environment – through the 7th to 9th centuries (McKerracher, 2018, 118, 120). Finally, it is notable that the settlement area samples contain a significantly lower proportion of rye (18%) than those from the malting complex (65%) (**Figure 6.7** and **6.8**). This may intimate that rye was particularly favoured for beer-making at Sedgeford.

Barley, like rye, tolerates adverse ecological settings – in barley's case, including wet and saline conditions such as prevail in the fens: proportionately abundant barley in 7th to 9th century samples at Ingleborough and Walpole St Andrew attests to fen farmers adapting crop choices to the local environment (**Figure 8.1**) (Hamerow et al., in prep.). Barley at Sedgeford may represent cultural-continuity with neighbouring fen-land cultivation practices, or, perhaps, be imported from that distinctive region.

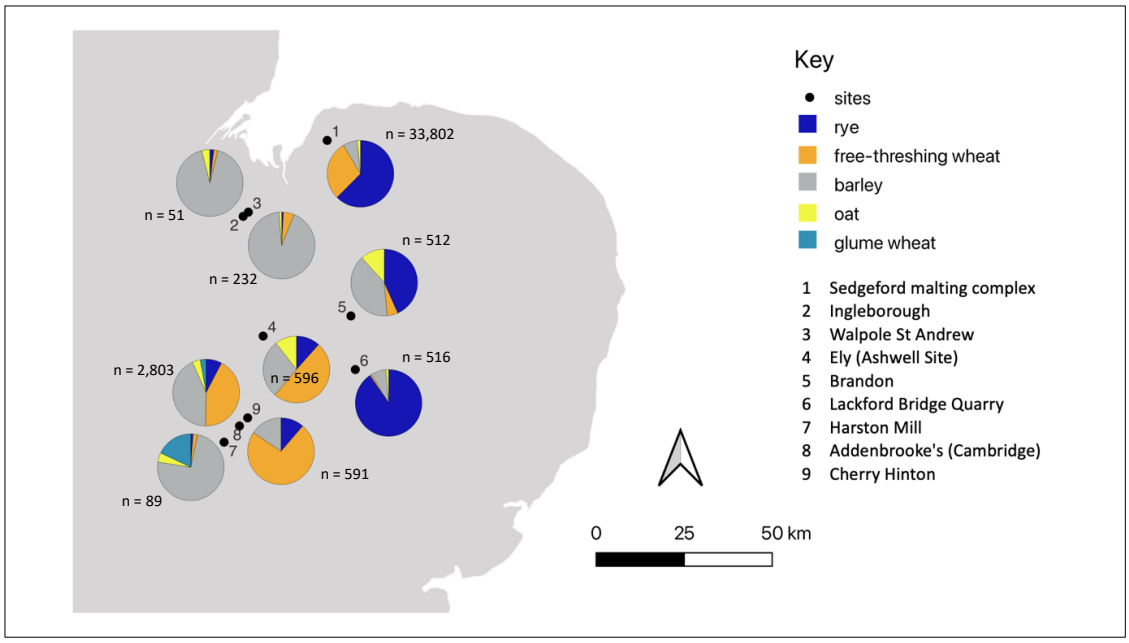

Figure 8.1 Cereal taxon proportions at sites in East Anglia dated to the 7th to 9th centuries, having dense samples (at least 30 charred items per litre). Assemblage size (number of grains; n=) is specified.[86]

Unusually for the era, analysis of the Sedgeford settlement assemblage revealed 10 grains tentatively identified as spelt – a glume wheat (McKerracher and Caroe, in prep.). Significantly, McKerracher suggests spelt, being more resistant to spoilage, was favoured by landlords for 'trade and tribute' and that its occurrence at the royal and monastic site of Lyminge, Kent; Bishopstone, East Sussex, an estate centre; and other 'high status' Mid Saxon sites justify spelt's being designated part of an 'elite site signature' (McKerracher, 2018, 122–123). Though very slight evidence, these ten spelt grains are consistent with Sedgeford's also being an elite site (McKerracher and Caroe, in prep.) (**section 8.6.2**).

[86] References for archaeobotanical data are (Mortimer, 2003; Ballantyne, 2005, 101–102, 153; Murphy, 2005, 247–249; Roberts, 2008, 111, 118–120; Murphy and Fryer, 2014, 325–327; Scaife, 2016, 192). 'Assemblage size' excludes indeterminate grains.

8.1.3 Chaff

It has been noted that the malting complex samples are grain-rich, chaff-poor, with varying proportions of weed seeds (these being generally of intermediate frequency and dominated by BFH 'type', see G. Jones), i.e., predominantly 'product' samples (**section 6.3** and **section 6.6.2**). Minimal chaff across the trench is consistent with, but does not necessarily imply, extra-site crop processing (Moffett, 1991, 8–9). Chaff and grains preserve differentially: with chaff rarely surviving fire (Boardman and G. Jones, 1990; Moffett, 1991, 8–9; Moffett, 1994a, 57; Hamerow, 2012, 155). 'Product' samples are common at archaeological sites. Of 81 Welsh corn-dryers having archaeobotanical remains, Comeau and Burrow identified clean or 'semi-clean' crops at 37, while virtually all samples in McKerracher's review of assemblages from Mid Saxon Upper Thames Valley and East Anglian sites are grain-rich 'product' samples. (McKerracher, 2018, 85; Comeau and Burrow, 2021, 114). Site-type (e.g., 'producer' or 'consumer') cannot be extrapolated from chaff abundance alone (Moffett, 1991, 8–9).[87]

8.1.4 Weeds

Five weed taxa abundant in the malting complex assemblage and pertinent to the emerging 'picture' of human-environment interaction at Sedgeford are considered here: *Bromus* (brome grasses, classified according to G. Jones' types as BFH), *Agrostemma githago* (corncockle, BFH), *Fallopia convolvulus* (black bindweed, BFH), *Anthemis cotula* (stinking

[87] Moffett (1991, 8–9) suggests that farms where crops are cultivated may have minimal chaff, whilst obvious 'consumer' sites (including urban areas) may import chaff for animal bedding, fodder, tempering and myriad other purposes.

chamomile, BHH) and *Raphanus raphanistrum* (wild radish, BHH) (**Table 5.4, Table 6.3** and **Figure 6.18**). Possible use of 'weeds' at Sedgeford as additives for beer making are explored in **section 8.4.6**.

Bromus seeds are near-ubiquitous in the malting complex samples. As 'BFH' type seeds, these can be removed only through hand-sorting. Hornsey hypothesises for Iron Age Danebury that *Bromus* seeds, with a high protein content, were tolerated or even 'encouraged' to grow alongside cereal crops, (and not extracted during crop processing) to 'bulk up' the harvest (Hornsey, 2003, 216). M. Jones notes that *Bromus* dominates some Iron Age charred assemblages (1981, 108), and cites Hubbard's argument that, in the Iron Age, *Bromus* may at times have been a crop in its own right (1975, in Jones, M., 1981, 108). It is feasible that Sedgeford's Mid Saxon maltsters, echoing the Danebury farmers, tolerated or even welcomed *Bromus* seeds as an addition to the harvested crops.

Fallopia convolvulus seeds are disproportionately abundant around kiln 1 (**Figure 6.19** and **6.21**). A common arable weed, which flowers late in the year (and hence is at a competitive advantage among spring-sown crops), this seed associates closely with wheat, which may be spring-sown (**sections 5.7** and **7.4**). Wheat grains are also disproportionately common around kiln 1. Hillman avers that abundant *Fallopia convolvulus* seeds implies potential 'up-rooting' of entire cereal plants, around which this plant twines, at harvest – however, it is difficult to see how it would be possible, using any large-scale harvesting method, to avoid harvesting black bindweed seeds in a field infested with this weed (Hillman, 1981, 149).

Kiln 1 has a distinctive archaeobotanical 'signature' and sample weed and crop spectra highly consistent with one another (**Figures 6.9** and **6.18**). However, kiln 1 samples are not distinct from other samples according to stable isotope analysis nor FWE. Wheat samples

from kiln 1 have the lowest variability in $\delta^{13}C$ values of any cereal taxon in any of the features studied (**section 7.2.1**). The most parsimonious explanation for these trends may be that plant material from kiln 1 represents a single, or small number of, wheat- and black bindweed-rich, well-cleaned 'batches' of crop from within the same farming regime as crops from the remaining kilns. The archaeobotanical distinctiveness of kiln 1 might be a result of (climate-, pest- or disease-induced) vagaries in the harvest, or maltsters adapting to changing preferences by 'experimenting' with malt 'recipes' (Blakelock and Caroe, in prep.).

Agrostemma githago (corncockle), in over 75% of malting complex samples, was also a common arable weed in Anglo-Saxon England, with flowers at the approximate height of cereal spikes – hence easily harvested with grains (Hall, 1981, 1–2). Corncockle grows best in autumn-sown fields and, Silverside asserts, is a common weedy contaminant of rye crops (1977, in Campbell and Robinson, 2010, 496), seemingly migrating across Europe with rye (Helbaek, 1966, 220; Krzywinski and Soltvedt, 1988, 47; Squatitri, 2019, 348). As a grain 'mimic', (BFH), corncockle is regularly resown with rye seed-corn, and arguably 'adapted' to rye cultivation (Krzywinski and Soltvedt, 1988, 47; Squatitri, 2019, 248). Correspondence analyses throughout this study testify to *Agrostemma githago* and rye being closely associated in malting complex samples (e.g., **Figures 6.37, 6.41, 7.13** and **7.14**).

Notably, corncockle (containing saponins, toxic to mammals) is poisonous if consumed, and the consumption of contaminated bread has even been recorded as causing fatalities (Hall, 1981; Hall and Kenward, 2015, 108). Modern maltsters reject crops contaminated with corncockle (Briggs, 1998, 252). Thomas Tusser, in his 1557 'Five hundred points of good husbandry', writes: '*For seed go and cast it; / for malting not so, /*

But get out the cockle, and then let it go', i.e., suggesting corncockle is the only weed seed that should be removed from harvested grains prior to malting (1557/1812, 46).[88]

However, G. Wilson found, in cesspits from medieval Chester, numerous *Agrostemma githago* seed fragments that had clearly passed through the human gut (1975, in Hall, 1981, 2). Additionally, Hall and Kenward (2015, 108) note that 19th century sources[89] present opposing views on whether boiling, baking or steaming *Agrostemma githago* seeds mitigates their toxicity – how fermenting would affect toxicity remains an open (and effectively un-testable) question. The possibility that corncockle-infested crop batches at the malting complex were burned and 'dumped' has been raised (**section 8.1.1**), yet relatively infrequent *Agrostemma githago* seeds in Trench 23 ditches does not support this (**Figure 6.22**). Might this (undoubtedly) noxious seed have had any perceived 'uses'? Corncockle is revisited in **section 8.4.6**.

As noted in **section 6.3.2**, *Anthemis cotula* has been widely recognised as an 'indicator' for heavy clay soils. However, a recent re-assessment suggests considerable caution is necessary in extrapolating soil type from *Anthemis cotula* in an assemblage – particularly where such surmises are founded solely on this species (Hamerow et al., in prep.).[90] Its relatively frequent occurrence at Sedgeford (in 16% of malting complex samples, and 28% of those from the settlement area) *may* signal cultivation of some crops here from areas beyond the local light soils (McKerracher and Caroe, in prep.). In contrast, *Raphanus raphanistrum* (wild

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[88] Further advice from commentator D. Hillman in this work (on crop processing) is, 'it may be worth the while to employ children in picking it fill, if it be but to take out the cockle' (Hillman, in Tusser, 1710, 122) – attesting to corncockle being a grain 'mimic'.

[89] Corncockle (now largely extinct in English fields) was here a common cornfield weed up to the mid-19th century (Hall and Kenward, 2015, 108).

[90] Kay notes that *Anthemis cotula* is 'also locally common on the heavier chalk soils' (Kay, 1971, 625), i.e., it does not grow exclusively on clay soils. Further, according to Adhikari et al. (2020, 316), *A. cotula* is an invasive, 'opportunistic' weed now growing on every continent– rather than a clay 'connoisseur' (Hamerow et al., in prep.). Further, the weed is the most commonly occurring species at sites across England in the medieval era studied by the FeedSax project– hardly a 'selective' indicator species (ibid.)

radish), in 18% of malting complex samples, is typical of sandy, acidic soils, comparable with those immediately surrounding Sedgeford (Murphy and Fryer, 2014, 328; McKerracher, 2018, 109). High frequencies of both taxa at Sedgeford are (with caveats) consistent with crops at the malting complex being sourced from more than one set of agricultural conditions.[91] Correspondence analyses presented in this study provide some evidence for separation between these two species in the malting complex assemblage – implying differing source areas (e.g., **Figures 6.39** and **7.13**).

8.2 What evidence is there for malting and brewing at Sedgeford and beyond?

First, the results of a review of sites in Britain dated to the Anglo-Saxon era with evidence for malting are presented in the **Descriptive Catalogue**. It is worth considering Comeau and Burrow's warning that, 'given the evident significance of ale in early medieval society and the fragility of the archaeobotanical evidence, [sites listed here are] almost certainly an under-representation of likely malting activity' (2021, 130).

Several sources of evidence cohere in suggesting that Sedgeford's Trench 23 represents a malting complex. Structural evidence at the site, as described in **section 4.3**, is entirely consistent with this being the area's main use – with structures corresponding to each stage of malting: a cistern (for steeping), several flat clay floors (germination floors) and a set of kiln features (malting kilns). Recovery of two iron hooks close to the cistern further

[91] In contrast, while *Anthemis cotula* seeds occur in over one quarter of the 'settlement area' samples, only a single *Raphanus raphanistrum* seed-head is found in this assemblage – see Appendix C II.

supports this having been a steeping tank inside which grains were suspended (**Figure 4.11**). No evidence for later stages of brewing has yet been recovered at Sedgeford: 'wooden tubs for cooling and fermenting' as recorded at monastery brewhouses at the Dissolution, for instance, and other assorted brewing equipment, would be unlikely to preserve, even if brewing did take place within the excavated area at the site (Rickett, 2021, 129). Alternatively, considering that malt, unlike un-hopped Anglo-Saxon beer, 'kept for any length of time' (ibid, 37), it is plausible that crop material intended for brewing was exported from Sedgeford as kiln-dried malt, and further processed elsewhere.

The thesis that Trench 23 represents a malting complex (although consistent with the structural evidence) emerged primarily from initial analysis of archaeobotanical remains (Wolff, 2017). Three sets of analyses have since been applied to charred grains from this part of the site to discern whether these show signs of germination: gross morphology-based assessment, GMM and SEM.

This study has developed novel methods for assessing levels of germination in a sample, based on external grain morphology as visible under a light microscope (**section 5.3.2**). This approach is effectual even for 'naked' grains, which dominate the assemblage at Sedgeford and in which germination has widely been considered very difficult to discern (**section 2.4**). According to these methods, nearly half (46%) of all assessed grains from Trench 23 are germinated (following proportional apportioning of indeterminate grains).[92] All but one sample (of 55) contain some germinated grains (**section 6.4**), and, on average, detached sprouts comprise ~4.0% of plant items per sample; these are also widely distributed

[92] Many of the grains classified as germinated show only slight evidence of germination, however 'slight' sprout growth is sufficient when germinating grains for malt (e.g. Stika, 2011a, 45; Crane and Murphy, 2019, 165).

across the trench. According to Lodwick (2017, 63), a broad distribution of evidence for malting (such as detached sprouts) in several samples across a site is suggestive of large-scale malting. In striking contrast, samples from the 'control' settlement assemblage show minimal evidence for germination.

Distribution of germinated grains and sprouts across the trench further supports its designation as a malting complex. For example, least evidence for germination occurs in samples from the steeping tank and nearby eastern ditch. This is attributable perhaps to as-yet unwetted (and hence ungerminated) grains being successively 'spilled' as crop material was suspended in the tank, and these then partly redeposited in the adjacent ditch (**Figure 6.26**).

The broad distribution of detached sprouts and germinated grains across the trench implies that each of the three main kilns was, at least some of the time, utilised for malting. Significantly, at least 11% of grains from each of the three main cereal taxa show clear evidence of germination, suggesting that each of these was malted (**Figure 6.25**). However, 19% of grains across the malting complex show no evidence for germination. Finding some ungerminated grains in hypothesised early medieval malting kilns at Uppåkra, Larsson *et al.* attribute these to the kilns' occasional use for corn-drying (2018, 1969). It is entirely plausible that Sedgeford's kilns also were sometimes used as 'standard' corn-dryers. If so, we cannot know whether these were purposely built to be multi-functional or used opportunistically for corn-drying between 'malt-firings' or in the summer malting 'off'-season (Hillman, 1982, 140; Rickett, 2021, 20).[93]

[93] Drying ungerminated grains in the kilns may even have been aimed at preparing 'adjuncts': ungerminated cereal grains deliberately added during mashing to reduce costs and/or contribute to the quality of beer finally produced e.g., by reducing haze in protein-rich beers (Bamforth, 2012, 12).

Evidence for germination in wheat grains from Trench 23, generated by T. Roushannafas using GMM, is wholly unprecedented (**section 6.7.1**) (Roushannafas, in prep).[94] Similarly, building on studies by Samuel, Heiss, Cordes and others (e.g., Samuel, 1996b; Heiss et al., 2020; Cordes et al., 2021), Y. Zhou, using malting complex grains, has found, for the first time, signs of germination in archaeological rye grains as discernible using SEM (**section 6.7.2**) (Zhou, unpublished).

As described in **section 2.4**, archaeobotanists have, in the past, variously specified 'threshold' proportions of grains displaying signs of germination in order for an assemblage to be reasonably judged to evidence malting e.g. van der Veen specifies more than 75% (1989, 305), though there is a lack of consensus on this question. The methods developed by the author and colleagues represent a novel, multi-stranded approach to discerning whether malting was taking place at a site, arguably more sophisticated than relying on achieving notional percentages. For, (though the proportion of Trench 23 grains showing clear evidence for sprouting falls significantly below, for instance, the van der Veen 75% threshold) surely these 'triangulated' results from archaeobotanical analysis, in addition to structural evidence from the trench, are, (even more so than at Roman-era Northfleet), nigh impossible to account for in terms of accidental 'wetting' of grains (Smith, 2011, 109). We can state with considerable confidence that Mid Saxon peoples at Sedgeford were deliberately germinating grains for malting.

[94] Krzywinski and Soltvedt (1988, 61), in a quantitative experimental study of charred germinated grains found these changed shape less during charring than ungerminated grains: length decreasing by 4% less, width increasing by 10% less and thickness increasing by 12% less. It has not yet been possible to discover if these results 'marry' up with Roushannafas' GMM results.

8.3 How were the cereals from which beer was malted and brewed at Sedgeford and beyond likely cultivated?

8.3.1 Intensity and disturbance

Chapter 1 has described the 'mouldboard plough package': a set of three fundamental changes traditionally theorised to be characteristic of early medieval agriculture – namely 'extensification', use of the mouldboard plough and crop rotation. As noted in **section 1.4.2**, across England and beyond, there was a marked tendency in the Mid Saxon era for farmers to 'extensify'. FWE indicates that crops from the Sedgeford malting complex were cultivated extensively (**section 7.3.1**). Evidence from isotopic analysis for low δ^{15}N values in malting complex grains – likely indicating these were grown with limited manuring (**section 7.2.2**) – is consonant with this understanding of farming at Sedgeford.[95]

Additionally, analyses indicate husbandry for crops malted in Trench 23 involved much mechanical disturbance (**section 7.3.2**). This, again, mirrors a trend to high levels of disturbance revealed at several Anglo-Saxon sites, including Stafford (West Midlands) and Lyminge (Kent) (Bogaard et al., 2022, 36). High disturbance is consistent with use of a heavy, animal-drawn mouldboard plough (Hamerow et al., 2020, 13; Bogaard et al., 2022). Faulkner (2022, 175) presents multiple sets of evidence for use of a mouldboard plough at Sedgeford, including numerous north-south plough marks on malting complex features beneath the plough-soil. As noted, (**section 8.1.4**), *Anthemis cotula*'s occurrence in the assemblage is consistent with heavy soils, which required tillage as then feasible only with a mouldboard

[95] We can conjecture that crops at the malting complex were manured with sheep/goat and pig waste – these being the most prevalent animals at the site in the Mid Saxon era (Davies, 2010a, 116).

plough. Indeed, by the 1086 Domesday survey, the settlement at Sedgeford is recorded is having five plough teams (ibid.).[96] In sum, evidence suggests the farming regime supplying the malting complex was an extensive system with relatively high levels of disturbance, the latter likely attributable to tilling with a mouldboard plough.

8.3.2 Cropping regime

Sedgeford's malting complex has (what might be termed) a 'diversified crop spectrum', with two major crops (rye and free-threshing wheat, together comprising ~92% of grains) and one minor (barley) all occurring near-ubiquitously in the samples analysed (Hamerow *et al.*, in prep.). Rye, wheat and barley may have been deliberately grown as a mixed crop, been subject to accidental or deliberate mixing or a combination of these (Banham and Faith, 2014, 36). 'Accidental mixing' might include post-depositional mixing; pre-harvest mixing through contamination of the seed-corn, or incursion of crop plants from neighbouring fields during cultivation; or mixing of grains during processing or storage (Diffey, 2018, 317; Hamerow et al., in prep.). The near ubiquity of all three crops in every sample is consistent with cultivation as a mixed crop; potentially a wheat-rye maslin, with some contamination by barley (see **section 8.4.1**).[97] However, the possibility that crops were cultivated singly (perhaps even in rotation) and then deliberately combined post-harvest for malting cannot be excluded.

[96] Faulkner (2022, 175) estimates one such team could plough between 60 and 120 acres per season. This is based on Banham and Faith's (2014, 54) estimation that a pair of oxen could daily plough an acre or so.
[97] Three crop mixed-crops are seemingly rare, but not unknown: Slicher van Bath (1963, 263) describes the French *terciel* or *bladum tercionarium* cultivated in the 'modern period' and comprising wheat, barley and oats.

Motivations for mixed cropping indubitably included sowing grains with differing ecological tolerances to increase security against harvest failure (e.g., Behre, 1992, 150; Banham and Faith, 2014, 36; McKerracher and Caroe, in prep.);[98] further, there is evidence for wheat/rye maslin being regarded as higher quality than pure rye (Slicher van Bath, 1963, 116). It is possible that Sedgeford-locality farmers were deliberately sowing some wheat with rye (whether at their own, or others' direction) to increase the perceived value of malt thereby created.

Table 8.1, building on an equivalent table in Hamerow *et al.* (in prep.), summarises expected features of an archaeobotanical assemblage, as discerned through various analyses, where crops recovered at a site were respectively cultivated as a mixed crop, as part of a two or three-course rotation, or separately. This is an expanded version of **Table 7.8**; **Table 8.1** also incorporates 'crop storage deposits' and 'crop processing by-products'. As discussed (**section 8.1**), crop deposits from the malting kiln features (arguably comparable to 'storage deposits') are consistently mixed, as are chaff and weeds ('crop processing by-products') across the trench. These trends coincide with those discussed in **section 7.5,** suggesting that crop carbon and nitrogen stable isotope values, disturbance levels (analysed using FWE) and crop sowing times (examined through correspondence analysis) as revealed for the malting complex are consistent with cultivation as a mixed crop (specifically, a maslin), or with two- or three-course crop rotation, but not with separate cultivation. However, an additional consideration: the clear associations in the assemblage of particular weed seeds with certain

[98] Behre (1992, 150) gives the example of rye and wheat being cultivated together to increase the likelihood of at least one good harvest, irrespective of that year's weather conditions, in Russia as late as the 20th century.

cereal taxa (black bindweed with wheat, and corncockle with rye) (**section 8.1.4**) would be consistent with crop rotation but does not support the 'maslin hypothesis'.

Evidence from isotopic analysis that crops at the site were grown in varied manuring conditions (**section 7.2.2**) is also, arguably, not inconsistent with crop rotation. Larsson tentatively attributes a similar trend at Uppåkra to the greater labour costs for farmers of transporting (heavy) manure to distant fields (Larsson et al., 2019, 13–15). Patterns of variability in δ^{15}N values imply grains were cultivated in heterogeneous conditions - either in several fields or, one can imagine, in a single field in successive seasons. A third possibility is that crops were cultivated in open fields with 'strips' (*selions*) differentially manured by different farmers (**section 1.4.2**). However, although these seem to have evolved slowly over several centuries, evidence for 'classic' open field farming systems generally considerably post-dates the Mid Saxon era, and such systems are concentrated in England's 'Central Province'; open field farming, in its 'classic' form, is thus an unlikely explanation for the isotopic trends observed at 7th-9th century, East Anglian, Sedgeford (Thirsk, 1964, 23; Oosthuizen, 2005, 166; Hall, 2014, 2–3; Rippon et al., 2014, 206–207; Williamson, 2018; Hamerow, 2022, 21; Williamson, 2022, 223).

Table 8.1 Expanded criteria for discerning whether remains of different crops in archaeobotanical samples were cultivated as a mixed crop, in rotation or separately, after (Hamerow, et al., in prep.)

Category	Mixed crop	2-course rotation	3-course rotation	Separate cultivation
Crop storage deposits	Mixed	Mixed or pure	Mixed or pure	Pure
Crop processing by-products	Mixed	Mixed or pure	Mixed or pure	Pure
Crop carbon and nitrogen stable isotope values	Compatible	Compatible	Compatible	Incompatible
Disturbance levels	Unclear	High	High	Unclear
Crop sowing times	Compatible	Compatible or contrasting	Contrasting	Compatible or contrasting

If crop rotation (though likely not part of an 'open field' system) were taking place at Mid Saxon Sedgeford, this would be remarkably early (**section 1.4.2**), though perhaps not unprecedented. There is, according to Hamerow *et al.* (in prep.), some hint of patterning in crop sowing times (an indicator for crop rotation, **section 7.4**) in correspondence analyses for the assemblage from West Fen Road, Ely (Cambs), dated to *c.* 720-1220, whilst isotopic results from Mildenhall (Suffolk) and Holmer (Worcs.), both dated *c.* 770-880 are not inconsistent with rotation.[99] It is noteworthy that some records from (later) documentary sources suggest that mixed crops (including maslins) were at times grown in rotation – for instance at Wisbech in the 14th and 15th centuries (Stone, 2005, 89–90).

As noted in **section 8.1.1**, dating evidence suggests kilns 1 and 2 are a generation older than kiln 3. However, kilns 2 and 3 have very similar crop 'spectra' (**section 6.3.1**), and

[99] However, the same set of research reveals that, at Mildenhall at least, there is limited evidence for seasonality in this era (Hamerow et al., in prep.)

analyses provide no (or minimal) evidence for differences in manuring (stable isotope analysis, **section 7.2.4**) or in intensity of cultivation or level of disturbance (FWE, **section 7.3**) between the respective kilns. This implies consistency in husbandry practices for crops provisioning the malting complex over its period of use.

8.3.3 Cultivation specifically for brewing?

As observed in **Chapter 3**, ale and beer were, in every way, deeply important to people of Anglo-Saxon England. Was this reflected in crop cultivation practices at Sedgeford? Preferential manuring of crops intended for brewing is potentially evidenced at a set of (geographically and chronologically distinct) sites where isotopic analysis has been conducted on charred grains. Styring *et al.* (2017, 373) find consistent preferential manuring of hulled barley at early Iron Age sites in southwest Germany, and attribute this to barley's being cultivated for beer-making. Similar claims are made for Early Bronze Age Archondiko in northern Greece; I suggest evidence for distinctively high δ^{15}N values in hulled barley at medieval Stafford (Staffs.) may be potentially tentatively similarly attributed (Nitsch et al., 2017, 122–123; Valamoti, 2018, 621–622; Hamerow et al., 2020, 603–604).[100]

As described in **section 7.2.4**, isotopic analysis reveals no equivalent evidence for preferential manuring of one crop from the Sedgeford malting complex over others. However, since there is significant evidence for germination in all three main crops (**section 8.2**), it is arguably not possible to know which crop(s) (if not all) were 'intended for brewing'. An isotopic comparison with grain samples from the settlement area would be instructive.

[100] High δ^{15}N values for hulled barley compared with rye, oat and free-threshing wheat at Stafford may alternatively simply reflect barley cultivation in soils more enriched in δ^{15}N (Hamerow et al., 2020, 603–604).

8.3.4 Sedgeford's place in the Mid Saxon agricultural 'revolution'?

As discussed in **section 1.4.2,** the idea of a Mid Saxon 'agricultural revolution' is controversial – archaeologists and historians have arguably long been too ready to identify 'revolutionary' change within their own period of interest (Williamson, 2022, 212–214). Recent research by Oxford's FeedSax group suggests no single period in medieval England saw truly 'revolutionary' transformation in agriculture: rather, there were gradual trends of cerealisation with some episodes of more notable change, for instance the 7th to 9th centuries (Hamerow, 2022) (**section 1.4.2**). Not until the 10th to 11th centuries is there persuasive evidence for widespread systematic crop rotation and mouldboard plough use, although these are earlier evidenced at some sites, from the 8th century onwards (ibid.).

The FeedSax group's three-fold so-called 'mouldboard plough package' has been identified as typifying changes (that *did* take place) in medieval agriculture (McKerracher and Hamerow, 2022). There is at least tentative evidence in the malting complex assemblage for each element of this 'package' being in place in the fields supplying Mid Saxon Sedgeford: the use of a mouldboard plough, extensification, and (conceivably) crop rotation.

Further, the very presence of a multi-kiln malting complex at Sedgeford is part of the emerging picture of renewed construction of specialised grain processing (e.g., watermills, corn-dryers and malting kilns) and storage features in Mid Saxon England (for the first time since the Romano-British era) from the 7th century (**section 1.4.2**) (Hamerow, 2012, 151–152). The recent FeedSax publication, despite questioning ideas of agricultural 'revolution', is unafraid to claim that documentary, archaeological (structural) and archaeobotanical evidence cohere in indicating an ongoing growth in capacity to store, process and consume crops from

the 7th until the 13th centuries (McKerracher, 2022c, 137). As noted in **section 8.1.1** the sheer richness of charred remains in the malting complex assemblage is consistent with a trend to sites rich with preserved plant material appearing also from the 7th century. These linked trends each indicate increased arable production in the period.

The malting complex assemblage moreover exhibits diversification in crop spectrum (**section 8.1.2**); diversification goes 'hand-in-hand' with growth in arable surpluses through careful matching of crop choices to local environmental conditions (McKerracher, 2018, 120). In sum, we can conclude that, if an 'agricultural revolution' can in any way be claimed to have taken place (with characteristics as described in **Chapter 1**) from the 7th century, Mid Saxon Sedgeford was very much a part of it.

Significantly, according to Crabtree, the advent of agricultural development in East Anglia predates the earliest evidence for Ipswich Ware and, we can extrapolate, for the *emporium* at Ipswich. She suggests it coincides, rather, with 'political consolidation of the Anglo-Saxon kingdoms around 600 AC.E.' (2014, 107).

8.4 What can be discerned about how beer was malted and brewed at Sedgeford and beyond?

8.4.1 Crop choice for brewing

As noted in **section 8.2**, there is evidence that all three major cereals in the assemblage (the commonest being rye, then wheat) were used for malting. This is arguably surprising, since brewing with both rye and wheat presents significant challenges.

In the modern era, sahti beer from Finland, kvass from northeastern Europe, and Bavarian roggenbiers are generally made with (at least) a proportion of rye grains, however, rye remains today widely considered difficult to brew with (certainly as the main cereal grain) (e.g., Kølster, 2011, 706; Wang et al., 2018, 50). Rye grains contain a high proportion of arabinoxylans, causing high wort viscosity and the so-called 'stuck mash' known to brewers, which impedes lautering (**section 2.3.1**, and **2.3.3**) (Hübner et al., 2010, 72). Further, being naked (i.e., hull-less) (**section 2.4**), sprouts detach readily from both rye and wheat grains during germination; damaged or lost sprouts cause germination to stop (Briggs et al., 2004, 29). Finally, rye and wheat have a higher protein content than barley, which can affect beer flavour and appearance, arguably detrimentally (Kølster, 2011, 706; König, 2011, 835).

Brewing with rye and wheat grains is not without advantages: having a thinner aleurone layer, each grain type absorbs and loses water more quickly than barley, reducing time requirements for both steeping and kilning; each is also reported to have higher potential 'extract values' (a measure of efficiency for sugar release during mashing) (Briggs et al., 2004, 29–30; Kølster, 2011, 706; König, 2011, 838). The lower proportion of rye in Sedgeford's settlement assemblage (**section 6.3.1**) is consistent with deliberate selection of rye for malting at Sedgeford. It is conceivable that maltsters were choosing rye for these known advantages, or alternatively to meet 'demand' for the spicier flavours of rye-dominated beer. If so, we can question how they responded to the challenges of brewing with rye.

It is possible that the small proportion of barley grains occurring near-ubiquitously in malting complex samples represents maltsters' deliberate choice to include (high-starch, low-protein) hulled barley as a minor brewing 'ingredient' amongst otherwise rye- and wheat-

dominated malt, for its perceived benefits in terms of reducing total protein content and (thanks to its husks) assisting with forming a filter bed during lautering.

8.4.2 Crop processing for malting / steeping

Harvested crop material requires a degree of processing (to remove chaff, weed seeds and, at a later stage, sprouts) before it can be used to generate beer. A new model describing crop processing for malting, involving a stage during which floating material is skimmed from the surface of water in the steeping tank, has been developed in **section 5.4.3** and tested in **section 6.6**. Though crop processing in the malting complex according to this model cannot be ruled out, analyses presented in **section 6.6** are, rather, consistent with G. Jones' 'conventional' model best describing crop processing here. It is worth being reminded of Krzywinski and Soltvedt's (1988, 62) assertion that, where crop material is 'contained' during steeping, for example suspended in sacking, skimming of chaff and buoyant seeds from the water's surface will not be possible. As noted, two iron hooks (**Figure 4.11**) have been recovered close to the Sedgeford steeping tank, and excavators hypothesise these were used for suspending grain sacks in water. Testing the 'traditional malting model' against archaeobotanical data from other sites where malting is evidenced would be highly instructive; data constraints (small numbers of samples) render comparisons with the (roughly) contemporaneous British sites at Higham Ferrers and South Hook largely unmeaningful. However, I posit that the model may have application across broader regions and timeframes (**Chapter 9**).

Whether or not crop preparation in Sedgeford's malting complex involved skimming from the steeping tank, it is, as stated (**section 8.1.3**), conceivable that early stages of crop

processing (which would have been conducted according to the conventional model)[101] may have taken place beyond Trench 23. If so, crop material arriving at the malting complex would already be grain-rich and depleted in chaff and light (aerodynamic) weed seeds, and in this case, 'skimming' chaff and buoyant seeds would be unnecessary.

Faulkner (2022, 173) hypothesises, plausibly, that the (once likely wood lined) water-ditches, formed from a diverted stream, running to the east and west of the malting complex gully, were the source of water in the steeping tank. As noted, malting (predominantly) with naked grains would likely have reduced the time needed for crop material suspended in Sedgeford's steeping tank to achieve the required (~42-48%) moisture content, to ~32 hours; modern maltsters caution against over-steeping rye (**section 2.3.1**) (Wang et al., 2018, 52). Shorter steeping 'turnaround' times for each crop batch may account in part for identification (to date) of only one potential steeping tank in Trench 23; the single tank potentially 'serving' several malt-houses.[102]

8.4.3 Couching and germination

As described in **section 4.3**, at least three, and up to six, clay germination floors have been identified in Trench 23. The germination floor associated with kiln 1 was clearly within a built structure ('malthouse 1'). Each floor may similarly have been housed within a malthouse structure. **Section 3.2.3** describes the way in which steeped grain would have been couched onto the respective floor by Sedgeford's maltsters, and then regularly raked and turned, with

[101] Off-site processing, for example at a local landholding, could not have involved 'steeping' grains in water, as this would preclude control of the germination stage of malting.
[102] Faulkner (2022, 173) also notes that steeping tanks were often (unlike the 'sunken' cistern already identified in the malting complex) at the time built above ground, and hence any additional tanks at Sedgeford would likely not have been preserved.

pile height varied according to ambient temperature and humidity. As outlined in **Table 3.2**, Muspratt suggests, in English climate, grains be left to germinate for fourteen days; alternate sources suggest a significantly shorter germination period (five or six days) (Muspratt, 1860, 238; Stika, 1996, 86). Modern maltsters aim to maintain consistent conditions (ventilation, temperature etc.) to ensure evenness of germination (**section 2.3.1**). Variability in germination levels among grains recovered from the malting complex suggests, unsurprisingly, some difficulty for Sedgeford's Mid Saxon maltsters in so doing (see Krzywinski et al., 1983, 153; Murphy, 1985b, 7).

As suggested in **section 8.1.1**, the lack of charred organic remains in the clay layer corresponding to each germination floor implies these were swept clean either by maltsters or by precipitation run-off. The few samples recovered from postholes on the edge of 'floor 2' have a higher frequency of germinated grains (55%), than the associated kiln (35%), consistent with the floor's being a germination floor and the corresponding kiln being occasionally used for 'conventional' corn-drying (**Figure 6.26**).

8.4.4 Kilning

Section 4.3 suggests, according to the Comeau and Burrow corn-drying typology (2021, 113), (first outlined in **section 1.4.5**), that all three kilns excavated to date most closely resemble an 'oval/circular' type. Each kiln would have comprised a hearth/firing area (in the kiln 'pit'), stoking area and drying floor, with the drying floor likely positioned over the shallow extension and constructed from straw, or a 'hair cloth', lain over sticks (**section 3.2.3**) (ibid, 122, 125). Kilning would take approximately two days (**Table 3.2**) (though Sedgeford's rye-dominated grains may have required less drying time, as noted), with the hearth regularly

stoked to maintain a suitable temperature on the drying floor and monitored vigilantly to avoid accidental fire. After each firing, the hearth would have been thoroughly raked to remove spent fuel and burnt grain, again to reduce fire risk (**section 3.2.3**).

Fuel-use in the kilns would have depended on availability; Rickett suggests each of wood, charcoal, peat, turf and straw were fuels used in medieval corn-dryers (Rickett, 2021, 130). It has been noted in **section 3.2.3** that fuel choice for kilning was believed to affect beer flavouring, and that straw was favoured. Whilst chaff would have burned quickly and been insufficient to fuel an extended hearth fire, available chaff might nevertheless have been added to the fuel – a potential further reason for the dearth of chaff in malting complex samples (Moffett, 1997, 80). One sample from the Higham Ferrers malting kiln flue contained much silicified free-threshing wheat chaff. This could not have been the kiln's main source of fuel but, Moffett hypothesises (2007, 166), may represent readily-burning material used to start the hearth fire.

Charcoal recovered from the malting complex (**section 6.3.3**) may be the remains of wood or charcoal used as fuel. However, daub remains from the site show abundant 'wattle-marks'. Likely some of the charcoal recovered, particularly in 'daub-rich' samples, represents burnt remnants of the wattle and daub superstructure of the various kilns (SHARP team, *pers. comm.*).

Following kilning, the malted grains would have been rubbed or pounded then sieved to remove sprouts, i.e., 'de-culmed', as suggested in the novel 'crop processing for malting' model (**sections 3.2.3** and **5.4.3**). Root sheaths and sprouts thus detached ('deculming by-product', DBP) might also have been used as fuel. Whether used as fuel and burned in a kiln hearth or 'dumped' as residue and burned in an accidental conflagration, DBP would have

burned rapidly and thus, the detached sprouts identified in malting complex samples likely significantly under-represent original totals.

8.4.5 Later stages of brewing

No evidence for later stages of brewing has yet been recovered at Sedgeford (**section 8.2**); Sedgeford's malt being 'whole-grain' rather than milled (fragmented) grist has also been noted (**section 8.1.2**). However, proximity to a mill, necessary for 'cracking' malt prior to mashing, would have been expedient (Campbell, 1994, 69). Domesday records five watermills in Sedgeford parish.[103] We cannot know how long these mills pre-date the survey; however, large pieces of (gritstone) millstone have been recovered at the Mid Saxon site (J. Jolleys, *pers. comm.*). Associations between both corn-dryers and water-mills, and 'elite' royal and monastic sites in the era, including in contemporary documents, are noteworthy (Hamerow, 2012, 152–154; McKerracher, 2018, 121). However, malted grain from Sedgeford was likely, at least in part, milled domestically using quern-stones (basaltic lava quern stones have also been recovered at the site) (**section 3.2.3**) (Ogden, 2021).

8.4.6 'Weed' seed additives?

The use of wide-ranging potential flavourings and preservatives in Anglo-Saxon era beer-making is described in **section 3.2.4**. It is unlikely that beer brewed from Sedgeford's malt would have contained hops, and I here propose, rather, that Sedgeford's maltsters deliberately added, or, more likely, tolerated growing amongst crops, seeds of both *Fallopia convolvulus* (black bindweed) and *Agrostemma githago* (corn-cockle), for their favourable

[103] This information is available at https://opendomesday.org/place/TF7036/sedgeford/ [Accessed 5.1.23]

properties for beer-making, including flavouring, perhaps ritual significance and even additional psychotropic effects.

Fallopia convolvulus (black bindweed)

Fallopia convolvulus is in places traditionally known as 'wild hops' (Grigson, in Hornsey, 2003, 311; Bond and Davies, 2007, 1). Wolff notes that the related species (also from the family Polygonaceae) *Reynoutria japonica* Houtt. (Japanese knotweed) is increasingly used in place of *Humulus lupulus* (hops) in 'novelty' beers by modern brewing companies (Wolff, 2017, 4). Further, Campbell (1994, 69) found, at Mid-Late Saxon West Cotton in Northamptonshire, 17 *Fallopia convolvulus* seeds in a sample alongside grains which were about one-third germinated – which she interprets as malted – when samples from surrounding contexts without evidence for germination contained no more than a single seed of the species. I hypothesise that crops infested with *Fallopia convolvulus* were deliberately selected for harvesting, and ultimately dried in kiln 1, because of the seeds' favourable properties for brewing.

Agrostemma githago (corncockle)

Tusser's suggesting 'cockle' be the only seed removed from harvested grains prior to steeping has been noted (**section 8.1.4**). However, in his 1812 commentary on Tusser's text, William Mavor ('honorary member of the Board of Agriculture') adds here, 'Cockle, indeed, is supposed to render beer more heady, though certainly less wholesome' (in Tusser, 1812, 47). Similarly, in his 1710 commentary on Tusser's work, D. Hillman writes, 'if the cockle be left

in, it will work, and some say make the drink the stronger' (Tusser, 1557/1710, 161), and (of cockle) 'malt him he works with the barley' (ibid., 71).[104]

The abundance of *Agrostemma githago* seeds across the malting complex indicates that Sedgeford's maltsters were not adhering to Tusser's advice (certainly, this species' seeds were not being removed before steeping). Samples rich with corncockle may be the residue of batches of grains deliberately burnt as 'contaminated' (**section 8.1.1**). However, Verberg asserts that brewers have, 'over the centuries' sometimes used additives for 'desired psychotropic or adulterating effects' (2020, 9, 17), and it is conceivable that the broad distribution of *Agrostemma githago* across the trench (**Figure 6.22**) is attributable rather to Sedgeford's maltsters either adding or tolerating corncockle seeds amongst their malt with the aim of producing a highly potent,[105] psychotropic beer.

8.5 How may the beer malted and brewed at Sedgeford and beyond have been consumed?

8.5.1 Scale of consumption

'Oceanic' or, following Rickett, 'enormous' beer consumption in Anglo-Saxon England has been noted in **section 3.3.1** (Joyce, 1903, 114; Salzman, 1913, 185; Finberg, 1972, 422; Rickett, 2021, 36). Further, there is some tentative evidence from isotopic studies not only for much beer consumption throughout the Anglo-Saxon era, but for particularly

[104] Darnell (*Lolium temulentum* L.) is a further common crop weed, from the family Poaceae, which has traditionally been known as 'cockle'; it is somewhat poisonous. A.S. Wilson (1873) suggests Tusser in these passages is referring to darnell. However, A. Fitzherbert in his 1534 'boke of husbandry' (contemporary with Tusser) describes 'cockle' as follows: 'cockle hath…v or vi floures purple colloure as brode as a grote, and the sede is rounde and blacke': he is here clearly referring to *Agrostemma githago* (1540, 29–30).
[105] 'Highly potent' is not intended to imply that corncockle made the beer more alcoholic.

heavy drinking from the 7th century: based on oxygen stable isotope analysis of tooth enamel from burial populations, Leggett *et al.* identify a potential 'beer event horizon' from this era, with shifts in isotope values perhaps attributable to (so-called) 'brewing and stewing' (2021, 18; see also Brettell et al., 2012). Sedgeford's maltsters contributed to the English peoples' gargantuan thirst for beer: Faulkner (2022, 173–174) surmises, based on a series of estimates, that malthouse 1 alone could have annually produced enough malt to brew beer for between 2,500 and 5,000 people.[106]

8.5.2 Feasting and symbolic significance

Beer was deeply significant for all England's peoples (rich and poor, old and young) in the era in terms of volume of consumption, but also socially and symbolically. If nothing else, it is undeniable that, for Anglo-Saxon peoples, as for all communities, 'drinking [was]… a significant force in the construction of the social world' (Dietler, 2006, 235). Alcohol is, as van der Veen and many others have observed, a, 'positive stimulant to festive occasions, a facilitator of social interactions and a status differentiator' (Mandelbaum, 1965; van der Veen, 2003, 418; Dietler, 2011, 180–181).

The considerable social, political and symbolic significance of feasting for Anglo-Saxon life has been described in **section 3.3.2.** The appearance of malting kilns at elite sites in late Roman Britain has been attributed to demand for beer for feasting, and the desire of local elites for control over the means of production (Gerrard, 2013, 257). It seems reasonable to

[106] This assumes an annual eight month 'season' for the malthouse, the capacity (based on medieval crop yield research) to process yields from 45 acres, generating 28 tonnes of malt, used to brew ~1,500 barrels or 400,000 pints of strong ale, or up to 800,000 pints of weak 'small beer'. Annual consumption assumes levels comparable to modern Britain: ~150 pints per year.

similarly account for the renaissance in corn-dryer (and malting kiln) construction from the 7th century. For Wales and Ireland, the concentrated period of corn-dryer construction began somewhat earlier – from the 5th century (**section 1.4.5**) – and it is posited that these kilns are clustered at estate centres, often potential assembly sites: consistent with use of processed crops (for example, malt) for either bulk storage or consumption at gatherings (Gleeson, 2018; Comeau and Burrow, 2021, 133).

There is no evidence from isotopic analysis for preferential manuring of one cereal taxon from the malting complex assemblage over others (**section 8.3.3**). However, since all three cereal taxa seem to have been used for malting, the only way to discern whether farmers were preferentially manuring crops for beer-making would be isotopic comparison with grains from the settlement part of the site, which, it seems, were not intended for malting, as a 'control' (**section 8.3.3**). Styring *et al* (2017, 357), finding evidence for preferential manuring of barley grains in Early Iron Age Germany, argue that this reveals the political significance of beer and feasting being played out in crop cultivation methods. Conceivably, the results of isotopic comparison of grains from Sedgeford's malting complex and settlement might engender a similar conclusion.

8.5.3 Ritual significance

Taking an anthropological perspective (and here writing about feasting in an African context, but surely applicable across time and space – most certainly to Anglo-Saxon England), Dietler describes, 'this property of fermentation as a quasi-magical transformation of food into a substance that, in turn, transforms human consciousness augments the symbolic value of alcohol in…aspects of rituals' (Dietler, 2001, 73). The potential symbolic

significance of 'heady' corncockle-rich beer which may have been produced from Sedgeford's malt (**section 8.4.6**) can only be imagined: ritual significance here cannot be ruled out (E. Standley and T. Martin, *pers. comm.*).

8.5.4 Material culture

Anthropologists widely claim that all forms of food and drink are a kind of 'embodied material culture': one which is destroyed through ingestion, but in such a way that it becomes 'part' of the human body and thus crucial to conceptions of identity (e.g., Passariello, 1990, 53; Dietler, 2006, 229; van der Veen, 2008; Tierney and Ohnuki-Tierney, 2012, 117, 121). Dietler further argues that consumption of alcohol, because of its psychotropic nature and resultant significance in ritual contexts, is often associated with a more 'emotionally charged' set of practices and beliefs than other foodstuffs or beverages; and, that the constant need to replenish alcohol as it is consumed creates a particularly close and significant relationship between the producers of crops for brewing and those who consume the finished product – an arena for the exercise of political power (Douglas, 1987; Dietler, 1996; Dietler, 2001; Wilson, 2005; Dietler, 2006, 232).

8.5.5 The story of beer consumption

Finally, it is arguable that drinking beer in the era was not only of inestimable significance to the peoples of Mid Saxon England but is also crucial to the 'story' of food and drink in England. Modern patterns of consumption were established in the medieval era, including the use of modern staples such as free-threshing wheat-bread and hopped beer, and relationships between consumer 'urban' areas and their 'producing' rural hinterlands (van der

Veen et al., 2013, 151). In light of this, van der Veen laments the infrequent referencing of archaeobotanical insights in writing on the period (ibid.).

8.6 What was the role of Mid Saxon Sedgeford and its malt in the wider socio-economic context?

As described in **Chapter 1**, the Mid Saxon period is widely recognised as having been an era of significant transformation in the lives of the peoples of early medieval England, with the establishment of kingdoms, emergence of elites (both secular and ecclesiastical), transitions in settlement hierarchy and structure, and (though arguably not a 'revolution') shifts in agricultural practice (**section 1.4**) (White, 1940, 151; Scull, 1993; Hansen and Wickham, 2000; Ulmschneider, 2000; Yorke, 2002; Blair, 2005; Loveluck and Tys, 2006; Rippon, 2007, 121; Rippon, 2010, 64; Williamson, 2018; Hamerow et al., 2020, 585). Mid Saxon Sedgeford has been claimed to 'typify' some of these transitions – for example in the apparent re-organisation of the settlement in this period (Faulkner, 2022, 167–168). There is some evidence that the 'de novo' Mid Saxon settlement at Sedgeford was constructed according to a 'short perch' grid-plan, as described in Blair's seminal works on planning in the Anglo-Saxon landscape (2018; Blair et al., 2020, 286). Faulkner (2022, 167–168) argues powerfully for this). Amongst other theorised novel Mid Saxon water-management and landscape-reorganisation at Sedgeford, there is indication that the river Heacham was partly canalised at this time (**Figure 4.2**) (ibid., 170).

However, the most notable feature at the site, evidencing significant transition in the organisation of local society, is unquestionably the malting complex itself. This is, with at least three malting kilns and up to six germination floors, surely more so than the single malting

kiln at Higham Ferrers, much 'too elaborate and substantial a structure to have been part of someone's domestic brewing operation' (Hardy et al., 2007, 204; Faulkner and Blakelock, 2020, 70).

8.6.1 A 'collection centre'?

The malting complex is seemingly incontrovertible evidence for transition from autarkic farming methods typical of the 5th and 6th centuries to specialised farming and cereal processing techniques. According to the distinctions established by van der Veen (1992, 99), Sedgeford could be classed as a 'producer' site, capable of producing a (malt) surplus. Archaeobotanical results presented in this thesis imply that crops malted at Sedgeford derived from several environmental settings. This is indicated by significant variability in carbon and nitrogen stable isotope values for single-grain samples, suggesting cultivation in different water availability conditions and 'conditions of manuring', respectively (**sections 7.2.1** and **7.2.2**); by the abundance of both *Anthemis cotula* seeds (indicative of heavy clay soils) and *Raphanus raphanistrum* seed-heads (this plant favouring acid-rich soils) (**section 8.1.4**); and by tentative evidence from 'outlying' carbon and nitrogen stable isotope values for sourcing of some crops from the coastal zone (**section 7.2.3**). Combined with the high grain content (or 'cleanness') of samples from the malting complex (**section 6.3**), alongside the consideration that plant remains are here mostly 'fine sieve product' (**section 6.6.2**), these results are together consistent with the suggestion that – as theorised for Higham Ferrers, Northamptonshire, and Uppåkra in southern Sweden – Sedgeford was a 'collection centre'. That is: crops harvested and 'cleaned', i.e., threshed, winnowed and sieved, by local farmers in the surrounding area were amassed at Sedgeford and processed into malt at the malting complex (Hardy et al., 2007, 203; Larsson et al., 2019, 17). Hardy *et al.* (2007, 204) suggest a greater

efficiency for farmers local to Higham Ferrers in bringing their harvested crops to a central place for processing – surely applicable also to Sedgeford.

8.6.2 Modelling the 'story' of Sedgeford's malt

Questions remain: who was 'managing' malting at Sedgeford? And by whom was Sedgeford's malt (once converted to beer) ultimately consumed? Two possible models, summarising the roles and relationships of actors potentially implicated in the 'story' of malt from Sedgeford, are presented in **Figures 8.2** and **8.3.** The first summarises a more 'traditional' understanding, founded largely on documentary evidence from Anglo-Saxon England (as presented in **Chapter 3**), and assumes a socio-economic setting in Sedgeford and surroundings which echoes the more general picture across England.[107] The second model is founded on newer evidence relating more specifically to 7th to 9th century northwest Norfolk; using recent excavations and novel methods, including 'ancient DNA' (aDNA) analysis and the archaeobotanical analyses conducted in this study, to present 'emerging' understanding of this essentially document-free ('pre-historic' (Blair, in press)) region of early medieval England. The models are, as far as possible, here tested against environmental, archaeological and archaeobotanical evidence, with the role of each 'actor' respectively identified examined in turn.

[107] J. Blair warns that textual evidence for feudal lordship and both lordly and royal tribute in the era is mostly derived from western parts of Anglo-Saxon England (particularly Wessex), and should not be 'blanket' extrapolated onto England's 'eastern zone' (in press).

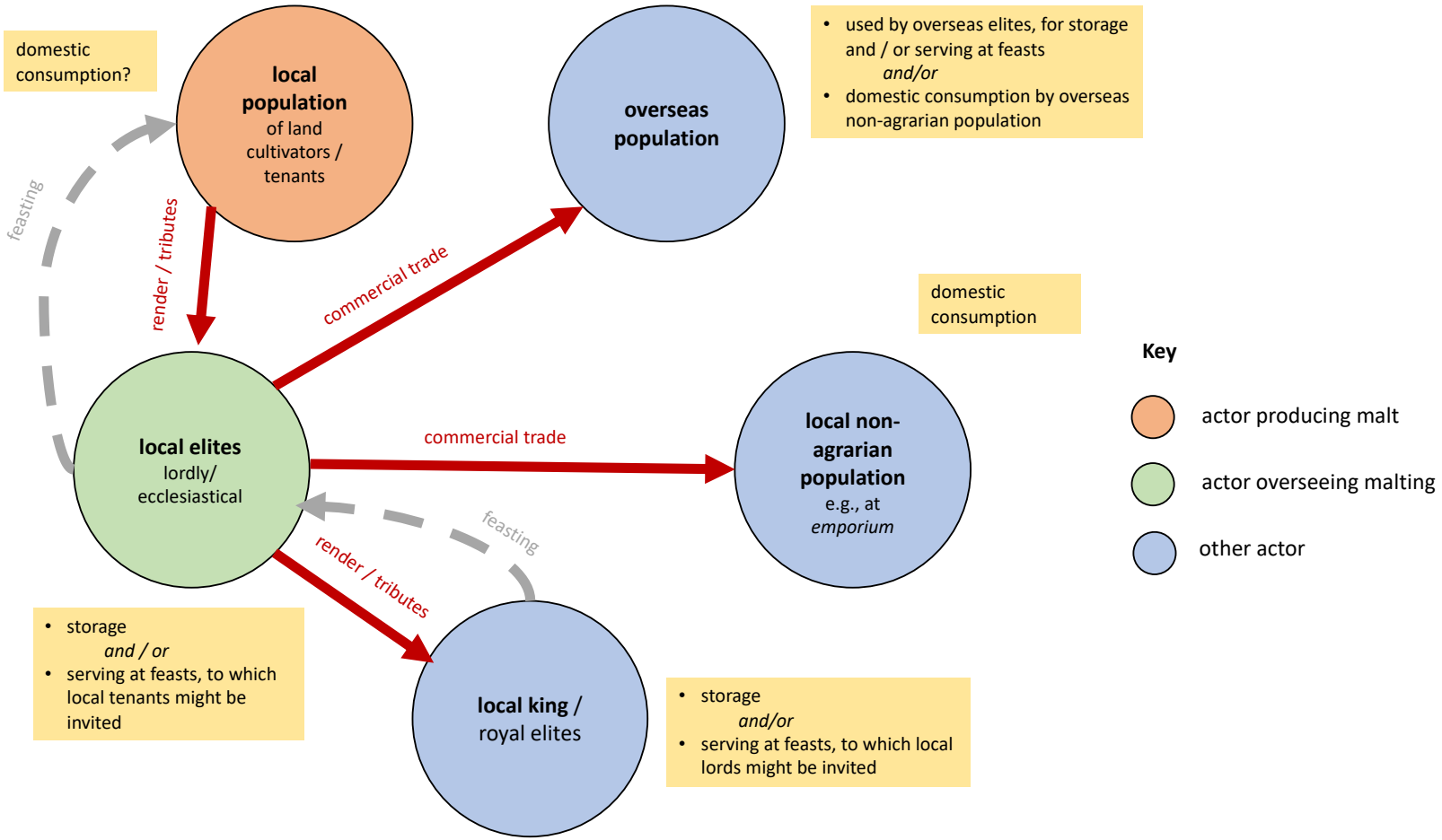

Figure 8.2 Model summarising potential 'story' of malt from Sedgeford, based on 'traditional' understandings

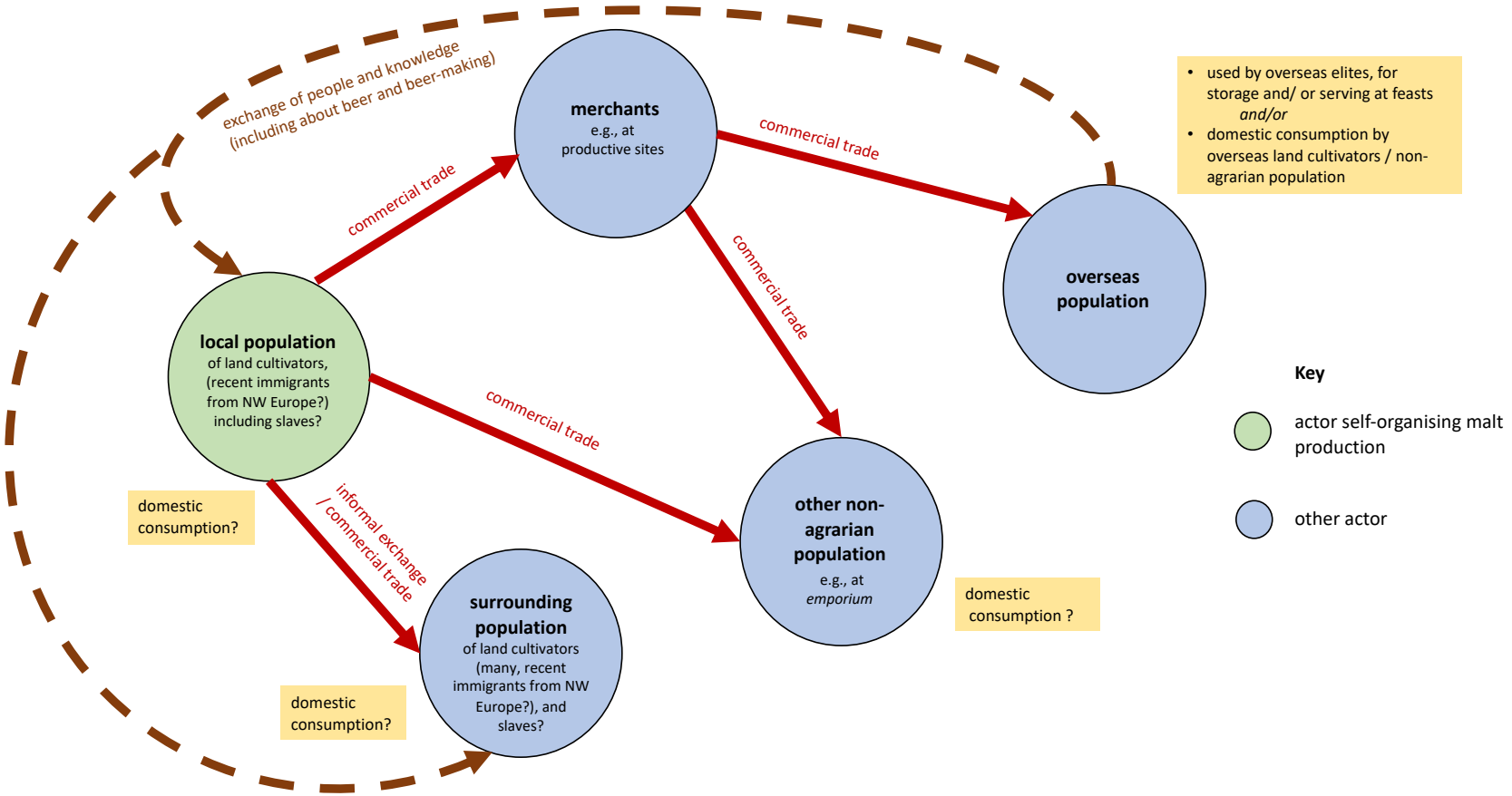

Figure 8.3 Model summarising potential 'story' of malt from Sedgeford, based on 'emerging' understandings of Mid Saxon northwest Norfolk

Local elites (lordly or ecclesiastical)

The 'traditional' model (**Figure 8.2**) proposes malting at Sedgeford was conducted by local land cultivators ('peasants') and overseen by local elites, extracting tributes in malt from the populace. Local elites are (perhaps conspicuously) missing from the second model (**Figure 8.3**).

The new level of organisation required in society to manage a 'collection centre' such as hypothesised at Sedgeford might seemingly render novel oversight of a local elite, whether secular or ecclesiastical, indubitable. It has been observed that sites fulfilling centralised collection functions in the era were generally estate centres, overseen by elites (Hamerow, 2012, 153–154; Blakeney, 2017, 95). Applicable to the malting complex, McKerracher writes, 'many of the…innovations in 7th to 9th century agriculture required a scale of investment (in both labour and raw materials) and a degree of planning which might have proved impossible without strong and stable lordship' (2018, 124). Further, Faulkner *et al.* (2014, 227) interpret evidence for extensive ditch-work, assumed to be boundary markers, constructed at Mid Saxon Sedgeford as implying novel private ownership and hence control of resources and the means of production by local elites. Indeed, G. Davies (2010b, 268, 328–29) (though himself conceding that distinguishing between ecclesiastical or secular elite-governed centres in the era is no simple matter) surmises, based on a review of Sedgeford's zooarchaeology, a shift from Mid Saxon ecclesiastical to Late Saxon secular oversight at the site.

Faulkner summarises thus his understanding of what he calls Sedgeford's Mid Saxon, 'agro-social revolution': 'the evidence…is best understood as an expression of the rise of lordship, the division of the land into great estates, and the imposition of labour services and food renders on a class of dependent peasant villagers', citing in support the extensive Anglo-Saxon documentary evidence for food (including malt and ale) renders and tributes paid to

elites (**section 3.4**) (2022, 178). In seeming agreement, if we assume, with G. Davies (2010a, 91, 114), that coin-finds represent individuals engaged in economic transactions, the notable lack of coinage at Sedgeford argues against direct trade between malt-producing land cultivators and, for example, local merchants.[108]

Whilst Sedgeford is not classed as a coin- or metal-rich 'productive site', discovery of two writing styli and vessel glass, along with (some, slight) evidence for spelt cultivation, and for then-sophisticated construction methods in malthouse construction (**section 4.3**), are arguably interpretable as, 'indication(s) of the supervising presence of an outside authority' (Davies, 2010a, 114; Jolleys et al., 2019, 76; Faulkner and Blakelock, 2020, 85). Based on associations between corn-dryers and seeming sites of assembly in Wales and Ireland, and consonant with extensive contemporary documentary evidence, Comeau and Burrow propose that the primary uses for bulk quantities of malt received by local elites were for storage or (brewing and) feasting (2021, 133).

Kings / royal elites

A third potential destination, in this era of kingdom-building, for local elites' tribute-derived malt would be the meeting of further tribute demands from royal elites. **Section 3.4** outlines evidence from royal charters for tributes in malt and ale made by elites to their respective Anglo-Saxon kingly superiors. Primary sources are unambiguous: the socio-political imperative to use (perhaps tribute malt-brewed) beer for hosting feasts was at least as strong for royal, as lordly, elites in the era (**section 3.3.2**).

[108] In Faulkner's view, there is, 'no evidence whatsoever…at Sedgeford' for, 'foodstuffs being produced and traded as commodities' (2022, 178).

However, the lack of primary sources renders all understandings of East Anglian kingship problematic (Yorke, 2002, 58–60), and recent research implies kings and kingship were less influential in northwest Norfolk. Indeed, Blair suggests (*pers. comm.*) that royal oversight of north Norfolk as late as the Mid-Saxon era was minimal (it is believed, as suggested in **section 1.5**, that royal control of Norfolk by the early Saxon Suffolk-based *Wuffingas* was a secondary development (Yorke, 2002, 70)).

Local land cultivators / tenants

An emerging perspective (**Figure 8.3**) would further suggest that Sedgeford's local populace had considerably greater agency than might be assumed. T. Williamson presents a controversial perspective on the socio-political setting of early medieval England entire, arguing, 'the critical role of lords in shaping medieval rural affairs…has never actually been demonstrated, in an English context at least' (2022, 233). Blair's related (slightly more nuanced) view is: 'it is time to abandon the image, so deep-rooted in both popular and academic writing, of a homogeneous Anglo-Saxon England made up of "lords" and "peasants"' (2018, 418). Both are convinced that the East of England was in this regard distinctive. Williamson, taking a notably 'environmentally deterministic' standpoint, suggests for East Anglia that climatic conditions conducive to cereal cultivation, combined with fertile soils, set it apart. In his view, reliable harvests in the east fostered rapid population growth, leading to fragmentation of landholdings (thereby fundamentally altering field systems). This, he claims, is why by Domesday there were more free peasants in the east (2013, 234, 238–239; see also Faith, 2012 on 'light manorialism' in Lincolnshire). For Blair, focusing on settlement structure particularly as revealed in excavations since *c.* 1990, 'archaeology provides nothing to encourage a "seigneurial" model…for eastern England' (2018, 218).

Further, stable isotope results from this study, which imply considerable variation in levels of manuring *within* fields supplying the malting complex (**section 7.2.2**) are, as Styring *et al.* argue based on similar trends in isotopic values for Iron Age Germany, 'consistent with agricultural decision-making at a local level rather than centralised control' (2017, 357).

Notably, it has been suggested that archaeologists are often 'over-eager' to classify Anglo-Saxon settlements as 'high-status' (Loveluck, 2007, 147; Hamerow, 2012, 101). Sedgeford's 'high status' material finds are undeniably meagre, and, as Ulmschneider contends (2011, 165), coins and glass are identified in many apparently low-status rural settlements from the era.

A question remaining to be discussed is the nature of the socio-economic relationship between the malting complex and settlement areas of the site at Sedgeford (**section 4.2**). The sparse calibrated radiocarbon dates available for the two areas (**sections 4.2** and **4.4**) are consistent with these having been in use concurrently, (although the malting complex's time of use may have slightly preceded that of the settlement).[109] No evidence for crop-storage facilities has yet been revealed in the malting complex, however, a larger, raised building in the settlement area is hypothesised to represent a granary (in which crop material could potentially be stored before and / or after malting) (E. Blakelock, *pers. comm.*). It seems almost certain that the settlement's population were among the groups consuming beer created from the site's malt. We can question also whether those running the malting complex day-by-day (whether with elite or local oversight), were residents of the settlement. Day-to-day management would have required only limited labour input, however, whether or not the larger workforce

[109] This suggestion is seemingly corroborated by ceramic evidence; with Ipswich ware, almost exclusively, recovered from the malting complex, whilst both Ipswich and (later) Thetford ware occur frequently in the settlement area (Faulkner, 2019).

necessary for both initial construction[110] and ongoing supplying (with harvested crops) of the malting complex were mostly, or entirely, residents of the settlement area is a moot question. It is also not (yet) known whether some or all of those (directly and indirectly) implicated in malting at Sedgeford, were buried in the adjacent cemetery.[111] In sum, to date, understanding of the ways in which the three areas of the site at Sedgeford excavated to-date interrelated remains elusive.

Non-agrarian population

With a clear capacity for surplus production (estimated settlement population being only 300 people) and proximity to transport routes (**sections 8.5.1** and **4.2**), it seems reasonable to propose, as, for example, does Hamerow for the early medieval rural centre at Dalem in Lower Saxony, that those in control of Sedgeford's malting (whether elites or local land cultivators) were engaged in commercial export and trade (in malt) with emerging 'consumer sites' – both within and perhaps beyond the East Anglian kingdom (2002, 137; Faulkner, 2022, 167). If nothing else, were Sedgeford's malt not brewed on-site, it must have been exported elsewhere for processing into beer.

Great comparative costs of transporting bulky goods overland as opposed to by water in the medieval era have been noted (**section 3.4**) (Unger, 2007, 59). Further, the superabundance of oyster shells recovered at Sedgeford (along with 'outlier' stable isotope values – **section 7.2.3**) are suggestive of regular contact with the coast (Davies, 2010a, 114).[112]

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[110] Faulkner estimates that 250 person-days of labour were required for the construction of a single malthouse (Faulkner, 2022, 177)

[111] Osteological analysis aimed at determining whether any of the human remains recovered from the cemetery to date reveal evidence of having worked the malting complex is planned (E. Blakelock, *pers. comm.*)

[112] Discovery of what has been identified as a whale bone at Sedgeford would seem to corroborate this (Wolff, 2017, 23).

We can imagine malt transported to the coast along the part-canalised river Heacham, perhaps to one or more 'productive sites' (**Figures 4.1-4.2**) and even by sea to the *emporium* at Ipswich (**Figure 1.2**) (Faulkner, 2022, 170). The notable abundance of Ipswich Ware recovered at Sedgeford (even compared with contemporaneous local sites)[113] implies entrenched connections with the *emporium* (ibid.).

Malt imported to the early trading settlement at Ipswich could have had two primary 'destinations': either consumption by the growing local non-agrarian population of craftspeople and merchants (theoretically not themselves able to malt domestically) there living, or further export, across the North Sea, to one or several among Ipswich's overseas trading partners.

Overseas population

Archaeological evidence clearly indicates that Ipswich was at this time actively engaged in international trade (e.g., Wade, 1988, 96; Scull, 2011, 203). The question as to how early 'bulk' goods such as cereals and malt were exchanged by sea in the early medieval era has been explored in **section 3.4**, as has Blair's conclusion, reviewing evidence on international trade from Mid Saxon *emporia*, that, 'it was as channels for bulk exports that they really mattered'; he posits also that, 'wool, cloth, lead, *grain* and even *preserved foodstuffs* could all have been major exports' (emphases mine) (2018, 166, 253). Important documentary evidence for significant international trade in malt 'throughout the thirteenth century and even earlier' (Carus-Wilson, 1962, 185) from the Wash port of Lynn, ~15 miles from Sedgeford, has also been highlighted (**section 3.4**). Applying these findings, Rickett concludes, 'therefore, malting and corn drying

[113] The abundance of Ipswich Ware finds at Sedgeford is estimated at one sherd for every 2.2m² excavated (estimated total finds to date are ~4,500 sherds) (Faulkner, 2022, 176).

were probably undertaken in the hinterland of the Wash ports' (2021, 37–38). Speculating as to whether a malting and brewing 'industry' in the 'eastern zone', meeting demands for international trade in the 13th century, might have extended back to the Mid Saxon era, when, as noted, northwest Norfolk was according to Blair a 'powerhouse' of the Anglo-Saxon economy (2018, 44) may be over-weighting the available evidence.[114] However, undeniably, discoveries at Sedgeford of both a Frankish coin and basaltic quern stone likely fashioned on the continent are indicative of international connections here in Mid Saxon times (Faulkner et al., 2014, 126; Ogden, 2021).

Cultural connections between East Anglia and northwest Europe in the Mid Saxon period have been highlighted (**section 1.5**). This is an active area of current research for archaeologists and historians of the Saxon east of England. It has been suggested, as noted, that the eastern zone may have been culturally closer, at the time, to littoral Scandinavia than to its own rural 'hinterland' in central and western parts of England (Blair, 2018, 44); contact across the North Sea, 'certainly…involved ideological interaction' (Carver, 1989, 149).

Significantly, recent research comparing ancient DNA (aDNA) sourced from the skeletal tissue of 460 individuals buried at sites across early medieval Europe and Anglo-Saxon England, including 20 from the Mid Saxon cemetery at Sedgeford, provides powerful evidence for ongoing movement of northern Europeans across the North Sea to Britain from the post-Roman era until the 11th century (Gretzinger et al., 2022, 118). On average, Anglo-Saxon human remains analysed had 76% northern European ancestry; this figure is higher in

[114] Blair observes that the small number of 'rich' excavations to date in the region, 'corroborate the impression of high-density activity in western Norfolk, facing the Wash' (2018, 289).

eastern England, with the Sedgeford individuals sampled each having over 95% northern European ancestry (ibid. 114, 115 Figure 3c, 116, extended data Figure 5b). The Sedgeford human remains are all interpreted as those of either immigrants or the direct descendants of immigrants (without admixture) (ibid.).

It is thus plausible that the abundance of rye at Sedgeford represents more than expedient adaptation by the area's farmers to local environmental conditions, and might in fact be an artefact of economic and cultural continuity with the North Sea-bordering continental zone, where rye was the dominant bread crop (Wolff, 2017, 10). I suggest that Sedgeford's farmers were influenced in their crop choice by counterparts in southern Scandinavia. Further, I hypothesise that interaction with northern Europeans involved one or more of the following: the local population of Sedgeford learning a 'taste' for rye-rich beer from their neighbours across the sea; exporting rye malt to lands with a demand for 'spicy' rye beer; or, finally (as aDNA research now suggests) themselves being recently arrived immigrants from northern Europe, importing the skills, as well as a partiality, for creating rye beer. Could Sedgeford's Scandinavian maltsters have been producing rye-malt to meet the demands of a surrounding population (in the 'eastern zone') of similarly recently-arrived countryfolk (**Figure 8.3**)?

Merchants

If Mid Saxon northwest Norfolk was dominated by Scandinavians and Scandinavian influence, surely it is to the social structures of these lands that we must look to understand contemporary local society? Blair has claimed (as noted), 'Scandinavian and English farming communities…belonged to the same socioeconomic world' (2018, 306). Recent research suggests early medieval farmers in southern Scandinavia lived alongside, rather than in

subjection to, military elites; whilst Icelandic sagas depict a society of slave-dependent farmer-merchants (Holst, 2014; e.g., Magnússon, 1999).[115] One 13th century saga describes a 9th century Icelandic merchant sailing to trade in England, and returning with wine and cloth ('Egil's Saga' c. 17 in Magnússon, 1999, 94). **Figure 8.3** hypothesises a key role for merchants in the 'story' of Sedgeford's malt.

Recent research is increasingly revealing the significant role both Frisian and Scandinavian merchants played in Mid Saxon society, with the distribution of e.g., Frisian *sceattas* suggesting their penetration even far beyond the 'eastern zone' (e.g., Faith, 2012; Laight and Metcalf, 2012). Whilst a merchant 'class' were deeply implicated in *emporia*-based trade, evidence also suggests that local Anglo-Saxons traded directly with merchants, beyond the *emporia*: Faith describes Frisian and Scandinavian merchants trading independently with 'free' and wealthy Lincolnshire farmers, whilst research indicates money-based exchange on the English south coast beyond the *emporium* at *Hamwic* (Faith, 2012; Costen and Costen, 2016; Blair, 2018, 166). Blair posits that some of the 'free laity' of the eastern zone, 'evidently prospered by producing – and presumably selling or exporting – commodities that must have included…grain [and malt?], but it is imponderable whether they did this independently, or as tenants or agents. They must have…interacted with [merchants] regularly' (2018, 305, my parentheses).

If mercantile trade between England and southern Scandinavia was two-way, we must surely ask whether the distinctively abundant rye (common on the continent) at Sedgeford could conceivably have been imported. Whilst an intriguing possibility, localised

[115] Contemporary Scandinavian society was highly slave-dependent (e.g., Skre, 2020), and Pelteret argues for the significant role played by slaves in Mid Saxon England: by the 11th century, according to Domesday (1086), enslaved people comprised 13% of the recorded population of Essex (1995, 204). It is entirely plausible that slaves were involved at Sedgeford in both cultivating crops and malting these for beer.

concentrations of Mid Saxon rye cultivation (as evidenced archaeobotanically) (**Figure 8.1**), a co-occurring weed assemblage typical for eastern England, and mean stable isotopic values consistent between cereal taxa, across features and over time in the malting complex (**section 7.2**) (implying crops cultivated in broadly comparable conditions, with variability suggesting no more than local heterogeneity), would seem to belie this.

The 'story' of Sedgeford's malt: Concluding thoughts

Recent research, as represented in **Figure 8.3** (the 'emerging' model), is displacing some long-held theories about the socio-economic context of the Mid-Saxon east of England, for instance the universal hegemony of lordly elites over a subjugated 'peasantry'. Whilst many (e.g. Faulkner et al., 2014; Faulkner and Blakelock, 2020; Faulkner, 2022) will understandably interpret available evidence as suggesting 'elite oversight' at Sedgeford, in line with the **'**traditional' model presented here (**Figure 8.2**), I find the bold new vision of social structuring in the 'eastern zone' (with Sedgeford at its heart) – a world of self-organising immigrant farmers independently trading with foreign merchants; a world very much 'looking east' – compelling and persuasive.

8.7 Summary

In the (later medieval) poem 'An Unfriendly Crowd' from the Welsh 'Book of Taliesin' is written of beer, 'I was drink for the king' (Williams and Lewis, 2019, 53). Building on the synthesis developed in this chapter, the subsequent, final chapter summarises the entire project, presents concluding remarks and proposes possible avenues for future research into malting, brewing and beer at Mid Saxon Sedgeford and beyond. Here, I ask, finally, whether 'a quart of ale' was, at Sedgeford, truly 'a dish for a king'.

9 CONCLUSIONS

Ælfric's 10th century Colloquy records: 'the ploughman gives drink (*sylð us…drenc*) as well as bread (*hlaf*)' (Garmonsway, 1991, 40, l.226). This work has, I hope, demonstrated that beer to drink was, for the peoples of Mid Saxon England, both practically and symbolically, every bit as important as bread to eat. Yet corresponding archaeobotanical evidence has been, to date, conspicuously lacking. Hence the particular significance of an assemblage from the earliest unambiguous multi-feature Anglo-Saxon malting complex, revealed at Sedgeford.

Archaeobotanical research, uncovering an abundance of germinated grains (a sign of malting), was the key 'missing piece', alongside structural evidence, underpinning the designation of Sedgeford's Trench 23 as a Mid Saxon malting complex. This work has 'triangulated' three practices – all, to varying extents, novel – for determining levels of germination among grains from the site. I have developed methods for diagnosing germination based on grain morphology as visible using a light microscope (a particular challenge for 'naked' grains, as abound at Sedgeford). Secondly, T. Roushannafas has used GMM to clearly, and excitingly, for the first time at any site, recognise germination in (free-threshing wheat) grains from the malting complex. Finally, Y. Zhou, using SEM, has revealed unprecedented evidence for germination in archaeological rye grains, again from Sedgeford. Sedgeford's was indubitably a malting complex. Further, I have presented in this study a new model for preparing (processing) crops for malting – an adaptation of G. Jones' 'classical' crop processing model, with potential wider application for future research.

Analysis of cereal grains and their co-occurring chaff and weed seeds has further demonstrated Sedgeford's place in the 'ploughman's tale': recent research by the University of Oxford FeedSax group questions the once widely espoused idea of a Mid Saxon agricultural 'revolution', however, Sedgeford emerges as an early precursor of constituent practices that

were central to longer term processes. Stable isotope analysis and FWE methods have generated evidence for all three components of the so-called 'mouldboard plough package' – use of a heavy plough, extensification of cultivation and, perhaps, early crop rotation – in the arable fields that supplied Sedgeford's malting complex. The richness of the malting complex assemblage, and its diverse crop spectrum (with rye most frequently occurring) also typify trends in arable farming nascent from the 7th century. Rye, though a minor crop throughout the Anglo-Saxon era, and rarely dominant in Mid Saxon assemblages, is well adapted to local environmental conditions in northwest Norfolk, and locally common. Tailoring crop choice to soil and climate type is a further feature of growing connection between Mid Saxon peoples and their land: farmers were, 'digging themselves in as never before' (McKerracher, 2018, 118). Significantly, Sedgeford is the only known Anglo-Saxon example of large-scale malting primarily with rye.

In northern parts of continental Europe, rye was, in this era, the main bread crop. Cultural and economic continuity between the so-called 'eastern zone' of Mid Saxon England and littoral regions of northwest Europe was such that Blair suggests eastern England was culturally more closely connected to the continent than its own 'hinterland' in central and western England (2018, 44). It seems the people of Sedgeford, where a Frankish coin and Germanic quern stones have been discovered, were looking east, connected by a canalised river to the North Sea and having deeply entrenched connections with the local international trading port at Ipswich. I have hypothesised that cross-oceanic cultural continuity may have extended to exchange of knowledge about crop choice, and economic continuity to exchange of (long-lived) rye malt with lands which may have welcomed the 'spicy' flavours of rye-brewed beer. Recent aDNA research suggests a distinct third possibility: that Sedgeford's population was (almost) entirely composed of recent immigrants from coastal northern

Europe, who imported both the skills and a predilection for creating rye-rich beer. It is entirely plausible that Mid Saxon Sedgeford was simultaneously, or at different times, in each of these ways connected across the North Sea with northern continental Europe.

Socio-economic transitions in Mid Saxon life ranged beyond field and furrow. This was an era in which both monastic and lordly elites were established, of shifting settlement structure and emerging market economies, facilitating trade at so-called 'productive sites' and at *emporia* such as Ipswich. It was a time of kings and kingdom-building. These were lords and kings who regularly bowed to social imperative in the holding of lavish feasts, fuelled by beer.

Results presented here are consistent with Sedgeford's having been a 'collection centre' for malting of crops harvested from surrounding arable land. A case can also be made for Mid Saxon Sedgeford, with its pair of styli, and vessel glass – with evidence for large-scale water-management, grid-planning and above all, with its extensive malting complex – having been overseen by an elite, whether ecclesiastical or secular. However, I propose that 'emerging' understandings of the socio-economic world of northwest Norfolk – which would suggest 'bottom-up' oversight of the malting complex by independent, slave-owning farmers trading directly with merchants – may better describe the 'story' of Sedgeford and its malt. Blair argues, forcefully, that the fen-edge region of Lincolnshire and northwest Norfolk was a 'powerhouse of the seventh to tenth century economy' (2018, 44). If so, this was a powerhouse in which Sedgeford, and its malt, had important parts to play.

Discoveries at Sedgeford including the abundance of malted rye, and the potential use/tolerance of particular 'weed' seeds as flavourings; a sense of Sedgeford's place in the emerging story of *ceorl*, *eorl* and coulter (Mid Saxon farming); as well as my further tentative hypotheses concerning the malting complex's place in local, regional and even international

cultural and socio-economic contexts, hopefully begin to 'fill-out' a useful and multi-dimensional picture of the earliest known such site in Anglo-Saxon England.

Additional helpful investigations beyond the range of the current project might include testing of residues lining some of the abundant Ipswich ware ceramic sherds found in the malting complex (as a means of revealing use patterns). Testing the 'traditional malting' model for crop processing here presented against other archaeobotanical assemblages evidencing malting, from Anglo-Saxon England and beyond, would be an obvious means of extending the current research. Further, both SEM and GMM analyses, referenced in this work, could usefully be extended to incorporate germinated grains of other species from the malting complex. Finally, here, much might be profited by expanding stable isotope analyses at Sedgeford: to incorporate analysis of grains from the settlement part of the site, as an instructive comparison with malting complex grains; and of tooth enamel and collagen from skeletal remains recovered from the site's Mid Saxon cemetery – which might, *inter alia*, complement aDNA research by indicating birth-place for some of Sedgeford's then population.

Already a site rich with discoveries, it seems that Mid Saxon Sedgeford and its malting complex have a great deal more to gift us. Can it be that, in the charred remains of 1200-year-old cereals and weeds at this perhaps 'elite' malting complex – arguably at the economic heart of the East Anglian Anglo-Saxon kingdom – we find a gift fit for a king? Or is it possible, rather, that scorched grains testify to the self-directed toil of immigrant agriculturists? Truly, tiny burnt seeds have rich stories to tell – of kings, *ceorls*, and the 'dishes' of ale served them.

DESCRIPTIVE CATALOGUE

Sites in Britain dated to the early medieval period with evidence for malting / brewing

The 'early medieval period' is here equated with the Anglo-Saxon era in England, defined (as per FeedSax convention) as *c.* 420 – *c.* 1030. Sites included are firstly those where the author contends, based on an assessment of archaeological and archaeobotanical data, that a reasonable case can be made that malting was taking place; secondly, other sites pertinent to the history of beer-making in the Anglo-Saxon era are listed.

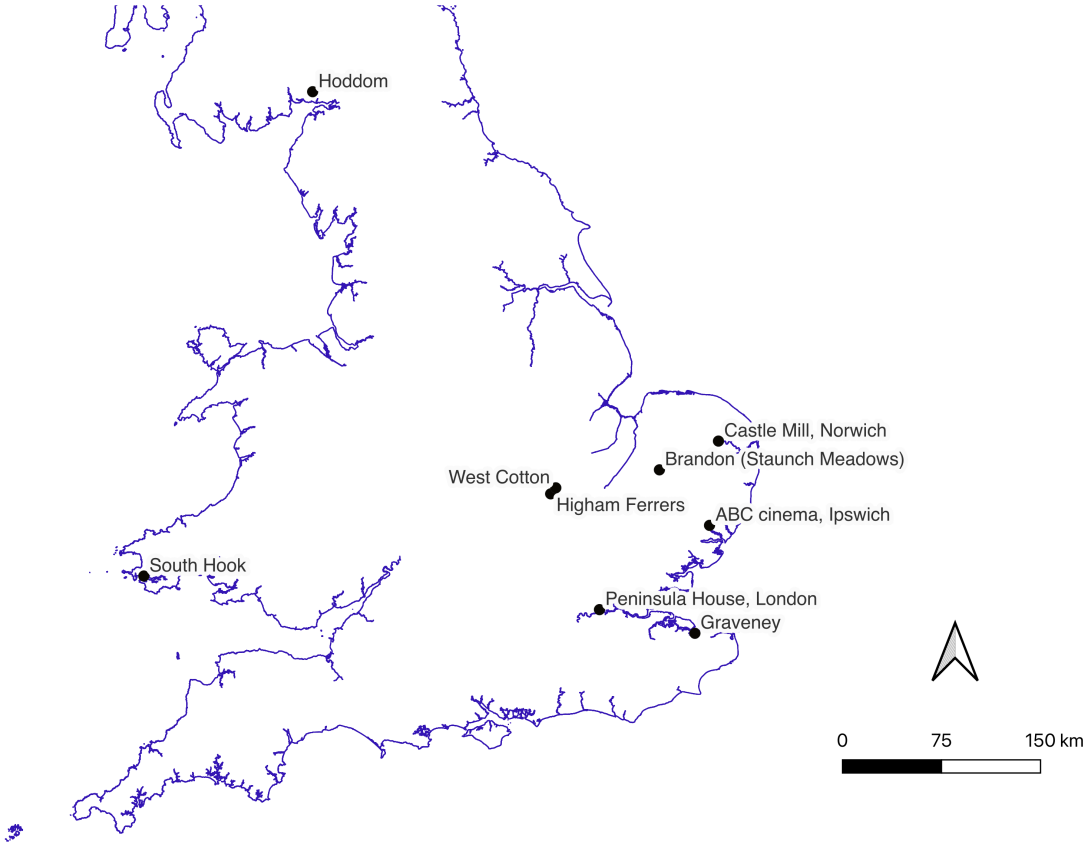
Data summary

Site	**Location** (National Grid Reference)	**Date** (century)	**Summary**	**Reference(s)**
Brandon (Staunch Meadows), Suffolk	TL 778 864	Mid 7th to mid 9th	A hypothesised 'high status' settlement. Ditch in southwest part of the site contained detached sprouts and fragmented grains, likely mostly barley, thought to be malt grist.	Archaeology: (Tester et al., 2014) Archaeobotany: (Murphy and Fryer, 2014)
Graveney, Kent	TR 053 627	10th	Remains of boat identified in saltmarsh/mud-flat area. Boat assemblage (including from between boat staves) included abundant fruit, bracts and bracteoles of hops. Hop pollen also identified. Abundance and location of hop remains suggests not locally growing wild species. Hypothesised boat used to transport hops, intended for brewing.	Archaeobotany: (Wilson, 1975)

Site	Location (National Grid Reference)	Date (century)	Summary	Reference(s)
Higham Ferrers, Northamptonshire	SP 959 684	Early 8th – mid 10th	Hypothesised to be tribute-centre for a royal estate. 'Monumental' (McKerracher, 2014a) corn-dryer, containing ~90% barley, of which ~1/3 germinated. Detached sprouts also frequent. Interpreted as malting kiln. Barley grain from oven radiocarbon dated to Cal AD 710-963 at 78% confidence.	Archaeology: (Hardy et al., 2007) Archaeobotany: (Moffett, 2007)
Hoddom, Dumfriesshire	NY 155 730	7th to mid 13th	Hypothesised to be ecclesiastical centre. Structural evidence for 14 corn-dryers. 14% wheat grains from one corn dryer germinated. Due to unevenness of germination, discounted as accidental germination, possibly following a wet harvest, (however, see **section 2.4**).	Archaeology: (Holden, 2006a) Archaeobotany: (Holden, 2006b)
Ipswich (ABC cinema)	TM 164 445	10th	Pit fill containing charred aggregates of plant material, identified as hops, and surmised to be intended for brewing.	Archaeology: (Scull, 2009) Archaeobotany:(Murphy, 1987; Murphy, 1991)
Norwich (Castle Mall)	TG 231 083	10th or early 11th	Sunken featured building, ceramically dated, had two hearths and charred assemblage comprising oats (54%), wheat (18%) and barley (4%). A 'high proportion' of oats and barley germinated (not quantified due to poor preservation). Hypothesised that hearths were used for malt kilning.	Archaeology:(Popescu, 2009) Archaeobotany: (Murphy, 2009)
Peninsula House, London	TQ 329 807	10th	Oven with mix of several cereals ('many' of which had sprouted) with some detached sprouts and abundant weed seeds, though little chaff or culm nodes. Possibility that grains were deliberately germinated dismissed because of abundance of weed seeds.	Archaeology: (Vince, 1991) Archaeobotany: (G. Jones et al., 1991)

Site	Location (National Grid Reference)	Date (century)	Summary	Reference(s)
South Hook, Pembrokeshire	SM 876 061	Late 7th to late 9th	Complex comprising 4 extended features identified as corn dryers. Spread of grain from 'cleaning out' of one feature comprised mostly barley, 12% sprouted and 57% with damaged embryo ends. Suggested to represent malted grains. Barley grain, surmised to be from final use of corn dryer, dated to cal.AD 680-880.	Archaeology: (Crane and Murphy, 2019) Archaeobotany: (Carruthers, 2019)
West Cotton, Raunds, Northamptonshire	TL 004 730	10th to 12th	Two kilns (one 10th and one potentially 12th century) had fills comprising mostly oats and barley (possibly grown as dredge), >40% of each sprouted. Claimed as evidence of malting.	Archaeology: (Chapman, 2010) Archaeobotany: (Campbell, 1994; Campbell and Robinson, 2010)

Map



Created using QGIS (accessed 28.11.22), using a Boundary Line™ ESRI® shapefile from OS OpenData, freely downloadable under the Open Government Licence.

APPENDICES

Appendix A: Malting and brewing instructions from a late 13th century poem

Anglo-Norman couplets by Walter de Bibbesworth (cited in Brears, 2008, 88) are here juxtaposed with a 19th century translation (Bickerdyke, 1886, 49).

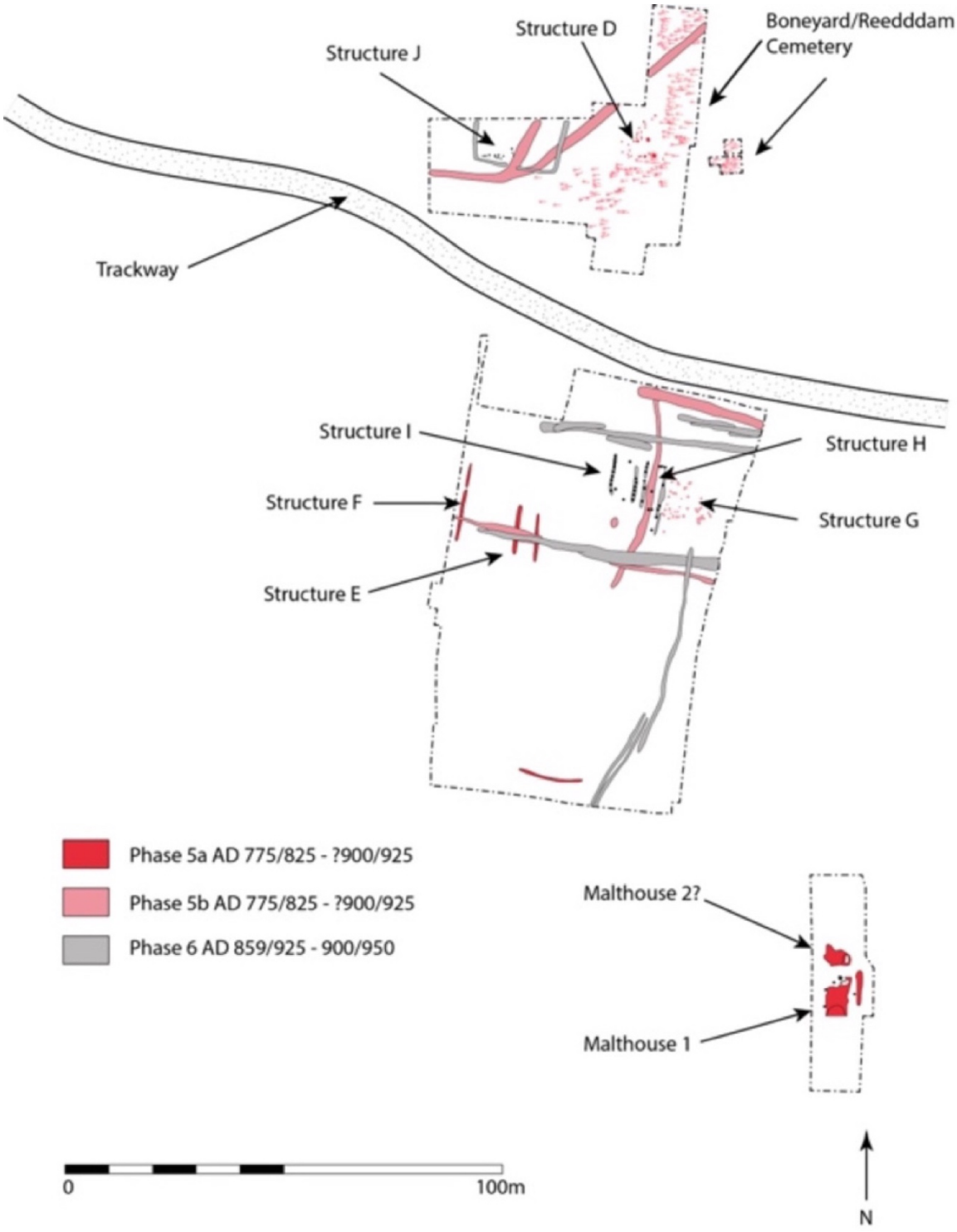
Seyoms ore entour cerveyse	*Ale shall now engage my pen*
Pur fere gens ben à eyse	*To set at rest the hearts of men*
Alumet, amy, cele lefrenole	*First my friend your candle light*
E kaunt averas mangés de brakole	*Next of spiced cake take a bite*
En une cuve large e leez	*Then steep your barley in a vat*
Cel orge là enfoundréz	*Large and broad take care of that*
E kaunt sera enfoundré	*When you shall have steeped your grain*
E le ewe seyt escouloé	*And the water let out drain*
Mountez sel haut soler	*Take it to an upper floor*
Si le festes nette baler	*If you've swept it clean before*
E là cochet votre blée	*There couch and let your barley dwell*
Taunke seyt ben germé,	*Till it germinates full well*
De cele houre appelleras	*Malt now you shall call the grain*
Brès, ke blé avant nomas	*Corn it ne'er shall be again*
Le brès de vostre mayn muez	*Stir the malt then with your hand*
En mounceus ou en rengeés;	*In heaps or rows now let it stand*
Pus le portez en un corbel	*On a tray then you shall take it*
Pur ensechuer au toral.	*To a kiln to dry and bake it*
Le corbel e le corbiloun	*The tray and eke a basket light*
Vous serviront au fusoyn.	*Will serve to spread the malt aright*
Kaunt vostre brez est molu	*When your malt is ground in mill*
E de ewe chaud ben enbeu,	*And of hot water has drank its fill*
Des bertiz ver cervoyse	*And skill has changed the wort to ale*
Par art contrové teise.	*Then to see you shall not fail*

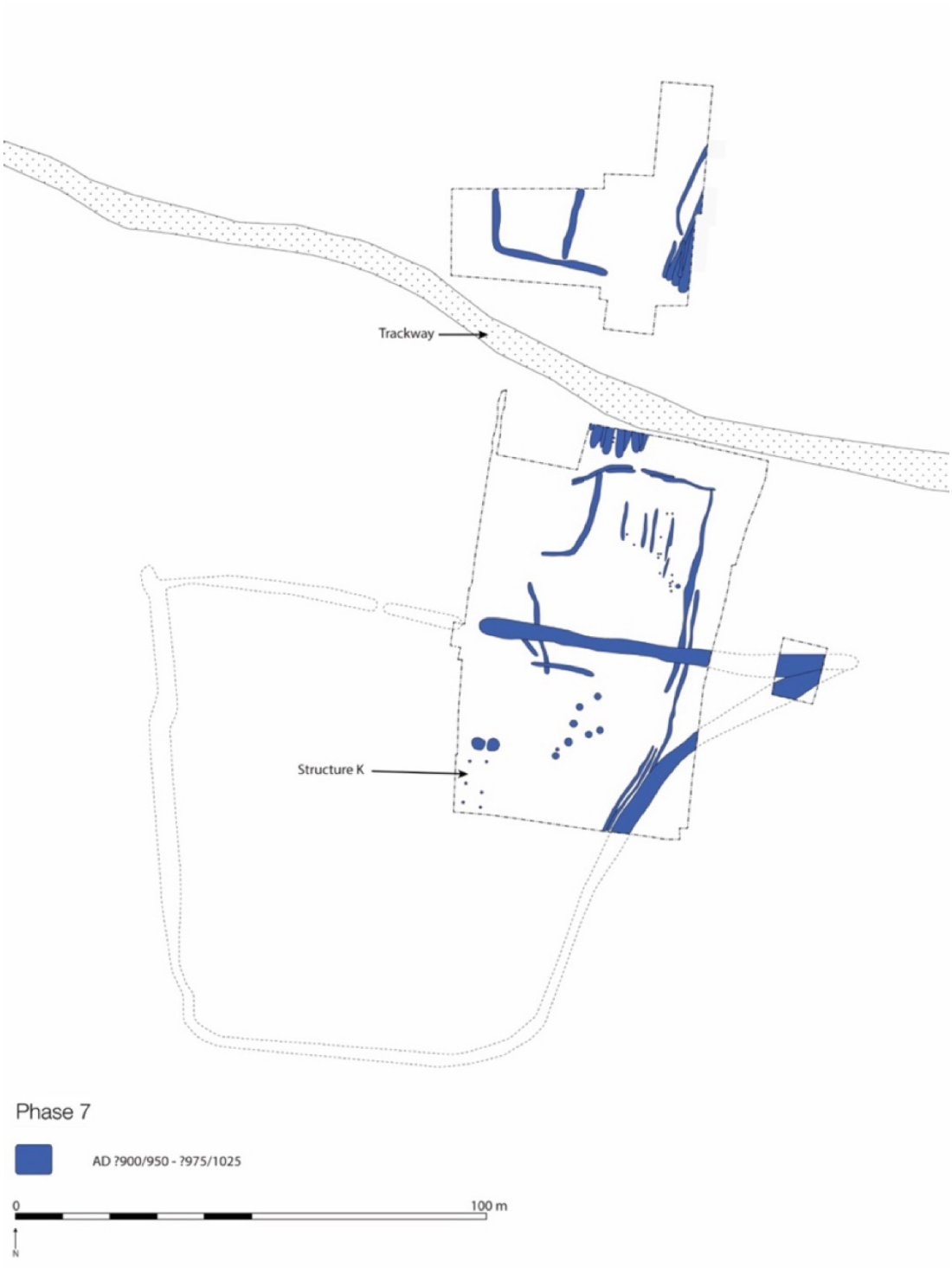
Appendix B: The Sedgeford Mid Saxon occupation sequence

A chronology identified based on stratigraphy and ceramic finds is as follows (Faulkner, 2022 Plate XIII):

Phase	Approximate date range
3	*c.* 650/700–725
4	*c.* 725–?775/825
5	*c.* ?775/825–850/925
6	*c.* 850/925–?900/950
7	*c.* ?900/950–?975/1025

Plans are reproduced with kind permission (Jon Cousins and Gary Rossin / SHARP).


Structure D
Boneyard/Reedddam
Cemetery
Structure J
Trackway
Structure I
Structure H
Structure F
Structure G
Structure E
Phase 5a AD 775/825 - ?900/925
Phase 5b AD 775/825 - ?900/925
Phase 6 AD 859/925 - 900/950
Malthouse 2?
Malthouse 1
0
100m
N


Trackway
Structure K
Phase 7
AD ?900/950 - ?975/1025
0
100 m
N

Appendix C: Archaeobotanical data

I Archaeobotanical data from the Sedgeford malting complex assemblage, showing all quantified items

Current interpretation is that all malting complex samples belong to Phase 5 (Faulkner and Blakelock, 2020, 70).[116]

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Context type		Layer or final kiln fill	pit fill	kiln fill	kiln fill	kiln fill	fill of cut into clay	cistern fill	kiln fill	cistern fill	layer	ditch fill	ditch fill	fill	layer	layer	layer	layer	layer
Sample size (litres)		**10**	**10**	**40**	**20**	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**20**	**10**	**70**	**20**	**10**	**10**	**20**
Total % sorted		**100**	**100**	**25**	**100**	**12.5**	**100**	**100**	**50**	**100**	**100**	**25**	**100**	**12.5**	**12.5**	**25**	**50**	**50**	**50**
	English nomenclature																		
CEREALS																			
Total cereal		1696	97	754	2097	1125	476	1170	592	381	412	372	590	824	853	721	780	1269	1101
Cereal indet.		200	21	88	120	84	84	216	77	160	213	108	155	362	113	228	289	104	200

[116] However, radiocarbon dating suggests Phase 5 may date to an earlier period than previously thought (**section 4.5**) (McKerracher, 2022b).

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Cereal indet. detached embryo with base		56	16	68	144	24	24	88		28		8	8	144	72	16	32	208	32
Cereal indet. detached embryo				28	24			32		16		8	8	16	16	32	40	16	
Total cereal chaff			3			4	40	8		12		72	16		24	4	160	32	
Cereal indet. chaff fragment			1					8		4		16					8	8	
Cereal indet. culm node			2										4						
Triticum L. (free-threshing)	wheat (free-threshing)	744	15	234	649	97	113	177	151	43	30	86	146	12	193	8	146	40	291
Triticum aestivum L. rachis node							24			4					8		8		
Triticum aestivum L. rachis internode																		24	
cf. *Triticum aestivum* L. chaff							8												
Secale cereale L.	rye	360	33	268	720	815	176	468	269	130	101	108	131	354	434	368	240	1052	416
Secale cereale L. rachis node												16	4		8		104		
Secale cereale L. rachis internode												24							

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Triticum L. (free-threshing) / *Secale cereale* L.	wheat (free-threshing) / rye	376	12	148	576	108	40	196	68	22	28	36	77	84	56	28	64	52	112
Hordeum vulgare L. total	barley		14	4		21	63	65	24	14	24	12	45	10	41	85	17	17	41
Hordeum vulgare L. hulled straight			6	4			10	8	8	8	8	2	9		8	16	1	8	16
Hordeum vulgare L. hulled twisted			6			21	29	29	16	6	16	10	35	8	25	56	16	5	25
Hordeum vulgare L. hulled indet			2			0	24	28					1	2	8	13		4	
Hordeum vulgare L. six-row rachis node							8					8					16		
Hordeum vulgare L. six-row rachis internode																			
Hordeum vulgare L. indet. rachis node																			
Hordeum vulgare L indet. rachis internode																			
cf. *Hordeum* L.																			
Secale cereale L. / *Hordeum vulgare* L.	rye / barley	16							1		2		4	2	8	4			

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Secale cereale L. / *Hordeum vulgare* L. rachis node										4		8	4			4	16		
Secale cereale L. / *Hordeum vulgare* L. rachis internode													4		8		8		
Triticum L. (free-threshing) / *Hordeum vulgare* L.	wheat (free-threshing) / barley							20	4	8	6	12	16		8		8	4	42
Avena L.	oat		2	12	32			8		4		2					16		
Avena L. floret base						4													
Avena / large *Poaceae*	oat / large grass		2		16	16		16				2	12		8			24	16
S. cereale L / *Avena* sp	rye / oat					8		20			8	8	16						
AMARANTHACEAE																			
Atriplex L.	orache family																		
cf. *Atriplex* L. core	orache family					8													
Atriplex patula L. / *hastata* L. / *prostrata* Boucher ex. D.C.	common orache / hastate orache / spear-leaved orache																		

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Chenopodium album L.	fat hen										8								
cf. *Chenopodium album* L.	fat hen														8				
Chenopodiaceae	goosefoot family			4			8	48		4	8		4			16	24		32
Chenopodiaceae core	goosefoot family																		
ASTERACEAE																			
Anthemis cotula L.	stinking mayweed															8			
Asteraceae	daisy family																		
Centaurea L.	knapweed																		
APIACEAE																			
Apiaceae	umbellifer family																		
BORAGINACEAE																			
Buglossoides arvensis (L.) I. M. Johnst.	corn gromwell																		
BRASSICACEAE																			
cf. *Alliaria* L.	garlic mustard															4			
Barbarea W. T. Aiton	winter cress																		

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Brassicaceae	cabbage family			4													8		
Brassicaceae in pod	cabbage family						4												
Brassica L.	cabbage/mustard							8								8			
Brassica L. / *Sinapis* L.	cabbage/mustard					8		8		12			4	32		8			
Brassica rapa ssp *campestris* (L.) A.R. Clapham	field mustard					16													
Raphanus raphanistrum L.	wild radish									2	2				0.125		8		8
CARYOPHYLLACEAE																			
Agrostemma githago L.	corncockle		1		8	32	20	24		8		16		48	32	36		104	8
Arenaria serpyllifolia L.	thyme-leaved sandwort																		
Silene L.	campion					8													
CYPERACEAE																			
Carex L.	sedge																		
CONVOLVULACEAE																			
cf. *Cuscuta* L.	dodder																		

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
FABACEAE																			
Vicia L. / *Lathyrus* L. (1-2mm)	vetch / lathyrus	8						4				16							
Vicia L. / *Lathyrus* L. / *Pisum L.* (>2mm)	small-seeded vetch / lathyrus / pea													2					
cf. *Vicia* L. / *Lathyrus* L. / *Pisum* L. (>2mm)	large-seeded vetch / lathyrus / pea								4										
Pisum sativum L.	common pea																		
c. f. *Pisum sativum* L.	common pea																		
Trifolium L.	clover																		
LINACEAE																			
cf. *Linum* L.	flax																		
JUNCACEAE																			
Juncus L.	rush																		
MALVACEAE																			
cf. *Malva sylvestris* L.	mallow															4			
ONAGRACEAE																			
Epilobium L.	willowherb																		
PAPAVERACEAE																			
Papaver L.	poppy					8											8		

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Papaver argemone L.	pale poppy					8													
Papaver somniferum L.	opium poppy																		
cf. *Papaver somniferum* L.	opium poppy																		
PLANTAGINACEAE																			
Plantago lanceolata L.	ribwort plantain				8					4									
Veronica hederifolia L.	ivy-leaved speedwell							8											
POACEAE	grasses																		
Avena fatua L. chaff	wild oat chaff					4													
Bromus arvensis L. / *hordeaceus* L. / *secalinus* L.	brome grasses	32	6	8	32	24	24	24	16	8	36	32	1	8	16	48	192	100	40
germinated *Bromus* L.	brome grasses																		
Phleum pratense L.	timothy grass									4	8		16	8	16		16		8
Phleum L.	timothy grasses												4		16	16	8	8	8
Poaceae > 1 mm	larger grass seeds																16		
Poaceae < 1mm	small grass seeds				8				8										

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Poaceae (small) rachis node / internode																			
Poaceae culm node							16												
POLYGONACEAE																			
Polygonaceae	knotweed family																		
Fallopia convolvulus (L.) Á.Löve	black bindweed	72		72	248	8		16								4	8		
cf. *Fallopia convolvulus* (L.) Á.Löve (achene)	black bindweed	104		48	232		8	8		12	8		4			12			
Fallopia convolvulus (L.) Á.Löve shell	black bindweed						8	8					1				8		
Polygonum aviculare L.	knotweed			4															
Rumex L.	dock / sorrel																		
PRIMULACEAE																			
cf. *Anagallis* L.	pimpernel																		
ROSACEAE																			
Rubus L.	blackberry/raspberry etc					16	8												
RUBIACEAE																			
Galium L.	bedstraw																		

Context / sample no.		17013	17018	17023	17026	19036	19046	19049	19061	19070	19073	23077 A	23302	23325	23333 slot 1	23340	23365	23370	23371
Galium verum L.	lady's bedstraw													8					
SOLANACEAE																			
Solanaceae	nightshade					16													
cf. Solanaceae	nightshade															8			
Hyoscyamus niger L.	henbane																		
URTICACEAE																			
Urtica urens L.	small nettle								16										
INDETERMINATE																			
Seed					16	4	8	120	16	24	18	16	32	40	8	32	8		8
Seed germinated					8														
Seedcoat							8				2		4	8	8	16	32		
Fruit stone									4										
Fruit skin fragment																			

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
Context type	layer	layer	ditch fill	layer	layer	pit fill	layer	ditch fill	layer	layer	spread	layer	layer	posthole	spread	fill	layer	kiln fill	layer	ditch fill
Sample size (litres)	**5**	**60**	**40**	**20**	**20**	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**10**	**20**	**10**	**20**	**10**	**20**	**18**	**10**
Total % sorted	**100**	**25**	**12.5**	**100**	**50**	**100**	**100**	**100**	**50**	**12.5**	**25**	**100**	**100**	**100**	**50**	**100**	**25**	**100**	**12.5**	**100**
CEREALS																				
Total cereal	205	1168	1429	568	640	461	367	640	728	1022	1488	600	1473	779	272	321	232	402	1812	189
Cereal indet.	40	249	337	187	148	194	169	180	233	72	352	184	232	184	162	130	88	127	304	84
Cereal indet. detached embryo with base	2	248	48	24	4	16	16	4	20	4	4	6	12	48			8	8	120	
Cereal indet. detached embryo			24			8	16	8	20	2	8	6	4	12			2	8	40	8
Total cereal chaff			88	16	24	24	16	12	64	4				24	32	16	32			16
Cereal indet. chaff fragment				8	8		16		16	2					8	4				
Cereal indet. culm node			32			8		4						8			8			4
Triticum (free-threshing)	66	93	483	98	79	38	55	138	339	346	275	163	508	45	12	18	20	117	49	19
Triticum aestivum rachis node														4						

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
Triticum aestivum rachis internode				8												4				
cf. *Triticum aestivum* chaff																				
Secale cereale	60	714	352	200	216	123	67	106	104	248	450	191	500	460	78	108	76	113	1298	35
Secale cereale rachis node			32		8	16			28					12	24	8	24			8
Secale cereale rachis internode			8						20											
Triticum (free-threshing) / *Secale cereale*	24	36	144	44	112	59	53	48	32	112	136	56	216	37	8	27	26	26	96	4
Hordeum vulgare total	13	48	89	33	57	27	11	41	10	240	259	2	9	25	10	23	16	6	57	27
Hordeum vulgare hulled straight	5	16	8	4	20	7		10	1	72	57	2		4	2	9	4	5	16	6
Hordeum vulgare hulled twisted	8	32	65	20	29	16	8	15	1	150	130		1	17	5	12	12	1	33	14
Hordeum vulgare hulled indet			16	9	8	4	3	16	8	18	72		8	4	3	2			8	7
Hordeum vulgare six-row rachis node			16							2										4

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
Hordeum vulgare six-row rachis internode																				
Hordeum vulgare indet. rachis node					4															
Hordeum vulgare indet. rachis internode					4															
cf. *Hordeum*																				
Secale cereale / *Hordeum vulgare*				4				1	8			2				6			8	
Secale cereale / *Hordeum vulgare* rachis node																				
Secale cereale / *Hordeum vulgare* rachis internode								8												
Triticum (free-threshing) / *Hordeum vulgare*	2	8	0.125	2		8	12	62	2		16			12	2	7	4	7	0.125	10
Avena			24		28	12		20		4			8			2	2	4		10
Avena floret base																				
Avena / large *Poaceae*		16	16	12	28	14		12		8		2					6			8

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
S. cereale/ Avena		20						44				2		16				2		
AMARANTHACEAE																				
Atriplex										4					4	4				
cf. *Atriplex* core																				
Atriplex patula / hastata / prostrata			8					4												
Chenopodium album								4		4		4			4	4			8	
cf. *Chenopodium album*																				
Chenopodiaceae	2				8	32	16	20		26						36		8	32	
Chenopodiaceae core											4		4							8
ASTERACEAE																				
Anthemis cotula				8			8						8			4		4	16	
Asteraceae					4															
Centaurea																				
APIACEAE																				
Apiaceae																				
BORAGINACEAE																				
Buglossoides arvensis																				

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
BRASSICACEAE																				
cf. *Alliaria*																				
Barbarea													8							
Brassicaceae	2				8						4									
Brassicaceae in pod																	2			
Brassica								8										4	24	
Brassica / Sinapis			16	8	8						8	4		8		5	6	28	64	1
Brassica rapa ssp *campestris*						8													16	
Raphanus raphanistrum			8			1									1				8	
CARYOPHYLLACEAE																				
Agrostemma githago	6	116	8	40	16	9					32	4	8	24	5	28		8	120	
Arenaria serpyllifolia																				
Silene																				
CYPERACEAE																				
Carex	4				8															
CONVOLVULACEAE																				
cf. *Cuscuta*																4				
FABACEAE																				
Vicia / Lathyrus (1-2mm)			8	8				8										2	8	4

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
Vicia / *Lathyrus* / *Pisum* (>2mm)		0.25	8										8							
cf. *Vicia* / *Lathyrus* / *Pisum* (>2mm)																				
Pisum sativum							2													
c. f. *Pisum sativum*																				
Trifolium																				
LINACEAE																				
cf. *Linum*																				
JUNCACEAE																				
Juncus																				
MALVACEAE																				
cf. *Malva sylvestris*																				
ONAGRACEAE																				
Epilobium													4							
PAPAVERACEAE																				
Papaver				8										4						
Papaver argemone																				
Papaver somniferum																			8	
cf. *Papaver somniferum*																			8	

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
PLANTAGINACEAE																				
Plantago lanceolata					4														8	
Veronica hederifolia		8																		
POACEAE																				
Avena fatua chaff																				
Bromus arvensis / hordeaceus / secalinus	18	120	40	36	108	78		16	24	34	16	12	20	56	18	33	44	16	32	6
germinated *Bromus*																				
Phleum pratense			24	24			8		4				4	4	24	32	32	12	72	24
Phleum		16	8	24				4				2		8		20		4	8	
Poaceae > 1 mm					4					8										
Poaceae < 1mm				16	20	16									8				8	
Poaceae (small) rachis node / internode					8															
Poaceae culm node			16		4									8						
POLYGONACEAE																				
Polygonaceae																				
Fallopia convolvulus		8	16	8	16	1	4			2		70	56	8		4		19	8	

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
cf. *Fallopia convolvulus* (achene)	2			16		16	8		8			65	252	8	4		10	16	8	
Fallopia convolvulus shell												28	40		4	5	2	4		
Polygonum aviculare				8																
Rumex				8																
PRIMULACEAE																				
cf. *Anagallis*																				
ROSACEAE																				
Rubus																				
RUBIACEAE																				
Galium																				
Galium verum																				
SOLANACEAE																				
Solanaceae																				
cf. Solanaceae																				
Hyoscyamus niger																				
URTICACEAE																				
Urtica urens																	2			

Context / sample no.	23372	23375	23505	23609	23621	23624	23643	23645	23647	23650 A	23650 B	23660	23662	23709	23710	23712	23714	23719	23722	23723
INDETERMINATE																				
Seed	2	40	16	8	24	43	32	17	8	2		38	16	32	16	84	8	4	184	40
Seed germinated		8											24							
Seedcoat			32					12	8		12		8	16	48		6	4	64	16
Fruit stone																				
Fruit skin fragment														4						

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
Context type	layer	fill	spread	layer	layer	layer	layer	layer	layer	layer	layer	layer	layer	layer	layer	layer	layer
Sample size (litres)	**5**	**14**	**15**	**10**	**20**	**7**	**10**	**16**	**20**	**20**	**18**	**20**	**20**	**20**	**20**	**20**	**20**
Total % sorted	**12.5**	**50**	**100**	**100**	**100**	**100**	**50**	**50**	**50**	**50**	**50**	**12.5**	**50**	**50**	**50**	**100**	**100**
CEREALS																	
Total cereal	968	1669	366	422	673	720	1085	638	659	915	1158	1497	526	833	915	187	115
Cereal indet.	252	545	102	131	205	280	417	125	113	157	345	208	125	84	76	29	21
Cereal indet. detached embryo with base	32	144	8	10	32	32	56	56	8	72	96	88	20	12	40		2
Cereal indet. detached embryo	12	40	8	4	8		8			48	40	8	8	20			
Total cereal chaff			8		48	72	32	56	64	136	168		24	20			1
Cereal indet. chaff fragment						16			8	56	32		8	12			
Cereal indet. culm node													8				
Triticum (free-threshing)	16	636	56	29	161	92	145	85	73	76	48	64	20	28	16	4	15
Triticum aestivum rachis node					8				8								

Context / sample no.	**23727**	**23754**	**23646 G/H7**	**23337 I6**	**23005 I8**	**23701 J5**	**23701 J7**	**23701 K6**	**23701 K8**	**23701 L5**	**23701 L7**	**23701 M6**	**23701 M8**	**23701 N5**	**23701 N7**	**23701 O6**	**23713 O8**
Triticum aestivum rachis internode											8						
cf. *Triticum aestivum* chaff										8							
Secale cereale	592	329	114	238	173	196	258	313	321	602	583	1185	285	621	731	136	66
Secale cereale rachis node					32	40	24	40		16	48		4				
Secale cereale rachis internode						8		16	24					8			
Triticum (free-threshing) / *Secale cereale*	84	88	20	12	36	56	105	40	68	8	140	16	64	56	80	10	6
Hordeum vulgare total	24	40	62	12	70	72	153	72	76	64	37	8	28	28	12	7	5
Hordeum vulgare hulled straight	4	16	16	8	9	21	40	12	8	12	12		4	4	8	2	1
Hordeum vulgare hulled twisted	12	8	22		37	31	65	32	48	24	21	8	16	12	4	2	2
Hordeum vulgare hulled indet	8	16	24	4	24	16	48	28	20	28	5		8	12		3	2
Hordeum vulgare six-row rachis node					8				8	24	24		4				

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
Hordeum vulgare six-row rachis internode										8	8						1
Hordeum vulgare indet. rachis node			8				8										
Hordeum vulgare indet. rachis internode																	
cf. *Hordeum*						4											
Secale cereale / *Hordeum vulgare*					4					8	4	8					
Secale cereale / *Hordeum vulgare* rachis node						8			16	24	40						
Secale cereale / *Hordeum vulgare* rachis internode																	
Triticum (free-threshing) / *Hordeum vulgare*		32	12						8					12			
Avena					24	24	8	4					4	4		1	2
Avena floret base											8						

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
Avena / large *Poaceae*					8	68			12		8	16	4	24	16		
S. cereale / *Avena*											1	8					
AMARANTHACEAE																	
Atriplex																	
cf. *Atriplex* core				4													
Atriplex patula / hastata / prostrata																	
Chenopodium album									8								
cf. *Chenopodium album*																	
Chenopodiaceae	20	8	8	2	32	240	344	32	24		104	16					2
Chenopodiaceae core				2													
ASTERACEAE																	
Anthemis cotula	4										8						
Asteraceae				4													
Centaurea																	
APIACEAE																	
Apiaceae								8									

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
BORAGINACEAE																	
Buglossoides arvensis																	
BRASSICACEAE																	
cf. *Alliaria*											8						
Barbarea																	
Brassicaceae					8	16										8	
Brassicaceae in pod																	
Brassica																	
Brassica / Sinapis		16	4	4	24				8								
Brassica rapa ssp *campestri*							8										
Raphanus raphanistrum								4									
CARYOPHYLLACEAE																	
Agrostemma githago	44	8	4	16	16	24		8	8	28	68	64	12	72	40	7	3
Arenaria serpyllifolia																24	8
Silene																	
CYPERACEAE																	
Carex																	

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
CONVOLVULACEAE																	
cf. *Cuscuta*																	
FABACEAE																	
Vicia / Lathyrus (1-2mm)			2			4						8					
Vicia / Lathyrus / Pisum (>2mm)				2													
cf. *Vicia / Lathyrus / Pisum* (>2mm)																	
Pisum sativum																	
cf. *Pisum sativum*																	
Trifolium											8						
LINACEAE																	
cf. *Linum*												8					
JUNCACEAE																	
Juncus						8											
MALVACEAE																	
cf. *Malva sylvestris*																	
ONAGRACEAE																	
Epilobium																	

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
PAPAVERACEAE																	
Papaver																	
Papaver argemone																	
Papaver somniferum																	
cf. *Papaver somniferum*																	
PLANTAGINACEAE																	
Plantago lanceolata			4					8							8		
Veronica hederifolia																	
POACEAE																	
Avena fatua chaff																	
Bromus arvensis / hordeaceus / secalinus	48	48	24	26	24	177	72	60	24	153	76	48	37	96	104	23	14
germinated *Bromus*						1											
Phleum pratense					8		8	8		8	8						
Phleum	8						8	16	8	16	24						
Poaceae > 1 mm						4											
Poaceae < 1mm		8	16	24	8	16	8										

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
Poaceae (small) rachis node / internode					88								8				
Poaceae culm node																	
POLYGONACEAE																	
Polygonaceae																	
Fallopia convolvulus	8	104	4			4	24										
cf. *Fallopia convolvulus* (achene)		104				8	8			8	8						1
Fallopia convolvulus shell		24															
Polygonum aviculare																	
Rumex																	
PRIMULACEAE																	
cf. *Anagallis*												8					
ROSACEAE																	
Rubus																	
RUBIACEAE																	
Galium																	1
Galium verum								8									

Context / sample no.	23727	23754	23646 G/H7	23337 I6	23005 I8	23701 J5	23701 J7	23701 K6	23701 K8	23701 L5	23701 L7	23701 M6	23701 M8	23701 N5	23701 N7	23701 O6	23713 O8
SOLANACEAE																	
Solanaceae																	
cf. Solanaceae																	
Hyoscyamus niger							8			8							
URTICACEAE																	
Urtica urens		8															
INDETERMINATE																	
Seed	36	8	8	2	256	24	48	56	8	40	32	24		24	32	32	24
Seed germinated																	
Seedcoat		8															32
Fruit stone																	
Fruit skin fragment	8											16					

II Archaeobotanical data from the Sedgeford settlement area assemblage, showing all quantified items

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Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
Context type		ditch	ditch	pit	posthole	undefined	pit	pit	pit	ditch	ditch	ditch	ditch	ditch	ditch	ditch	undefined	undefined	ditch
Sample size (litres)		**30**	**30**	**20**	**30**	**10**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**	**30**
Phase		**6**	**3**[117]	**7**	**7**	**U**	**U**	**7**[108]	**U**	**U**	**U**	**U**	**U**	**U**	**U**	**U**	**U**	**U**	**U**
	English nomenclature																		
CEREALS																			
Cereal indet.		80	66	221	149	64	294	224	100	662	304	264	271	124	136	326	40	134	87
Cereal indet. rachis node									8	4									
Cereal indet. detached embryo with base		8		24				8											

[117] Radiocarbon dating suggests an earlier date than the assigned phase (McKerracher, 2022a).

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
Cereal indet. detached embryo								16		5			2		1				
Cereal indet. chaff fragment				8				16		2									
Cereal indet. culm node												8	1						
Triticum L. (free-threshing)	wheat (free-threshing)	113	15	43	59			506	29	65	32	32	14	13	13	29	18	31	18
cf. *Triticum* L. (free-threshing)						24													
Triticum L.	wheat						24		58	57	24	40	16	11	7	11	9	19	14
cf. *Triticum* L.							1			23									
Triticum cf. *spelta* L.	spelt wheat									5			3	1				1	
Triticum L. rachis node									24	5			1	2	1			1	
Triticum L. rachis node (hexaploid type)					8			16	2							6			
Triticum L. / *Hordeum vulgare* L.	wheat/barley	12	2					8											
Secale cereale L.	rye	19	40	252	46		8	42		45		72	39	15	19	31	2	7	7

Context / sample no.		**15158**	**15187**	**15262**	**15355**	**15229**	**15467(A)**	**15467(B)**	**15467(S)**	**22048A**	**22048B**	**22048C**	**22048D**	**22048E**	**22048F**	**22048DOG**	**22086**	**22106**	**22180**
Secale cereale L. rachis node								16											
Secale cereale L. rachis internode								33											
cf. *Secale cereale* L.						16			2	28	16	8	14	10		18	5	3	
Secale cereale L. / *Avena* L.	rye / oat	4	12	24	82			160											
Secale cereale L. / *Hordeum vulgare* L. rachis node					8														
Secale cereale L. / *Triticum* L. free-threshing	rye / wheat (free-threshing)	28	9	73	16		8	40											
Hordeum L.	barley	7	8	24	15		20	35		50		24	40	8	18	24	2	11	9
Hordeum vulgare L. hulled straight			2	4	7			9		20			1	1		3	4	1	
Hordeum vulgare L. hulled straight germinated						8													

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
Hordeum vulgare L. hulled twisted		3	2	18	2		4	18		6						1		1	
Hordeum vulgare L. hulled indet.		4	4	2	6			9											
Hordeum vulgare L. six-row rachis node				8				8											
cf. *Hordeum* L.							8			23	8	32	14	7	4	16	2	7	8
cf. *Hordeum* L. (small)																			1
cf. *Hordeum* L. rachis node									2										
Avena L.	oat	4	7	24	32		145	17	4	81		56	32	25	10	37	7	14	
Avena L. germinated																1			
cf. *Avena* L.						8	307		8	232	216	200	99	42	24	87	6	54	9
Avena L. / large *Poaceae*	oat / large grass	4						41	26			1	7						
AMARANTHACEAE																			
Atriplex L. / *Chenopodium* L.	orache family / fat hen									2			1						
Chenopodiaceae	goosefoot family			32															

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
ASTERACEAE																			
Anthemis cotula L.	stinking mayweed									7			17	1	1			1	
Centaurea cyanus L.	cornflower					8				3									
Centaurea L.	knapweed			8															
BETULACEAE																			
Corylus avellana L. nutshell fragment	hazel												1						
BRASSICACEAE																			
Brassica L. / *Sinapis* L.	cabbage / mustard							8											
Raphanus raphanistrum L.	wild radish												1						
CARYOPHYLLACEAE																			
Agrostemma githago L.	corncockle		1	16										1					
cf. *Agrostemma githago* L.	corncockle									4						3			
Silene dioica (L.) Clairv.	red campion									11			6	1				1	1

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
CYPERACEAE																			
Cyperaceae	sedges																1		
Carex L.	sedge									1									
FABACEAE																			
Vicia L. / *Lathyrus* L. / *Pisum* L. (>2mm)	large seeded vetch / lathyrus / pea		2		2	1				25	8	13		3	3	16	3	8	
cf. *Vicia* L. / *Lathyrus* L. / *Pisum* L. (>2mm)	small seeded vetch / lathyrus / pea	6																	
Vicia L. / *Lathyrus* L. (1-2mm)	vetch / lathyrus		4						2	6		8	1			2		7	
Pisum sativum L.	pea			4						1		3	6		1				
cf. *Pisum sativum* L.	pea		1	1						1		16							
Vicia faba L.	broad been									1									
cf. *Vicia faba* L.	broad bean									2					1				1
LINACEAE																			
cf. *Linum usitatissimum* L.	flax															1			

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
POACEAE																			
Bromus L.	brome grasses	4		8															
cf. *Bromus* L.	brome grasses									12									
Bromus hordeaceus/secalinus L.	brome grasses									15			14	13	1				
cf. *Bromus hordeaceus/secalinus* L.	brome grasses						8					8	8			21	1	3	
Phleum pratense L.	timothy grass							8											
Poaceae (>2mm)	larger-seeded grasses									9				2					
Poaceae (<2mm)	small-seeded grasses									4			1		1	10		2	
Poaceae (small) rachis node										5					2	3			
Poaceae (small) rachis internode										1									

Context / sample no.		15158	15187	15262	15355	15229	15467(A)	15467(B)	15467(S)	22048A	22048B	22048C	22048D	22048E	22048F	22048DOG	22086	22106	22180
Poaceae (small) floret base									2	1									
Poaceae culm node									2										
POLYGONACEAE																			
Fallopia convolvulus (L.) Á. Löve	black bindweed									5			1		1	1	3		
Polygonum aviculare L.	knotweed	16		8															
Rumex L.	dock / sorrel									7		8		1		4	1		
RANUNCULACEAE																			
Ranunculus L.	buttercup															1			
ROSACEAE																			
cf. *Prunus* L. fruit stone	plum / cherry												1						
INDETERMINATE																			
Seed		16	42	84		8		16		17			14	5	3	5	5	3	3
Seedcoat fragment												8							
Fruit stone/nutshell fragment										4			4			1		1	5

Appendix D: Stable isotope data

Carbon and nitrogen stable isotope data for single-grain samples from the Sedgeford malting complex

Tables structured *after* Szpak *et al.* (2017 Appendix A)

DA and DB correspond to 'duplicate A', and duplicate B', respectively.

$\delta^{13}C_{VPDB}$ and $\delta^{15}N_{AIR}$ correspond to normalised $\delta^{13}C$ and $\delta^{15}N$, respectively.

All values are rounded to 2 decimal places *after* Szpak *et al.* (2017).

Session 1

Position	Sample	Type (standard type/sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
17	LEUCINE	Check	0.94	-28.27	6.56	-28.12	6.72	50.35	9.88	5.95
41	LEUCINE	Check	0.99	-28.20	6.27	-28.05	6.43	58.81	11.53	5.95
51	LEUCINE	Check	0.96	-28.29	6.24	-28.14	6.40	50.12	9.78	5.98
73	LEUCINE	Check	0.96	-28.31	6.16	-28.16	6.31	46.21	8.96	6.02
84	LEUCINE	Check	0.94	-28.03	6.30	-27.88	6.45	84.92	16.70	5.93
18	P2	Check	0.76	-28.19	-1.70	-28.04	-1.61	68.40	7.78	10.26
42	P2	Check	0.78	-28.14	-2.04	-27.99	-1.95	64.46	7.14	10.53
52	P2	Check	0.80	-28.17	-1.91	-28.02	-1.83	67.60	7.59	10.39
74	P2	Check	0.74	-28.15	-2.15	-28.00	-2.06	53.74	5.78	10.84
83	P2	Check	0.81	-28.01	-2.19	-27.86	-2.10	67.88	7.42	10.67

Position	Sample	Type (standard type/sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
11	COW	Calibration	1.00	-24.53	7.69	-24.35	7.86	42.96	15.58	3.22
33	COW	Calibration	1.10	-24.58	7.82	-24.39	7.99	40.42	14.73	3.20
50	COW	Calibration	1.06	-24.47	7.78	-24.29	7.94	38.59	13.99	3.22
58	COW	Calibration	1.08	-24.54	7.82	-24.35	7.99	42.58	15.56	3.19
86	COW	Calibration	0.99	-24.45	7.79	-24.26	7.96	46.34	16.86	3.21
12	SEAL	Calibration	1.00	-12.81	15.93	-12.50	16.16	42.78	15.46	3.23
34	SEAL	Calibration	1.13	-12.91	15.93	-12.60	16.16	41.25	15.04	3.20
49	SEAL	Calibration	1.06	-12.84	15.89	-12.53	16.13	39.84	14.48	3.21
57	SEAL	Calibration	1.04	-12.87	15.75	-12.57	15.99	39.65	14.46	3.20
85	SEAL	Calibration	1.03	-12.77	15.79	-12.46	16.02	43.09	15.66	3.21
15	ALANINE	Calibration	1.03	-26.98	-1.56	-26.82	-1.47	41.28	16.02	3.01
23	ALANINE	Calibration	1.08	-26.98	-1.58	-26.82	-1.49	46.77	18.08	3.02
31	ALANINE	Calibration	1.11	-26.97	-1.66	-26.81	-1.57	42.63	16.38	3.04
39	ALANINE	Calibration	1.04	-27.23	-1.86	-27.07	-1.77	32.57	12.63	3.01
47	ALANINE	Calibration	1.15	-26.97	-1.59	-26.81	-1.50	40.89	15.74	3.03
55	ALANINE	Calibration	1.08	-27.11	-1.62	-26.95	-1.53	41.93	16.25	3.01
63	ALANINE	Calibration	1.06	-27.18	-1.85	-27.02	-1.76	37.70	14.66	3.00
71	ALANINE	Calibration	1.00	-27.03	-1.73	-26.87	-1.64	36.83	14.26	3.01
79	ALANINE	Calibration	1.09	-27.08	-1.64	-26.92	-1.55	42.38	16.60	2.98
87	ALANINE	Calibration	1.11	-27.03	-1.67	-26.87	-1.58	41.75	16.25	3.00
92	ALANINE	Calibration	1.07	-27.02	-1.69	-26.85	-1.60	41.14	16.01	3.00
9	SED01A	Sample	2.59	-21.92	2.77	-21.72	2.89	41.74	2.55	19.08

Position	Sample	Type (standard type/sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
10	SED01C	Sample	2.48	-21.00	1.57	-20.80	1.68	44.05	2.85	18.05
13	SED01E	Sample	2.62	-22.44	5.37	-22.31	5.49	44.72	4.46	11.71
14	SED01G	Sample	2.61	-21.36	0.84	-21.23	0.92	46.23	3.94	13.68
19	SED01J	Sample	2.59	-20.99	0.65	-20.77	0.73	45.68	3.22	16.54
20	DA_SED02A	Sample	2.65	-20.85	1.00	-20.63	1.07	47.40	3.44	16.07
21	DB_SED02A	Sample	2.64	-20.99	0.85	-20.78	0.91	46.32	3.42	15.79
22	SED02B	Sample	2.55	-21.14	0.72	-20.94	0.78	48.55	3.66	15.49
25	SED02H	Sample	2.60	-20.67	2.05	-20.46	2.17	49.55	5.07	11.40
26	SED02I	Sample	2.60	-20.98	4.42	-20.78	4.55	48.23	3.72	15.15
27	SED04A	Sample	2.59	-20.68	2.86	-20.49	2.99	50.20	4.44	13.18
28	SED04C	Sample	2.56	-20.90	4.14	-20.73	4.27	51.09	3.70	16.11
29	SED04G	Sample	2.50	-21.90	1.99	-21.76	2.11	36.67	2.21	19.35
30	SED04I	Sample	2.57	-19.68	2.45	-19.53	2.57	49.09	3.44	16.62
35	DA_SED05A	Sample	2.59	-22.30	2.29	-22.09	2.39	43.72	3.85	13.25
36	DB_SED05A	Sample	2.60	-22.18	1.96	-21.97	2.05	46.88	4.07	13.45
37	SED05B	Sample	2.65	-22.03	2.79	-21.82	2.88	46.57	4.01	13.56
38	SED05C	Sample	2.52	-21.32	-0.15	-21.11	-0.09	44.31	3.68	14.03
43	SED05D	Sample	2.60	-21.07	4.56	-20.82	4.76	45.82	4.44	12.05
44	SED05E	Sample	2.61	-21.11	3.75	-20.85	3.96	47.59	4.11	13.53
45	SED06A	Sample	2.58	-23.21	2.36	-22.97	2.58	37.11	2.39	18.11
46	SED06B	Sample	2.61	-23.74	7.46	-23.49	7.74	41.92	2.67	18.30
53	SED06F	Sample	2.56	-23.94	2.01	-23.78	2.12	46.54	2.22	24.44

Position	Sample	Type (standard type/sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
54	SED06G	Sample	2.61	-24.68	1.88	-24.52	1.99	41.97	2.33	21.03
59	SED06I	Sample	2.56	-23.79	2.98	-23.64	3.09	44.41	2.42	21.43
60	SED07A	Sample	2.57	-21.04	1.73	-20.87	1.81	29.20	1.55	21.91
61	SED07B	Sample	2.53	-20.36	3.28	-20.20	3.37	35.27	2.11	19.50
62	SED07C	Sample	2.54	-22.80	3.89	-22.68	3.99	35.90	2.05	20.45
65	SED07H	Sample	2.62	-21.94	2.46	-21.72	2.62	32.38	1.73	21.90
66	SED07I	Sample	2.52	-19.92	2.27	-19.68	2.46	38.32	2.85	15.69
67	DA_SED08A	Sample	2.61	-21.82	1.50	-21.59	1.71	36.08	1.87	22.46
68	DB_SED08A	Sample	2.54	-21.76	1.87	-21.52	2.12	36.01	1.83	22.90
69	SED08B	Sample	2.48	-20.24	1.42	-19.98	1.70	42.37	3.22	15.36
70	SED08F	Sample	2.64	-21.22	4.45	-20.96	4.79	40.25	2.30	20.45
75	SED08G	Sample	2.56	-20.95	4.88	-20.72	4.98	34.87	2.20	18.47
76	SED08I	Sample	2.53	-21.80	2.61	-21.57	2.68	29.80	1.56	22.25
77	DA_SED09A	Sample	2.53	-23.19	3.25	-22.97	3.31	38.78	2.15	21.00
78	DB_SED09A	Sample	2.62	-23.12	2.81	-22.90	2.86	43.30	2.47	20.48
81	SED09C	Sample	2.60	-22.83	3.78	-22.62	3.89	41.98	2.97	16.52
82	SED09D	Sample	2.57	-23.31	1.58	-23.11	1.66	43.68	1.83	27.88
89	DA_SED09F	Sample	2.51	-22.42	6.38	-22.22	6.57	43.95	3.31	15.48
90	DB_SED09F	Sample	2.57	-22.32	6.09	-22.13	6.30	44.05	3.23	15.92
91	SED09G	Sample	2.62	-24.37	0.73	-24.21	0.93	43.40	1.60	31.65

Session 2

Position	**Sample**	**Type** (standard type / sample)	**Mass (mg)**	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	**%C**	**%N**	**Atomic C:N**
14	LEUCINE	Check	0.99	-28.19	6.69	-28.06	6.64	52.61	10.26	5.98
29	LEUCINE	Check	0.92	-28.02	6.51	-27.85	6.50	56.15	11.05	5.93
52	LEUCINE	Check	0.98	-28.31	6.64	-28.08	6.60	45.63	8.87	6.00
74	LEUCINE	Check	0.96	-28.28	6.66	-28.00	6.71	57.23	11.16	5.99
90	LEUCINE	Check	0.96	-28.32	6.43	-28.07	6.48	52.83	10.28	5.99
108	LEUCINE	Check	0.99	-28.26	6.54	-27.95	6.61	56.43	11.00	5.98
13	P2	Check	0.84	-27.97	-1.62	-27.83	-1.67	65.76	7.30	10.51
28	P2	Check	0.84	-27.95	-1.87	-27.77	-1.89	65.72	7.44	10.30
51	P2	Check	0.75	-28.08	-1.58	-27.85	-1.62	65.55	7.25	10.54
73	P2	Check	0.77	-28.16	-1.80	-27.90	-1.77	70.30	7.83	10.48
89	P2	Check	0.80	-28.11	-1.63	-27.86	-1.60	74.08	8.22	10.51
107	P2	Check	0.81	-28.00	-2.28	-27.72	-2.24	61.57	6.80	10.56
11	COW	Calibration	1.00	-24.37	7.93	-24.32	7.93	43.31	15.69	3.22
21	COW	Calibration	1.08	-24.34	7.72	-24.20	7.71	44.00	16.03	3.20
41	COW	Calibration	0.99	-24.42	8.00	-24.33	8.04	38.94	14.22	3.20
67	COW	Calibration	1.03	-24.44	7.92	-24.35	7.92	43.53	15.84	3.21
78	COW	Calibration	1.01	-24.49	7.79	-24.33	7.89	40.75	14.81	3.21
99	COW	Calibration	1.13	-24.47	8.00	-24.37	7.98	42.98	15.64	3.21
12	SEAL	Calibration	1.09	-12.64	16.13	-13.07	16.13	44.62	16.13	3.23
22	SEAL	Calibration	1.04	-12.73	15.95	-13.04	15.93	40.36	14.73	3.20

Position	Sample	Type (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
42	SEAL	Calibration	1.12	-12.89	16.12	-13.26	16.18	41.42	15.02	3.22
68	SEAL	Calibration	1.08	-12.65	16.18	-13.03	16.18	43.41	15.81	3.20
81	SEAL	Calibration	1.01	-12.84	16.10	-13.19	16.16	41.94	15.27	3.21
98	SEAL	Calibration	0.98	-9.66	16.07	-10.14	16.09	39.44	14.49	3.18
15	ALANINE	Calibration	1.14	-27.04	-1.46	-26.97	-1.54	40.07	15.55	3.01
23	ALANINE	Calibration	1.04	-27.07	-1.47	-26.82	-1.52	42.53	16.52	3.00
31	ALANINE	Calibration	1.08	-26.90	-1.60	-26.81	-1.65	41.29	15.99	3.01
39	ALANINE	Calibration	1.05	-26.99	-1.54	-26.79	-1.52	41.06	15.90	3.01
47	ALANINE	Calibration	0.98	-27.03	-1.58	-26.91	-1.56	42.75	16.53	3.02
55	ALANINE	Calibration	1.03	-27.06	-1.66	-26.89	-1.78	36.41	14.14	3.00
63	ALANINE	Calibration	1.07	-27.03	-1.67	-26.76	-1.55	42.47	16.46	3.01
71	ALANINE	Calibration	1.15	-27.03	-1.58	-26.86	-1.66	42.61	16.50	3.01
79	ALANINE	Calibration	1.08	-27.11	-1.55	-26.85	-1.46	40.08	15.60	3.00
87	ALANINE	Calibration	1.00	-27.09	-1.66	-26.93	-1.64	42.65	16.47	3.02
95	ALANINE	Calibration	1.11	-27.09	-1.57	-26.92	-1.49	39.80	15.41	3.01
103	ALANINE	Calibration	1.12	-27.00	-1.51	-26.82	-1.62	41.80	16.14	3.02
111	ALANINE	Calibration	1.10	-27.07	-1.64	-26.78	-1.56	38.11	14.75	3.01
115	ALANINE	Calibration	1.04	-27.11	-1.61	-26.92	-1.56	38.08	14.75	3.01
9	SED10A	Sample	2.54	-20.73	4.02	-20.78	4.04	39.83	2.88	16.12
10	SED10D	Sample	2.60	-20.84	5.27	-20.91	5.28	42.90	4.54	11.03
17	SED10E	Sample	2.52	-22.83	3.88	-22.78	3.90	45.39	2.28	23.23
18	SED10G	Sample	2.65	-21.32	2.22	-21.32	2.23	44.87	2.14	24.43

Position	Sample	Type (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
19	SED10H	Sample	2.63	-20.53	5.37	-20.55	5.37	40.85	3.78	12.60
20	SED11A	Sample	2.60	-20.36	2.99	-20.38	2.98	44.35	4.97	10.42
25	SED11D	Sample	2.59	-21.58	2.40	-21.60	2.42	46.46	4.25	12.75
26	DA_SED11E	Sample	2.50	-19.60	3.58	-19.71	3.59	43.14	4.58	10.98
27	DB_SED11E	Sample	2.55	-19.58	3.65	-19.71	3.65	42.77	4.53	11.02
30	SED11G	Sample	2.56	-21.56	5.32	-21.67	5.29	47.61	3.35	16.59
33	SED11I	Sample	2.64	-19.77	7.14	-19.84	7.18	39.46	3.03	15.18
34	DA_SED12A	Sample	2.59	-24.05	0.62	-23.96	0.64	39.92	3.10	15.04
35	DB_SED12A	Sample	2.61	-24.02	1.22	-23.93	1.25	41.14	3.29	14.59
36	SED12B	Sample	2.58	-22.55	5.82	-22.52	5.86	46.45	5.81	9.33
37	SED12E	Sample	2.60	-18.97	10.77	-19.08	10.81	43.57	4.67	10.89
38	SED12F	Sample	2.53	-22.52	3.51	-22.50	3.54	37.14	2.28	18.97
43	SED12J	Sample	2.48	-22.66	5.07	-22.66	5.11	43.63	2.61	19.53
44	SED16A	Sample	2.59	-22.62	2.27	-22.63	2.30	47.92	2.02	27.74
45	SED16B	Sample	2.49	-22.48	3.72	-22.52	3.75	48.16	2.44	23.05
46	SED16C	Sample	2.52	-19.19	11.11	-19.36	11.16	43.44	3.51	14.45
49	DA_SED16F	Sample	2.65	-22.61	0.89	-22.57	0.90	43.72	2.34	21.75
50	DB_SED16F	Sample	2.56	-22.59	0.85	-22.56	0.83	45.83	2.47	21.61
53	SED16H	Sample	2.53	-21.30	4.45	-21.34	4.38	46.86	2.49	21.96
54	SED17A	Sample	2.48	-21.07	2.59	-21.12	2.50	43.36	3.33	15.21
57	SED17B	Sample	2.51	-22.55	0.86	-22.50	0.90	45.63	2.67	19.91
58	DA_SED17C	Sample	2.54	-22.57	0.86	-22.51	0.91	46.80	2.60	21.01

Position	Sample	Type (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
59	DB_SED17C	Sample	2.50	-22.54	1.45	-22.48	1.52	47.49	2.66	20.83
60	SED17D	Sample	2.54	-19.95	3.74	-19.98	3.83	47.38	4.02	13.75
61	SED17E	Sample	2.62	-21.18	5.03	-21.15	5.14	43.92	5.73	8.95
62	SED18D	Sample	2.58	-22.15	4.67	-22.08	4.79	44.96	3.43	15.30
65	SED18E	Sample	2.65	-23.11	5.19	-23.05	5.21	37.12	1.83	23.69
66	SED18G	Sample	2.58	-22.74	8.03	-22.71	8.04	49.36	5.70	10.11
69	SED18I	Sample	2.54	-23.27	4.88	-23.23	4.84	44.36	2.71	19.09
70	SED19A	Sample	2.52	-22.03	5.07	-22.05	5.02	49.12	3.49	16.42
75	SED19B	Sample	2.65	-19.86	3.20	-19.91	3.26	47.10	3.03	18.14
76	SED19C	Sample	2.57	-20.33	7.79	-20.35	7.87	46.00	2.65	20.28
77	SED19D	Sample	2.58	-21.56	2.88	-21.53	2.96	50.11	2.65	22.09
82	DA_SED20C	Sample	2.61	-21.18	3.75	-21.21	3.78	46.01	2.90	18.50
83	DB_SED20C	Sample	2.64	-21.16	3.80	-21.20	3.83	46.36	2.85	19.01
84	SED20D	Sample	2.54	-20.92	3.38	-20.98	3.41	42.53	2.94	16.87
85	SED20E	Sample	2.56	-21.51	5.33	-21.55	5.37	43.53	4.02	12.63
86	SED20H	Sample	2.51	-23.03	3.13	-23.03	3.15	47.15	3.16	17.41
91	SED21C	Sample	2.58	-24.80	3.16	-24.69	3.21	45.56	1.90	28.02
92	SED21E	Sample	2.59	-21.81	3.60	-21.83	3.66	48.46	3.23	17.52
93	SED21G	Sample	2.63	-23.42	4.27	-23.38	4.34	47.41	1.96	28.16
94	SED21H	Sample	2.65	-23.98	4.76	-23.92	4.84	44.46	1.90	27.29
97	SED18J	Sample	2.57	-24.51	5.17	-24.40	5.18	37.49	1.64	26.70
100	SED19H	Sample	2.54	-20.61	5.21	-20.66	5.17	43.93	3.21	15.99

Position	Sample	Type (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
101	DA_SED20G	Sample	2.50	-21.43	3.34	-21.46	3.27	46.09	3.52	15.28
102	DB_SED20G	Sample	2.66	-21.45	3.23	-21.48	3.14	40.20	3.10	15.14
105	SED28J	Sample	2.52	-20.43	12.28	-20.46	12.34	45.38	2.56	20.69
106	SED29J	Sample	2.61	-21.49	-0.31	-21.47	-0.27	42.71	5.05	9.88
109	SED30I	Sample	2.61	-23.09	3.34	-22.98	3.41	44.98	2.53	20.73
110	SED31D	Sample	2.61	-20.89	0.53	-20.85	0.61	39.07	2.71	16.83
113	SED32I	Sample	2.57	-22.29	1.94	-22.26	1.98	43.54	2.97	17.08
114	SED33E	Sample	2.59	-23.52	2.15	-23.46	2.20	46.34	2.21	24.49

Session 3

Position	Sample	**Type** (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
18	LEUCINE	Check	0.97	-28.28	6.88	-28.07	7.01	52.15	10.26	5.93
35	LEUCINE	Check	0.98	-28.23	6.59	-28.03	6.72	56.06	11.02	5.93
52	LEUCINE	Check	0.94	-28.40	6.63	-28.23	6.76	49.96	9.73	5.99
61	LEUCINE	Check	0.92	-28.41	6.65	-28.10	6.73	54.53	10.67	5.96
17	P2	Check	0.82	-28.08	-1.72	-27.88	-1.63	62.89	7.17	10.23
34	P2	Check	0.84	-28.03	-1.66	-27.83	-1.57	67.16	7.63	10.28
46	P2	Check	0.77	-28.00	-1.79	-27.88	-1.60	71.14	7.91	10.50
60	P2	Check	0.80	-28.20	-1.55	-27.92	-1.49	68.42	7.65	10.43
11	COW	Calibration	1.08	-24.35	7.66	-24.21	7.85	44.92	16.31	3.21
19	COW	Calibration	1.09	-24.62	7.93	-24.41	8.07	40.98	14.97	3.19
27	COW	Calibration	1.13	-24.55	7.75	-24.33	7.91	32.68	11.86	3.21
58	COW	Calibration	1.09	-24.53	7.93	-24.27	8.05	43.42	15.89	3.19
12	SEAL	Calibration	0.98	-12.67	15.71	-12.53	15.96	44.28	16.16	3.20
20	SEAL	Calibration	1.02	-12.82	15.87	-12.58	16.05	39.41	14.41	3.19
33	SEAL	Calibration	1.15	-12.72	15.90	-12.48	16.08	41.08	14.98	3.20
59	SEAL	Calibration	1.03	-12.85	16.07	-12.55	16.22	41.64	15.19	3.20
15	ALANINE	Calibration	1.02	-26.93	-1.81	-26.90	-1.59	46.30	17.92	3.01
23	ALANINE	Calibration	1.08	-27.13	-1.62	-26.92	-1.54	39.06	15.16	3.01
31	ALANINE	Calibration	1.06	-27.10	-1.85	-26.89	-1.72	41.61	16.12	3.01
39	ALANINE	Calibration	1.13	-27.00	-1.68	-26.81	-1.60	43.41	16.80	3.01

Position	Sample	Type (standard type / sample)	Mass (mg)	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	%C	%N	Atomic C:N
47	ALANINE	Calibration	1.15	-27.09	-1.68	-26.98	-1.48	42.37	16.45	3.01
55	ALANINE	Calibration	1.14	-27.16	-1.62	-27.02	-1.53	41.70	16.25	2.99
63	ALANINE	Calibration	1.11	-27.22	-1.59	-26.87	-1.56	40.74	15.82	3.00
67	ALANINE	Calibration	1.14	-27.04	-1.75	-26.81	-1.74	40.39	15.63	3.01
9	SED28B	Sample	2.61	-22.51	4.91	-22.31	5.06	49.72	2.90	20.00
10	SED28D	Sample	2.58	-21.18	2.44	-21.01	2.59	52.33	3.22	18.96
13	SED28E	Sample	2.65	-20.82	5.10	-20.73	5.32	46.79	3.66	14.91
14	SED28G	Sample	2.65	-20.74	3.34	-20.67	3.57	44.74	3.08	16.97
21	DA_SED29C	Sample	2.51	-22.09	1.53	-21.87	1.63	42.62	3.27	15.19
22	DB_SED29C	Sample	2.65	-22.05	1.58	-21.83	1.68	43.02	3.38	14.86
25	SED29D	Sample	2.52	-22.34	4.94	-22.12	5.07	42.10	3.93	12.49
26	SED29H	Sample	2.63	-19.85	1.32	-19.63	1.44	43.47	4.40	11.53
28	SED29I	Sample	2.65	-22.04	3.47	-21.82	3.62	45.32	3.93	13.46
29	DA_SED30C	Sample	2.48	-25.02	4.74	-24.81	4.90	66.71	5.85	13.30
30	DB_SED30C	Sample	2.56	-22.60	4.72	-22.39	4.88	44.14	3.50	14.73
36	SED30D	Sample	2.65	-22.24	3.89	-22.02	4.00	45.30	2.76	19.17
37	SED30E	Sample	2.64	-24.88	4.51	-24.68	4.63	43.15	2.16	23.30
38	SED30F	Sample	2.62	-22.47	4.30	-22.26	4.41	45.32	3.00	17.62
41	SED031A	Sample	2.65	-20.52	3.20	-20.31	3.33	42.58	3.71	13.38
42	DA_SED31B	Sample	2.49	-23.25	0.85	-23.06	0.99	46.10	2.14	25.11
43	DB_SED31B	Sample	2.60	-23.20	1.11	-23.03	1.26	46.93	2.13	25.66
44	SED31C	Sample	2.55	-21.62	2.06	-21.46	2.24	47.00	2.15	25.47

Position	**Sample**	**Type** (standard type / sample)	**Mass (mg)**	$\delta^{13}C_{raw}$	$\delta^{15}N_{raw}$	$\delta^{13}C_{VPDB}$	$\delta^{15}N_{AIR}$	**%C**	**%N**	**Atomic C:N**
45	SED31F	Sample	2.65	-22.89	3.54	-22.74	3.74	46.33	1.89	28.65
49	DA_SED32C	Sample	2.65	-19.82	2.36	-19.60	2.48	48.60	4.53	12.51
50	DB_SED32C	Sample	2.55	-19.77	2.32	-19.57	2.44	49.00	4.52	12.65
51	SED32E	Sample	2.62	-21.44	0.77	-21.25	0.87	44.68	2.84	18.39
53	SED32F	Sample	2.59	-22.11	6.63	-21.94	6.76	43.25	2.73	18.50
54	SED32H	Sample	2.57	-20.93	1.34	-20.77	1.45	46.95	3.16	17.34
57	SED33A	Sample	2.57	-23.40	2.79	-23.16	2.89	43.14	2.06	24.43
62	SED33B	Sample	2.64	-22.53	2.75	-22.19	2.80	41.83	2.05	23.82
65	SED33G	Sample	2.64	-24.02	3.59	-23.80	3.68	44.65	1.97	26.51
66	SED33J	Sample	2.60	-22.58	2.70	-22.35	2.76	50.71	2.53	23.37

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