

An investigation of differentiation between Cornwall and Devon based on history, surnames, and Y-chromosomes

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Abstract

Understanding genetic diversity among human populations can help uncover their histories. In 2015 the 'People of the British Isles' (PoBI) study of autosome-wide diversity revealed subtle but significantly different genetic clusters, including a clear distinction between the neighbouring counties of Cornwall and Devon; it proposed that Bodmin Moor and the River Tamar had formed a barrier between the two. This thesis uses a combination of historical, onomastic, and genetic approaches to investigate differentiation in this region in more detail.

A survey of the historical literature examines whether Cornwall has been isolated from the rest of England and the Continent. Evidence from archaeology, historical documents, and place-names shows that both Roman and Anglo-Saxon influence on Cornwall was less than that on Devon, supporting the idea of Cornish distinctiveness at least over the last two millennia. However, the historical record also shows abundant evidence for Cornwall's connectedness with the nearby nations of Ireland, Wales, and Brittany.

Based on census and parish records, research was undertaken to analyse the specificity and persistence over time of surnames of the people of the Bodmin Moor region between 1702 and 1881. This showed a lack of regionally-specific names, and clear evidence of input from Devon and the rest of England.

Analysis of the male-specific Y chromosome examined whether the autosomal Cornwall-Devon distinction seen in the PoBI study was also reflected in paternal lineages. Surname-ascertained samples were recruited from Bodmin Moor and supplemented with PoBI samples. DNAs were analysed with short tandem repeats and single nucleotide polymorphisms. Population genetic analysis supported Cornish distinctiveness, with Bodmin Moor more closely related to Devon. Differences are compatible with lower Anglo-Saxon influence on west Cornwall. Co-analysis with other datasets clusters Cornwall most closely with Wales and Ireland and supports affiliation with Brittany, while Bodmin Moor and Devon more closely resemble other English populations.

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Chapter 1 Introduction

The genetic diversity of human populations varies throughout the world and is affected by population movement and contact with, or isolation from, other populations. Characterising a population's genetic structure can provide insights into past demographic processes affecting the history of populations and the ways in which natural selection has acted upon them. Migrations and invasions in historical times have played an important role in shaping current patterns of genetic diversity, and studying this diversity can illuminate the histories, ancestry, population movements, and behaviours of the groups involved.

Evidence of the cultural impact of historical events can be uncovered using archaeology, place-names, and linguistics, but there is often debate about the corresponding influence of these factors on the demographics of the population. However, analysing the genetics of modern populations can offer an independent approach to recognising the impact of past migrations and colonisations.

A brief history of the use of genetic markers in population studies

The first genetic markers used to uncover population histories included blood groups (Menozzi et al., 1978) which were used to map patterns of variation in different regions of the world; this led to new hypotheses for the spread of agriculture in Europe via migration of farmers from the Near East (Cavalli-Sforza et al., 1993). In the 1980s DNA fragments were used to map out the patterns of variation at global and continental scales: maternally-inherited mitochondrial DNA was shown to have African roots, consistent with a recent origin of modern humans in Africa (Cann et al., 1987), while work done on the male-specific Y chromosome came to similar conclusions (Thomson et al., 2000). The sequencing of autosomal DNA segments also supported the out-of-Africa model for the recent origins of modern humans (Yu et al., 2002).

More recently, methods to assess variation at a genome-wide scale have allowed unbiased analysis of population diversity and relationships, revealing genetic clusters that correspond to continental regions (Rosenberg et al., 2002). Genome-wide variants were also analysed within European populations with indigenous ancestry; when genetic differences between individuals were plotted in two dimensions using principle component analysis, this showed a pattern resembling a map of Europe and demonstrated population structure at a within-continent scale, in which geographical distance was the main factor structuring the variation (Novembre et al., 2008). This offered the promise that recent migrations from one part of Europe to another (e.g. from the Continent to the British Isles) could in principle be detectable.

The People of the British Isles study and the singularity of Cornwall

The British Isles have been the recipient of countless immigrations and invasions during at least the last 2,000 years of recorded history, and doubtless through many more years of prehistory (Cunliffe 2012). Did these events simply involve changes in leadership by ruling elites or did they involve mass population movements? And did any invading populations leave a genetic signature on the current population of the British Isles?

To help answer these questions, a 2015 study in *Nature* (Leslie et al., 2015) studied the genomes of people who had local ancestry from different regions of the British Isles and found a striking coherence between geographical location and similar ancestry based on genome-wide variants. These variants were analysed in a way that detects subtle differences between genome types – these genetic differences within and between populations are known as population structure. The study attempted to interpret local clusters of genetic types in terms of contributions from migrating groups from elsewhere in Europe (described in more detail in Chapter 2). Among other localised features, the study found a distinct difference between people with ancestry from Cornwall compared to those with ancestry from Devon, neighbouring counties that make up the south western-most peninsula of England. The authors of the study pointed to a possible correlation of the genetic boundary

between the two counties with the natural geographical features of the region, such as the River Tamar and the rough upland area of Bodmin Moor. The suggestion was that these features could have acted as physical barriers inhibiting migration into Cornwall and leading to different amounts and types of immigration between the two regions. This observation of a Cornwall-Devon differentiation provides the motivation for the investigations carried out in this thesis.

Cornwall has had a long history of being considered different from the rest of England. Despite becoming part of the Anglo-Saxon empire in the 10th century, parts of Cornwall retained the Cornish language and customs until the 18th century; even today, some continue to fight for Cornish independence from the UK. Cornwall's location on the tip of the southwest peninsula may have added to a sense of separation from the rest of England, and other aspects of the Cornish landscape may have compounded this feeling, such as the vast, uncharted region of Bodmin Moor which lies at the forefront of the county, close to the border of Devon. The moor had no roads until the mid-19th century, and bad weather and dangerous peat bogs made it extremely difficult to cross- perhaps shielding the county from invaders arriving from the east. In contrast, Cornwall has been highly connected to other countries, via the sea, for thousands of years. All these factors could have led to the perception of Cornwall as a county different from the rest of England; there are many conflicting opinions about the nature and causes of Cornish distinctiveness - could genetic analysis of the population offer any resolution to this debate?

This thesis examines the question of Cornish 'difference' and what part Bodmin Moor played, if any, in contributing to this difference. It also looks at how Bodmin Moor may have affected the contact and therefore genetics of its surrounding communities, as well as between Cornwall and Devon itself - did it act as a boundary separating the two populations, thus contributing to the genetic divide seen in the autosomal data? Given that the male-specific Y chromosome generally shows higher geographical differentiation than autosomal markers within the same populations (Jobling & Tyler-Smith 2003), it might be expected that the genetic boundary between Cornwall and Devon would be even more strongly reflected in

their paternal lineages. In order to determine this, patrilineal surnames and local ancestry were used in the Y-chromosome variation analysis to see if there are any significant differences between the populations of Devon, Bodmin Moor, and mid/west Cornwall.

This project was conceived as an interdisciplinary investigation involving the areas of history, surname studies, and genetics, and was co-supervised by an academic geneticist and an academic landscape historian. The research undertaken, as reflected in this thesis, includes a historical investigation focused on the isolation (or otherwise) of Bodmin Moor and Cornwall in general, a study of the surnames of Bodmin Moor, and a molecular genetic analysis of male DNA samples through a comparison of Devon, Bodmin Moor, and Cornwall, and then in a broader context, employing genetic data from elsewhere within Britain and the Continent.

1.1 Cornwall

The aim of this chapter is to create a historical and geographical context for the events that shaped the genetics of the current population of Cornwall and Devon. In doing this, the dichotomy that is found in much of the literature about Cornwall is revealed, namely the opposing views regarding Cornwall's alleged isolation versus its connectedness with the outside world- aspects which could have affected the genetic diversity of the population.

Bernard Deacon (2007, p.1), a writer and academic based at the Institute of Cornish Studies, begins his book on the history of Cornwall with the assertion that "Cornish history is a battleground." Throughout Cornwall's written history, there has been a conflict between two opposing models of thought. On one hand Cornwall has been seen as having a separate historical narrative from the rest of England: Philip Payton (1996), professor of Cornish Studies at the University of Exeter, contends that in each historical period, Cornwall's experience has been highly individual when compared with that of the English 'centre' or the rest of Britain. This school of thought considers Cornwall a separate nation and its people a separate ethnic group, more akin to the Celtic regions of Wales and Scotland than to the English. Deacon (2007) attributes this stance to the survival of a Celtic-speaking population

which existed until the end of the 18th century; Deacon (p.4) believes this factor is also responsible for the fact that Cornwall remains “the one part of England where not all indigenous inhabitants automatically describe themselves as English,” but rather claim their nationality as Cornish. In 2014, Cornish distinctiveness did receive formal recognition: Cornish people were granted ‘national minority’ status by the UK Government under the terms of the Council of Europe's ‘Framework Convention for the Protection of National Minorities’ (UK Gov 2014), meaning they had the same status as other Celtic minorities – the Scots, the Welsh, and the Irish - within the UK. Cornish history, culture, and language were key factors influencing the decision.

Much of the debate on Cornish ‘difference’ centres on the idea that the current inhabitants of Cornwall are descended from the Celtic-speaking ‘native’ British tribes that resisted integration with many of the invaders who came and settled in the British Isles- such as the Romans, the Anglo-Saxons, and the Vikings- until the 10th century when they were forced to join the Anglo-Saxon kingdom of the newly-unified England (Deacon 2007). Until this time, they had retained their own Celtic-based language and culture and were considered a distinct ‘race’, seemingly resisting influence from the changing mainland cultures despite almost 1,000 years of foreign rule by various groups. The neighbouring county of Devon, on the other hand, became thoroughly integrated into mainland society and lost its Celtic-based language and culture hundreds of years earlier than Cornwall, beginning with its submission to Roman rule around 50AD and then its assimilation into Anglo-Saxon England around 700AD.

The other side of the debate does not recognise Cornwall's distinctiveness as a nation or a unique people, stressing that for over 1,000 years Cornwall has been an integrated county of England, and much more Anglicised than the other Celtic-speaking nations of Wales and Scotland. J.P.D. Cooper (2003, p.3), lecturer of Early Modern history at the University of York, argues that by at least the 15th century, Cornwall was located within England’s “national imagination” as well as its administrative and judicial framework - and that it is the similarities between ‘English’ Devon and ‘Celtic’ Cornwall that stand out, rather than the differences. Some attribute Cornwall’s stance on their alleged racial difference as a product of recent

nationalism in order to promote a political agenda (Deacon et al., 2003) while others, such as Mark Stoye, professor of Early Modern English history at the University of Southampton, believe that the Cornish have a long history as a 'separate people' whose culture, politics, and religion are British rather than English (Stoye 2002). Cornwall has been portrayed in these opposing ways, both by its natives as well as outsiders, for most of its known history and the truth probably lies somewhere in between. Can a study of the genetics of the modern-day populations of southwest England contribute new evidence to this debate?

1.2 Cornwall's reputation

Many historical as well as current writers describe the county of Cornwall as being 'isolated,' 'remote,' and sometimes not even part of England. The image of Cornwall as a wild and uncivilised periphery of the mainland (see figure 1.1) has a long history: for many, England appeared to terminate at the Tamar River which, for over 1,000 years, has been the historical as well as legal boundary between Cornwall and its neighbouring county of Devon. Cornwall was considered, by those on the east side of the border at least, as out of the reach of civilisation and carrying a questionable reputation: folklore warned that even the Devil avoided Cornwall as he had no wish to be made into a squab pie, which was the fate of anyone who ventured west of the Tamar (Deane & Shaw 1975). In 1506 a Venetian diplomat stuck in Cornwall during a storm described it as "a very wild place which no human being ever visits, in the midst of a most barbarous race so different in language and customs from the Londoners and the rest of England that they are as unintelligible to these last as to the Venetians" (Griffiths 2003, p.181). Their reputation still hadn't improved by the 18th century, when tales of men who wrecked ships in order to loot their cargo enforced the image of a lawless people living on the edge of civilised behaviour as well as on the edge of the land (Deacon 2004). As for the Cornish point of view, many regard themselves as the original British people, descendants of the Celts, and inhabitants of a land set apart- where the English can still be seen as not just strangers but as foreigners (Wade 1928).

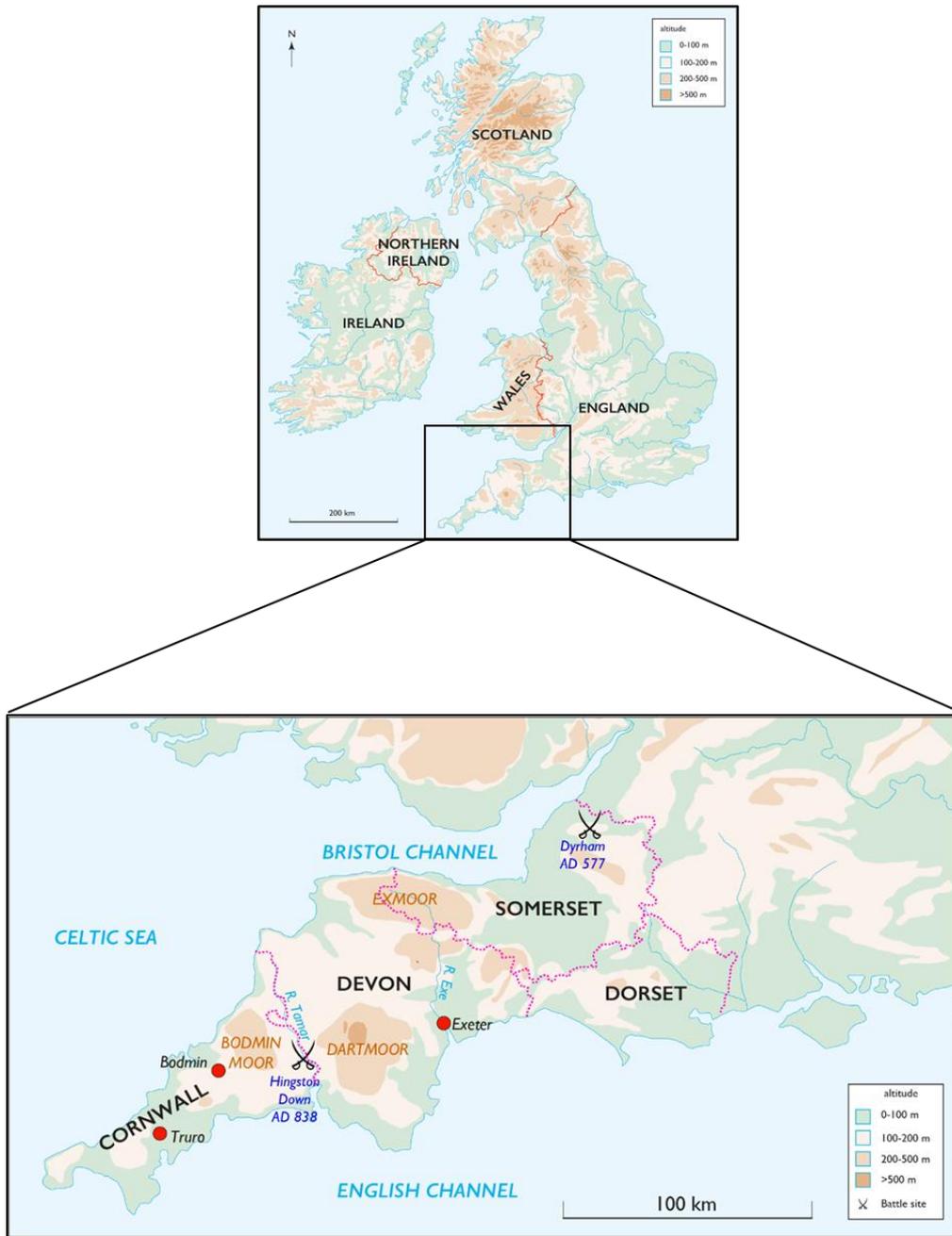


Figure 1.1 Map of the British Isles and the southwest peninsula Adapted from Cunliffe (2012). County borders are outlined in pink. Major battles affecting Cornish history are shown, as are the major towns and moors in Cornwall and Devon.

1.3 Cornwall's landscape

“Cornwall is different in scenery, customs, and climate” from the rest of England (Hammond 1967, p.5) – so begins a 1967 tour guide of Cornwall. But much of Cornwall's reputation of being different from England is also due to its marginal location. Stoye (1997, p.22) calls

Cornwall “the most remote and inaccessible county in southern England” due to its being almost completely surrounded on all sides by water - the River Tamar spans 61 miles, almost the entire length of the Devon-Cornwall border, making Cornwall almost an island. Writing in 1603 while on a tour of his native Cornwall, antiquarian Richard Carew (1953, p.83) described it as “the farthest part of the realm,” “... enwrapt with the sea on all sides, except towards Devonshire, and there bounded by the River Tamar, which in a right line runs almost from sea to sea.” Carew believed that these characteristics of the Cornish landscape may have helped to deter or delay any invasions arriving overland from England.

Adding to Cornwall’s inaccessibility was the fact that until 1837 there were very few roads leading to Cornwall from the rest of England. The phrase ‘out of the world and into Bodmin’ described the difficulty of reaching Cornwall by land - Bodmin being the first town past the vast wilderness of Bodmin Moor, and still extremely inaccessible from the “world” - meaning England (Wade 1928, p.160). And while reaching Cornwall via overland routes may have been difficult, once there, it was not much easier to travel throughout the county itself. In a 1754 article for a London-based magazine, Cornwall was described as having “... the worst roads in all England, a great part of which are intolerable” (Axford 1975, p.25). Cornwall did not get paved roads until the 1940s and even today, many of the roads are just high-banked paths which have evolved out of ancient trackways built for a horse and cart or for driving animals to market, with the course they take determined by the topography of the landscape (Balchin 1983).

The geology and topography of Cornwall and much of the southwest peninsula (which also includes Devon and Somerset), are different from the rest of England and this may have contributed to differences in how their inhabitants settled on the land (Payton 1996). In contrast to the broad valleys and open countryside of most of England, Cornwall has both deep valleys and areas of high ground, forming a more fragmented landscape. This leads to the main settlement pattern being one of dispersed hamlets comprised of a few farmhouses joined by narrow lanes which are seemingly unplanned and created based on local needs, with many just leading from farm to farm (Balchin 1983). In contrast to the larger Anglo-

Saxon villages found in most of England, travel writer J.H. Wade (1928, p.3) describes Cornish towns and villages as “small, isolated, and peculiar... either wedged into the nooks and crannies of the coast and estuaries or mounted on the tops of hills above the wooded valleys.”

Cornwall has some of the highest ground in England. These upland areas make the lower ground, where most settlements are located, difficult to access, and can create isolated areas shielded from outside influence (Todd & Fleming 1987). Whyte et al. (2004) believe that these enclaves each have the potential to develop a distinctly local culture which can be reflected in the diversity of dialects spoken throughout Cornwall. A 1978 survey by the Institute of Cornish Studies found that throughout Cornwall many different dialects (words, pronunciations, and grammar) were still very localised and existed within a small circumference (North et al., 1980); these regional forms of speech were especially preserved within the agricultural communities which make up Cornwall's oldest industry. This was attributed to a lack of immigration or contact with outsiders, along with other factors such as local settlement patterns, historical administrative divisions, ancient linguistic frontiers, and natural barriers such as rivers, marshes, and upland moors (North et al., 1980). Any of the above aspects of the Cornish landscape could have contributed to keeping segments of the population protected from incoming invaders, thus affecting the genetics of the population overall.

1.4 Cornish language

While Stoye (1997) believes that Cornwall's remoteness, its scattered pattern of settlement, and its unique history all helped to differentiate it from the rest of England, he states that above all, it was the language which set the county apart. Despite being part of England from the 10th century, the Cornish language was spoken in parts of Cornwall until the 18th century when English became the dominant language, spread by immigration as well as by the introduction of Protestantism which banished the use of Latin and Cornish within the Church.

The Cornish language belongs to the Brittonic branch of the Celtic language known as P-Celtic and is most closely related to Breton and Welsh; the Goidelic branch, which is known

as Q-Celtic, developed into Gaelic (Irish, Scottish, and Manx) (Price 1984). Exactly when these languages first arrived in Britain is a subject of debate: the previous language of the inhabitants may have been pre-Celtic (as is suggested by a few Scottish river names (Price 1984)), but it is thought that Celtic speech first arrived in Britain from the Continent in the early Bronze Age around 2,000BC (Cunliffe 2012), and then developed into the Brittonic and Goidelic branches during the Iron Age (after 800BC) (C. Thomas 1973).

Any information on the languages spoken in Britain is due to Greek (from 325BC) and Roman (up to 500AD) historians who had contact with the British Isles (Jackson 1953). Their writings indicated that Celtic languages were spoken all over the British Isles and Western Europe until the Roman Empire brought in Latin (Deacon 2007), although Celtic languages continued to be spoken in some parts of the British Isles. When the Anglo-Saxons began arriving at the end of the 5th century AD, the peoples of England, Wales, and south Scotland spoke the Brittonic form of the Celtic language, while Gaelic was spoken in Ireland, the Isle of Man, and the rest of Scotland (Trudgill 1984). But in 577AD the Anglo-Saxons divided the territory held by the native Britons in the west and north into three separate areas and the British language diverged from this point, splitting into Welsh, Cornish, and Cumbrian (in the north), which died out soon after (Price 1984).

The Anglo-Saxon language of Old English replaced the Celtic languages throughout Britain almost completely by the 7th century; this was partly due to the Anglo-Saxons renaming the places they settled in, which helped to cement the language while also maintaining their identity and power (Rose & Preston-Jones 1995). English was also the language of trade so anyone who wanted to participate had to speak it, and because the Anglo-Saxons appear to have entered at all levels of the social hierarchy, this brought the English language to all levels of British society. By the 9th century, English was spoken up to the Welsh border in the west and the Devon border in the south-west; beyond that, the native languages of Welsh and Cornish were retained for a few hundred years.

In 1350 Cornish was still spoken by most people except in the eastern parts of Cornwall, but by 1450 the county was almost equally divided between Cornish and English speakers (Stoyle

2002). Beginning in the early 16th century, the Protestant Reformation brought in an English-language prayer book, as opposed to the Latin one that the Cornish church had been using. Soon Cornish was the dominant language in only west Cornwall (Payton 1996) and by the end of the 17th century only fishermen and market-women still spoke it in the southern-most parts of the county, and the decline accelerated after that (Padel 1988). Cornish was still spoken in fishing villages, perhaps due to the contact with Breton speakers from Brittany, but had died out by 1800, except for a few words of dialect in the far west still in use (Padel 1988), although there have been attempts at a revival of the language in recent years.

Deacon (2004) believes that with the demise of the Cornish language, there was no equivalent decline in Cornish identity- instead, this was increasingly expressed by attachment to territory rather than to the spoken tongue: he refers to the link between Cornish-language surnames and Cornish place-names as “echoing a wider connection between people and place” (Deacon 2004). Price (1984, p.309) puts it most aptly when he quotes 19th century Cornish- language scholar Henry Jenner: now the Cornish language only exists in the form of “idioms, provincialisms, words and phrases, and still more apparently, in the names of every hill, farm, river, rock, stream, or well, and of the descendants of those who once spoke it.”

1.4.1 Cornish Language Place-names

Although Cornish was spoken until the 18th century, there are virtually no writings in Cornish- only a few manuscripts and medieval plays. The only remnant of the language is in Cornish-language place-names and surnames, and this “faint but constant echo of the county's non-Englishness” (Marsden 2014) has played a vital part in attempts to reassemble the vocabulary and structure of the Cornish language. Place-names in Cornwall are predominantly Celtic and Cornwall is the only English county where Celtic place-names outnumber English ones- 30% of Cornish place-names begin with the Cornish-language element ‘tre-’ (meaning ‘settlement or homestead’ (Padel 1988)), and the majority of the rest incorporate other Cornish- language elements. Many Cornish-language surnames are taken from place-names and begin with the prefix ‘tre-’ (discussed fully in Chapter 3).

With about 1,200 examples in total, place-names starting with 'tre-' occur almost throughout Cornwall, as shown in figure 1.2 below. They extend up to the county boundary marked by the River Tamar, except towards the north- and south-east where the names are more similar to those of Devon: here the most common place-names contain the Old English element '-tun,' which the Anglo-Saxons used to denote their newly established settlements (Rose & Preston-Jones 1995). In Devon, by contrast, there are only three 'tre-' place-names, two of them near the boundary with Cornwall; the overall concentration of Celtic place-names in Devon is virtually the same as in the other counties of England, where they remain a tiny minority (Padel 2007).

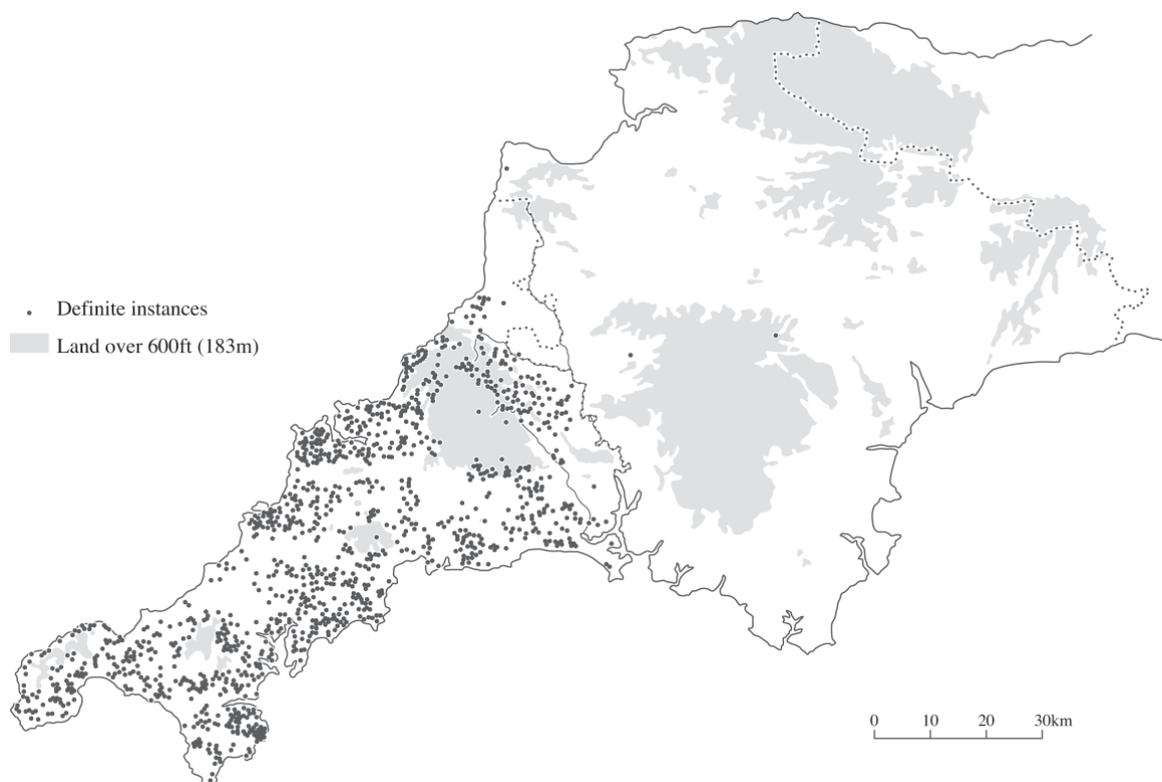


Figure 1.2 *Distribution of place-name element 'tre-' (Padel 2007) The majority are in Cornwall, only three are found in Devon*

1.5 History of Cornwall and its connections

Cornwall's location on the periphery of England, its challenging overland routes and convoluted inner topography, and its distinctive language all may have given it a reputation of isolation and separateness. But while Cornwall may be seen as comparatively isolated from the perspective of the rest of England, it has never been so in relation to nations overseas. Cornwall has over 300 miles of coastline and the sea is never more than 20 miles away at any point (Cornwall Council 2019), and these have been key factors in its relations with the outside world. W.G.V. Balchin (1983), author of *The Cornish Landscape*, believes that sea-borne cultures have altered Cornish history more significantly than influences from England – whereas land communications to and within Cornwall were difficult well into the 19th century, its many estuaries, ports, and rivers have allowed Cornwall to sustain maritime links for thousands of years with Europe, the Mediterranean, and especially its Celtic-speaking neighbours in the Atlantic Sea Zone: Ireland, Wales, and Brittany.

1.5.1 Prehistory

Although Britain was populated prior to the last Ice Age, no humans survived the glacial period. Archaeological evidence (Cunliffe 2012) suggests that after the Ice Age ended (around 9,600BC), Palaeolithic hunter-gatherers entered the British peninsula, which was still joined to Continental Europe by land, from two routes: over land from north-eastern France, Belgium, and Germany, and by sea, from the Atlantic Sea Zone countries of western France and Brittany. The Atlantic Sea Zone countries were part of a trade route that exchanged goods, culture, new technologies, and people, tracing back to the 5th millennium BC (Cunliffe 2012), and therefore would have had great influence on some of the earliest settlers of the British Isles. Figure 1.3 shows a timeline of the known history of Cornwall.

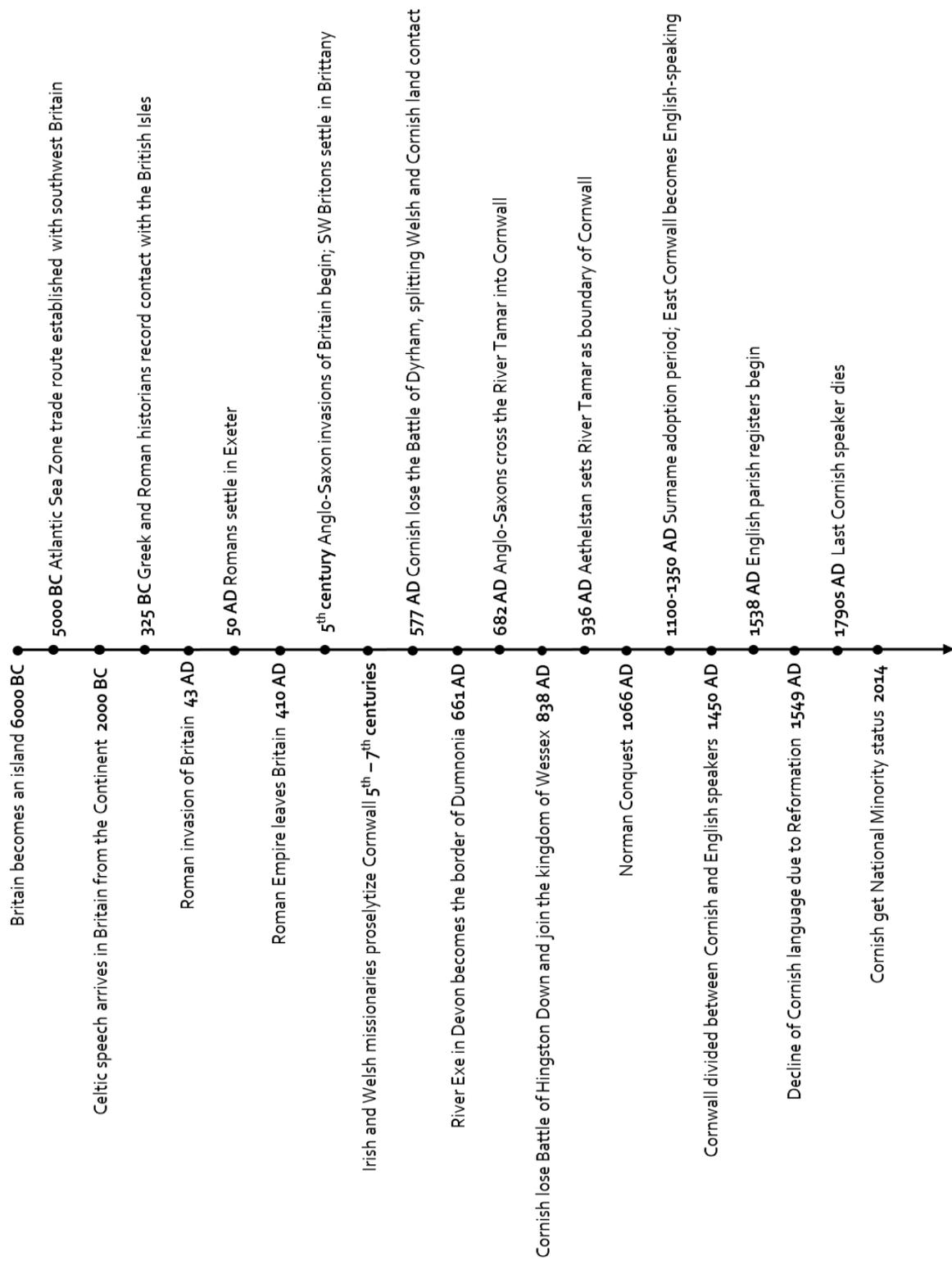


Figure 1.3 Cornish history timeline

Around 6,000BC Britain became an island and by 5,000BC Britain was well populated by hunter-gatherer communities (Cunliffe 2012). British archaeologist Barry Cunliffe (2012) cites evidence from 4,200–3,800BC which suggests movements of people from southern Brittany into Ireland, coastal Wales, western Scotland, and possibly south-west Britain. The evidence includes burial monuments in Britain and Ireland also found in a region of southern Brittany, structures which are among the earliest megalithic tombs found in the British Isles. Figure 1.4 shows the same type of tomb monuments found in Ireland, Wales, and Cornwall, but not the rest of England.

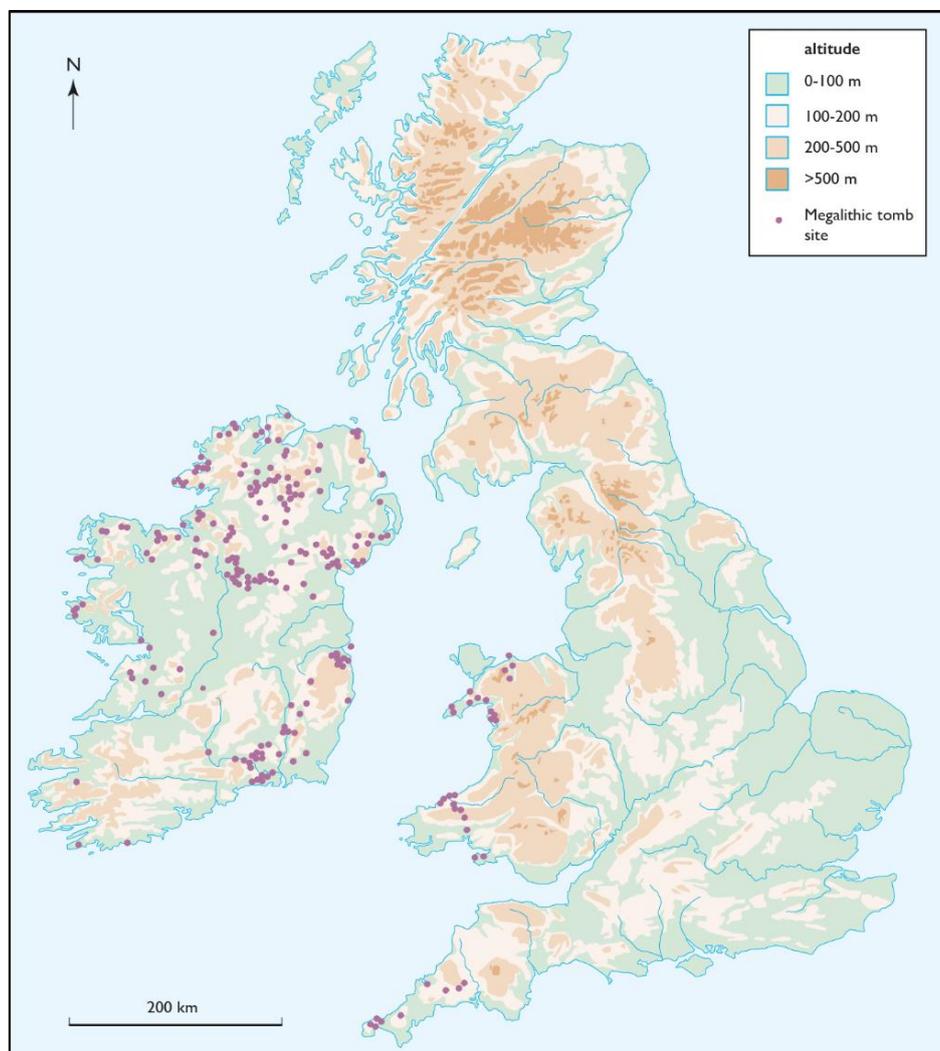


Figure 1.4 *Megalithic tombs in the Atlantic Sea Zone* Adapted from Cunliffe (2012). The Atlantic Sea Zone countries shared culture and technology with SW Britain

By the Bronze Age (2500BC- 800BC), Payton (1996, p.42) describes Cornwall as a “window to a wider world” due to its sea trade of tin and metal goods. He believes that any claims that the Cornish are parochial or inward-looking have always been false: there is extensive archaeological evidence revealing trade in metals with the Atlantic Sea Zone countries- Ireland, Wales, Cornwall, and Brittany all had copper, tin, and gold, and the south-west of Britain and Brittany were in especially close contact during the 2nd millennium BC (Cunliffe 2012). F. E. Halliday (2001), author of *History of Cornwall*, observes that, based on the lack of material evidence found from the Bronze Age, while the Tamar River appears to have isolated Cornwall from the rest of England, the north Cornish coast was a port for Irish traders on their way to France, and there were trade routes from the Mediterranean to Brittany and Scotland. Due to this Atlantic seaboard traffic, Halliday believes that Cornwall had more in common with the cultures across both Channels than with that beyond the Tamar in England. There is also evidence of prehistoric trackways which reveal a major path across Cornwall linking the English Channel on the south coast to St George’s Channel on the north coast, which is thought to have been a Bronze and Iron Age trade route between Brittany and Ireland, used in order to avoid travelling by sea around the peninsula (Balchin 1983).

Much of the trade between Cornwall and other nations would have been due to the abundance of Cornish tin. Tin was an essential component of making bronze but it was rare throughout most of Europe, except for in Cornwall and Brittany (Cunliffe 2012). As far back as the 5th century BC, the Greek historian Herodotus mentions the existence of tin-rich islands in the Atlantic known as the Cassiterides (Cunliffe 2012), which some have taken to mean the Isles of Scilly off the west Cornish coast (Deane & Shaw 1975); in the 4th century BC a Greek geographer wrote about mining tin at Land’s End, in the far west of Cornwall, which was then sold to Gaul (Halliday 2001). There has also been much debate about the location of the famous offshore semi-island of Ictis which was described as a tin-trading centre in the 1st century BC, although there may have been a number of ports on the south coast of Cornwall and Devon being used for trade at this time (Cunliffe 2012). Pytheas, an explorer from Marseille, made a first-hand study of Britain in about 320BC, witnessing the tin trade between Cornwall and Gaul, and from this moment Britain enters written history.

Until written records existed, the only information regarding the inhabitants of the British Isles comes from limited archaeological evidence. During the Iron Age and probably much earlier, it is thought that Britain was populated with Celtic-speaking tribes who had come from the Continent and intermarried with the natives (Cunliffe 2012), although it is also possible that Celtic influence was spread just through the language and culture rather than through the movements of people (Davies 2000). The Romans, who had been warring with the Gauls on the Continent, noted that the inhabitants of Britain spoke a similar language to the Continental Gauls and so referred to them by the term 'Galli,' from 'Gaels,' which is what the Gauls called themselves; the word 'Celt' comes from the Greek 'keltoi' meaning 'strangers,' and came to be used interchangeably with the term 'Gaul' during this time (Davies 2000). It is possible that the British Celts were related to the Gauls. Agricola, a Gallo-Roman general during the Roman conquest of Britain in the 1st century AD, wrote that the people of Britain physically resembled the Gauls, either due to a common origin or common climatic conditions, and noted that they also shared the same rituals and religious beliefs and spoke a similar language (Cunliffe 2012). The 16th century antiquary William Camden, author of the first comprehensive topographical survey of England, also thought that the British were a branch of the Gauls, based on a comparison of their languages, customs, and religion (Cunliffe 2012).

This belief that Britain was a Gallic nation led to an attempted invasion in 55BC: Rome was still at war with the Continental Gauls and the Roman emperor Julius Caesar believed the best way to subdue them was to also take control of the related Celtic tribes in Britain. Although he did not succeed, he documented their tribal names in Latin, as shown in figure 1.5. One of these tribes in the southwest was referred to as the 'Dumnonii' who are thought to have inhabited the lands covering the Isles of Scilly, Cornwall, Devon, and western Somerset (Munn 1976). During this time refugees from Caesar's armies arrived from Gaul and Belgium (Johnson 1990), such as the Veneti tribe from Brittany, who settled in Cornwall (Halliday 2001).



Figure 1.5 Tribes of Celtic Britain Adapted from Davies (2000) and Cunliffe (2012). The Dumnonii tribe inhabited part of the southwest peninsula

1.5.2 Roman influence on Cornwall

During the Iron Age, Rome and the Mediterranean bought tin from Cornwall. After his brief foray into Britain, Caesar had established political links and trade with the ruling houses and it was this contact that eventually led to the Roman invasion in 43AD, when the documented history of Britain begins. In the British Isles the Romans were met with various tribes who, although they shared a language group, were not a homogenous nation, but had distinctive regional cultures (Gearey et al., 2000), with probably limited population movement between them (Harvey et al., 1986). The Romans created a political and social infrastructure throughout most of Britain but outside of the Romanised towns, the British natives still lived

in the Celtic manner, mainly in hamlets with small hedged fields, and also retained many of their local customs (Halliday 2001). While Cornwall was technically part of the Roman Empire - called 'Cornubia' by the Romans, according to the 2nd- century Roman writer Ptolemy (Deacon 2007)- very little of the Roman way of life reached them: the Romans' administrative presence stretched only as far west as the city of Exeter in Devon and this allowed the Dumnonii to retain their autonomy, including their language and culture (C. Thomas 1973). Throughout the rest of England and Wales there were Roman towns and villas, industry, military forts, and trading centres, but west of the River Exe there were none of the usual features of Romano-British life such as major roads or permanent settlements (Besnier 1924). There are inscriptions bearing Roman emperors' names, which implies that these areas were part of the Roman Empire (C. Thomas 1973), as well as coins and paved courtyards, but there are no settlements or burial sites (Payton 1996). There are a few sites in Cornwall that show traces of Roman settlements, but this could mean that natives were trading with the Romans or living there using Roman pottery and coins, as by the mid-3rd-century Roman money was being used in Cornwall; this is in contrast to areas east of the River Exe where coins from all periods have been found. Payton (1996) believes that this implies that the Romans never settled in or occupied Cornwall but had contact mainly through commerce. After 200AD when Rome's supply of tin from Spain was depleted, they mined tin in west Cornwall where many Roman coins have been found, but Halliday (2001) believes that they reached the area by sea, leaving the inner lands of Cornwall untraversed. Figure 1.6 shows the lack of Roman towns and fortifications in Cornwall.

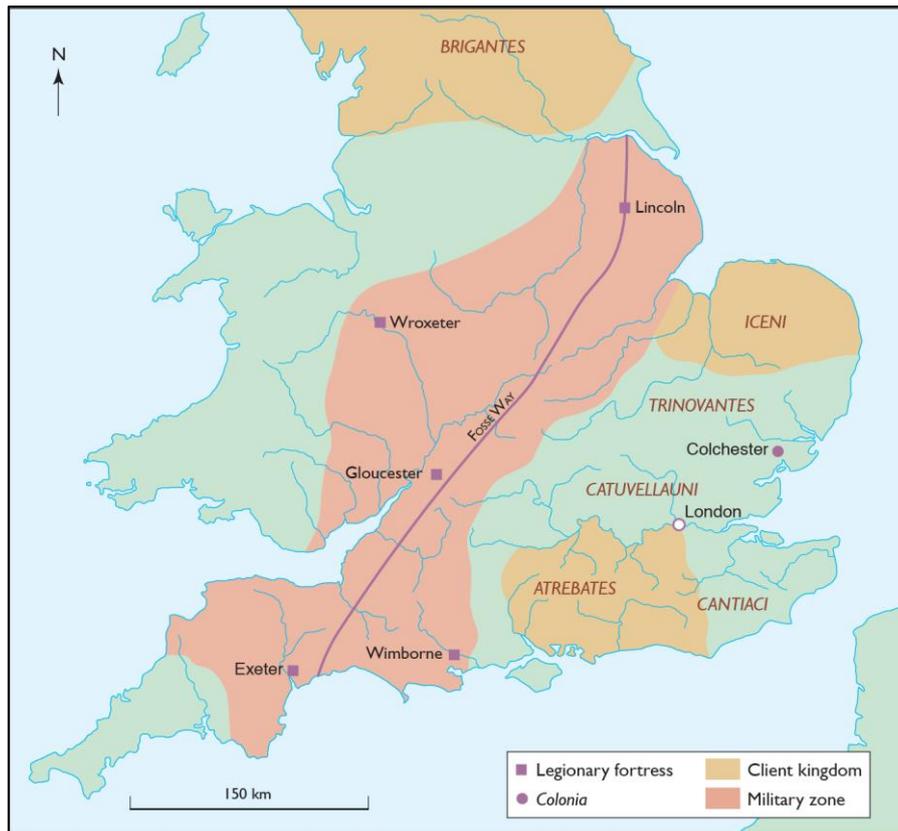


Figure 1.6 Roman Britain (Cunliffe 2012). The Romans did not expand far into Cornwall

Why the Romans didn't expand into Cornwall is a subject of debate. One reason could be that their supply of tin came from Spain so they had no need for Cornish resources - while Cornish tin had been mentioned in pre-Roman literature, no writer during the Roman Empire references tin from this area (Besnier 1924). The lack of Roman expansion could also be due to the fact that west beyond Exeter lay 368 sq miles of the rough uplands of Dartmoor, and then upon reaching Cornwall, 100 sq miles of Bodmin Moor – areas that were difficult to cross due to the lack of roads and the challenging topography. Perhaps these areas were natural stopping points for the Romans, leaving the lands between Exeter and the west coast of Cornwall relatively devoid of Roman culture. For whatever reason, when the Roman Empire left Britain in 410AD, the collapse of the infrastructure did not affect Cornwall to the extent that it did the rest of Britain. The Dumnonii, along with many of the other Celtic tribes outside of the Roman-settled areas in Britain, had retained their cultural identity and way of life during Roman rule (Turner 2006) and so when it ended, these areas were once again ruled by their tribal chieftains.

1.5.3 Contact with Ireland and Wales

Since prehistory, Cornwall has had close contact with Ireland and Wales, as the north coast of Cornwall lay along their overland trade routes to the Continent. Oliver Padel (2013b), a specialist in Cornish and Welsh studies, states that there are at least three documented immigrations from Ireland occurring between the 5th to the 16th centuries.

In the 3rd-4th centuries the Irish were raiding Wales and Cornwall and in the 5th century, Irish Christian missionaries, later called 'saints' by the Church, evangelised to the Cornish people who had retained Christianity after Rome retreated and whose Celtic traditions had become intertwined with Christian ones (Halliday 2001). The extent to which the Irish settled in Cornwall at this time is unclear since most of the datable inscriptions indicating an Irish presence are from the 6th century (Cunliffe 2012).

By the 6th-7th centuries, Welsh missionaries arrived via the north Cornish coast (Pearse 1983) and Irish missionaries were building monasteries in Cornwall, Wales, and Brittany, erecting chapels around the springs and wells that were worshipped by the Celtic population (Balchin 1983). Figure 1.7 shows holy sites in Cornwall named after Irish, Welsh, and Breton saints, the most famous of whom is the Irish St. Piran, the patron saint of Cornwall. St. Ives Bay, which is the nearest accessible landing from Ireland on the north coast of Cornwall, was named after the Irish saint Ia (Pearse 1983).

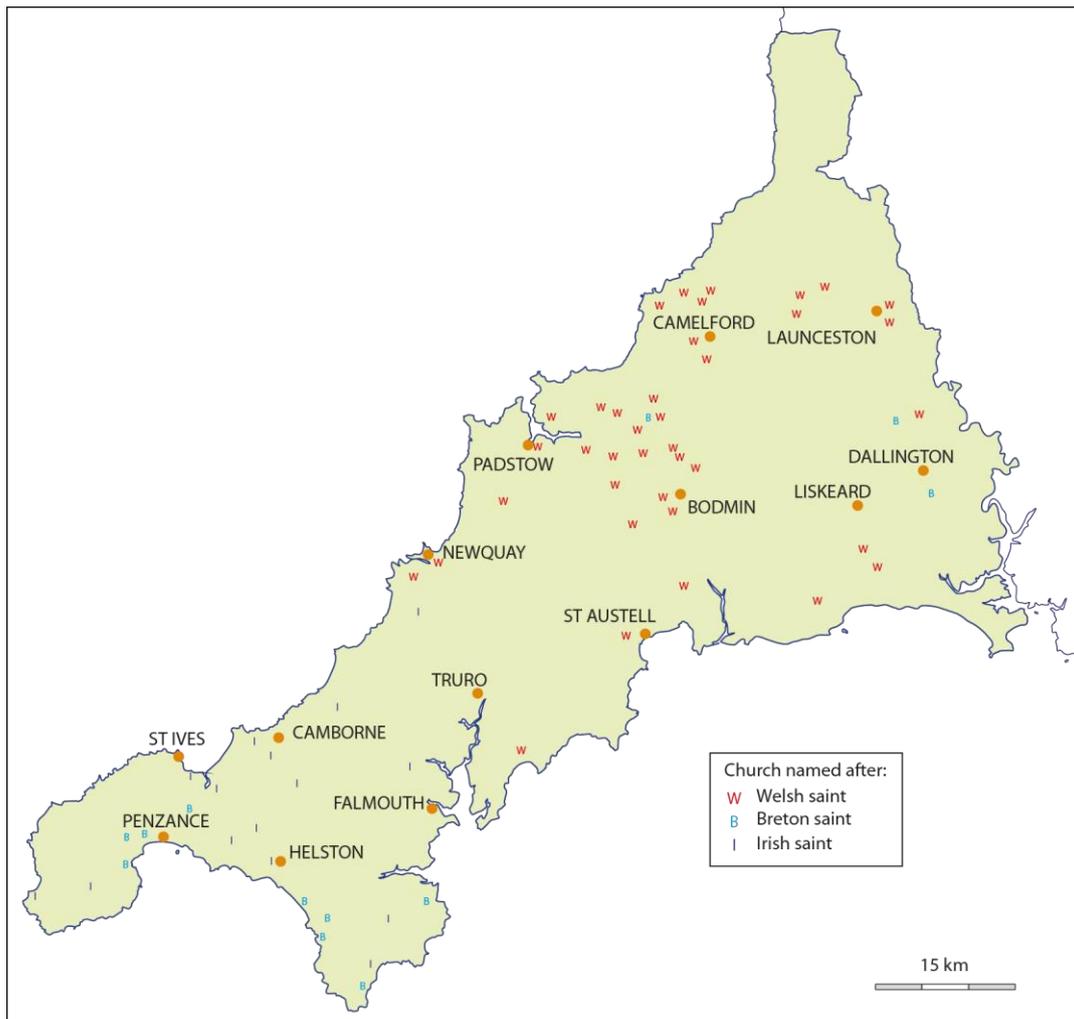


Figure 1.7 Saint sites in Cornwall Redrawn from Pearse (1983). Many of the holy sites were near the coasts, as the missionaries arrived from both north and south coasts

In addition to the monasteries, the Irish also left written monuments behind. During the 5th-6th centuries, Christian stones inscribed with the Ogham script, an early form of Irish writing, appeared in northeast Cornwall, and stones with Irish-language names written in Roman letters were found across the southwest peninsula (Padel 2013b). There are also standing stones with bilingual Irish/Latin inscriptions from the 5th-7th centuries near the north coast town of Padstow, suggesting that the Irish population was becoming integrated into the local Brittonic-speaking society of Cornwall (Padel 2013b).

There is additional documentary evidence of Irish habitation in Cornwall in the 12th-13th centuries in the form of taxation rolls, which list surnames containing variations of the word 'Irish' or 'Ireland' (Oliver Padel, personal communication), as well as surnames containing the Cornish word for 'Irishman' - from the Middle Cornish 'gwythel' or 'gothel' (Padel 1985b). There are also names of Irish slaves in Cornwall freed in the 10th century, Victorian-era documents listing Irish names as migrant labourers in Cornish mines (Padel 2013b), and in the 16th century the north-coast town of Padstow was recorded by antiquary John Leland as being "full of Irish men" (Padel 2009, p.14).

1.5.4 Contact with Brittany

Britain and France share a prehistory as part of the 'Atlantic fringe' of Europe (Payton 1996) which is seen in their archaeology and paleoclimatology, with Cornwall and Brittany sharing particularly close links. Their landmasses, now separated by approximately 100 miles of the English Channel (see figure 1.8), were once joined, and in more recent aspects of their history, their language, culture, and place-names are closely related, and their flags were inverses of each other until 1532 when Brittany became part of France.



Figure 1.8 Brittany and Cornwall (adapted from Google maps) Now separated by approximately 100 miles across the English Channel, their landmasses were once joined

Much of Brittany is coastline: before the 6th century AD, Brittany was known by the native Gauls as 'Armorica,' meaning 'the country near the sea' (Cunliffe 2012). According to Bede, an 8th century British monk who wrote extensively on British history, tradition held that the first people to settle in Britain originally came from Armorica (Cunliffe 2012). Thereafter, maritime contact between the two regions continued throughout the ages: there were more sailing routes to Brittany and Wales than overland routes to England throughout most of known Cornish history (Wilcox 1999); during the Bronze Age, Cornish tin was shipped to Armorica (Halliday 2001); during the Iron Age, axes from Armorica were imported into southwest Britain (Cunliffe 2012); and in the 1st century BC 'the Western Britons' were thought to have aided the natives of Armorica against Caesar's armies (Carew 1953). There were numerous migrations both ways between the southwest peninsula and Armorica, and after the Anglo-Saxons invaded Britain, Armorica became known as 'Brittany' due to all the British settlers who fled there (Franklin 2006). The first of these emigrations was written about 70 years after the fact by British chronicler Gildas in 540AD, describing how in 470AD the native British "sought lands beyond the seas with great lamentation" (James 1999); another emigration occurring around 510AD is also mentioned. However, author and archaeologist Simon James (1999), among others, has challenged Gildas' writings on the basis that they are a work of Christian polemic using Biblical allegories, rather than an accurate historical narrative.

However, Cunliffe (2012) believes that the exodus referred to by Gildas was just a continuation of the process of migration that had already been occurring for many centuries and that the duration of the migration to Brittany and its causes may have been more complex than Gildas acknowledged. The archaeological evidence shows that Armorican ports were in direct contact with the ports on the south coast of Britain, at least from the 3rd century AD, continuing a long tradition of maritime interaction going back into prehistory which would have included the movement of people. Based on linguistic and place-name evidence in Brittany, most of the incomers were thought to have come from Devon and Cornwall, the area which was called Dumnonia at that time: some of the earliest Breton kingdoms created were called 'Domnonée' and 'Cornouaille' (Cunliffe 2012). During these

migrations to Brittany, the language spoken in the two regions was the same; it then differentiated into Breton and Cornish beginning in the early 7th century (Johnson 1990), after the last migration to Brittany. Even as late as the 11th century, Cornish and Breton were mutually intelligible (Jackson 1953) due to their constant trading contact across the English Channel; in fact, Padel (2007) describes Wales, western Brittany, and much of Cornwall as a single cultural and linguistic region until 1200AD. However, Cunliffe (2012) notes that more recent work has questioned the significance of the linguistic evidence, arguing that the native inhabitants of Armorica probably already spoke a Gallic dialect closely related to the Celtic language spoken in western Britain throughout the Roman period; this may imply that the emerging Breton language, rather than being introduced by Dumnonian emigrees, was indigenous Gallic strengthened by the British Celtic spoken by the immigrants.

Contact between Cornwall and Brittany continued in the 11th century when a large group of Bretons settled in Cornwall via the Norman Conquest (Pattison 2008); their names are known because they are recorded as landowners in the Domesday Book. Count Alan of Brittany became Earl of Cornwall in 1140 (Deane & Shaw 1975) and in the 15th century there was an influx of Breton craftsmen into Cornwall (Deacon 2004); Padel (personal communication) states that in the first half of the 16th century there were Bretons living in almost every parish of the western half of Cornwall. However, although Brittany remained independent from France until 1532 (Payton 1996), by the early 16th century England was becoming Protestant while Brittany and France remained Catholic, so Cornish-Breton links were not as easily maintained (Payton 1996).

Cornwall and Brittany also had continuous contact via the Irish missionaries who passed through both regions: several parishes in Mount's Bay on the south coast of Cornwall have churches named after Breton saints, as this was the sailing point between the two countries, and seven saints who had been associated with Cornwall have early cathedrals named after them in Brittany (Pearse 1983). Thus there was sustained contact between the two regions - via Christian communities and pilgrims, trade exchanges, and population movements, continuing off and on for 1,000 years after the first recorded exodus to Brittany; Deacon

(2007) believes that this must have been a reminder to the Cornish people of what an independent Celtic nation could be.

1.5.5 Contact with other nations

In the 5th-7th centuries Cornwall imported wine, oils, and pottery from the Mediterranean and Byzantium, as seen from the evidence at Tintagel on Cornwall's north coast (Padel 2013b), which has the most pottery from this time than any other site in Britain (Johnson 1990). During this time the Celtic church in Cornwall was also in contact with Greece and the near East, as seen by the adoption of the Greek cross at this time, while the rest of England was still under the influence of the pagan Saxons.

1.5.6 Anglo-Saxon invasions

During the Roman period the lands comprising Cornwall and Devon had been an administrative sub-division of Rome, known as *Civitas Dumnoniorum* ('Dumnonii citizens'), which formed a loose association of assorted tribes rather than a unified cultural or political entity (Franklin 2006). The Dumnonii were ruled by a decentralised network of local chieftains and this may have helped them to retain their civil infrastructure when the Roman administration collapsed in 410AD (Deacon 2007). At this time the other native British kingdoms were fighting off invaders from the Continent who arrived mainly on the east coast, which became known as the 'Saxon shore' due to the frequent invasions beginning in 300AD (Svensson 1987).

Very little is known about post-Roman Britain – the main source of information is due to a collection of manuscripts known as the *Anglo-Saxon Chronicle*, which was not written until the late 9th century (Balchin 1983). The *Chronicle* records that the conquest of Britain occurred in stages over the centuries following the departure of the Roman Empire: between 450AD-850AD Angles, Saxons, and Jutes arrived on the southern and eastern shores of Britain from the Danish peninsula and northwest Germany, bringing with them a new language, place-names, material culture, and cereal crops (Halliday 2001). The number of Anglo-Saxons who

entered Britain during this time is unknown, but archaeological evidence suggests there was a significant level of immigration into south-eastern England during the 5th century, equalling possibly 10 – 20 per cent of the native British population (Cunliffe 2012). The natives were either killed, absorbed into the new population, or fled to the peripheries of the island- Wales, Scotland, or the southwest peninsula (Deacon 2007)- areas that would remain under the control of the native Britons for the next few hundred years, even as the Anglo-Saxons started forming independent kingdoms that would eventually unify into one kingdom of England. Figure 1.9 below shows the parts of Britain still inhabited by Celtic tribes during the early Anglo-Saxon era; the territory of Dumnonia still covered most of the southwest.

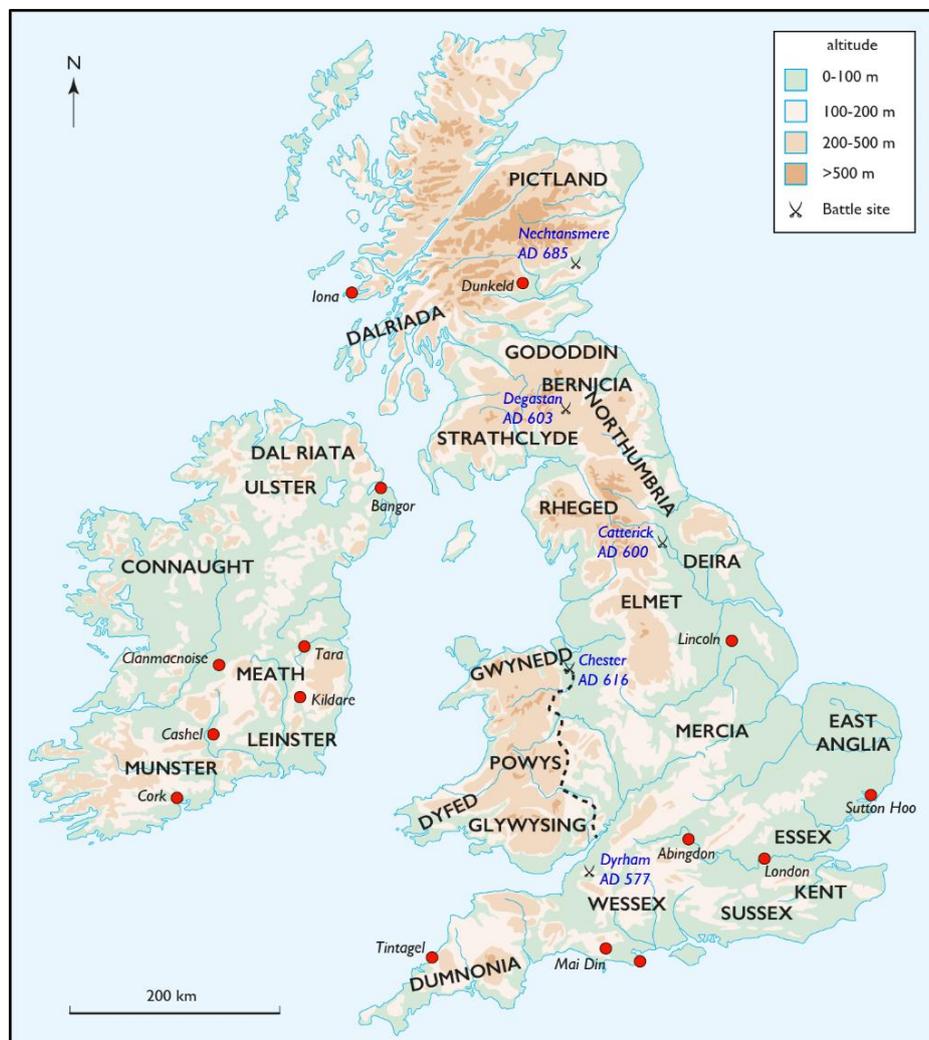


Figure 1.9 Map of early Anglo-Saxon Britain Redrawn from Davies (2000). Anglo-Saxons settled in the east, while Dumnonia still covered the southwest peninsula, and other Celtic tribes inhabited the western and northern parts of Britain

The Anglo-Saxons first settled in the east then continued to spread north and westwards throughout Britain. During this time, Cornwall remained in close contact with the Celtic nations surrounding it - Ireland, Wales, and Brittany – due both to their proximity as well as to their growing Christianity, which the Anglo-Saxons had not yet adopted. But in 577AD, the native Britons lost the Battle of Dyrham (see figure 1.9 above) to the Anglo-Saxons who, according to the *Anglo-Saxon Chronicle*, “put the Britons to flight as far as the sea” (Rippon 2012, p.305). This resulted in the division of the territory that lay between Wales and Cornwall, and from there the two Celtic areas lost contact by land. By 661AD the border of Dumnonia had been pushed further into Devon to the River Exe, and by 682AD the Anglo-Saxons had crossed the River Tamar and settled in north Cornwall, thus pushing the border even further westwards (Payton 1996). This border lasted until 838AD when the native Britons lost the Battle of Hingston Down in southeast Cornwall (see figure 1.1), and the lands of Dumnonia were forced to become part of the kingdom of Wessex. Figure 1.10 below shows a clear divide between the Anglo-Saxon and Celtic areas of Britain up until the 7th century.

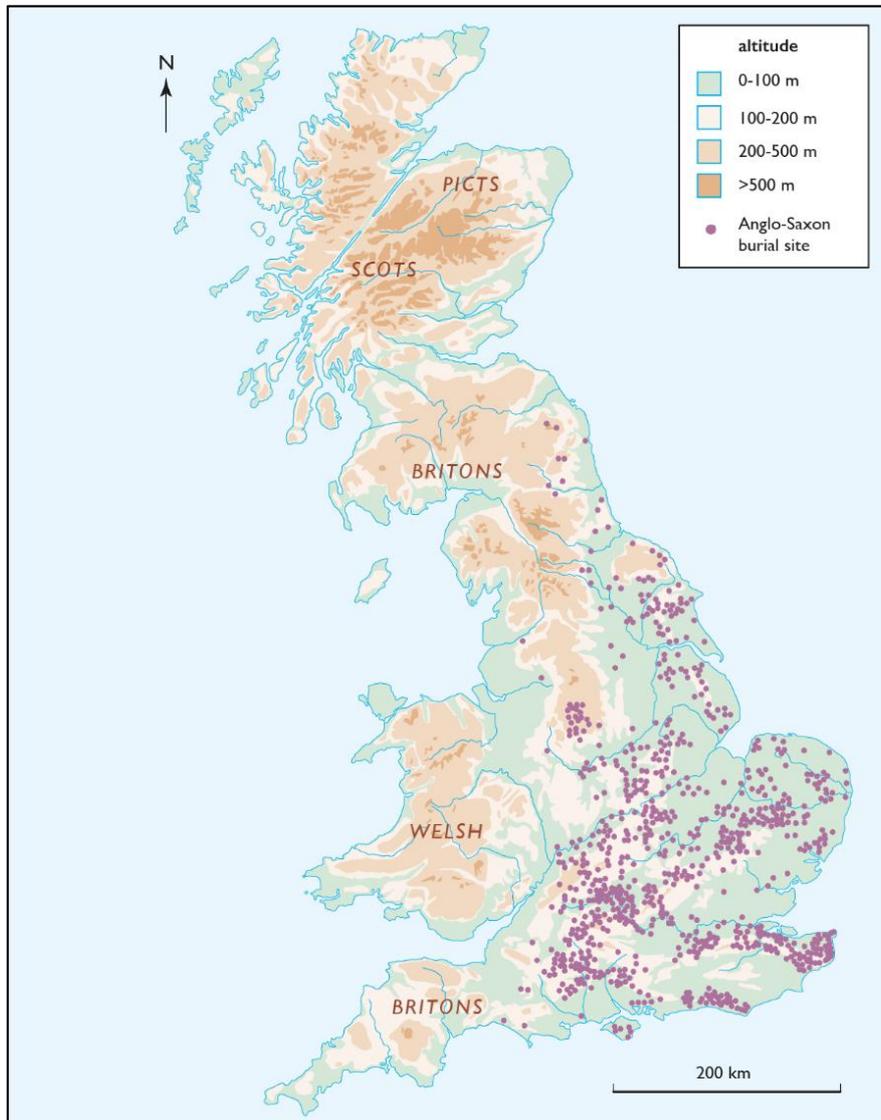


Figure 1.10 Anglo-Saxon settlements in the 5-7th centuries (Cunliffe 2012). The Celtic areas of Britain remained Saxon-free until the 7th century

During the 8th century, Danish, Norwegian, and Swedish Vikings had begun raiding the coasts of Britain but did not set up permanent settlements until the 9th century (Deacon 2007), when they were restricted to a part of eastern England that became known as the Danelaw; however, from 1016-1035AD the Danish king Canute ruled all of England. Yet the 20 years of Danish rule had little effect on Cornwall - there were sporadic attacks along the north coast and up the Tamar River and into Devon, but by 1042AD Edward the Confessor became the next English king and the Saxon incursion into Cornwall experienced little interruption (Halliday 2001).

After the Romans had departed Britain, the loose confederation of tribes that existed in the southwest grew into the Kingdom of Dumnonia. Although Cornwall had joined the Anglo-Saxon kingdom of Wessex by the early 9th century, native kings continued to rule Cornwall according to British laws and customs until 875AD when their last king died (Svensson 1987). The territory of Dumnonia shrank even further in 936AD when King Athelstan of Wessex expelled the remaining British natives in Exeter and banished them to beyond the River Tamar (Higham 2007). He set the east bank of the river as the boundary between Anglo-Saxon Wessex and Celtic Cornwall – a frontier which still marks the division between the two counties today - thus creating the political and territorial border of what Payton (1992, p.46) calls "the geo-political unit - modern Cornwall."

The native Dumnonians were known as the 'West Welsh' by the Saxons- the word 'Welsh' stems from 'wealas,' the Saxon word for foreigner or stranger, and is the origin of the '-wall' in Cornwall. Any natives, or 'wealas,' residing in the kingdom of Wessex had been considered an ethnically and legally distinct lower-class group according to late 7th century laws, until at least 900AD (Padel 2007); laws after this time don't mention a separate status of the British, which Padel (2009) thinks infers that they were by then considered legally English. However, the Bodmin Manumissions, a series of 10th century documents listing the names of slaves being freed by the Anglo-Saxons, contain mostly Celtic names, implying that the slaves were of native ancestry (Padel 2009); in the 1086AD Domesday Book, Cornwall and Devon are listed as having the highest number of slaves of all the southwest counties, which may have been members of the native British population (Kelly 1934).

By the mid-10th century, Cornwall was fully administratively assimilated into the newly-united Kingdom of England. However, King Athelstan did not manage to subjugate the Cornish people completely and in fact might have protected them from complete assimilation (Padel 2013b): by fixing the boundary at the Tamar in 936AD, he had halted Anglo-Saxon settlement (albeit temporarily), thus preserving the Cornish language and place-names. In 944AD Cornwall was still considered a separate area inhabited by Britons, and in 994AD King Aethelred created an independent Cornish diocese (Padel 2009); despite being officially part of the Kingdom of England at this time, Payton (1996, p.87) maintains

that it was still a “union without integration” and that Cornwall retained its cultural character even throughout the next 500 years.

The Anglo-Saxon expansion into Cornwall was gradual: Balchin (1983) suggests that the rough upland areas of the southwest peninsula- Exmoor, Dartmoor, and Bodmin Moor- may have kept the Saxons from expanding further west too quickly. In most parts of Cornwall the incursion consisted of only a small number of Anglo-Saxon landowners, while the native population remained substantially unchanged (Padel 2009); this is in direct contrast to the Anglo-Saxon settlement of Devon and other parts of England where the linguistic and place-name evidence shows a substantial influx of Anglo-Saxon settlers, which caused a major change in culture and presumably the genetics of the population. Figure 1.11 below shows that in 1086AD, over 200 years after Cornwall became part of England, English place-names were still confined to east Cornwall, probably due to observance of the county boundary of the River Tamar.

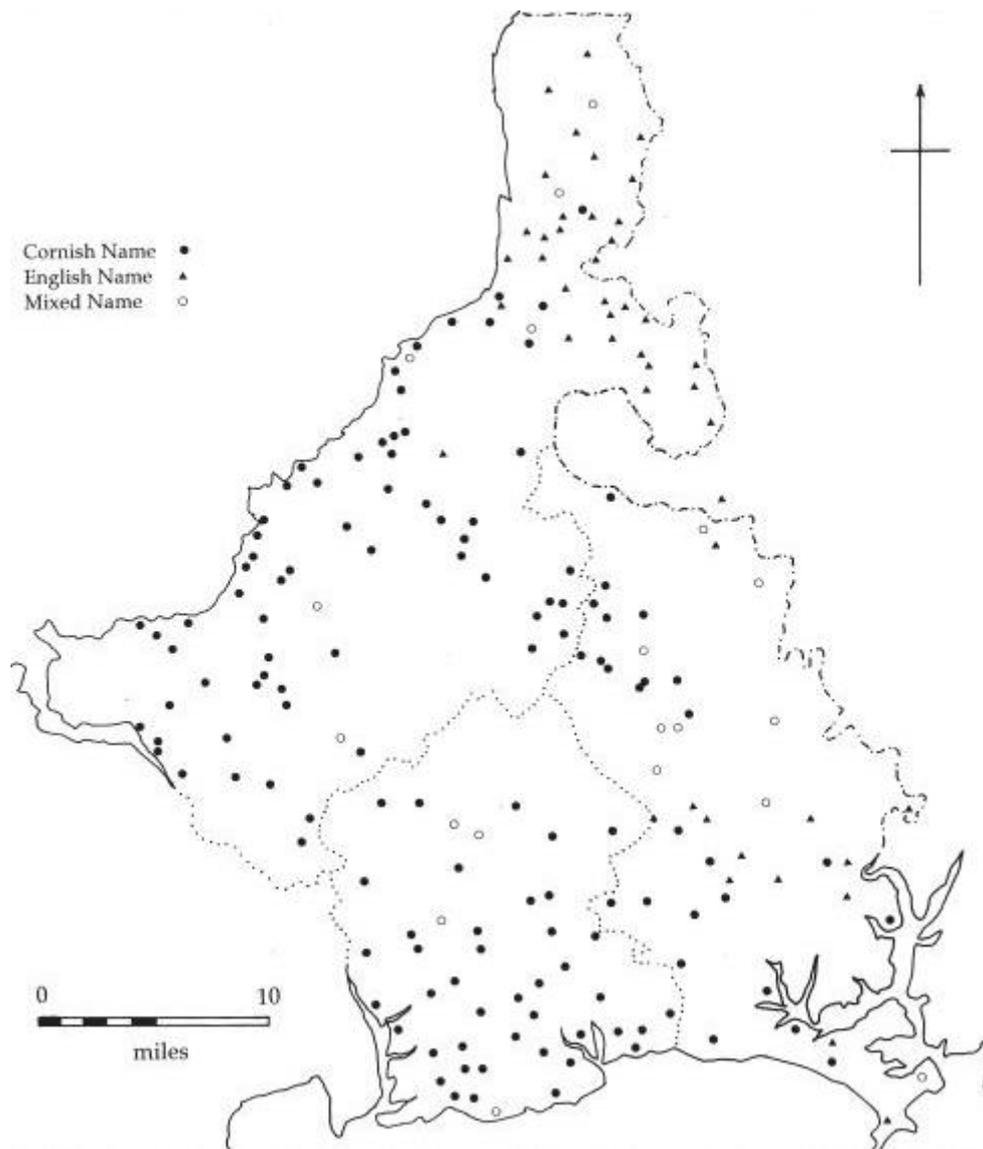


Figure 1.11 *Cornish and Saxon place-names in east Cornwall in 1086 AD (Padel 2007). The right-hand boundary is the River Tamar, the official border between Devon and Cornwall. The left-hand boundary designates the counties comprising east Cornwall. English names remained restricted to east Cornwall for the first 200 years of Anglo-Saxon rule in Cornwall; most of them are close to the Devon border*

1.5.7 Norman influence following the Conquest

In 1066AD William of Normandy became king of England. The Norman Conquest consisted of only a small group of elites from northern France and therefore resulted in relatively little population movement into Cornwall and all of England (Halliday 2001). At this time, Cornwall was rural with a few large English villages and one big market town at Bodmin in east Cornwall, but most of its population still lived in dispersed hamlets and farmsteads. The

population of Cornwall was mainly native British, despite being under the cultural, linguistic, and administrative control of a limited number of Anglo-Saxon landowners (Padel 2009).

According to the Domesday Book, William the Conqueror's taxation survey of property throughout England compiled in 1086AD, the population of Cornwall was approximately 29,000 inhabitants (Cornwall Parish Register Index 2016), with most of the population concentrated in the eastern part of the county (Deacon 2004). Cornwall was a poor county with small estates and only six mills at this time, whereas Devon had 99; of all the counties recorded in the Domesday Book, Cornwall has the fewest entries, and the population was very sparse, with: "just over two men to the plough-land as compared with nearly four in Derbyshire" (Victoria History of the Counties of England 1924, p.53). There is no mention of Cornish tin-working in the Domesday Book and there was very little arable land to attract the Normans (Ditmas 1973), who only built one castle in all of Cornwall, as opposed to the many they built in Devon (Hoskins 1959). Cornwall at this time probably still consisted of mainly native British inhabitants: the Domesday Book records 350 place-names in Cornwall, of which fewer than 50 are English, 93 begin with the Cornish prefix 'tre-', and many of the others are Cornish landscape terms (Turner 2006).

The Normans increased trade with the Continent throughout England, and this led to new towns being formed in Cornwall and Devon. During this time transport in the southwest was largely through the coasts or inland rivers, as opposed to land routes. But while maritime trade flourished, British historian and writer Edith Ditmas (1973, p.511) describes Cornwall as still extraordinarily isolated from the Norman centres of administration in London and Winchester, which allowed it to maintain a certain "aloofness" from the rest of England. She attributes this to the fact that west of Exeter the road system was either non-existent or too crude for wheeled vehicles; as for travellers on foot, there were dirt paths but these involved crossing the "dreaded wastes" of Dartmoor and Bodmin Moor with their "sudden bewildering mists and the dangers of bog and marsh" (Ditmas 1973, p.511).

1.5.8 Cornwall in the mid- to late-Medieval period

By the 13th century, although Cornwall was still essentially rural, it was becoming more open to outsiders: it now had an extensive network of towns and markets, and only on Bodmin Moor would people have had to travel more than six miles to the nearest market (Johnson 1990). There were new trading ports with goods arriving from Ireland, Brittany, France, and Spain (Johnson 1990), while many foreigners from across the sea were coming to reside in Cornwall: a 1327 taxation roll for the south coast town of Penryn was equally divided between natives and foreigners, whereas in other coastal towns there were more foreigners than natives (Rowse 1969). In 1439 in the south coast town of Fowey, one-third of the property holders were foreigners, listed as Irish, French, and Dutch. Bretons were still the largest foreign element in south Cornish towns until the 16th century when both the Protestant Reformation and the subsequent decline of the Cornish language stopped the flow of migration from Brittany (Rowse 1969). Rowse believes that even into the 16th century, Cornish towns were different from most other English towns due to the high proportion of foreigners they had residing in them, despite the fact that most Cornish towns were the size of villages compared to the rest of England.

Population numbers before the 1801 census can only be estimated using historical sources which utilise indirect evidence and, depending on the criteria used, different scholars have produced different figures. The numbers cited in this thesis are from the Cornwall Parish Register Index website (Cornwall Parish Register Index 2016) whose sources include documents outlining property-holdings and taxation; later population numbers were back-estimated based on the annual totals of Anglican baptisms, burials, and marriages collected in the 1801 census. These are subject to wide margins of error especially due to the fact that the number of baptisms, burials, and marriage rates was not constant, and even if the rates had been constant, parish register coverage was not comprehensive; in addition, the spread of dissenters from the Protestant Church in the 18th century meant that many baptisms were not recorded in Anglican registers (Wrigley 2007). Most of the population numbers used from this source were cross-checked with those cited by Deacon (2004) - who presumably used different sources or methods- and were found to be comparable.

There was increasing economic and population growth in Cornwall throughout the 14th century: by 1348, the population had expanded to approximately 108,000, although soon after, due to an outbreak of plague, it decreased to approximately 62,000 in 1377 (Cornwall Parish Register Index 2016). The population soon rose again as the Cornish economy began to diversify, employing thousands in occupations such as wool manufacturing, stone quarrying, shipping, and the export of tin (Johnson 1990), still a staple of the Cornish economy. Mid-12th century records show Cornwall trading tin with the Basque country and during the 13th-14th centuries Cornwall was the main source of tin being exported to all the parts of the world open to European commerce, including the Far East (Pearse 1983). In 1337 tin output was at its highest due to funding England’s war with France; goods were also imported from Portugal, Spain, France, Belgium, the Netherlands, and Germany. Figure 1.12 below shows medieval tin trade routes originating from Fowey on the south coast of Cornwall.

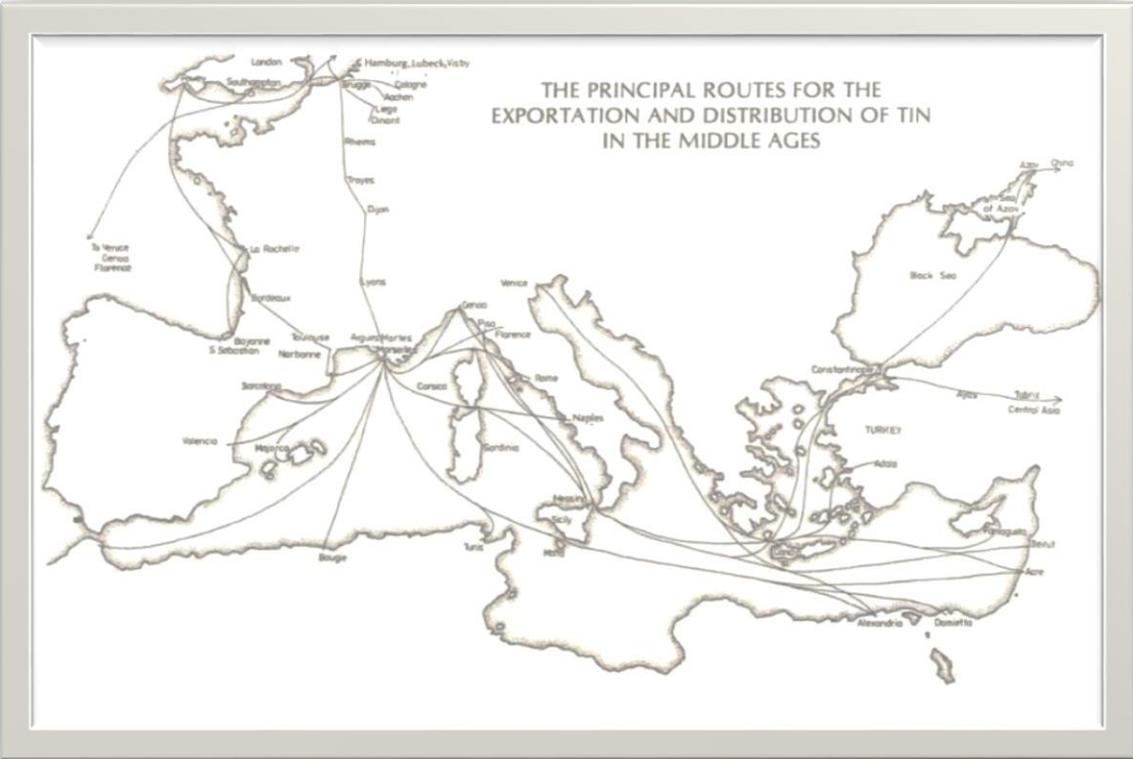


Figure 1.12 Medieval Cornish tin-trade routes (Pearse 1983). The south coast of Cornwall was a port for international tin trade routes

While the tin-trade flourished, Pearse (1983) believes that Cornwall's fisheries were an even bigger part of their economy. In the 12th century, merchants from Basque country were granted exclusive rights to purchase fish from the south Cornish coast in order to supply the busiest medieval pilgrimage route to northwest Spain; records also show frequent fish exports to parts of southwest France and the Mediterranean throughout 14th century (Pearse 1983). By the mid-16th century, Cornwall was on a trade route with the Americas, the Mediterranean, and the Orient, exporting fish, slate, and tin, and it occupied a strategic position for England's wars with the Continent (Kelly 1934). In the early 17th century goods listed in Cornish shops imply an exchange of commodities with the southwest region, London, and the Continent (C. North 1995). By the mid-18th century, fish exports to Italy, Spain, and Portugal were at their peak and in return, Cornwall imported salt from Spain, Brittany, and France for use in curing their own fish (Pearse 1983).

While Cornwall was in constant contact with overseas countries throughout Middle Ages, Payton (1996) believes that it still experienced a considerable independence from the English government. During the 14th century the English Crown had established two special administrative bodies in Cornwall - the Duchy of Cornwall, which managed the landholdings in the county, and the Stannary organisation, which was, in effect, a mini-government based around the rights of the tinning industry and which gave special privileges to miners from both Cornwall and Devon. Payton (1996) believes that both of these institutions gave Cornwall an atmosphere of semi-territorial independence and indeed, many Cornish people believed that the Duchy and Stannaries implied a semi-autonomous status for their region which, no doubt, encouraged a distinct sense of identity apart from that of England. However, Cooper (2003) acknowledges that although the Duchy and Stannaries were central to the independent political culture which existed in the southwest region during the 16th century, he believes they provided only an illusion of autonomy to the Cornish people.

Despite its population growth and extensive maritime contacts, Rowse (1969) believes that during the Middle Ages, Cornwall was still a remote and forbidding county to most Englishmen, due to its distance from the main centre of administration in London. During the

late Middle Ages, Cornwall still held the status of a county separate from that of England: at the battle of Agincourt in 1415 the Cornish fought under their own banner separate from the English troops; when Elizabeth I died in 1603, Cornwall had its own flag alongside that of England, Wales, and Ireland representing one of the dominions she ruled over. Stoye (1997) believes that even into the early modern period (just after the Middle Ages), many Cornish people still had a separate sense of Cornish ethnic identity and continued to regard Cornwall not as an English county but as a British country, despite their forced assimilation into England five centuries earlier.

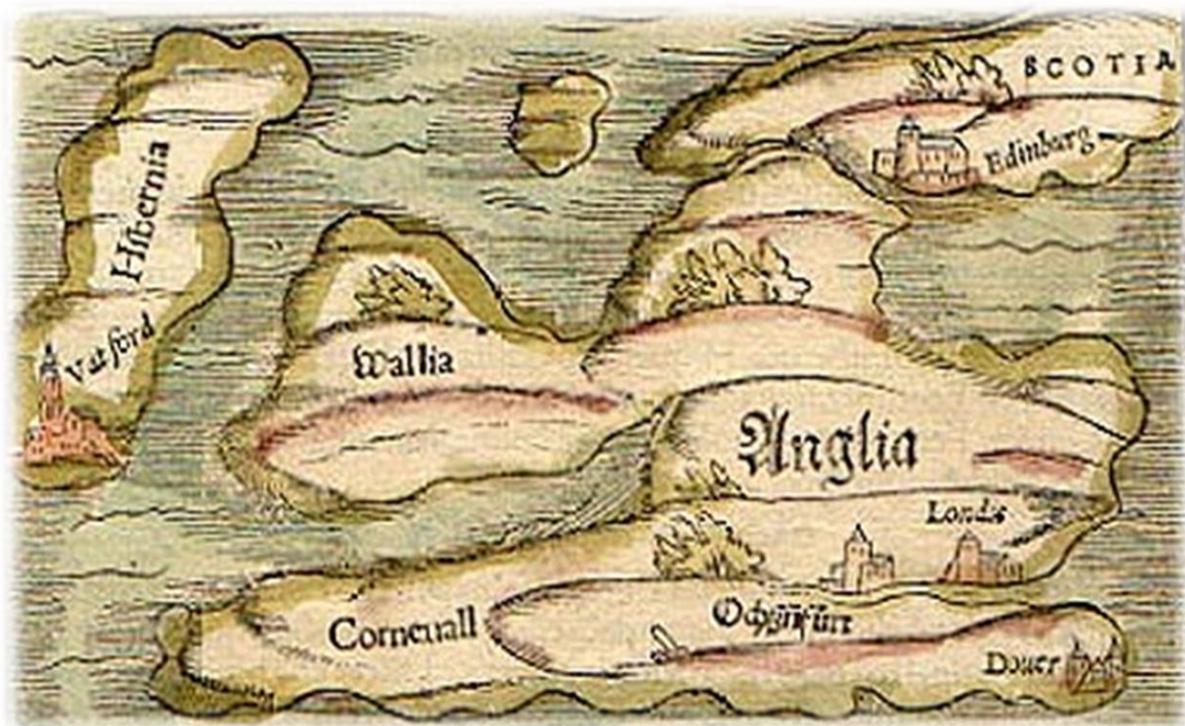


Figure 1.13 Late Medieval map of the British Isles (<http://www.cornwallheritagetrust.org>). Cornwall, like the other Celtic nations, is shown as a separate region from England

Stoye (1997) believes that foreign observers also saw Cornwall as a distinct area with a character of its own (as the map in figure 1.13 above shows). Cooper (2003) agrees that during the 16th century, both foreign and English travellers were struck by Cornwall's different language, customs, and culture from those of England. In 1485 an Italian cleric writing a history of England stated that "The whole country of Britain is divided into four parts, whereof the one is inhabited by Englishmen, the other of Scots, the third of Welshmen, the fourth of

Cornish people ... and which all differ among themselves either in tongue, either in manners, or else in laws and ordinances" (Griffiths 2003). In 1506 a Venetian diplomat noted that Cornwall was treated as a separate division of the English kingdom, "like Wales", with its own language and customs (Griffiths 2003, p.180) which he believed affected their sense of identity and integration within England; in 1538, a French ambassador described England as such: "The kingdom of England is by no means a united whole, for it also contains Wales and Cornwall, natural enemies to the rest of England, and speaking a [different] language" (Stoyle 2002, p.42).

Johnson (1990) also maintains that Cornwall was still very much a county with a distinctive identity in the late Middle Ages: Cornish was still spoken in the west, although the tin industry had moved from east Cornwall to the west and with it came English- speakers looking for work (Price 1984). However, Stoyle (1997, p.28) proclaims 1648 as "the last stand of traditional Cornishness": Parliament was launching assaults upon Cornish traditions and rituals by destroying the holy wells and standing stones which were distinctive features of the Cornish landscape, while their local games and pastimes were discouraged. This "cultural offensive" (Stoyle 1997, p.28) was felt most in the far west, where the Cornish language was by now confined to a small group of fewer than 40 parishes, and by 1660 the Cornish language was dying even in its last western strongholds. As it did so, Stoyle (1997, p.28) believes that the Cornish sense of racial difference also died, and by the early 18th century "Cornwall was at last part of England."

1.5.9 Cornwall during the Post-Industrial Revolution age

By 1750 the population of Cornwall had risen to approximately 128,000 (Cornwall Parish Register Index) due to the tin and copper mining boom- Cornwall had more tin, which was rarer than copper or iron, than anywhere else in Europe at this time, which not only encouraged immigration to the area but allowed people to get married earlier and therefore have more children (Deacon 2004). However, fluctuations in the price of minerals made it an unreliable occupation resulting in only periodic employment and by 1841 mines were closing. Soon after, foreign mines began to threaten Cornwall's dominance in the mining trade - there

had been over 173 copper mines in Cornwall but they collapsed when copper prices fell- and tin mining could not sustain the county (Thomas 2007), all of which led to overseas migration and population decline. Mass emigration had also occurred in the agricultural areas across the county, due to low wages, poor harvests, and diminished access to common lands for grazing, while the growth of British colonies overseas required labour in the form of British immigrants (Deacon 2004), and so the population continued to decline. The 1851 census records the population at over 355,000, though Cornwall was still predominantly rural with the largest towns housing only 13% of the total population (Deacon 2004). But in 1856 a railway bridge was built over the River Tamar, thus exposing Cornwall to the "second English invasion" (Wade 1928, p.9) and, according to Balchin (1983), causing it to at last lose its isolation from the rest of England.

1.5.10 Conclusion

As the above evidence shows, in contrast to its reputation of being isolated and cut off from the rest of the world, Cornwall has always been widely connected with many other cultures and nations- from their prehistoric trading contacts which continued throughout the Middle Ages, to their more recent seafaring and Continental wars- all of which have kept Cornwall in close touch with Western Europe and beyond. Cornwall's location on a peninsula and its maritime nature have left it constantly open to immigration and many of these traders or visitors would have settled and made Cornwall their home; therefore the ethnic and genetic makeup of the population of Cornwall, even from early times, has been far more diverse than its reputation has allowed.

But the question remains- is Cornwall different than England? To some, the southwest region as a whole is similar- to others, England begins at the Tamar. Throughout its known history, much of Cornwall has had close contact with Devon, from the sharing of their tribal lands of Dumnonia, to the occupations of mining, tin trading, and transhumance which have transcended county lines; however, in more recent times, the two counties have had very different immigration histories. Looking at both these connections and divisions may help to explain the similarities or differences in the genetics of the two populations.

1.6 Devon

The county of Devon, located on the southwest peninsula, is bounded by Cornwall to the west, Somerset to the northeast, and Dorset to the southeast (see figure 1.1). It has two separate coastlines - the Bristol Channel and Celtic Sea to the north, and the English Channel to the south - both of which have played a major part in the history of the county. Both coasts have many navigable rivers and bays sustaining over 40 fishing towns and ports (Stanes 2000) supporting seaborne trade and immigration throughout the county.

Like Cornwall, for most of its known history Devon's maritime contacts were more easily sustained than its overland contacts with England, as roads were not fully developed to reach the southwest region until the early 20th century. Devon's coastlines lay in the path of Christian missionaries who, during the 5th-6th centuries, travelled between Ireland, Wales, Devon, Cornwall, and Brittany, building chapels and monasteries (Hoskins 1959). Many of these missionaries later became the patron saints of Devon and Cornwall, with many churches dedicated to them scattered along their coastlines (Stanes 2000) (see figure 1.7 for map of Saint sites in Cornwall).

Devon's coasts have also connected it to wider events in the outside world: during the 12th century Crusaders set sail from the south coastal town of Dartmouth, and Devon was on a major trade route with Bordeaux and Aquitaine which Henry II had recently acquired; in the 16th century Devon was a key location in sighting the Spanish Armada and in 1620 the Pilgrims left from Plymouth, on Devon's south coast, to sail for North America (Stanes 2000).

Along with its extensive coastlines, the topography and settlement patterns of Devon are also similar to those of Cornwall - the inland terrain is mostly rural and hilly, described by landscape historian W.G. Hoskins (1959) as a landscape made by peasants: pre-industrial, with small fields and high banks used as boundaries; any big villages were mainly agricultural with isolated farms and settlements scattered around them (Hoskins 1959).

Devon is home to Dartmoor which is the largest open space in southern England at 368 sq miles and includes the largest area of granite in Britain. The topography of Dartmoor is similar to that of Bodmin Moor in that it produces minerals and metals, and from the 12th century Devon's economy was partially based around producing tin (Fox 2012). Devon's economy also relied on an extensive trade in wool and cloth during the 15th century which gave rise to many markets, thereby opening Devon to extensive contact with outsiders (Hoskins 1959).

Devon shares a prehistory with its neighbours in the southwest: the region was inhabited by hunter-gatherers from about 6,000BC, then by the early Iron Age became home to the Dumnonii who inhabited the lands stretching from western Somerset to Cornwall (Stanes 2000). But after this, the histories of Devon and Cornwall diverge: in the ensuing centuries, while Cornwall retained its language and Celtic culture largely due to its lack of Roman and Anglo-Saxon immigration, Devon was invaded and settled by Romans, Anglo-Saxons, Vikings, and Normans, and as a result, much of its original native population was either lost or absorbed into the new population.

In pre-Roman times most of the natives in Devon lived in dispersed farming settlements, as opposed to villages; the east Devon town of Exeter was a centre of trade, as deduced by the quantity of coins and pottery from Gaul and possibly the Mediterranean found there (Hoskins 1959). When the Romans occupied Exeter in 50AD they named it '*Isca Dumnoniorum*' meaning 'Exeter, capital city of the Dumnonii' (Hoskins 1959); it had been a small town but it soon became the Roman administrative centre for the southwest, with streets, marketplaces, public buildings, major roads, and a port on the south coast (Hoskins 1959).

During their almost 400 years of occupation, the Romans expanded no further west than Exeter, which was the terminus of a major frontier road (Deacon 2007) (which still exists today as the Fosse Road). Roman Exeter continued its trade with the Mediterranean and Gaul, but outside of the city there were few signs of Romanisation- native life had been allowed to carry on as long as it adhered to Roman rule, and when the Romans left Britain in 410AD the

kingdom of Dumnonia re-emerged, with tribal kings ruling the lands of Cornwall, Devon, and parts of Somerset once again (Deacon 2007).

Starting in around 450AD Devon was invaded by Anglo-Saxons who, by 577AD, had won a pivotal victory against the native Britons of the southwest, further expanding Anglo-Saxon territory westwards (Hoskins 1959). Padel (2007) posits that Devon was thinly populated at this time, possibly because many of the natives from both Devon and Cornwall had already fled to Brittany from the ensuing Anglo-Saxon invasions. Padel (2007) believes, therefore, that the Saxons found a landscape with plenty of space for expansion, as is indicated by the many settlements with Anglo-Saxon names that imply new foundations, such as 'Newton' - the Saxon element '-tun' denoting a town or settlement. The Anglo-Saxon takeover of Devon is reflected in its place-names which are almost entirely Old English (see figure 1.14 below) - the number of Celtic place-names in Devon, excluding river names, is less than 1% of the total and this suggests that the Celtic language did not survive very long in Devon after the Saxon takeover (Padel 2007).

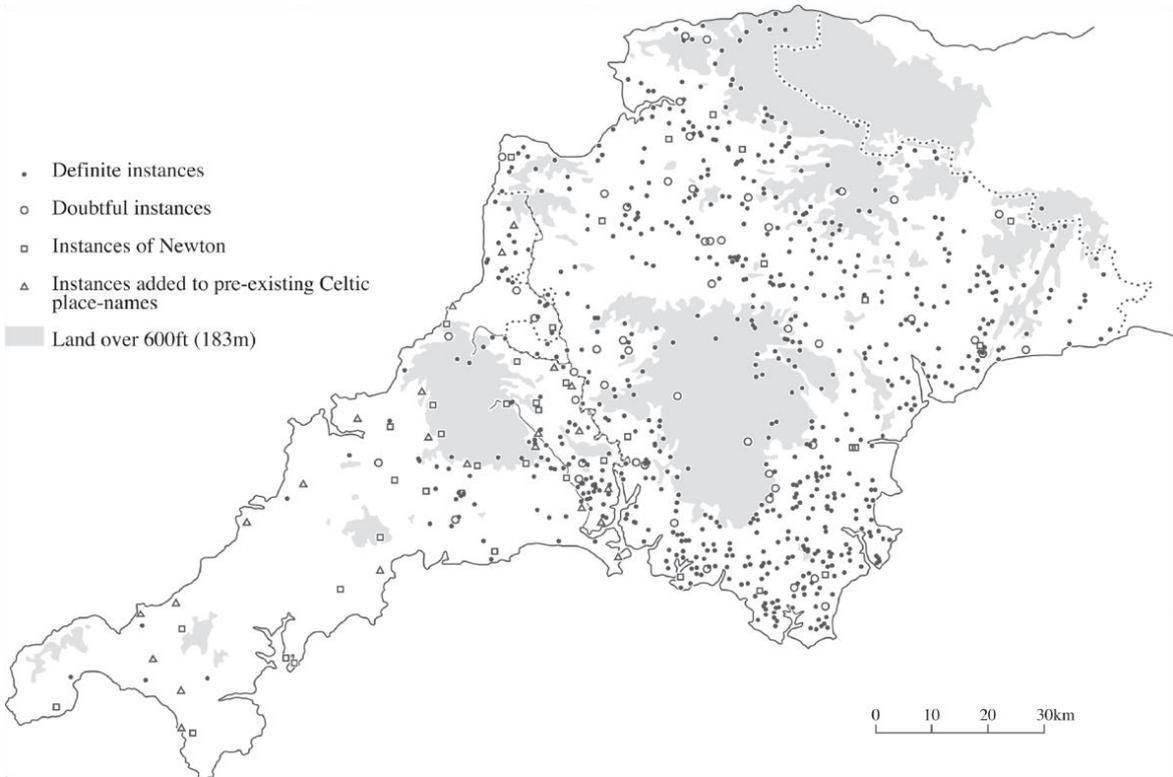


Figure 1.14 Distribution of the English element '-tun' (Padel 2007). There are significantly fewer '-tun' names in Cornwall than in Devon

Devon was fully conquered by the Anglo-Saxons by the late 7th century, although Stephen Rippon (2012), landscape archaeologist at the University of Exeter, believes that the invasion was a political takeover and not a mass migration. He bases this on the finding that there was no significant change in land use in Devon in the 4th-7th centuries, which would have occurred had there been masses of people exploiting the land; instead there was the continued use of the Roman-era isolated enclosures used by the native British, and the re-occupation of Celtic hillforts. Even so, by 682AD the kingdom of Dumnonia existed only in Cornwall, and the remaining Dumnonii in Devon became partially assimilated as a lower-class people within the newly forming Anglo-Saxon kingdom of Wessex. However, by 936AD the remaining natives had been banished across the River Tamar by King Athelstan, who had designated it as the 'West Welsh' border, just as he had set the territory of the North Welsh at the Wye River, separating Wales from England (Higham 2007). Devon became a frontier between the native Britons and Anglo-Saxon Wessex and was thereafter constituted as a shire of the kingdom of England (Stanes 2000).

Raids by Danish Vikings had occurred sporadically along the coasts of Devon and Cornwall throughout the 9th - 11th centuries; in 876AD they invaded Exeter but did not settle there in any great number, although in 1003AD they destroyed it, and England was under Danish rule for 50 years thereafter (Hoskins 1959).

Soon after the Normans arrived in England in 1066AD they inhabited Exeter, which became the biggest market town in the county, and within a few generations the Normans had built 20 castles in the vicinity (Hoskins 1959). At the time of the Domesday Book in 1086 the population of Devon was estimated to be between 60-80,000, with 9,000 farms and 1,200 manors (Hoskins 1959). By this time, all the Saxon landowners in Devon had lost their lands to only six Normans - as in the rest of England, the area was ruled by a small group of Norman aristocrats and was not subject to an enormous invasion, thus leaving the Saxon population intact.

In 12th century Henry II acquired regions in southwest France and many ports were built in Devon and Cornwall to support this relationship, creating two of Devon's largest towns based around the rivers that flowed into the south coast sea, Dartmouth and Plymouth. Tin was discovered on Dartmoor and there was much trade and immigration between Bristol, Ireland, Brittany, France, and Spain (Hoskins 1959).

In the 14th century outbreaks of plague destroyed a large proportion of the population, tin-mining ceased, and land was abandoned across Devon. This ended serfdom but had less of an effect in Devon and Cornwall than elsewhere in England since in the southwest many men were tanners or colonised the open moorlands, as opposed to being serfs (Stanes 2000). In addition, during the 14th-16th centuries, Devon had one of the fastest-growing economies in England due to the cloth industry (Altenberg 2003) and it became a centre of production and trade (giving rise to the common surname 'Tucker' which was a regional term for the person who trod on the cloth to soften it). When wars with France began, however, the cloth trade died although many dockyards were created (Hoskins 1959). In his early 18th century tract *Tour thro' the whole island of Great Britain*, Daniel Defoe (1927) noted that Exeter held the greatest market in England, with wool being shipped to Holland, Portugal, Spain, and Italy; Devon also traded with the North American colonies and Newfoundland (Hoskins 1959).

The Industrial Revolution never came to Devon or anywhere in the southwest, as there was no coal there to power the mills, but Devon had many of its own traditional industries to sustain it: while many people left to work in factories in the north of England, farming remained and Devon had tanning and cloth-making. However, these soon declined, as did trade, due to the French wars and loss of the American colonies, and therefore Exeter lost its status as a major port (Hoskins 1959). By the late 19th century the Tamar railway bridge was built, connecting the southwest to London and opening Devon up to the rest of England (Stanes 2000).

Before the Romans invaded Britain, Devon and Cornwall experienced a joint history through the sharing of their tribal lands of Dumnonia. But from there, their histories diverge: while

the two counties still had contact with the same overseas nations through trade and religious exchange, the influx of Romans and then Anglo-Saxons into Devon drove the boundary of Dumnonia further westwards until finally the border between English Devon and Celtic Cornwall was set at the Tamar River. This political border defined a cultural and physical territory for the native Britons west of the Tamar which may have helped to preserve or protect their Celtic language and culture- and possibly the genetics of the population- from English influence. But was there also a physical barrier that helped shield Cornwall from overland invaders for the past two millennia? The results of the People of the British Isles study have given new life to this debate and point to the region of Bodmin Moor in east Cornwall as a possible barrier that may have contributed to the genetic difference between Devon and Cornwall (Leslie et al., 2015).

1.7 **Bodmin Moor**

1.7.1 Landscape

Located just 10 miles west of the Devon border, Bodmin Moor (shown below in figure 1.15) is a rough upland area of almost 150 square miles, which presents a formidable barrier to anyone trying to enter Cornwall on foot.



Figure 1.15 Bodmin Moor (adapted from en.wikipedia.org). Bodmin Moor is located close to the Devon border; it includes some of the highest land in Cornwall

Uplands are defined as rough unenclosed areas over 300 metres in altitude, where the climate, topography, and land use all differ from the adjacent low-lying farmland (Herring 2008). Reaching 420m at its highest point, Bodmin Moor contains some of the highest land in Cornwall; due to this high altitude, it is one of the wettest uplands in Britain, experiencing lower than average temperatures, excessive cloud cover, and an average annual rainfall of 177cm, compared to the 89cm at the north coast which is only 7 miles away. It also has the greatest range of humidity in the county, with low cloud and hill fog covering the moor for long periods and in all seasons (Johnson et al., 1994). The combination of high rainfall and fog along with low temperatures produces acidic soggy soil, making it difficult to grow most food crops in these upland areas (Whyte et al., 2004).

Due to its high altitude, Bodmin Moor is fully exposed to the strong winds coming from the Atlantic Ocean which hinder tree growth; any trees that do survive tend to grow stunted and twisted (see figure 1.16). This lack of trees leads to the somewhat barren landscape of the

moor and as a result there is very little to block the wind. Many shelters on the moor were constructed with this in mind: most prehistoric hut entrances on the moor face south while any west-facing ones have protected entrances (Johnson et al., 1994); some medieval longhouses on the moor were built on an oblong platform with its long axis at right angles to the hillside to best protect them from the wind and rain (Dudley & Minter 1962).



Figure 1.16 Moorland trees (photo by the author). Trees on the moor grow stunted due to the windy environment

Underneath the grasslands Bodmin Moor is an island of granite which has produced the abundant rock tors (such as the one in figure 1.17 below) and debris which cover the moor and influence the vegetation that grows there. The granite bedrock forms shallow basins which prevent rainwater from draining and this leads to thin, acidic soil which makes agriculture difficult - the only vegetation sustained on the moor is heather, gorse, bracken, and peat (Johnson et al., 1994), which is made of compressed dead plants that gather in the bogs and swamps that form in the undrained basins (Hey 2000b). But although the underlying granite has prevented successful farming, it has provided the moor's inhabitants with other economic opportunities: fissures in the granite expose minerals such as tin, copper, silver, lead, and iron, plus chalk and china clay (Todd & Fleming 1987). Bronze Age inhabitants of

the moor utilised these metals to make tools and jewellery, and the mining of these metals and minerals has continued to be one of the main occupations of the moor until recent times (Munn 1976).



Figure 1.17 Sharp Tor (photo by the author). One of the many granite masses covering Bodmin Moor

1.7.2 Settlement patterns

"We have in Cornwall Rocks of that grandeur, remarkable shape and surprising position, as can leave us in no doubt but that they must have been the Deities of people addicted so much to the superstition of worshipping Rocks" William Borlase, 1754

The above quote could have been meant specifically for the landscape of Bodmin Moor. With its 150 square miles of grassland and natural granite outcrops, Bodmin Moor is the largest section of Cornwall's 'Area of Outstanding National Beauty.' But scattered throughout the moor, alongside the natural rock formations, and despite its inhospitable environment, are

also man-made monuments created from the granite of the moor by the inhabitants of the land over the past 4,000 years (Herring 2008).

Bodmin Moor has been the subject of detailed archaeological surveys and is one of the best-recorded upland landscapes in England (Johnson et al., 1994). The moor's remoteness and marginality have ensured the survival of its many archaeological sites and features (Payton 1996) which have lain mainly undisturbed because most of the moor has not been inhabited continuously, due to its lack of use as agricultural land. Axford (1975) describes the past on Bodmin Moor as being conspicuously present: there are signs of human habitation in the form of ancient relics, settlement sites, field systems, and ceremonial monuments, stretching from the prehistoric, medieval, and post-medieval periods to more recent industrial remains (Johnson 1990). Balchin (1983) likens the landscape to a historical document, a palimpsest in which the writings of different ages are layered on top of each other, with each layer partially visible. Figure 1.18 below shows man-made structures on Bodmin Moor from time periods spanning thousands of years, demonstrating that the moor has been an area of habitation over many millennia.



Figure 1.18 *The Hurlers* (photo by the author). A Bronze Age stone circle with a Victorian engine-house in the background

Cornwall has more nationally protected 'Scheduled Monuments' (a protected historic building or site) than any other county in England and many of these are on Bodmin Moor: there are Bronze Age hut settlements and stone circles, Celtic hill forts, transhumance huts, abandoned clay pits, tin quarries and engine houses, Medieval, Elizabethan, and Victorian farmhouses, and over 300 miles of ancient boundaries in the form of fields, hedges, and stone walls (Johnson et al., 1994). The placement of many of the prehistoric monuments and relics in relation to the landscape and to each other is thought to be intentional, as they are aligned on axes with other visually prominent landscape markers, such as the high rock tors across the moor (Tilley 1996). Many of these monuments were incorporated into the everyday lives of the inhabitants: Altenberg (2003) has found that most medieval settlements on the moor were located within 50m of a prehistoric feature such as a boundary, field, remains, or monuments, sometimes incorporating them into their structures.

Bodmin Moor's prehistory

After the last Ice Age, Bodmin Moor was inhabited by bands of Palaeolithic and Mesolithic hunter-gatherers who followed the rivers and tributaries up onto the moor (Tilley 1996); hearths and chipping floors found on the moor imply a nomadic hunting economy (Balchin 1983). During the Neolithic period, from 3,500BC- 2,300BC, there is evidence of woodland clearance on the moor along with ritual and ceremonial monument construction. During the Bronze Age, from around 2,400BC- 500BC, a cultural transformation of the landscape began in the form of monuments and permanent settlements (Tilley 1996). One example is the 'Cheesewring' (see figure 1.19 below), a natural rock outcrop situated on a defensive granite hillfort called Stowe's Pound which, on a clear day, has views of both north and south coasts as well as Dartmoor in Devon, 16 miles away. This hillfort was extensively inhabited during the Bronze Age, as seen by the remains of the many stone huts scattered along the hillsides, and is also thought to have had ritual significance (Johnson 1990).



Figure 1.19 *The Cheesewring* (photo by the author). A natural granite outcrop that had monumental significance in the Bronze Age

During the middle to late Bronze Age, from about 1500 to 800BC, the British climate became warmer and drier which made large tracts of uplands available for colonization (Cunliffe 2012) - trees grew on Bodmin Moor again and the land became fertile and suited to farming. People lived in stone huts, used metal tools, grazed their animals on the moor, and cultivated fields using stones from the moor to build boundary walls; they also constructed henges, stone circles, burial barrows, and tumuli (Tilley 2010).

The climate became cooler and wetter towards the end of the Bronze Age, and widespread bogs began to form on the moor (Johnson et al., 1994); peat grew extensively and the grassland became more acidic and difficult to farm again and by the late Iron Age the moors were abandoned for lowland areas and were only used as summer pasture (Axford 1975). Between 550BC- 350BC, Celts from the Continent settled on and around the moor (Svensson 1987); some of their settlement sites are shown below in figure 1.20.

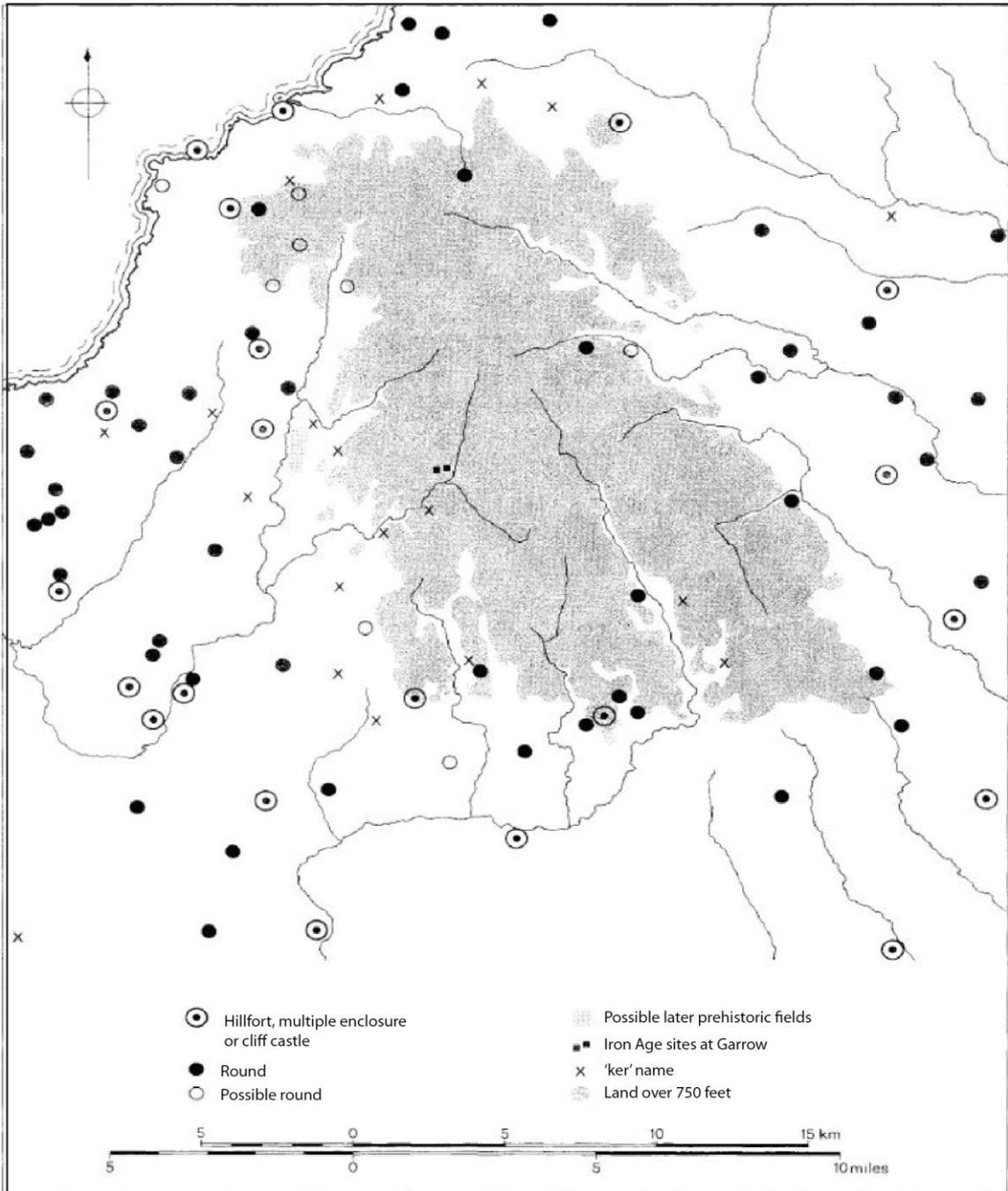


Figure 1.20 Bodmin Moor Iron Age sites (Johnson et al., 1994)

Medieval Period

While the uplands remained uninhabited, the fringes of the moor began to be resettled starting in 1000AD, in the form of dispersed settlements sharing communal farming strips (Herring 2008). The current pattern of settlement today around the edges of the moor and along its river valleys is directly descended from the organisation of the landscape stemming from this period (Johnson et al., 1994).

In 1086 the moor was still uninhabited: the Domesday Book records it as being manorial waste (Axford 1975) and pasture used for seasonal grazing and fuel (Rose & Preston-Jones 1995); there are only three manors listed as being on the moor itself, with the rest located on the lower ground nearby (Tilley 1996). The Domesday Book also describes the bigger English settlements, located in the east and south-eastern lowland districts of the moor, as being more heavily populated than the areas where the Cornish lived, in isolated farmsteads and hamlets around the moor (Munn 1976).

From the 11th century onwards, due to population growth and a milder climate, many new permanent settlements were formed around the moorland edges and in the river valleys (Johnson et al., 1994). This occupation of the upland areas occurred in stages (Axford 1975), as can be discerned by the names of the settlements: as people started expanding upwards into the more marginal grounds, they named their settlements 'Newton' (meaning 'new settlement or town' in English) or 'Trenoweth' (meaning 'new settlement' in Cornish) (Padel 1988). This is a common name of outlying farms in many moorland parishes that are found on high ground away from the main settlement; these farmhouses did not gather in clusters but were scattered, each with their own enclosed land, indicating a pastoral rather than an arable economy (Axford 1975).

Between the 12th- 14th centuries there was general economic and population growth in Cornwall, resulting in land shortages which led to settlement into the far upland areas of the moor- in 1327 a farm was recorded at a height of 274m (Padel 1985a). Archaeological

evidence of mid-13th century hamlets on the moor indicate that the inhabitants lived on farmsteads sharing communal open land, each with a longhouse to live in, corn-storage, barns, and a garden which faced away from the communal centre (Herring 2008).

A market economy existed in the towns around the moor at this time and trade networks created a demand for agricultural produce (Altenberg 2003), so large areas of the moor were farmed for oats and rye which, unlike wheat or barley, can stand acid soil, high rainfall, and low summer temperatures. Even rough ground for grazing was in high demand and this led to boundary disputes and the move to enclose the common land (Jones & Essex 1999). The arable moorland edges were colonised by small groups who settled in hamlets and the surrounding land, both arable and rough, was enclosed and farmed communally (Whyte et al., 2004). However, in the mid-14th century, the population declined due to plague outbreaks and many of the hamlets on the moor became abandoned (Johnson et al., 1994).

Industry on Bodmin Moor

Due to the decrease in population, much of Bodmin Moor became used for animal rearing rather than farming, because this required fewer labourers, who were now scarce. By the 16th century the moor's tin deposits were exhausted and poor road conditions made transport of goods from the mines difficult; the parishes around the moor became more thinly populated once again and by the 19th century there was neither a local skilled workforce nor a developed industrial infrastructure in any of the surrounding towns. For those few farming families remaining on the moor, the living continued to be a difficult one, requiring the help of neighbours to assist with seasonal tasks during crucial parts of the farming year in order to sustain a living (Herring 2008).

In 1837 copper was discovered on Bodmin Moor and it soon became the world's main producer, making mining a successful industry once again. Most of the villages that are on the southeast side of the moor were built during this time for the mine workers; this includes St. Cleer, where the population grew from 774 in 1800 to almost 4,000 by 1861 (Axford 1975).

But by 1890 both the tin and copper industries were outpriced by foreign competition and the moor communities struggled once again, with the population of east Cornwall decreasing drastically due to emigration brought on by the collapse of the mining industry (Munn 1976). Figure 1.21 shows an old engine house on the moor, one of the last remnants of this previously flourishing area.



Figure 1.21 Engine house (photo by the author). One of the many abandoned engine houses on the moor on a misty day

1.7.3 Place-names

While the Domesday Book and other resources cannot present a full picture of settlement patterns on and around Bodmin Moor prior to the Norman Conquest, place-name evidence can help fill in the gaps. There are both Cornish and English place-names in the farms and villages around the moor (see figure 1.22 below) which can help reveal when they were

established: Cornish place-name elements, such as 'tre-' (meaning farm or homestead), 'bod-' (meaning settlement), and '-hendre' (meaning permanent or winter settlement), were used to coin new place-names only until 1100AD, after which English became the dominant language spoken in east Cornwall (Padel 1988).

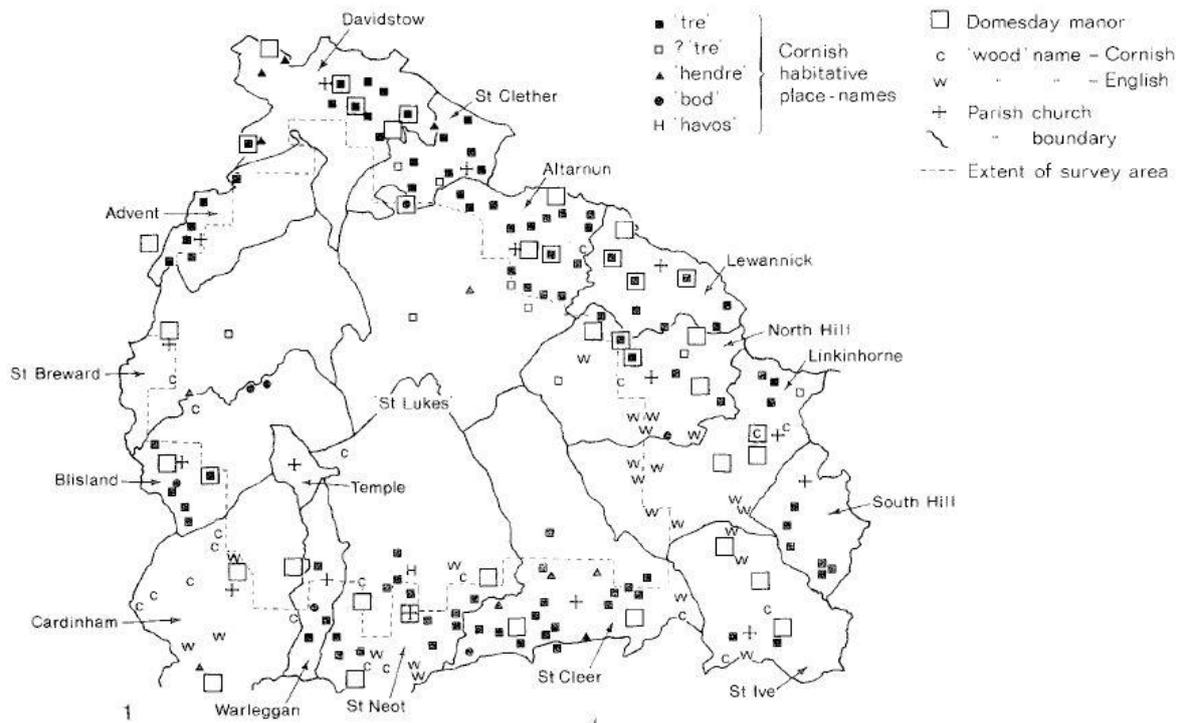


Figure 1.22 Cornish place-names around Bodmin Moor (Johnson et al., 1994).

Place-names can reveal what the landscape was like at the time of settlement: 'tre-' names in the eastern Bodmin Moor parish of Linkinhorne form a ring at the edge of the moor, but the gap is filled with English place-names suggesting a previously wooded environment, such as '-wudu, -bearu, -leah, -stoc' (Johnson et al., 1994). This implies expansion that occurred after the 11th century into areas that were cleared of trees, probably in order to establish new settlements. The place-names in the south-western parish of Cardinham show that the area has very few settlements dating from before 1100AD, probably due to the abundance of

woods that covered the land, as is demonstrated by the names containing the Cornish place-name elements '-cos' and '-kelli,' meaning 'woods' and 'grove' (Johnson et al., 1994).

Place-names can also help deduce how the land was used: the early medieval 'tre-' place-names in the northern-most parish of Davidstow show that the settlements were laid out around 800m apart on the valley slopes on either side of the river Inney, so that each farmstead could use the arable land on the slope, the grazing on the upland moor area, and the fishing in the river (Johnson et al., 1994). Additionally, there are both Cornish and English place-names on the moor which describe the herdsman's shelters used during the summer transhumance (seasonal grazing of cattle), which were built up until the 12th century (Herring 2008). For example, the villages of St. Breward and St. Neot have place-names relating to this practice- they contain the Cornish element '-havos' which means 'summer dwelling.' A change in these place-names show that these previously seasonal ('-havos') settlements developed into permanent hamlets: the largest number of '-hendre' (winter/permanent dwelling) names in Cornwall are found around the edges of Bodmin Moor, and Padel (1988) has interpreted this change from '-havos' sites to '-hendre' sites as an indication of permanent colonisation of the area. Place-names containing the element '-havos' in the Domesday Book also imply that some previously seasonal settlements had become permanent dwellings by 1086AD, as shown by the fact that they are listed with their fixed populations and their number of plough lands (Fox 2012), as well as the fact that the '-havos' name only survived when it became a permanent dwelling (Altenberg 2003).

1.7.4 Reputation

As described above, most of the permanent settlements were just off the moor, with good reason. The absence of arable farmland and the expansive and uncharted landscape leading to a lack of human habitation can give uplands the reputation of being remote, empty wildernesses cut off from the civilised world. These marginalised areas can be the source of all manner of myths and legends, including the many Cornish folk tales which take place in rough, isolated uplands (Whyte et al., 2004). One locally famous example is that of the

restless spirit called Tregagle who shrieks his penitence as he flees across Bodmin Moor from pursuing devils whose cries can be heard on windy nights, at the height of the fiercest storms (Axford 1975).

Franklin (2006) has found that in medieval landscapes, in the southwest in particular, many folktales and myths pertain to areas seen as isolated or remote by the surrounding communities, with special significance given to moors due to their tendency toward sudden changes in weather involving mists and fog. Landscape historian Harold Fox (2012) notes that the vast uplands of Dartmoor in Devon are seen by the surrounding lowlanders as a marginalised environment- an example of what Franklin (2006, p.177) calls "external views" created by outsiders in relation to unfamiliar areas. Fox (2012) references the 'otherness' of Dartmoor in Arthur Conan Doyle's *The Hound of the Baskervilles*, where the bogs and mist threaten outsiders and only the locals can get around them: the city-dwelling Sherlock Holmes is warned to avoid crossing "the long, low curve of the melancholy moor" "in those dark hours when the powers of evil are exalted" (Doyle 1902, p.17, p.88).

Moors were considered marginal by the Christian church and they especially objected to the ancient pagan monuments (Altenberg 2003), many of which still exist on Bodmin Moor. To counteract these pagan influences and tame the uncivilised nature of the moors and their residents, the Church erected stone crosses and chapels in conspicuous positions in the landscape to impose the presence of Christianity, in order to integrate the local people into the church or possibly "as a crusade against the unknown" (Altenberg 2003, p.110).

Even without these supernatural connotations, for those who actually braved the moors, the landscape itself could be a source of desolation and despair. On his tour of Britain, Defoe (1727, p.93, 99,255) travels across the "endless" north English moors which he describes as the "most desolate, wild, and abandoned country in all England," with an "inhospitable terror...all barren and wild." As for Bodmin Moor in particular, there are "no trees, no lanes, no cluster of cottages or hamlet, but mile upon mile of bleak moorland, dark and untraversed..." (Du Maurier 1936, p.13).

Wade, in his 1928 *Rambles in Cornwall* (p.166), describes Bodmin Moor as “lone, silent, and doure.” Axford (1975, p.10) describes it as a bleak and endless wasteland which “conveys a sense of loneliness and isolation quite out of proportion to its size, and until recent years, those who lived on it were in a world of their own.” Cowles (1934) puts it more matter-of-factly: Bodmin Moor is haunted. Garrow Farm, shown below in figure 1.23, is one of the abandoned settlements on the moor providing a distinct aura of melancholy and complete isolation.



Figure 1.23 Garrow Farm (photo by the author). All that is left of the abandoned medieval settlement on Bodmin Moor

The moor’s bad reputation was not completely unfounded, as traveling across it could be dangerous due to the bad weather, lack of visibility, and the extensive peat bogs- low-lying areas of wet marshland that look deceptively like solid ground but can be as dangerous as quicksand. These hazards were compounded by the complete lack of roads across the moor, along with no signposts, nor even stones to mark the way; bridges were not paid for by the county, so crossing any rivers on the moor added to the difficulty (Axford 1975). Travellers

were dependent on verbal instructions of how to cross the moor, using topographical markers to find their way through the repetitive bleakness of their surroundings and not get lost after dark or end up in the peat bogs. There had been an old Norman horse trail leading across the moor, but by 1743 it was indiscernible – it was recorded that the Methodist preacher John Wesley was unable to follow it to get to the nearest town of Bodmin (Folliott-Stokes 1912). Things improved in the latter half of the 18th century: a wheel-friendly road was constructed in 1750, and in 1754 an innkeeper at Bodmin had direction and distance stones erected at quarter-mile intervals across the moor. Soon after, toll gates were paid for by users and set up through the moor and a direct route across the middle of it was created (now the A30 motorway), replacing a bridle path so “indeterminate and dangerous” that travellers “made out their wills before attempting the journey” (Axford 1975, p.25). The first mail coach crossed the moorland road in 1799 (Munn 1976) and by 1851 there was a paved road across it. However, even in 1934, the road which crossed the moor was still considered “rough” - after much wandering along the “terrible roads,” Cowles (1934, p.33) finally managed to find the main highway to travel on.

Sticking to the road was vital- Wade (1928, p.167) found that Bodmin Moor had worse peat bogs than Dartmoor- “bottomless quagmires” - and described the moor as a witch’s cauldron “brewing up the worst weather Cornwall can produce.” Even when following the main road, Hey (2000b, p.202) states that in inclement weather travelling across the moors was immensely difficult, with many a burial register recording “strangers lost in the snow” who were not found on the moors until springtime. Even with a modern map today it can be difficult to follow the sparse trails due to high vegetation or snow (Altenberg 2003), especially when the fog rolls in (as shown in figure 1.24 below). In the 1930s, the writer Daphne Du Maurier described losing her way on Bodmin Moor on horseback, miles from home in either direction, where the woods she thought only five miles distant were a mirage, with crags, boulders, and valleys barring her progress, and any trails leading only to streams and marshland bogs. Then a storm broke, fog descended, and she lost all sense of direction, with “nothing on all sides but waste and moor”- she “had never known greater despondency” (Du Maurier 2007, p. 139, 137).



Figure 1.24 Misty Moor (photo by the author). The mist comes in thick and fast on the moor, although the cows don't seem to mind

1.7.5 Parishes

The difficulties involved in crossing the moor would have resulted in limited population movement between the communities in areas separated by large stretches of moorland. In addition, the unit of the parish itself could have contributed to the voluntary separation between the inhabitants of adjacent communities. Many of the current parish boundaries in England today were constructed by the Anglo-Saxons and are over a thousand years old; they originated as administrative units which later became a form of local government overseeing the 'moral' behaviour of the people living within it (Fletcher 2003). In the Middle Ages much of a person's social and communal identity was linked to what parish they belonged to, with major occasions such as births, baptisms, and church-going celebrated primarily within the

parish (Altenberg 2003). Boundaries were often bordered by significant landscape features designating the outer limits of the parish, and the act of 'perambulating' or 'beating the bounds' was a significant event in the parish calendar and seen as a way of asserting and recording these boundaries for future generations; it was also important in building a sense of community and confirming what Fletcher (2003, p.186) calls "the commonality of what lay within." Parishes could be insular units - as well as regulating the social norms of the community, the parish instilled a sense of local identity as well as loyalty to a place. People often married within their parish boundaries and this could be taken to the extreme- Snell (2006) presents many examples of English parishes in 16th - 18th centuries where those from outside the parish were called 'foreigners' and regarded with suspicion or even violence.

Currently Bodmin Moor lies within the bounds of 12 parishes, shown below in figure 1.25, all of whose farms have rights of common pasture on it (Johnson et al., 1994) and which together cover an area of about 250 square miles. These are: St. Neot, St. Cleer, Linkinhorne, North Hill, Altarnun, St. Clether, Davidstow, Advent, St. Breward, Blisland, Cardinham, and Warleggan. These parish boundaries have been in place at least since medieval times and some of them for over a thousand years: the Domesday Book lists holdings in two of the parishes, 'Blisland manor' with its 40 villagers and 20 farmers, and St. Neot, which had been held by clergy until 1066 (Morris et al., 1979).



Figure 1.25 Bodmin Moor parish map (adapted from Cornwall County Council; Gary Crossley, personal communication). The 13 parishes surrounding Bodmin Moor; St. Ive is not included in this study

Johnson et al. (1994) note that the medieval use of the moor affects the interactions of the surrounding parishes today: no towns were developed within the parishes and most of the parish churches were built outside the moor- so for the inhabitants of the moorland parishes, it was a long walk to church and even further to the nearest market (Johnson et al., 1994). But journeys between neighbouring parishes could be difficult too, with many of the hamlets being hard to reach on foot due to the large stretches of moorland between them. Gary Crossley, in his University of Oxford PhD thesis about kinship networks on Bodmin Moor, has found historical evidence for minimal population movement between some of the Bodmin Moor parishes, particularly those divided by large tracts of moorland. This lack of movement is demonstrated by what he calls “surname dynasties” (Gary Crossley, personal communication) which show the existence or lack of certain surnames in adjacent parishes. For example, in the 1851 census for the Bodmin Moor parish of St. Neot, there were seven surname dynasties heading an average of nine households each, while three of these surnames were not found at all in the adjacent parishes of Altarnun or Blisland. Another

example is of the parish of Altarnon, which shares long boundaries with Blisland, St. Breward, and St. Neot, yet had only three heads-of-household born in any of those three parishes. Crossley (2018) believes that this tendency for people to marry within their own parish was magnified by the relative isolation enforced by the stretches of moorland between the parishes. This separation between adjacent areas is also demonstrated in a 1978 study of regional farming dialects which found that the parishes on the east side of Bodmin Moor pronounced the word 'stackyard' differently than those on the south side of the moor (North et al., 1980); they are separated by less than 10 miles but it is mainly across open moorland.

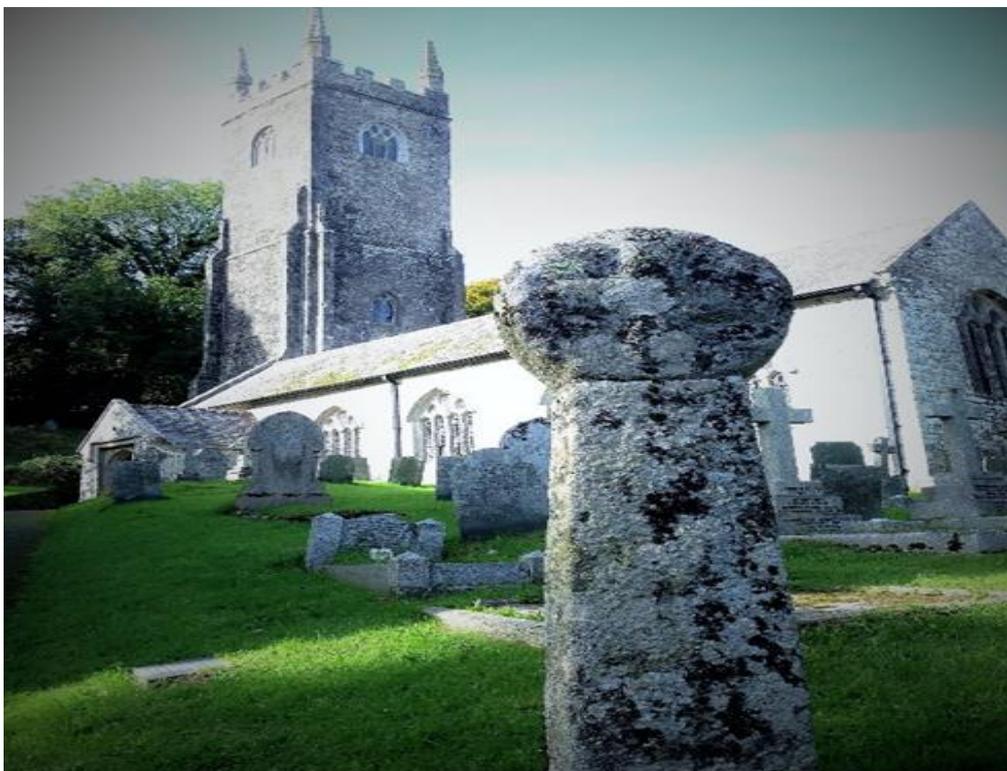


Figure 1.26 Altarnon church (photo by the author). Nestled in a moorland valley, its churchyard contains a mixture of Celtic and Christian monuments

Other areas around the moor were hard to reach due to the vagaries of the landscape. Two villages on the moor's edge, Davidstow in the north and Minions in the east, are both situated 300m above sea level making them the highest villages in Cornwall, while St. Breward, located in the north-western side of the moor, lays claim to the county's highest inn. North Hill is a village on a hill on the edge of a deep valley, and St. Cleer is an enclosed settlement high enough to allow views of Dartmoor over 16 miles away. The parish of Altarnon consists

of 15,000 acres of mainly open moorland; its church, shown in figure 1.26, lies within the tiny village in a secluded valley. Warleggan, whose name means 'the high place on the moor,' (Cornwall Guide 2019) is bounded by small rivers and was considered "the most remote place in Cornwall" (Axford 1975, p.139) until 1953 when it finally got a road leading to it. The church in the parish of St. Clether is located a mile from the village and can only be reached by a footpath across a meadow; the church itself has a stream running through it. The parish of Blisland is bounded by Bodmin Moor's two main rivers and one-third of it is moorland, with a few scattered cottages interspersed among the marshes, while St. Breward is surrounded on three sides by rivers and moorland on the fourth, with plenty of deterrent marshland surrounding the highest point on the moor at 420m; one resident proudly stated that "to get here you need to cross the moor or use a bridge." The southern-most parish of St. Neot is bounded by rivers on three sides and moorland on the fourth. Axford (1975, p.164) states that "the bulk of its population form an indigenous group": many of the families living there today have been there for generations, with several of the names found on gravestones from the last few hundred years appearing in this study; the same is true for most of the other parishes as well. Figure 1.27 below shows a cottage built on land in the parish of Altarnon owned for hundreds of years by the ancestors of one of the study's participants.



Figure 1.27 Joll's Ground cottage (photo by the author). Land in the parish of Altarnon previously owned by the ancestors of one of the study volunteers', surname 'Joll'

1.7.6 Connectedness

Despite its bad reputation and the difficulties of accessing many of the villages surrounding it, Bodmin Moor had its visitors both from near and afar. Altenberg (2003) states that although the natives of medieval-era Bodmin Moor lived mainly confined to their own farms or hamlets, they were not immobile and solitary: many moved between different settlements, as farms were often leased rather than owned, and even the most isolated places around the moor would be in contact with tanners, itinerant traders, people grazing their cattle, and religious pilgrims en route to the monastery in the town of Bodmin. The moor's inhabitants also relied on neighbouring farms to help with tasks such as harvesting, hay-baling, or carrying the dead across the moors to the nearest burial ground; according to Herring (2008), this shows the marginality, relative poverty, and lack of readily available capital among the farming communities of Bodmin Moor. Faith (2011, p.86), describing farms on Dartmoor, agrees that the farming lifestyle in general was interdependent upon others in

the immediate community, stating “we should not envisage any kind of farm at any period, however isolated, without being aware of the invisible networks in which it was enmeshed. The great boundary walls speak of communal effort. So does the management of the moor: this literally goes with the territory.”

The parish church and markets were also central places to meet other people from within approximately a five-mile radius (Altenberg 2003). By 1542 there were six towns in Cornwall, four of which were located less than 10 miles from Bodmin Moor, and by 1602 all four had weekly markets (Brayshay 1996). The town of Bodmin, six miles from the southwest side of the moor, had “the most famous market in the whole of Cornwall” (Carew 1953, p.185), along with a monastery which was the site of many pilgrimages, with many travelling across the moor to get there. The town of Launceston, eight miles from the north-east edge of the moor, has been a centre for trade since Norman times and, being close to the Devon border, was an area of continuous interaction between people from the two counties. In her novel *Jamaica Inn*, Du Maurier (1936, p.135) describes Launceston as having a “brighter, more abandoned spirit about [it]; the crowd was greater and the voices mixed... Devonshire and England were across the river. Farmers from the next county rubbed shoulders with countrywomen from east Cornwall...”

In fact, although they lived in a more isolated manner than their urban counterparts, the residents of Bodmin Moor could not make a living without contact with the outside world, because the economy of the moor was not self-sustaining. Miners had to leave the moor to sell their tin, as the tinning industry had been tightly controlled since at least 1200AD, meaning that its products had to be traded in registered towns (Deacon 2007), farmers had to leave the moor in order to sell their goods in the nearest market town, and people had to purchase items from the outside that they couldn't produce from the moor's resources. These activities would have created social networks expanding outwards from the moor communities, for at least the past 1,000 years since the towns were created (Herring 2011).

In addition, Bodmin Moor provided the locals with an income which was almost completely dependent on contact with outsiders, through the practice of transhumance, the act of bringing livestock from afar to graze throughout the summer months. Bodmin Moor at one point contained most of Cornwall's common land – at 18,000 acres (Axford 1975), it was used for grazing by many in the county, as well as those from further afield. Remnants of transhumance huts dating from before 1000AD have been found (Johnson et al., 1994), from possibly as early as 600AD (Gearey et al., 2000). Fox (2012) believes that transhumance must have occurred earlier than the 7th century due to the presence of farms incorporating the place-name element 'hendre' meaning 'permanent farmstead.' This word is shared with the Welsh language, thus implying that they were named before the two languages split in the 7th century when Anglo-Saxon settlement prevented contact between the two peoples.

The practice of transhumance on the Cornish moors by people from other counties continued throughout the Middle Ages: as Carew (2004, p.101, 107) noted in the 16th century, "In times past the Cornish people gave themselves principally... to the seeking of tin and neglected husbandry, so as the neighbours of Devon and Somerset shires hired their pastures at a rent and stored them with their own cattle," while "the Devon and Somersetshire graziers feed yearly great droves of cattle in the north corner of Cornwall." Pounds (1973) describes the practice of 'summering on the down,' where cattle from outlying districts were pastured by moorland edge farm owners, some from over 20 miles away (Hey 2000b).

Landscape archaeologist Peter Herring (2011) states that the moors were a vital component of Cornwall's economy since prehistoric times: he believes that access to rough ground has been important to farming communities since the Bronze Age, citing the lanes that still lead to 2nd- millennium BC sites on the eastern parts of Bodmin Moor. Transhumance would have played an integral part in mixed farming systems in terms of keeping the moor well-grazed and not overgrown. Herring has calculated that it would take 3,000 households with five cattle each to maintain the open landscape character of the moor - this would require cattle from all of the moor's estates plus many more – and therefore the practice of transhumance would have spread far and wide around the moor, involving many outsiders. Many of the

transhumance huts are situated in clusters implying that other tasks such as milking, making cheese and butter, and spinning, knitting, and shearing wool were done while pasturing the cattle (Herring 2011); Fox (2012) refers to the same configuration of huts on Dartmoor and reasons that as the moorlands provided summer pasture for thousands of cattle from the Devon lowlands, people would have spent the entire summer living on the moor while grazing their livestock and pursuing other tasks.

Overall, the historic and landscape evidence show that in spite of its challenging topography and the difficulty in reaching its settlements, Bodmin Moor was not seen as a wasteland by the families living around it, but as an area they relied upon to survive. And although it may be seen as a peripheral region with limited worth from the point of view of outsiders, the moor was not as economically and socially marginal as is often supposed: the landscape was an integral part of the economy and culture of the surrounding communities, even more so during the Middle Ages than today.

People have inhabited Bodmin Moor for thousands of years, and many of the medieval-era families who lived and farmed on the fringes of the moor have descendants who still live there today, as is demonstrated by the surnames that have been there for centuries. The interactions of the moor's inhabitants with the outside world are also reflected in the surnames that existed, but also changed, in the Bodmin Moor parish records throughout the 300 years discussed in this study (see Chapter 4). Many of the names proved to originally be from across the border in Devon and even further afield. So should Bodmin Moor be seen as a dividing line between Cornwall and Devon- or is it an area of cohabitation and connectedness? The next chapter discusses whether Y chromosomes can help uncover this question.

Chapter 2 Genetic tools for studying human population history

This chapter will introduce the genetic variation in different components of the human genome and illustrate how these have been used to study population history. The main focus will be on the Y chromosome, since this is the tool applied in this thesis. Mitochondrial DNA will be discussed briefly, before a discussion of autosome-wide SNPs and how these have been used to investigate the history of the British Isles in particular.

2.1 The characteristics of the Y chromosome

The Y chromosome is the smallest of all the human chromosomes, at around 60 million base pairs long, and makes up only about 2% of the male genome. It carries approximately 80 genes which are all mostly involved in male-specific functions (Jobling & Tyler-Smith 2003).

Only males carry a Y chromosome because of its dominant role in male sex-determination, while everyone has an X chromosome, and females have two. The male-specific region (MSY), also known as the non-recombining region (NRY), is shown in figure 2.1. It makes up 95% of the Y chromosome's length and does not cross over during meiosis; crossover occurs only at the tips of the Y and X chromosomes, referred to as the pseudoautosomal regions (PAR₁ and 2). PAR₁ is located at the tip of the short arm of the Y chromosome and is approximately 2.7 Mb in length while PAR₂ lies at the tip of the long arm and is around 320 kb in length. Therefore, most of the Y chromosome (the MSY) is passed down intact from father to son, although gradual mutations occur over time which differentiate Y-chromosome lineages through time. These variations can be studied, differentiating males and the populations in which they reside (Jobling et al., 2013), and allowing the study of past male behaviours. Together with studies of maternally-inherited mitochondrial DNA (mtDNA), such studies can show how males and females behaved differently, for example in movement between social groups (Wilkins & Marlowe 2006).

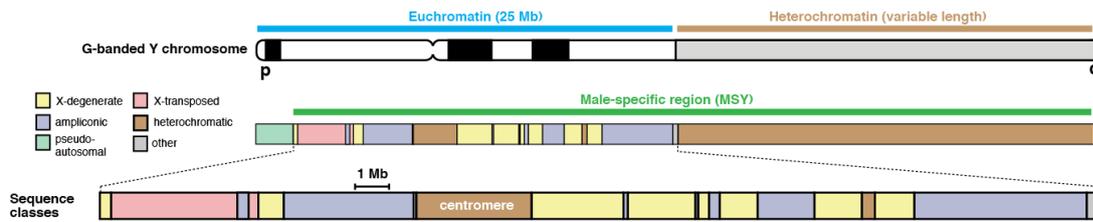


Figure 2.1 Structure of the human Y chromosome At the top is an ideogram of a G-banded Y chromosome. Below is a representation of the different sequence classes, including remnants of X-chromosome similarity, highly repeated regions (ampliconic), and the pseudoautosomal regions. Adapted from (Jobling & Tyler-Smith 2017).

This variation on the Y chromosome makes it very useful for tracing its inheritance. Whereas after a few generations of inheritance the shared portions of the autosomal genome between a pair of individuals decrease exponentially, the Y chromosome does not experience that loss of signal and the differences between generations via the male line accumulate only as fast as the mutation rate of the variants being compared (Calafell & Larmuseau 2017).

The male germ-line is highly subject to mutations because of the relatively high number of cell divisions in spermatogenesis (Crow 2000), so the Y chromosome might be expected to be more variable than other chromosomes. However, the MSY has a smaller effective population size than other chromosomes (one quarter of that of autosomes) so is prone to genetic drift, outweighing the increased mutation rate and thus lowering its diversity (Jobling & Tyler-Smith 2003). Genetic drift also has the effect of increasing the differentiation between populations, an effect that is exacerbated by predominant male behaviours including patrilocality (Burton et al., 1996) (the tendency of males to remain close to their birthplaces on marriage). Together, these effects make the MSY the most geographically-differentiated locus in the genome (Seielstad et al., 1999).

2.2 Molecular markers for MSY diversity

There are two types of molecular markers that are widely used to distinguish Y-chromosome types - Short Tandem Repeats (STRs), and Single Nucleotide Polymorphisms (SNPs) - both of which differ in their mutation rates and properties. Knowledge of mutation rates is crucial for estimating the time to the most recent common ancestor of groups of Y-chromosome

haplotypes in evolutionary studies, for interpreting the relationship between presumed relatives in genealogy testing, and for some aspects of interpretation of evidence in forensics. There are a few thousand STRs on the Y chromosome, of which about 200 have been well characterised (Ballantyne et al., 2010). Advances in next-generation sequencing (Jobling & Tyler-Smith 2017) have allowed the identification of tens of thousands of SNPs.

2.2.1 STRs

STRs (also known as microsatellites) are tandemly repeated arrays of short (2-7-bp) DNA sequences, repeated from 10 to 30 times, that mutate rapidly through changes in repeat unit number. STRs are estimated to cover about 1% of the total human genome on both the autosomes and the sex chromosomes (Zhivotovsky et al., 2004). Of the few hundred Y-STRs characterised, sets of 17-27 STRs are usually used, in a single polymerase chain reaction (PCR) multiplex, to analyse Y chromosomes. The resulting set of repeat unit numbers at a set of STRs is called a Y haplotype. Given these numbers of STRs and the average mutation rate per STR of one mutation every 500 generations (Ballantyne et al., 2010) (10^{-3} per STR per generation), most haplotypes in a population sample will be unique (Kayser 2017).

The mutation process of STRs is thought to be due to DNA replication slippage, usually involving single-step increases or decreases in allele length. STR evolution can be described by a stepwise mutation model which allows an STR to vary at a fixed rate independently of repeat length and with the same probability of expansion and contraction (Kimura & Ohta 1973). However, studies of large sets of autosomal STRs in pedigrees (Sun et al., 2012) reveal more subtleties: for example, mutation rates increase with repeat unit length (tetra nucleotide STRs have faster mutation rates than dinucleotide STRs) and shorter alleles are more likely to gain repeats, while longer alleles are more likely to lose repeats. Most analyses of Y-STR data rely on a simple single-step model and often employ an average mutation rate across STRs.

Given knowledge of the mutation rate, an attempt can be made to date the time to the most recent common ancestor (TMRCA) of a set of Y-STR haplotypes. Various different methods

have been developed for this, from simple approaches that use the mean number of mutational steps to the root of a haplotype tree (Forster et al., 2000), to sophisticated Bayesian coalescent methods (Drummond & Rambaut 2007). One problem has been how to treat mutation rates: the 'pedigree' rate as determined in father-son pair analysis is well known, but given the possibility of back mutation that characterises STRs, this rate may be too fast for ancient lineages so the suggestion has been made to use an 'evolutionary' rate, about three times slower, that accounts for such back mutation (Zhivotovsky et al., 2004). Studies where Y chromosomes are both sequenced and STR-typed (Hallast et al., 2015) suggest that, for young lineages ($\leq 10,000$ years), the pedigree rate is more reliable.

Because of the highly recurrent mutation at Y-STRs, phylogenetic representations of Y-STR haplotypes cannot be done using bifurcating trees. Therefore the most common means of representing haplotype relationships is via networks (particularly median-joining networks) (Bandelt et al., 1999), which can incorporate the reticulations representing recurrence. Such networks are useful tools for considering the population distribution and history of Y haplotypes and will be used in this thesis. An example is presented in the sections below.

2.2.2 SNPs

SNPs are the most abundant type of polymorphisms in the human genome and are estimated to occur at 1 out of every 1,000 bases within a given genome (1000 Genomes Project Consortium 2012), with tens of thousands known on the Y chromosome (Poznik et al., 2016). SNPs include base substitutions, single nucleotide insertions, and single nucleotide deletions, all which mutate slowly via DNA damage, base misincorporation, and incorrect repair. SNPs usually exhibit only two alleles: the ancestral and derived states (as judged by comparison with a chimpanzee orthologue). The frequency of this type of mutation is very low: approximately 9×10^{-10} mutations per base per year as measured in sequenced families for the MSY (Helgason et al., 2015). Thus, it is usually assumed that the derived allele resulted from a unique event in human evolution. This is true for >95% of known Y-SNPs, though some are known to be recurrent.

A set of Y-SNPs together defines a haplotype, but this is generally referred to as a haplogroup, to distinguish it from a Y-STR haplotype and to reflect its relative stability. Haplogroups can be arranged into a bifurcating tree using the principle of maximum parsimony. Such trees have been developing since the mid-1990s (Jobling & Tyler-Smith 1995), with increasing numbers of SNPs and increasing information about the ancestral state from chimpanzee sequencing (Hughes et al., 2010). An example of such a tree is presented in figure 2.2.

2.3 Applications for Y-chromosome diversity studies

The entire Y chromosome can act as one highly variable patrilineal marker because all variants (including STRs and SNPs) are inherited together as a haplotype. This variation can give insight into evolutionary processes and population movements and structure based on Y chromosome lineages defined either by SNPs (haplogroups), by STR haplotypes, or by a combination of these.

Analysis of Y diversity has a range of different applications such as forensic analysis, genetic genealogy, disease susceptibility, the causes of male infertility (Jobling & Tyler-Smith 2017), and evolutionary studies such as the analysis of population structure, migration, and admixture (King & Jobling 2009a). Some of these that are relevant to this thesis are discussed below.

2.3.1 Forensic genetics and the development of STR multiplexes

The use of STRs in DNA "genetic profiling" was developed in the early 1990s (Urquhart et al., 1995), following on from the minisatellite-based identification methods invented by Alec Jeffreys in 1984 (Jeffreys et al., 1985). The male-specificity of the Y chromosome made Y-STR profiling an attractive idea in forensics, particularly in cases involving mixtures of male and female DNAs (Roewer & Epplen 1992). One problem with such analysis is that patrilineally-related males generally share the same Y haplotype. Attempts to increase discrimination among males has driven increases in the number of STRs used for analysis: forensic efforts to

discriminate even among close male-line relatives have sought 'rapidly-mutating' STRs (Ballantyne et al., 2010), which have mutation rates as high as 5×10^{-2} per generation, and a combination of 13 of these distinguishes a good proportion of father/son pairs thanks to mutation (Ballantyne et al., 2014). The nine initial STRs defining the 'minimal haplotype' (Kayser et al., 1997) grew to the 17 STRs multiplexed together in the Y-filer kit (Thermofisher). In turn this grew to the 23 STRs in the PowerPlex Y23 kit (used in this thesis), and the 27 STRs in the YFiler Plus kit, six of which are rapidly mutating.

2.3.2 Use of the Y chromosome in studying population histories

Population genetics is used to understand the factors affecting evolutionary change and the amount of genetic variation within and between populations. This variation is generated by mutations and shaped by natural selection, genetic drift, and gene flow, all of which are influenced by historical or demographic events and are reflected in patterns of diversity which can be measured by the allele frequencies between populations.

Different parts of the genome have different effective population sizes because not all genomic loci are equally represented in all individuals. As mentioned above, the Y chromosome has only one quarter the effective population size of an autosome (and one third that of the X chromosome) because for every one Y chromosome that can be inherited, four different autosomes and three different X chromosomes can. Because of its small effective population size, the Y chromosome is more prone to genetic drift, the extent of which depends on population size and admixture with other populations, which leads to lower SNP diversity overall.

SNP mutations that accumulate in a particular Y chromosome lineage can be used as markers to distinguish individuals or groups from one another based on male-line ancestry. The history of these mutations can then be constructed in a haplogroup tree showing how all the Y chromosome types throughout the world are related to each other, with each branch sharing its own mutations specific to that haplogroup. Some SNPs may have deep origins and be shared by many men, others may be more recent and found mainly in specific

geographical regions, whereas others may be so recent that they are confined to a single family or even a single individual. An example of a haplogroup tree is shown in figure 2.2, together with the distributions of the haplogroups in global indigenous populations.

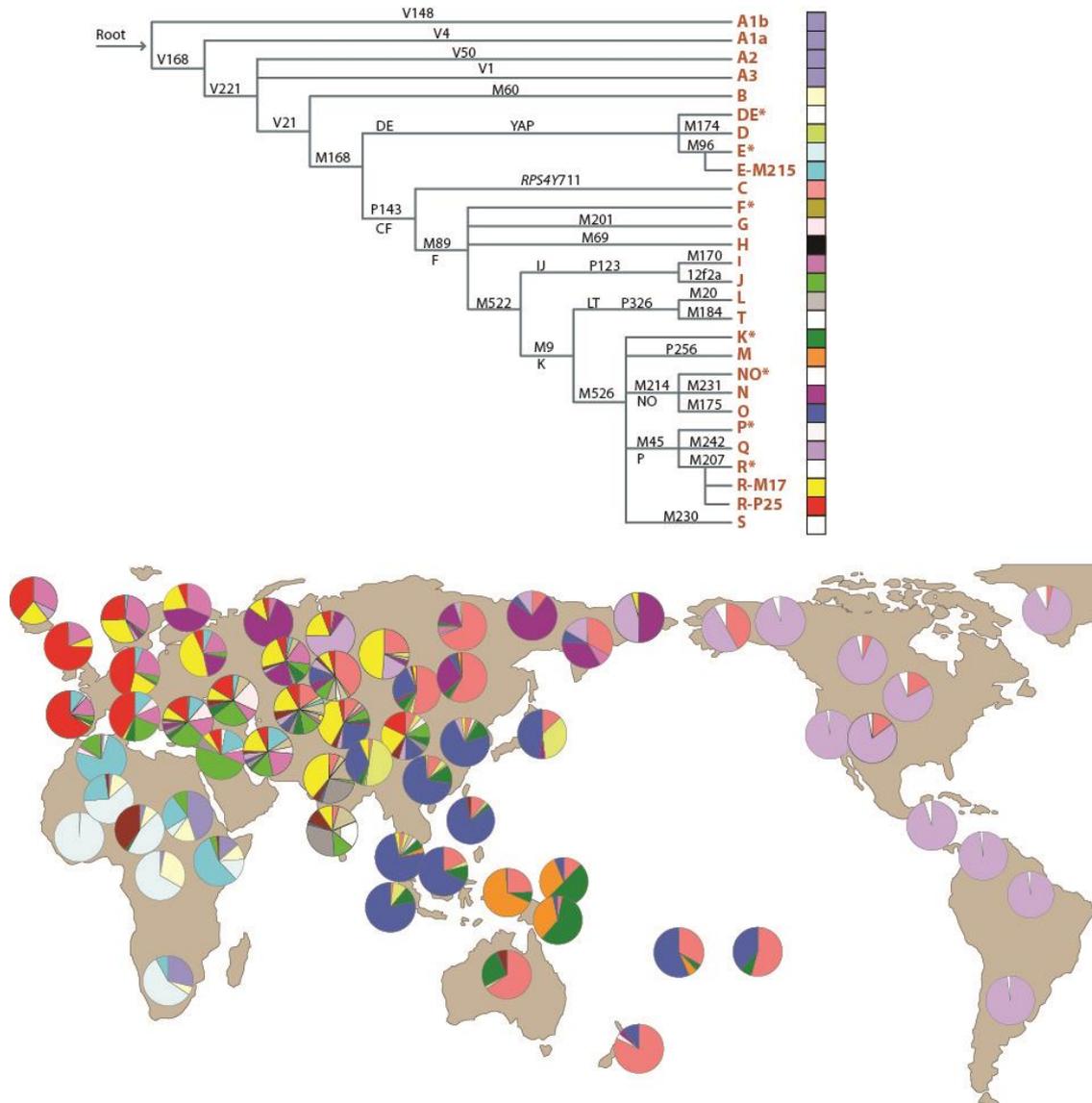


Figure 2.2 Y-chromosomal phylogeny and haplogroup distribution Top: simplified version of the Y-chromosomal phylogenetic tree. The major clades are indicated on the tree, together with the names of key variants defining the branches. Haplogroup names are shown at the ends of the branches and are assigned a colour corresponding to the colours used on the map below. Bottom: geographical distributions of Y-chromosomal haplogroups. Each pie chart represents an indigenous population sample, with the haplogroup frequencies indicated. Adapted from (Jobling et al., 2013)

The phylogenetic tree of the Y chromosome (Y Chromosome Consortium 2002) shown in figure 2.2 is based on ~600 SNPs and contains 311 distinct haplogroups. The human genome

was first sequenced in 2003 and since then, tens of thousands of SNPs have been found through developments in sequencing technology, increasing the resolution of the haplogroup tree enormously. One example is from the 1,000 Genomes Project (1000 Genomes Project Consortium 2012) which incorporates sequence data from 1,244 Y chromosomes from 26 populations and has identified 65,000 polymorphisms (figure 2.3). In such trees, branch lengths are proportional to time, since many SNPs are ascertained in an unbiased way. This gives insights into the ages of haplogroups and into male-lineage expansions that have occurred relatively recently, and provides a date for the Y-chromosome MRCA of around 190,000 years in Africa.

Colombians from Medellin, Colombia; ESN, Esan in Nigeria; FIN, Finnish in Finland; GBR, British in England and Scotland; GIH, Gujarati Indian from Houston, Texas; GWD, Gambian in the Western Divisions in the Gambia; IBS, Iberian population in Spain; ITU, Indian Telugu from the United Kingdom; JPT, Japanese in Tokyo, Japan; KHV, Kinh in Ho Chi Minh City, Vietnam; LWK, Luhya in Webuye, Kenya; MSL, Mende in Sierra Leone; MXL, Mexican ancestry from Los Angeles, United States; PEL, Peruvians from Lima, Peru; PJI, Punjabi from Lahore, Pakistan; PUR, Puerto Ricans from Puerto Rico; STU, Sri Lankan Tamil from the United Kingdom; TSI, Toscani in Italia (Tuscans from Italy); YRI, Yoruba in Ibadan, Nigeria. Adapted from: Jobling & Tyler-Smith (2017)

As illustrated by the two figures above, distribution of Y haplogroups across populations is characterised by high levels of geographic specificity so examining their global distributions can help uncover genealogy and population history, including past migrations, colonisations, and admixture events. The diversity within SNP-defined haplogroups can then be more fully explored by using STRs to further subdivide each haplogroup. A corollary of this is that STR haplotypes can be used to predict haplogroups (Khubrani et al., 2018): each haplogroup was founded by one man, with a unique STR haplotype, and further diversity has arisen since, via mutation.

As noted above, networks can be used to represent the variation and relationships among STR haplotypes. An example of a network within a particular haplogroup is shown in figure 2.4 below:

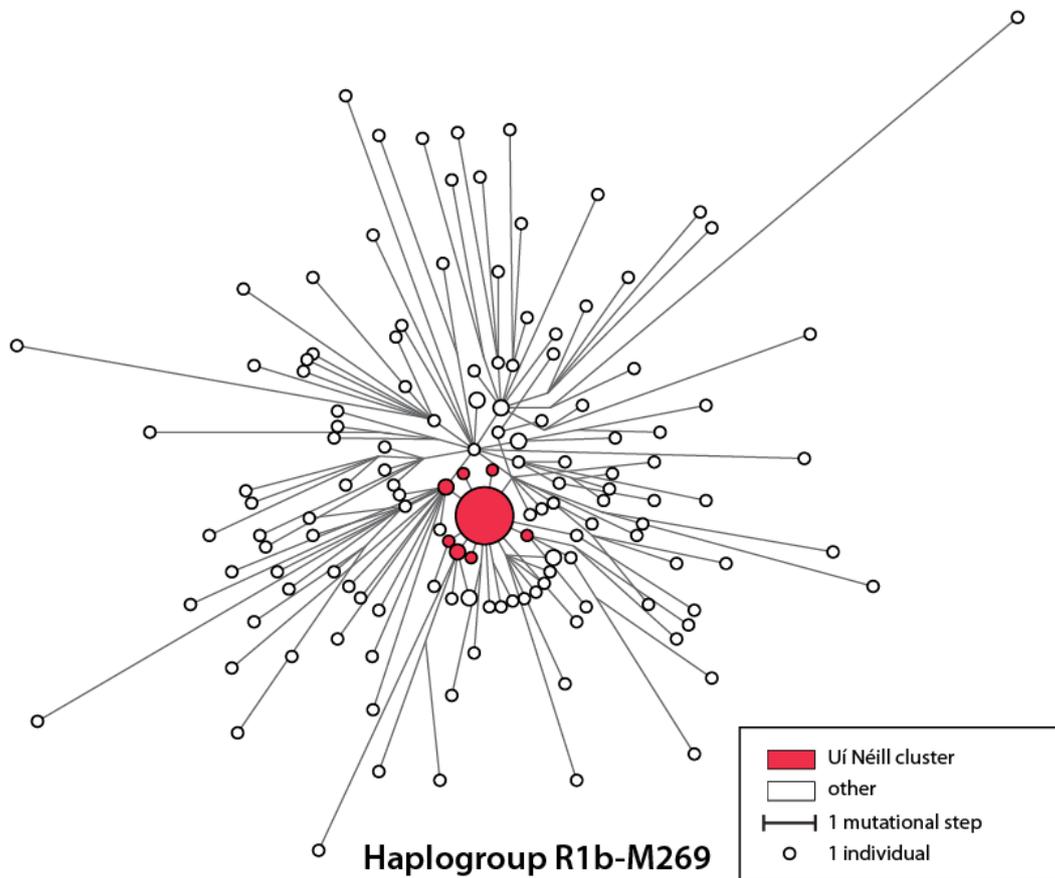


Figure 2.4 Example of a median-joining network Circles represent Y-STR haplotypes based on 17 STRs, with area proportional to sample size, and lines between them proportional to the number of mutational steps. Red colour in this case highlights an Irish expansion lineage ascribed to the medieval chieftain Uí Néill, as shown in the key, bottom right. Note the generally star-like form of the network (suggesting expansion) and that most haplotypes are unique (1 individual circles). Adapted from (Moore, et al., 2006).

Because of its strong geographic differentiation, the Y chromosome has been used to uncover past population structure even on a local level. One such study showed that the British Isles has experienced different paternal histories depending on the different parts of Britain that different immigrant groups have settled in (Capelli et al., 2003). Another study has shown the extent of population replacement by Anglo-Saxons of the native British, demonstrating that British genetic survival varied across Britain, with low levels in England, but high levels in Wales (Weale et al., 2002).

2.3.3 Surname studies

The Y chromosome, because of its patrilineal inheritance, is a natural tool to investigate the biological relatedness among males who share paternally-inherited surnames. This thesis used surnames in the recruitment of volunteers for DNA sampling, and this section provides the background on the surname-genetics relationship.

Understanding population structure

Hereditary surnames contain information about relatedness within populations. The use of surnames in genetic studies dates back to 1875, when Charles Darwin's son used them to estimate the degree of inbreeding in populations due to first-cousin marriages. More recently, they have helped to track disease in epidemiological studies and, by sampling modern populations, have been used to uncover the structure of past human populations which have been obscured by recent migrations and expansions (Jobling 2001). By using surnames, human genetic diversity can be studied at much more local scales than was previously possible with the use of genetic or linguistic information alone (Mateos 2014).

Surnames can also be used to study genetic population structure in terms of endogamy and relatedness within and between populations, or through the analysis of migrations and cultural interactions (Jobling & Tyler-Smith 2017). One way of doing this is through the use of Y chromosome mutations and inheritance.

Y chromosome markers in surname studies

Surnames are inherited paternally in most cultures and so both the surname and the Y chromosome should show common ancestry through the male lineage. Although most of the Y chromosome is inherited unchanged from father to son, mutations occur over time which can be used to distinguish individuals from one another; the use of markers with different mutation rates make it possible to uncover relatedness throughout different time frames, starting from the individual and family level to the surname and population level. For

example, due to the mutation rate of STRs, slightly different haplotypes with the same surname could imply the sharing of a common ancestor, because only a few of the STRs could have mutated (generally by one repeat, either forwards or backwards) during the 700 years since surname establishment. Additionally, the slower mutation rate of SNPs allow the classification of a more distant common ancestor before the advent of surnames; males who differ at even one of these SNPs cannot share common ancestry within the last few thousand years, and therefore not within the time that surnames have been established (King & Jobling 2009b).

While inherited surnames can act as models of the genetic structure of male populations, the correlation between a surname and a particular Y-chromosome is not always a direct one. The influence of non-genetic factors on surname models must be taken into account, such as adoption, extra-pair paternity (illegitimacy), and maternal surname inheritance. In addition, the surname must have a unique origin in order to link it to a specific Y chromosome type, although names can differ in pronunciation and spelling while their underlying Y chromosome lineage will remain the same (Lasker et al., 1985). For example, an early study by Sykes & Irven (2000) demonstrated that different groups of men carrying the 'Sykes' surname had different Y chromosome haplotypes, implying that they were descendants of different founders of the surname which therefore did not have a unique origin; nonetheless, their Y chromosome diversity was limited compared to controls. King et al. (2006) compared pairs of seemingly unrelated British men with the same surname and found that signals of co-ancestry were stronger in rarer surnames, which are more likely to have one originating founder (Jobling 2001). King et al. also found that the chance of sharing a Y chromosome haplotype amongst British men with the same surname was 100 times greater than within the general population, and for "rare" surnames - designated as those names with below 5,000 bearers - the probability of two men with the same surname sharing a common ancestor was 50%.

King & Jobling (2009b) analysed 40 British surnames for their estimated haplotype diversity and number of founders; results showed that in Britain, the more frequent surnames tended

to have more diverse Y-chromosomal haplotypes. Studies have also found that in England (King & Jobling 2009a) and Spain (Martinez-Cadenas et al., 2016), if two men share a surname, the probability of also sharing a Y-chromosome haplotype is inversely proportional to the frequency of the surname in the population; this is because common surnames, which were founded many times, have high haplotype diversity, whereas rare ones tend to have low diversity (King & Jobling 2009b).

One way of tracing ancestry using a combination of surnames and genetics is through the use of Y chromosome inheritance. The genetic structures of past human populations may have been obscured by recent migrations and can be observed only indirectly by inference from modern samples, but the link between an inherited cultural marker such as the patrilineal surname and a genetic marker such as the Y chromosome provides a way to use modern individuals as a proxy for populations at the time of surname establishment in England approximately 700 years ago.

This technique was utilised by Bowden et al. (2008) who used the Y chromosomes of current populations in northwest England as a model for populations that existed at the time of surname establishment, in order to uncover the genetic legacy left by the Vikings in that area. Men who had ancestors living in the area for two generations were compared with independent samples with the same residency criterion, but in addition bore surnames known to exist in local medieval lists. The Y-chromosomal haplotypes of these two sets of samples were significantly different and showed that the men carrying the local surnames were more likely to show high collective Scandinavian ancestry than were the men without such surnames. This suggests that access to the Y-chromosomal diversity of past populations might be possible through the selection of modern-day samples based on surnames known to exist in a particular region during the medieval period (Bowden et al., 2008), an idea which is the basis for this thesis.

2.4 Mitochondrial DNA as a tool for population history studies

Mitochondrial DNA is transmitted maternally to offspring of both sexes and can also be used to uncover population histories, providing a matrilineal counterpart to the Y chromosome. The high mutation rate, female-line inheritance, high copy number per cell, and lack of recombination make mtDNA a useful marker in population genetics. It allows investigation of female-specific processes, and its low effective population size leads to higher genetic drift compared to the autosomal chromosomes, and therefore higher geographic structure.

Most of the mitochondrial genome mutates at 10x the rate of nuclear DNA (Soares et al., 2009), but within the control region (the non-coding "D-loop" which ensures replication) hypervariable segments (HVS) 1 and 2 are even more subject to mutation, at a rate of 5×10^{-6} per base per generation, and are highly informative for pedigree studies.

There is no recombination in mtDNA, so this allows the exploration of genealogical relationships among individuals or groups by studying the frequency differences of matrilineal clades among populations at the continental and regional level. Sequencing the entire mtDNA genome can help uncover patterns that have arisen over thousands of years, although due to the highly variable mutation rate of the various regions of the mitochondrial genome, accurate split dates of the mitochondrial clades are not always clear. The root of the human mtDNA variation derives from a single female ancestor (Cann et al., 1987) who lived approximately 100-200,000 years ago in Africa (Kivisild 2015).

Compared to the estimates based on autosomal data, the observed differences in mitochondrial sequences among populations on a global scale are significantly higher and second only to the differences based on Y chromosomes, with Africa showing the highest within-region diversity (Lippold et al., 2014). However, while there is an abundance of extreme local male-lineage expansions (Poznik et al., 2016), which confirm the difference between male and female demographic histories (Karmin et al., 2015), mtDNA shows less extreme demographic shifts due to the existence of prevailing patrilocality, such that the genetic differences among populations are typically higher for the Y chromosome than for

mtDNA, although this effect has been mostly noticed at local rather than global scales (Wilder et al., 2004).

2.5 Using Autosomal DNA to study population histories

Autosomal DNA is inherited equally from both parents. With advances in genome-wide technologies, including SNP chips and whole-genome sequencing, large-scale analyses of autosomal DNA have become prevalent, as opposed to the earlier locus-specific autosomal studies. One example of an autosome-wide analysis is the People of the British Isles project ('PoBI') (Leslie et al., 2015) which attempted to uncover and interpret the genetic structure of the indigenous British population. The PoBI study provides the motivation for the central aim of this thesis – to examine the historical and genetic evidence for differences among the populations of southwest England, specifically Cornwall and Devon.

2.5.1 The PoBI study and its findings

The degree of replacement of the native population of the British Isles due to immigration and invasions has been a subject of debate for many years. Recent studies (Leslie et al., 2015) have demonstrated that comparing the types of genetic variation in the British Isles with populations on the European Continent can reveal which European groups settled in Britain, based on the similarities of parts of their genomes. These similarities can also uncover population structure on a more local level, such as between regional counties within Britain. While earlier studies had shown some regional variation in allele frequencies genome-wide, population structure within Britain is relatively limited. In order to investigate a more fine-scale population structure in the UK, PoBI sampled 2,039 'indigenous' men and women from across the UK whose four grandparents were born within 50 miles of each other and in a rural area of the British Isles, as rural areas are assumed to be more homogeneous than urban areas. Because each individual contains subsets of the chromosomes of their four grandparents, the DNA from these grandparents were effectively being sampled, while also being linked to a relatively specific location in Britain. The average birth date of the grandparents in this study was 1885, thus providing a "genetic snapshot" of Britain at a time

prior to the population movements later in the century; the underlying assumption in the study was that the relative genetic structure of these rural regions has remained comparatively stable up until that time, so the genetics of the local population today could effectively represent the past population structure of each region.

The genetic tool employed by the PoBI project was a set of about 500,000 common SNPs, typed using a SNP-chip. The large number and genome-wide distribution of SNPs provides a relatively unbiased 'average' picture of variation descending from many independent ancestors. Each of the 2,039 individuals was genotyped and computational methods were applied to detect population structure. Conventional methods based only on allele frequencies of SNPs (such as the program ADMIXTURE (Alexander et al., 2009)) are useful in clustering geographically coherent groups at the continental scale, but at a more local scale such as that of the British Isles, they produce only limited information - detailed genetic structure is undetectable. In the PoBI dataset, ADMIXTURE differentiated clusters of individuals from Orkney and Wales from other samples and from each other, but revealed little further discernible structure within the Isles (Leslie et al., 2015).

A more refined method called fineSTRUCTURE (Lawson et al., 2012) was then applied, which detects segments of the genome that are inherited together in linkage- this can help detect relatedness between the genomes of individuals. This method accounts not only for SNP frequencies but utilises genome-wide patterns of haplotype similarity between individuals by using linkage disequilibrium (LD), i.e. how SNP alleles associate with each other along chromosomes. Taking into account LD is more informative for population structure than looking at each locus separately because it assesses inherited blocks of alleles which have not yet been broken down by recombination, and this in turn infers recent ancestry.

Taking account of LD, Leslie et al. (2015) uncovered subtle levels of genetic differentiation in the British population. The method can define clusters hierarchically, as shown in the tree within figure 2.5: the deepest branch points reflect the split between Orkney and Wales, as was seen in the ADMIXTURE analysis. Without referring to geography, individuals were

assigned to one of seventeen genetic clusters (designated by the different colours in figure 2.5). The geographical distribution of the clusters is based on the placement of each individual, as a cluster-specific symbol, at the centroid of their grandparental places of birth on a map. The fact that the symbols cluster together in a largely non-overlapping pattern illustrates clear population structure, which could be due to the relative isolation of the populations from each other as well as reflect the differing patterns of migration and admixture from populations outside the UK.

The clusters reveal the clear distinction of Orkney; a division between north and south Wales; the separation of northern England, Scotland, and Northern Ireland from the rest of England; and separate clusters corresponding to Cornwall and Devon. The data also shows great genetic heterogeneity among the areas of Britain that have been sometimes classed together as 'Celtic.' For example, the cluster pertaining to Cornwall- which is often classified as a Celtic area and therefore might be expected to resemble other Celtic clusters- is quite different from that of the Welsh or Scottish clusters, and is much closer genetically to that of Devon and central/southern England, as can be seen from its location in the tree in figure 2.5. In addition, Devon has its own cluster which, as shown by its location in the tree, is closer genetically to central/southern England than to Cornwall. Just as striking as these finely differentiated local groups is a dominant widespread (red) cluster, comprising 51% of the samples, which covers central and southern England and extends up the eastern coast to north Yorkshire; the homogeneity of this cluster implies considerable freedom of movement within it.

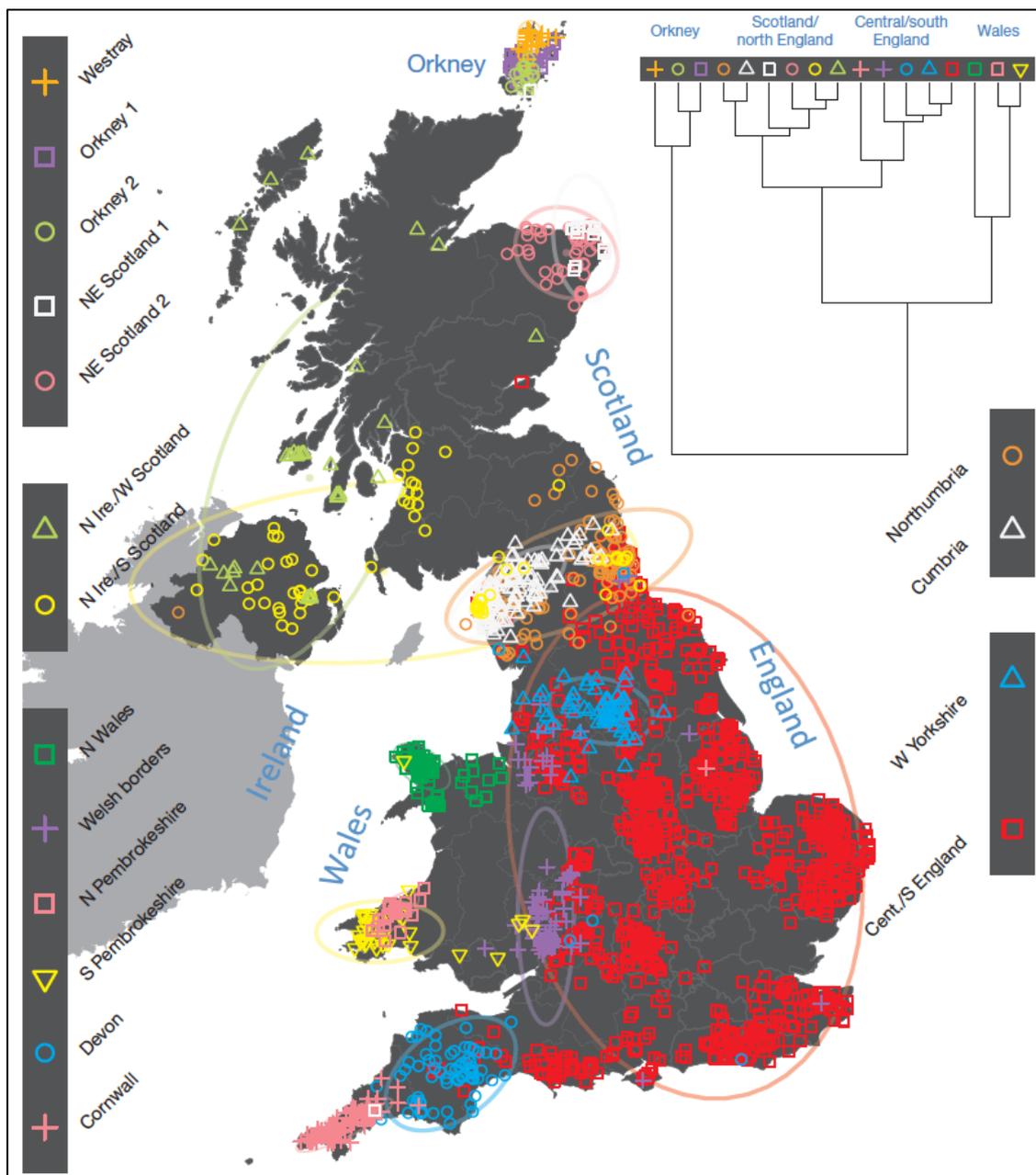


Figure 2.5 People of the British Isles genetic map Clustering of 2,039 UK individuals into 17 clusters based only on genetic data. The coloured symbol representing the genetic cluster to which the individual is assigned is plotted at the centroid of their grandparents' birthplaces. The tree (top right) depicts the order of the hierarchical merging of clusters (Leslie et al., 2015).

The genetic origins of the clusters were also investigated in terms of possible sources from outside the British Isles. To represent these sources, a set of 6,209 individuals, collected for a medical genetics study at different European hospitals, was used. Analysis using fineSTRUCTURE defined 51 geographically-differentiated European groups, whose

contributions to the PoBI clusters could then be considered to provide an 'ancestry profile' for each cluster (discussed further in section 6.1.1). Some European groups are components of many or all of the PoBI clusters- these are interpreted as relatively ancient contributions; some are prominent in only a limited number of clusters- these were interpreted as relatively recent contributions. The fact that Norwegian groups comprise about 25% of the ancestry of the largest Orkney cluster was regarded as validation of the approach, given Orkney's history as part of the kingdom of Norway during the Middle Ages.

Analysis of the major central/southern English cluster suggested a contribution of about 35% ancestry from a north-west German group that was interpreted as the result of Saxon migrations; this same group did not contribute at all to the Welsh clusters. However, by considering the lengths of the genomic segments contributed, which decrease in size with each generation since the original admixture event occurred, this contribution was dated to 858AD (95% confidence interval: 802-914 AD) - more than two centuries later than the major period of Saxon migration. This was explained on the basis that 'a migration event is likely to precede any subsequent population admixture, possibly substantially so, if the migrants mate largely within the migrant group for some time after their migration.' This interpretation has been explicitly challenged by Kershaw & Røyrvik (2016) who suggest that the north-west German input might instead reflect Danish Viking contributions, for whom the late date fits better.

The clusters that are of particular interest for this thesis are those in Cornwall and Devon: first, they are clearly distinguished from each other, and second, as the tree in figure 2.5 shows, the split between the Cornwall and Devon clusters is deep within the tree- it is the fifth split out of 17- signifying a substantial difference between the two clusters which is comparable to or greater than that of the difference between the northern English and Scottish samples, or between the islands of Orkney. According to Leslie et al. (2015), this difference is most probably due to the slightly greater contribution of Saxon DNA into Devon. The authors of the PoBI study also noted a strong correlation between the genetic clusters and some natural geographical boundaries, with the boundary between Cornwall and Devon

closely matching the 1,000-year old county boundary of the River Tamar, and Bodmin Moor, as seen below in figure 2.6.

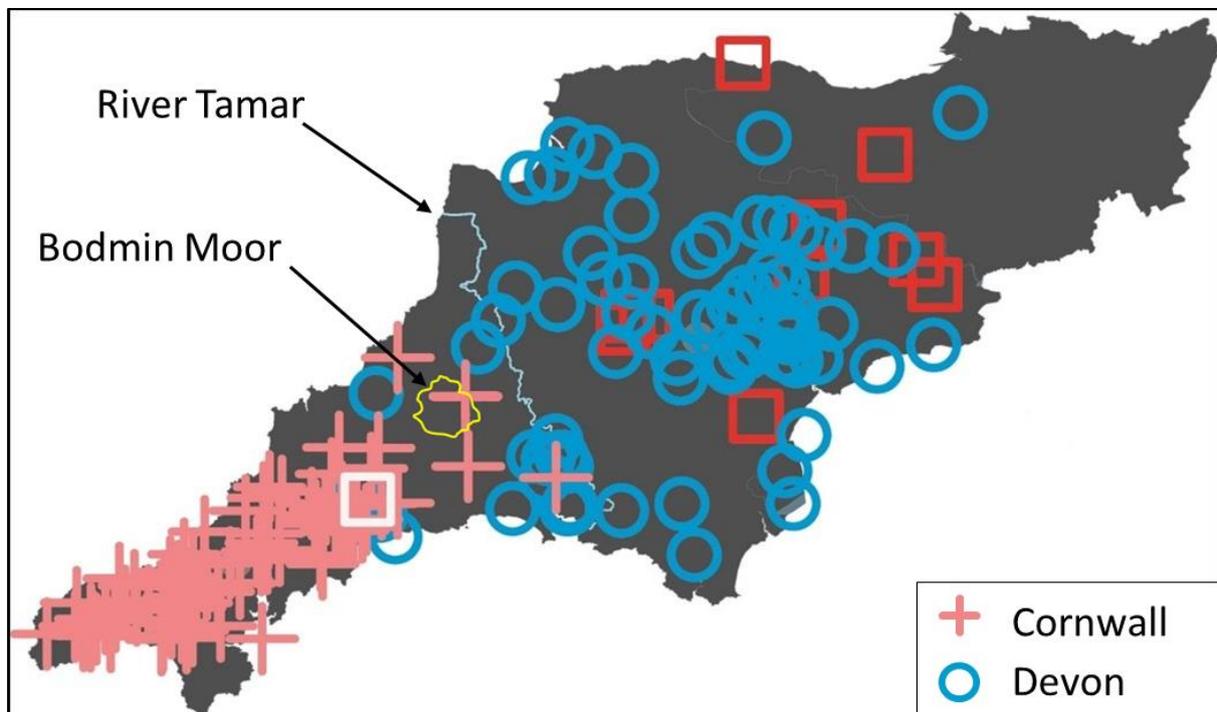


Figure 2.6 The Cornwall/Devon divide (adapted from Leslie et al., 2015) There is little overlap between the Cornish samples and the Devon samples. The red squares in Devon represent individuals with ancestry from Central or South England. The single white square found in Cornwall represents a lone sample whose genome does not match their genealogy: their genome is most similar to those found in NE Scotland, but located on the map at the centroid of their grandparents' birthplace in Cornwall. This could be due to a sampling error or a case of unknown adoption; there are other such discrepancies found in the PoBI dataset. It is notable that most of the Cornish samples are from mid- or west Cornwall, as opposed to the east Cornwall/Bodmin Moor area.

The PoBI finding of distinct Cornish and Devonian autosomal clusters is striking and raises a number of questions. Given the generally higher differentiation of Y-chromosome lineages than autosomal lineages, is the autosomal cluster boundary also reflected in different patterns of Y haplotypes? Could this suggest a male-mediated process that underlies the cluster formation? Is the status of Bodmin Moor as an apparent boundary region reflected in its Y lineages? Can the histories and distributions of surnames in the region support this idea, and can surnames be used as a sampling tool for Y lineages? This last question is addressed in the following chapters.

Chapter 3 History of surnames

3.1 How surnames arose

The development and spread of hereditary surnames in England was a slow and complex process occurring over several centuries, which varied in different parts of the country and between social classes (Hanks et al., 2016). The earliest hereditary family names in England are recorded in some Norman families after the Conquest in 1066AD (Hanks et al., 2016), with many using the title from their lands in Normandy as surnames. Surnames became common amongst the nobility in the south of England in the 12th century and the majority of landholding families throughout all of England had acquired hereditary surnames by 1250, usually taking the name of the place in which they resided; this helped to solidify their position as hereditary property owners and assured their tenure (McKinley 1990). Thereafter, traders and merchants began using surnames along with peasants and free men, with the countryside and the northern counties acquiring them last (Hey 2000a).

Before the use of hereditary surnames, people bore non-hereditary 'bynames'- defined as any second or qualifying name (Postles 1995)- in addition to their forename. Bynames were coined mainly in Middle English and consisted of either nicknames, the father's first name, the bearer's place of origin, or their occupation (Reaney 1967). During the 12th and 13th centuries the use of bynames spread down through the social classes, from the lower gentry to free tenants and finally to the unfree peasantry. By the Hundred Rolls of 1280, which listed householders and tenants of the land, everyone listed had a personal, but not hereditary, byname (Beddoe 1971), and by the middle of the 14th century almost everyone had a byname (Hanks et al., 2016). Non-hereditary names still existed in northern towns, but by the mid-15th century almost every person in England had a hereditary surname (Hanks et al., 2016).

Theories regarding the reason for the adoption of hereditary surnames are varied and somewhat inconclusive, and hindered by the fact that not all levels of society had their names documented - most of the earliest written records mention only landholders and taxpayers (McKinley 1990), representing only the wealthier segment of the population (Postles 1995). Some proposed reasons for the adoption of surnames include population growth, an increase

in population mobility and migration, and other societal changes. A widely accepted theory (Redmonds 1972) attributes the origin of hereditary surnames to the demands of manorial record-keeping and the need to strengthen claims to land when courts across England started recording property or land transactions during the 13th century, for peasants as well as for nobility- the king could now keep track of his various subjects in terms of transfers of land. So whereas previous efforts to identify people often consisted of "long-winded descriptions attached to a personal name" (Reaney & Wilson 1995, p.xlvi), surnames made official record-keeping easier and more efficient.

Another common theory is that bynames grew into hereditary surnames in order for landholders to consolidate their position as hereditary property owners (McKinley 1990), although this was mainly among the landowning class where surnames changed from each generation- the oldest son would inherit the land title/ surname while younger sons took the names of the smaller estates allotted to them. However, Reaney (1967) believes that rights to land were not necessarily dependent on having stable surnames, citing the lack of fixed surnames that existed in Wales as an example; Hey (2000a) also cites examples of 13th-14th century property documents which list people without even a byname. Instead, Reaney (1967) believes that the pet names and nicknames which are used as modern surnames today (see section 3.2.4 for examples) suggest that they arose out of the community- what people called each other in their daily interactions, rather than what official clerks wrote down (which would have been a more formal version of the name often written in Norman French or Latin). So many surnames today are what Matthews (1966, p.59) calls "natural survivals of the spoken word"- living examples of the nicknames and familiar forms that people bestowed upon each other in their day-to-day lives; as McClure (1981, p.63) observes: "we do not name ourselves but are named by others."

Another view of the origin behind the need for surnames is that by the 1300s, there was a limited selection of forenames in use which caused the need for a new method of identification (Redmonds et al., 2011), especially for the nobility and administrators who needed to identify people inheriting property. Mateos (2014) believes this need for

identification could explain why surnames are transmitted patrilineally in European countries as opposed to through the maternal line, which was not linked to property. During the period when surnames were being coined and becoming hereditary family names, major changes were occurring in the personal names that the English were using. Until the beginning of the 13th century forenames had been either English or Norman, with some words or names borrowed from the Old Scandinavian languages used by Viking settlers in the late 9th- 11th centuries (Hanks et al., 2016), but by about 1250 almost all of these names had been replaced by Continental names used by the Norman rulers. But whereas the Anglo-Saxons and Vikings had used a wide range of personal names, the Normans used only a few: in 1379, 82% of male forenames were comprised of only five names, as recorded in Hallamshire, Yorkshire (Hey 2000a); McClure (2014) has found that from the mid-13th to the mid-18th centuries, the names John, Thomas, Robert, Richard, and William accounted for over 70% of the male population of England. So when hereditary surnaming in England began to grow during the 13th century, these were the last few generations bearing Anglo-Saxon personal names, and the choice of other (Norman) names was extremely narrow (Hanks et al., 2016). However Reaney (1967) believes that a shortage of forenames was not the main reason surnames arose: based on lists of names in medieval subsidy (taxation) rolls, he found that the variety of forenames in use during the surname period was extensive and included both English and Scandinavian personal names, many of which are in existence today (Reaney 1967). Alternately, McClure (2014) has found that in late 14th- century England there were probably fewer than a thousand forenames in use.

Women were mainly given bynames later than men and until 1400 the names women used after marriage remained fluid, as the rules were not fixed: some women took their husband's name, some continued to use their father's name or other bynames, while others took their mother's given name, or used nicknames. There were also female versions of some occupational names (see section 3.2.3) but these would not have survived as surnames, as their children would have taken their father's name. For a time in the north of England women could be known by the addition of '-daughter' after a name, equivalent to '-son' for men, but this custom had disappeared by the 1500s. The practice of taking the husband's byname or surname only became general after 1400, a possible indication of greater dependency on men

and, as Deacon (2015) says, a reminder that surnames can tell us about a lot more than simply the history of a particular family.

3.2 Types of surnames

All surnames were originally fluid and meaningful - they described a relationship or the place a person lived or their occupation or personal characteristics, all of which can change over time. When surnames became inherited they suddenly became fixed and meaningless (Padel 2012), so by the 15th century, most surnames were no longer accurate descriptions of the individual. Almost all English surnames can be classified into four main types which originally described the bearer of the name: relationship names, toponymics (place of origin or dwelling), occupational names, and nicknames (Reaney & Wilson 1995).

3.2.1 Relationship names

The vast majority of relationship names derive from the personal name of a father, mother, or some other family member, and less often, a master's name. Patronymics (surnames derived from the father's given name) are the most common relationship names; some examples are Davis, Dawson, Evans, Harris, Harrison, Jones, and Watson. Surnames deriving from the mother's name (matronymics) are less frequent, often stemming from the given name of a woman who had been widowed and who outlived her husband for a long enough time to become an established figure in a neighbourhood; they might also have originally have been used as a way to describe heiresses or long-term widows (Mateos 2014). Examples of matronymics include Madison (from Maud), Emmott (from Emma), and Marriott (from Mary). Patronymics took different forms depending on what region of England they originated in: sometimes they had no suffix and just used the given name as the surname (ex: Richard), sometimes they had the suffix '-s' attached to the given name (ex: Richards), and sometimes they used the suffix '-son' (ex: Richardson). All three forms were in use in late medieval England but were found in different proportions throughout the country and at different social levels. Patronymics with no suffix were the earliest type of relationship name to become hereditary and were most common in the south of England. Patronymics with the suffix '-son' were more common north of the Midlands and were used mainly by small free

tenants, whereas in regions to the south, free tenants acquired surnames with an '-s' at the end of a personal name (Reaney 1967), replacing the suffix-less type; these were especially common in the south, the southwest, and the West Midlands, where they still predominate (Hey 2000a).

The '-s' added to the end of surnames is first found in peasants or servants who did not have hereditary surnames until the end of the 13th century and when they required them, used their masters' names and added the suffix '-s'; if a saint's name was being used as a surname, the final '-s' meant 'son of' (Lasker et al., 1985). Some occupational names also acquired the patronymic suffix '-son', such as Clarkson, Cookson, and Smithson, in the early 15th century. Names with the terminal '-s' often alternated with forms without it, seemingly randomly, for example: Wilkins and Wilkin (Hanks et al., 2016). McKinley (1990) has found the additional '-s' in parish registers from 1550-1650 affixed to surnames that came from a personal name which had existed for centuries without the '-s' but then arbitrarily ended up acquiring one; this also occurred in some topographical names (see section 3.2.2), implying that this was not just the possessive form of the name but perhaps due to a regional form of speech. Many early listings of names with the additional '-s' appear in the 13th century for women, so it is possible that it was a feminine suffix, but it probably just designated dependency, as the wife/daughter/or servant of a man (Matthews 1966).

The Cornish language had its own forms of patronymics, different from the English system, used especially in West Cornwall: they either used two personal names to designate 'son of, grandson of,' which was similar to the Welsh system, or they added the suffix '-o, -ow, -oe, -ou, -a, -y' to a personal name, indicating 'children or kin of' (Charnock 2015). This resulted in some native Cornish surnames, such as Jose, Santo, or Bennetto, being presumed Spanish; however, these names were first recorded in Cornwall in the 1540s, before any Spanish shipwrecks had occurred in the British Isles (White 1981). Some English surnames had an '-a' added to them when they were adopted into the Cornish dialect, for example 'Jacka' or 'Tomma' (Postles 1995).

3.2.2 Place names

Place names, or toponymics, describe where a person lived or came from; they include both *locative* names, which are derived from names of specific places, and *topographic* names, which are derived from general landscape features (Postles 1995). Most toponymic names originated with men who took on the name of their village or hamlet when they left it to find work in a nearby town (Hanks et al., 2016). The Hundred Rolls of 1280, which can be seen as an early form of the census, show that many people from the same village used the name of the village as their surname at this time (Beddoe 1971).

Locative names are the most common type of toponym, often given to outsiders to describe where they came from, such as their village or county, or the name of their house, farm, estate, castle, or manor. Because land and tenancy were often inherited, locative surnames were among some of the oldest hereditary surnames, originating from at least the 12th century (Hanks et al., 2016). McClure (1979) has noted that the distribution of toponymic surnames seemed to depend on the position and wealth of the individual, which determined their ability to move: locative names were most common among the landholding classes, and it was only after the feudal system broke down that men from unfree families were generally able to migrate to find work and thus to acquire locative surnames. McClure (1979) has found that in any 13th or early 14th-century document listing tenants in an English town, usually at least half of the surnames are derived from the names of other towns or villages; in the 14th century locatives were the most common type of surname in three-quarters of the 16 counties surveyed in western England (Rogers 1995). Many locative names include the Anglo-Saxon suffix '-ton', meaning town or settlement, which was used as they expanded in all directions, giving rise to toponymic surnames such as Newton, Norton, Sutton, Easton, and Weston.

Initially most migrants with locative surnames moved to towns within a 20-mile radius of their hometown, although the surname soon spread. Lasker et al. (1985) have found that the number of instances of a locative name is inversely proportional to the size of the place it came from - more people are named after smaller towns than larger ones because people

tended to leave small towns and move to bigger ones for work. An example of this is the surname 'London' which, despite being the most populated city in England, had only 1,481 bearers in 1881, whereas 'Kent,' which is an entire county and was only slightly more populous than London, had 12,594 bearers of the surname (Archer 2015).

Topographical names come from a geographical landscape feature, such as Hill, Woods, or Coombe (one of the surnames in this study, from the Anglo-Saxon word for 'valley,' borrowed from the Celtic 'cwym' (Padel 1988)); they can also describe the location of a person's dwelling place in their village, such as Green or Townsend. Many topographical names had originally been preceded by a preposition such as 'atten,' 'atte,' or 'del' - meaning 'at' 'of' or 'from' - but these had mainly disappeared by the 14th century, although some prepositions became fused to the topographic term, such as in Atwood, Bywater, and Underhill (Hanks et al., 2016).

Topographical names are very common and became surnames when new settlements were created near an identifiable landscape feature, and the inhabitants adopted the name of their settlement as their surname (Redmonds 1972); many topographs were coined in the 13th-14th centuries when people were expanding into previously uncultivated upland areas and converting them into agricultural land (Redmonds 1972). Some topographical names have regional distributions due to the fact that many features of the landscape were referred to in the local dialect. For example, the topographical surname 'Rigg' comes from northern England, reflecting how they pronounce the word 'ridge'; it has a totally different distribution to that of the surname 'Riggs,' (Hey 1997) found primarily in the south, which is not topographical.

Topographic surnames were often taken by or given to serfs or freemen, as opposed to aristocrats who took locative names based on the name of the entire village or estate they lorded over (Hanks et al., 2016). As Matthews (1966, p.277) points out, the upper-class Normans may have owned most of the land during the surname period, but "it was the English who lived and worked among the Hills, Dales, Meadows, Groves, and Wells and spoke of them in their native tongue" - and hence ended up with the surnames reflecting this.

Most topographical names in use today end in '-s,' such as Mills, Brooks, Bridges, Downs, Groves, and Woods. Some exist without the '-s' but it is rare- however, up until the 1500s, they were more common without the '-s' and acquired it only after several generations of being a hereditary name. Between the 16th-17th centuries the '-s' seems to have been arbitrarily added to topographical names throughout England, with some non-topographical names also experiencing this (Rogers 1995). McKinley (1990) suggests that this was due to local customs of pronunciation- as all written words begin with speech, he believes that the name wouldn't have been written this way unless it had been pronounced this way.

3.2.3 Occupational names

Occupational surnames identified people based on their job or position in society. Many of them are very common, with the most frequent ones being derived from occupations that were in use throughout England at the time of surname stabilisation (McKinley 1990), such as 'Smith,' the most common surname in England (Archer 2015). This category of surnames reflects the huge growth in urban economic activity from the late 12th century onwards which led to the rise of big cities and market towns which imported goods and provided services (Hanks et al., 2016). Most of the main trades at the time gave rise to surnames that still exist today, such as Chandler (seller of candles), Sumner (court official who issued summonses), Taylor, Marchant (merchant), Chapman (an itinerant seller of goods), and Spicer. The cloth trade also gave rise to many occupational names: wool was carded (Carder), spun (Spinner), and the threads woven into cloth (Webb, Webber, Webster, or Weaver); the raw cloth was cleaned by Fullers, Walkers, or Tuckers (depending on where in England the job was being done) and dyed by Dyers, Listers, and Waders (Hanks et al., 2016). A small number of surnames ended in '-ster', such as Baxter, Brewster, Dexter, and Webster, which is an Old English suffix that originally denoted a female (baker, brewer, dyer, or weaver, respectively) but by the time hereditary surnames were formed from these names, the distinction of gender was no longer present.

Occupational surnames often have no single point of origin and are generally less regionally-distributed than other types of surnames, although the same job in different regions may be called different things. For example 'Walker', 'Tucker', and 'Fuller' all mean someone who

softens cloth by treading on it (Redmonds 2004), depending on where in England you are- 'Walker' arose in the northeast, while 'Tucker' arose in the southwest, so these surnames show a regional distribution. Occupational surnames can often be traced to areas where they have the greatest density, although these types of names were given only if the trade in question was unusual enough to distinguish a person. For the more common occupational surnames in use today, such as Smith, although the trade was practised all over England, there would have been only a few smiths per village so the name would have been discriminating enough. In contrast, the lack of agriculturally-termed surnames demonstrates that these occupations were too common to distinguish the man holding that job. For example, when sheep farming became a common occupation, there were many bearers of the surname 'Shepherd' throughout Britain; however, in areas where there were too many shepherds, there are no people with the surname 'Shepherd,' as this would not have distinguished them from one another (Matthews 1966).

3.2.4 Nicknames

Nicknames describe a person's physical or moral characteristics or personality traits, for example: Short, Black, White, Swift, Goode, Truman, and Wilde. Nicknames can also take the form of diminutives, by adding a suffix or a prefix to a forename to make it a surname, such as: '-ett', '-kin', '-cock': Bartlett, Dawkins, Hitchcock, Jenkins, and Littlejohn. The surnames derived from nicknames can be as regionally distributed as place-names: for example, the forename Robert was popular all over England, but the diminutives of it - Robson, Dobson, Robbins - are found primarily in different parts of England (Hey 1997). While nicknames are the least common type of surname today, in late medieval England there was a much greater variety of them. Postles (1995) attributes the decline of nickname surnames to medieval-era population expansion: as towns grew, so did occupational surnames, while locative surnames and nicknames declined due to the loss of small settlements and communities, which McClure (1981) believes are the types of communities that gave rise to nicknames.

3.3 Surname origins and distributions

Surnames can reveal aspects of the society and time period in which they were formed, such as social structure, language and dialect, and regional jobs and landscape terms. The study of surnames can also help to uncover many questions that are relevant to this study, such as when and where a surname originated, if it is related to other similar names, and if it has a single origin or arose in more than one place or family.

The frequency and distribution of surnames today can help explain their origins but can be confounded by various factors. For example, throughout the Middle Ages the pronunciation of surnames was constantly changing due to linguistic differences (Reaney & Wilson 1995) – an immigrant to a new area may have borne an unfamiliar name that would be pronounced, and therefore spelled, differently when outside of their native dialect. So the modern form of many existing surnames is not necessarily the original form of the name, but instead may be a phonetic spelling recorded by a source unfamiliar with the original dialect (Reaney & Wilson 1995). This can have a great impact on genealogical and genetic studies in terms of tracing the origin of surnames and the question of relatedness amongst seemingly similar names (discussed further in Chapter 4).

In the 14th century there were more unique surnames in use in England than there are today despite the fact that the population was less than one-tenth of the size (Hey 1997). Because a large number of surnames were each used by a smaller number of people, surname historian David Hey (1997), previously at the University of Leicester's Centre for English Local History, believes that many English surnames have a single-family origin. This hypothesis seems to be supported by the 1881 census which records the population of England and Wales as almost 26 million (Schurer & Woollard 2000), sharing amongst them 420,000 different surnames. This gives an average of only approximately 60 bearers per name- so in England it was, and still is, "very common to possess an uncommon surname" (Redmonds et al., 2011, p.2).

The theory of surnames arising from single-family origins is also reinforced by the current regional distributions of the majority of English surnames: Hey (1997) has found that despite the mobility of the population in recent times, modern telephone directories show that every part of Britain still has its distinctive surnames, and that they appear to be concentrated in the area where they originated approximately 700 years ago. These surname distributions can be visualised using *The British 19th Century Surname Atlas* software (Archer 2015) which uses data from the 1881 census to show the regional distributions of all surnames in Britain at that time (see Chapter 4 for examples).

Mapping modern surnames has confirmed beyond doubt that the majority of English family names have moved relatively short distances over the centuries, in some cases staying very close to their places of origin (McClure 2014), and Hey (2000) has found that every county still has its own distinctive set of family names, many going back to the medieval period. People moved, but not very far, unless it was to London. While documents from this time show that many of the names listed are derived from the names of other towns or villages, most of these moves were over very short distances: McClure (1979) has found that at least half the place-name surnames in mid-13th century documents from various parts of England imply migrations of distances no greater than 8 miles. Deacon (2004) agrees that prior to the 19th century, people usually relocated no further than to the next parish, while Postles (1995, p.3) describes people's migration as "localised and circumscribed" and often based on kinship ties. Hey (1997) describes people's movements as being within comfortable travelling distance of where they were born, usually no more than 10-20 miles in radius, and bounded by the nearest market towns. He has also found that although the composition of parishes changed, a number of families remained rooted in the same general area for centuries and this may have helped to retain the local traditions and habits, along with the major regional accents that still exist within short distances in England today (Hey 1997).

3.4 Cornish Surnames

Out of the 46,000 surnames found in the *Oxford Dictionary of Family Names in Britain and Ireland* (Hanks et al., 2016), about 200 are classified as Cornish. Most of these names are

defined by having an etymology in the Cornish language, along with a smaller number of names which are derived from place-names that are unique to Cornwall, whether of Cornish-language origin or not.

3.4.1 Surname history in Cornwall

Hereditary surnames began stabilising in English-speaking east Cornwall sometime in the 14th century, slightly later than in most parts of England (Deacon 2004), while in the Cornish-speaking west, the process took longer. While some families had hereditary surnames by the 15th century, an unknown percentage of surnames was still unstable well into the 16th century and perhaps later, as the west Cornish people still used their own naming customs and patronymics until the 16th century (Deacon 2015).

3.4.2 Cornish name formation

The majority of Cornish surnames are either locatives or patronymics - there are far fewer Cornish occupational and nicknames (Padel 1985a). But most surnames found in Cornwall are not Cornish-language names- as with the rest of England, the Norman Conquest had an effect on Cornish personal names and therefore their future surnames. Cornish-language personal names had been in use in Cornwall up to the 10th century, but even at the lowest levels of society people throughout Cornwall had begun adopting Anglo-Saxon (English) personal names, or used both a Cornish and an English personal name (Padel 1985a); by the time of the Norman Conquest in the 11th century they mainly used just English personal names, and then eventually switched to using Norman names (Hanks et al., 2016). By the 13th century, Cornish documents show that almost half of all male forenames were of Norman origin, and by the time surnames were forming in Cornwall in the 14th century, the Cornish language was rarely used, except by the lower classes (Deacon 2004), so most Cornish surnames that were formed around this time are not Cornish-language names. Some native Cornish families could also have acquired English or Norman surnames by having worked on an estate that was owned by Anglo-Saxons or Normans, and then adopted the name of the manor as their surname (Hey 1997).

3.4.3 Cornish patronymics

The adoption of surnames in the Cornish-speaking west continued at least through the 16th century and at this time the most common method of assigning surnames was through patronymics. Although these patronymic surnames originated with Cornish men who bore (mostly) Norman forenames, many of them have come to be regarded as typically 'English' surnames (Deacon 2004) because they were so common throughout England. Some of these names are among the most frequent surnames historically found in Cornwall: in 1881 the top three most common surnames in Cornwall were Williams, Thomas, or Richards (Archer 2015) - all Norman first names. So, according to Deacon (2004, p.90), if a Cornish person has one of these surnames, "the likelihood that your ancestors were Cornish-speaking is as high as, if not higher than, if you have a Cornish locational name."

3.4.4 Cornish toponyms

Locative surnames are another common type of surname found in Cornwall, and Deacon (2004) believes that the distribution of this type of surname shows how much Cornwall differed from other parts of Britain: Cornwall as a county has the highest proportion of local place-name surnames in England - in 1327, 47% of surnames were locative (Padel 1985a) - with Devon coming in second. Most of these locative names pertain to small hamlets or farms, as opposed to villages or parishes (Svensson 1987), because when surnames were forming in Cornwall, people lived primarily in scattered settlements which are known to have a high proportion of locative surnames (Padel 1985a); the majority of these were formed from the Cornish language. According to Padel (2013a), no example of a Cornish- language topographical name has yet been found; any Cornish- language surnames which appear to be topographical are actually locative, in that they are derived from an existing place-name (Padel 2013a) rather than a landscape feature.

3.4.5 Cornish-language names

The traditional Cornish saying proclaims that "By Ros-, Car-, Lan-, Tre-, Pol-, and Pen-, you shall know Cornish men." These Cornish-language place-name elements (meaning,

respectively, 'heath, fort, enclosure, farm or homestead, pool, and headland') can be formed into toponymic surnames when used in conjunction with a personal name, an adjective, or the name of the farm where people lived or worked. Examples of this are the names 'Trenance' which means 'farm in the valley' or 'Polglaze' which means 'green pool.'

Charnock's 1870 book on the etymology of Cornish surnames (Charnock 2015) lists up to 500 surnames with the most common prefix, 'Tre-,' and 106 with 'Pen-.' But by the 1881 census fewer than 5% of people in Cornwall had surnames beginning with Tre-, Pol-, or Pen-, varying from less than 2% in the east to over 10% in the west (Deacon 2015); furthermore, Deacon states that today, at most you'll only know about one in 20 Cornishmen (or women) by these criteria. Whereas both Irish and Scottish names number up to 2,000 each in the *Oxford Dictionary of Family Names in Britain and Ireland* (Hanks et al., 2016), Redmonds et al. (2011) attribute the low number of Cornish names at least in part to the large-scale emigrations that occurred from Cornwall in the 19th century due to the failure of the mining industry which was their main economy.

3.4.6 Spelling in Cornish names

Of the more than 46,000 surnames in the *Oxford Dictionary of Family Names in Britain and Ireland* (Hanks et al., 2016), over half are variant spellings of others, because the spelling of surnames in England was not standardised until the 19th century. At the time surnames were stabilising in England, people of all classes were illiterate and could not spell their own names, or spelled them inconsistently. Regional accents were also stronger before immigration made dialects more similar, so parish clerks unfamiliar with the name would have spelled it as it sounded, and these variations created new spellings. Some of these phonetic spellings would have been interpreted to match more familiar-sounding names in the local dialect (McClure 2014): for example, the modern surname 'Beaglehole' comes from the Cornish-language term 'bugel hal' (meaning 'herdsman of the moor') (White 1981), which was then changed into the more familiar-sounding words by English-speakers.

The earlier the record the more spelling variations there are and, according to McClure (2014, p.112), during the mid-15th to 18th century English spelling was “more inconsistent, erratic, and ambiguous than it ever had been or ever would be.” In the 19th century the spelling of surnames began to be standardised, but even then minor changes were sometimes deliberately made to differentiate one branch of a family from another: a report published in 1856 states “until a comparatively recent period, an entire disregard of uniformity and precision in the mode of spelling family names prevailed, even amongst the educated classes...this was apparently less the result of carelessness than of affectation or design” (Rogers 1995, p.14). The now universal practice of fixed surname spelling is a relatively recent event and these current spellings are frequently the arbitrary outcome of a long period of written and spoken variability (McClure 2014).

The spelling of Cornish surnames was even less consistent than in the rest of England because during the time that surnames were forming in Cornwall, the Cornish language had been in decline and most of the population was illiterate, leading to great variability in the spelling of surnames (White 1981). In addition, due to the scarcity of texts written in Cornish, the spelling is very inconsistent, with many different representations of vowels, consonants, and all sounds (Trudgill 1984). As Hicks (1982, p.13) cautions, “if you haven’t heard the Cornish language spoken, you would be unaware of the actual names of things”: he gives the example of two different official documents from 1841 which list the same place as both ‘Trekick’ and ‘Kerkek.’ Hicks (1982, p.13) has also noted that often the older generation of Cornish people “display complete disregard for which form of their surname to use from one generation to the next, or even within individual lifetimes.” All of these spelling inconsistencies can make (and indeed have made) the use of surnames in ancestry studies such as this one very complicated. Examples of the particular issues with Cornish spelling variations in this study are given in Chapter 4.

3.4.7 Cornish surnames not really Cornish

White (1981) cautions that some of the names often classified as of Cornish origin may be from any number of incomers to the region over the years leading up to and during surname

stabilisation, such as the Irish, Welsh, Scottish, Bretons, English, and French, who became assimilated and whose names were changed in the successive spellings, or who may have adopted Cornish forms of their names. For example, in the 15th century there was an influx of Bretons into Cornwall (Deacon 2007), many of whom brought surnames which are now considered 'Cornish,' both due to the similarity of the languages of the two regions and the fact that these names have been present in Cornwall for many hundreds of years.

There is conversely some loss of Cornish-language names: as surnames were forming at the same time that English was replacing Cornish, those recording the surname may have translated the spoken Cornish name into its English version. Due to this, English occupational or nicknames were also widely found in Cornish-speaking areas, although this does not necessarily mean that their bearers were English-speakers (Deacon 2015). For example, the Cornish occupational surname 'Angove' - from 'ang hof' meaning 'the smith'- became 'Smith,' while the nickname 'Angwyn' – meaning 'white-haired' - became 'White.'

3.4.8 Tracing Cornish surnames

The majority of Cornish-language surnames derive from place-names in Cornwall, but these locative surnames are not a good guide to either the etymology of the surname or the location of its origin. Since so many Cornish surnames were formed by using a limited number of Cornish-language prefixes- such as the 500 surnames beginning with 'Tre-' listed by Charnock (2015) in 1870- it is inevitable that many of these names occur in more than one location, thus making it difficult to trace the origin of a particular surname (Deacon 2004). An example is the Domesday Book which, in 1086AD, listed many places beginning with 'Tre-,' some of which are still in existence today- however, the original location of many of these place-names is unclear, as the names are repeated throughout the county (Morris et al., 1979). Another example is the locative surname 'Trenoweth,' meaning 'new settlement,' which, by 1881, had well over 100 bearers found all over Cornwall (Archer 2015), presumably in places where a new settlement had been established during the time of surname stabilisation.

In addition, what Padel (1985a) refers to as a 'distinctive Cornish naming practice' makes tracing the origins of Cornish surnames even more difficult. He believes that, starting in the 14th century when surnames were forming in Cornwall, the overwhelming majority of Cornish people with place-name surnames bore the names of the farms where they were currently living, rather than where they originally came from. He bases this on records showing that the majority of place-name surnames were found in the parish the name originated in: if someone moved his residence at that date, he would probably have changed his surname to match where he moved to. In the rest of England it has been shown that a place-name surname was acquired usually after a person had moved away from the place, in order to describe where they were from- but in Cornwall it indicated the current residence of the person (Padel 1985a); Padel believes that this is evidence that fixed surnames did not yet exist on a wide scale in Cornwall. This is also supported by Carew (2004, p.125) who noted that as late as the 17th century the Western Cornish, like the Welsh, "entitle one another with his own and his father's Christian name and conclude with the place of his dwelling...through which means diverse gentlemen and others have changed their names by removing their dwellings, as Trengove to Nance, Bonithon to Carclew...and many others."

Based on documents showing when people with locative surnames are not found living at the farms indicated by their surname, Padel (1985a) believes that by the mid-16th century most people no longer changed their surname every time they moved- although as late as 1569 in Devon there are records of bynames that still had not become hereditary, such as 'John the miller' and 'Giles the baker' (Deacon 2004). Even into the 19th century, Padel (1985a, p.85) finds evidence of what he calls an "intriguing" number of people who were residing in the parishes where their surnames were derived; he states that "the general impression is of a very strong feeling [in Cornwall] that it is 'right' to bear the name of your dwelling as a surname" (Padel 1985a, p.85).

Overall, Cornish surnames can be confounding when trying to uncover their derivation, place of origin, or the ethnic make-up of their bearers; Cornwall is also under-represented in regards to the extensive surname surveys that are available for other English counties. These

factors all have implications for tracing the origin of a Cornish surname or family (as is discussed in Chapter 4). Padel (2012) makes the point that, due to the complexities surrounding Cornish naming practices, even if there is only one place in Cornwall with a particular name, you cannot be sure that everyone bearing that surname is related or even from that location. Deacon (2004, p.177) sums it up best when he says "Cornish [locative] surnames may record only the loot, by a Norman, of the estate of a Saxon, who dispossessed the heir of a Cornishman, who founded it and gave it his own name with Tre- before it; while the Cornish founder's heirs may still walk among us bearing perhaps, like so many Celts in Wales, some name such as Williams, Thomas or Richards."

Chapter 4 Analysis of the surnames of eastern Cornwall as tools to inform population sampling

4.1 Premise

As different surnames can have different regional distributions within England, and there is a demonstrable link between surnames and Y chromosome haplotypes (King & Jobling 2009b), it follows that Y chromosome variants should also be regionally distributed. Hey (1997) has shown that distinctive surnames are still most commonly found close to their place of origin and that many surnames still appear to be concentrated in areas where they originated 700 years ago; this is due to the fact that most population movement has been mainly over short distances (McClure 1979), with women usually moving greater distances than men, often for marriage (Burton et al., 1996). This means that individuals whose surnames are localised to a specific area are more likely to have ancestry from that area through the male lineage, and that these individuals should be more representative of the region in terms of genetic structure over long periods of time.

Charles Phythian-Adams (1987, p.27), of the Centre for English Local History at the University of Leicester, found that the British population was relatively immobile. Even as late as 1861, most people still moved mainly within their county boundaries and an “overwhelming majority” of people in England and Wales were living in the county in which they were born: according to the 1851 census, of the just over 17 million people in England and Wales, 80% were living in the county of their birth. He specifically noted that the region encompassing Cornwall and Devon was especially immobile and that there was a “manifest lack of demographic integration” (p.29) between the two counties, which he attributed to “the invisible line of the county boundary [acting] as a real barrier to geographic mobility” (p.30). In 1841, 95% of the people living in Cornwall had been born there, which was the highest proportion in the nation, with Devon at 90%, thus demonstrating that there was little migration between the two adjacent counties. By 1861, 92% of the people residing in Cornwall had been born locally- still the highest of all the English counties (Phythian-Adams 1987).

Like most of England, Cornish migration patterns were mainly to the next parish or town, but unlike the rest of England, Cornish people did not move to London in great numbers- this is based on data from a migration study which shows that between 1147-1350AD there were no Cornish place-name surnames recorded in London, in contrast to names recorded from every other part of England (McClure 1979). Low numbers are also recorded for migration into Cornwall from the rest of England- in 1327, only 0.5% of tax-payers in Cornwall bore names that were clearly not Cornish- and most of these were from Devon (McClure 1979).

In 1890, H. B. Guppy published *The Homes of Family Names*, which lists surname distributions in all the counties in England. He surveyed mainly farming families whom he believed were the most stable segment of society and found that many surnames have a statistically significant association with particular counties. Guppy (1890, p.11-12) classified those names which were mostly confined to a specific county as “peculiar names” and he found that Cornwall and Devon were, more than anywhere else in England, “a factory of family names” with the “peculiar” names (including almost 1/3 of the names in this study- see table 4.4) making up 40% of the surnames in the region. More recently Winney et al. (2012) found that within the ‘People of the British Isles’ sample set, Cornwall had the highest proportion of regional surnames.

Supporting this is work from Kandt et al. (2016) which further analysed the surnames of DNA donors to the PoBI project. They used an isonymy-based clustering analysis that also considered pairwise co-ancestry based on the genetic data of Leslie et al. (2015). This highlighted eight hierarchical regions of the UK that exhibit population structure based both around surnames and genetic structure. Cornwall and Devon together formed a “highly distinctive” (p.562) region based on shared surnames and genetic structure, and then split into two separate clusters based on the same criteria. This is the most consistent region of all the areas sampled, meaning that they are distinct from other isonymy groups, but also that the isonymy groups within them are relatively homogeneous, implying that they represent the population structure in the sample particularly well. Cornwall and Devon also displayed a

high level of confidence that their isonymy groups represent population structure (Kandt et al., 2016), as shown in figure 4.1.

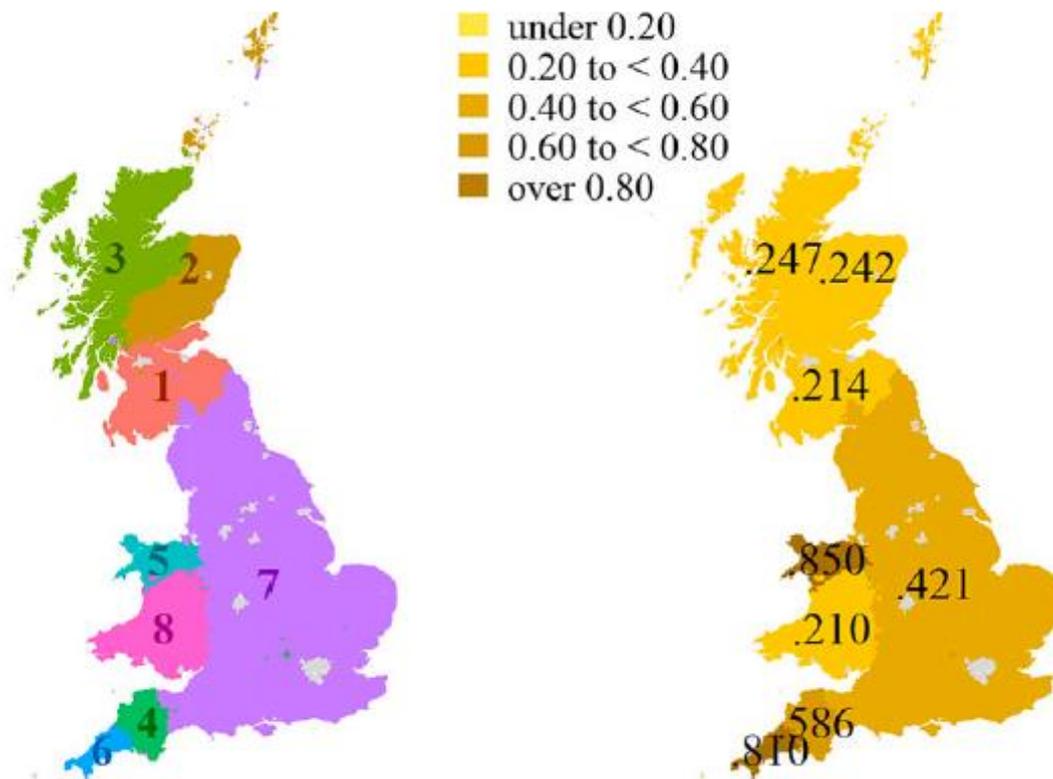


Figure 4.1 Britain split into eight isonymy regions based on population structure (Kandt et al., 2016)
Cornwall displays the highest level of confidence in its population structure

4.2 Choice of surnames for sampling

4.2.1 Criteria

The highly localised distribution of Cornish surnames could help to enhance the signals of Y-chromosomal population structure, if these surnames are used in the recruitment of DNA donors. Based on this premise, surnames distinctive to Bodmin Moor were sought as a basis for the sampling of males, with the aim of analysing their Y chromosome diversity, and for comparison with samples from other parts of Cornwall and from Devon. This sampling was motivated by the surname-based sampling approach of Bowden et al. (2008), and by the

observations of Leslie et al. (2015) regarding the boundary between Cornish and Devonian autosomal clusters.

Initially, the aim was to sample men bearing surnames that have been found continuously in the Bodmin Moor area from 1702 to the present (to represent continuous male-line ancestry) but which also were found in greater frequencies there than in the rest of Britain. This factor was based on the premise that surnames unique to a specific area may give rise to distinctive Y chromosomes, due to both the effect of patrilocality as well as to genetic drift, which increases the effect of patrilocality. Because patterns of Y-chromosome variants are not expected to change substantially during the time period under consideration (approximately 500 years, since the beginning of parish records), the group of men that make up the sample population can be seen as a proxy for their paternal ancestors who were living in the Bodmin Moor area from the time that parish records began in this part of Cornwall.

Along with bearing specific surnames, the other criterion for the men to participate in the study was that their paternal grandfather had to have been born in one of the twelve parishes that contain part of Bodmin Moor within their boundaries and whose farms have rights of common pasture on it, as defined in *An Archaeological Survey of Bodmin Moor* (Johnson et al., 1994) (except for the parish of St Ive, which is not included in the study because no accessible ancestry information exists for it). The twelve parishes included in this study are Advent, Altarnon, Blisland, Cardinham, Davidstow, Linkinhorne, North Hill, St. Cleer, St. Clether, St. Breward, St. Neot, and Warleggan.

4.3 Sources used to find surnames

4.3.1 Parish records

Surnames have existed in parts of east Cornwall from as early as 1327AD (Padel 1985a), but there are very few written records from that time and none which are comprehensive. It was not until 1538 that official records started being kept in every county in England, when Henry VIII ordered clergy to record church ceremonies (rather than births and deaths) which included every baptism, marriage, and burial performed in the parish (Kitson 2009). Despite

this, not all clergy complied with this mandate - some recorded burials but not baptisms for many years or vice versa, and some areas had no entries at all for many years. Many records from this time have also been damaged or lost- according to the National Index of Parish Registers (Wilcox 1999), only 17 parish registers date from 1540, and only 208 from before 1800; most registers are imperfect and incomplete, with entries or entire pages missing. Many of the registers do not contain information before 1558, but after this time there were also copies of the records made, known as the Bishop's Transcripts, which often exist when the original records have been lost. In some parishes there are gaps during the English Civil Wars (1642-1651) until after the Restoration in 1660 (Devon County Council 2016). Currently most parish records and Bishop's Transcripts are kept in county record offices; the original Cornish records are kept in the Record Office at Truro and were lent to the Cornwall Family History Society for transcription, who then provided them to the website FindMyPast (FindMyPast 2016) for their use in publication online. FindMyPast has transcribed the parish records of births and baptisms from 1538 until 1875, depending on availability of the original records. The records include all children baptised (usually within a month of their birth), including Protestants and Methodists, as baptism continued to be practiced through the Protestant Reformation (Kitson 2009).

Before the censuses began in the 19th century, parish registers provided a way to calculate population statistics. The parish records were used in this study to find the surnames of everyone baptised in the Bodmin Moor parishes during a designated time frame based on the availability of the records. The earliest available records for the twelve parishes used in this study range from 1548 to 1702, and all of the online parish records end at 1875 or earlier because at this time the census was used instead. The records are not all continuous, with some missing pages or entire years, but eleven of the parishes have continuous records from the years 1702-1782; the exception is the parish of North Hill which has records only up to 1772. Therefore, the criterion for including a surname in this study was that it should be found in one of the twelve parishes surrounding Bodmin Moor during the 80-year timespan (70 years for North Hill) from 1702-1782, based on the parish records on the FindMyPast website.

4.3.2 1881 census

The UK census is a governmental survey that gathers detailed information about national demographics in order to assist in the regional distribution of resources. It has taken place every ten years since 1801 with the exception of 1941, and 1921 in Ireland. The 1881 census has been fully transcribed and published by volunteers from the Church of Latter-day Saints in the US; it provides the names and place of residence for approximately 26 million people, with a total of 420,000 unique surnames.

The distribution of surnames throughout Britain can help assess how local a surname is by comparing the relative frequency of the surname in a given region to the overall frequency of that surname in Britain as a whole. In order to identify any surnames that were specific to the Bodmin Moor area, the census (Schurer & Woollard 2000) was used in this study to discern the surnames of everyone who resided within the Bodmin Moor parishes in 1881, how many bearers there were of each surname, and the total number of bearers of those same surnames throughout Britain. This would thus help to identify any surnames that were found in higher frequencies in Bodmin Moor than in the rest of Britain and, presumably, these localised surnames would be more likely to show a regional Y-haplotype structure.

4.4 Justification of time periods used

In choosing surnames, the assumption was that a surname found in the twelve parish registers during the 1702-1782 time period which was also found in the parishes in 1881 (as per the census) represented a continuous line of male descent. This assumption was necessary because the parish records from 1783- 1875 (leading up to the census) are highly sporadic, so it would not have been practical to use them: if this timespan had been included as a criterion for continuous ancestry, many of the 'continuous' names from the period spanning 1702-1782 (and then also found in 1881) would necessarily have been excluded from the final list, resulting in substantially fewer surnames to recruit for the project. However, because most study participants provided genealogical information at least through the 19th century, the continuity of their ancestry was supported in this way to make up for the missing years of parish registers.

As there is no recent census transcribed, the 1996 electoral rolls were originally consulted, in order to make the final list of names more 'continuous' to the current day; however, it only lists names that have greater than 10 bearers, and this would have led to the exclusion of 24 names. It was therefore decided not to use the rolls as a resource and instead to rely on the genealogies provided by the volunteers to ensure they fit the ancestry criteria.

As mentioned previously, an earlier time span of parish records was not used because the majority of parish records were not comprehensive before 1701. Thus, the sample population consisted of men whose paternal ancestry can be traced to the Bodmin Moor area from at least 1702 until the current day.

4.5 Limitations of sources used to find surnames

4.5.1 Parish records

There are a number of limitations regarding the use of parish records as a comprehensive source for all surnames existing in a parish during a specific time period, all of which could have affected the selection of surnames for the study and therefore the final results. They are listed as follows:

i) Parish registers are not a comprehensive record of births or baptisms

There will inevitably be some surnames that are not accounted for, as many babies died before baptism. Additionally, while baptism remained a sacrament and continued throughout the Protestant Reformation, some 'non-conformists' (such as Quakers and Baptists) dissented from the Church of England from the 17th century onward, so would not have baptised their babies in the parish churches; and after the act of 1753, dissenters (except Quakers and Jews) could not marry in Church of England chapels so there are few marriage registers for these groups as well. It has been estimated that by 1800, parish registers contain only about two thirds of Britain's births and deaths (Kitson 2009).

ii) Birth parish does not always equal baptism parish

Baptisms were not always carried out in the village in which the child resided, but instead in the nearest or next church where baptisms were due to take place, often in a neighbouring parish, since they often occurred based on specific dates of the Catholic calendar (Kitson 2009). Additionally, Crossley (2018) has noted the regular use, between 1813 and 1837, in the Bodmin Moor parish of St. Neot, of neighbouring parishes for baptisms- mainly Warleggan and St. Cleer which are on either side of St. Neot- probably because they were easier to get to from some moorland dwellings. There is one documented case of this from one of this study's volunteers whose paternal grandfather actually resided in the town of Bodmin when he was born but was baptised in the Bodmin Moor parish of Warleggan and so appeared in the relevant records for this study. It is likely that there are more unidentified cases of this in the sample population, so some surnames (and therefore Y chromosomes) may be included that did not actually originate in the relevant parishes. Additionally, while the paternal grandfathers may have been born in one of the relevant parishes, many earlier paternal ancestors were from parishes outside the region.

iii) Incomplete records for many years

The parish records are sporadic for many years, especially during the reign of Mary Tudor (1553–1558) and during the Civil Wars up to the Restoration (1642–1660), when they were less systematically kept (Devon County Council 2016). Due to this, the longest continuous time span that had a complete set of records did not occur until the 80-year period from 1702-1782, with the exception of the parish of North Hill, which is missing a period of 10 years from 1772-1782. Because the parish records after 1782 were not consulted, the names (and therefore Y chromosomes) recruited for the study in 2016 may not be from the same 'continuous' paternal lines, since they are not accounted for between the years 1783-1881. Therefore, the assumption that the paternal lines under consideration are continuous through 1881 and up until today is based only on the genealogical evidence provided by the volunteers.

iv) Surnames may have not been hereditary during the time period used

There remains the slight possibility that surnames had not completely stabilised in all parts of Cornwall during the time period used and therefore a name listed in a parish register may

not have persisted as a hereditary surname. When parish registers were introduced in 1538, most families had only had a surname for three to four generations maximum (Dark 1998) and it is possible that they were not yet hereditary; in addition, Cornish naming practices were more fluid than in the rest of England (as discussed in section 3.4).

v) Surnames not necessarily local

In the early 19th century the population of Bodmin Moor increased, especially in the eastern mining parishes of St. Cleer and Linkinhorne which showed a significant increase in population from the agricultural parishes (Crossley 2018). In the agricultural parishes, Crossley (2018) found that around two-thirds of household heads were born on Bodmin Moor, while the mining parishes had large numbers of inhabitants from elsewhere in Cornwall. A more robust method for surveying local names would have been to focus on agricultural parishes rather than mining parishes, because it may be that the farming areas were generally made up of more local families who remained tied to the land for many generations (Guppy 1890).

vi) Accuracy of transcriptions/ spelling variations

As with any transcribed record, there is the question of accuracy. The modern spelling of surnames today is due to what was written in the parish registers by clerks who may have lacked the local knowledge of regional accents needed to record the names accurately, so there may be names that had a common origin but were spelled so differently that they appeared to be totally separate names. This would affect the frequency count of the name throughout the parishes and therefore the final selection of surnames. The effects of spelling variations on this study is discussed fully in section 4.7.2.

4.5.2 1881 census

The census, while the most comprehensive survey of all inhabitants registered as residing in a specific region at the time, also has some factors that can contribute to errors.

i) Limits of time period used

The 1881 census was the last officially documented listing used for any name in this study until 2016 when the living male relatives were recruited as participants, so the names used for recruitment may not be from 'continuous' male lines. However, the genealogy provided by each volunteer was relied upon to fill in the missing time period between 1881 and 2016, although it was not formally checked.

ii) Record of residency, not births/baptisms

While the parish registers were a record of all baptisms in the parish, which usually occurred in the birth parish, the census recorded everyone who resided in the parish at the time it was taken. So anyone with a relevant surname who was living in the parish in 1881 would not necessarily be related to an earlier family with the same surname, and thus the paternal line may not be continuous.

iii) Accuracy of transcriptions

As the census was transcribed by Americans, there could be further spelling errors from those not familiar with either English or Cornish names.

iv) Names only included if held by over ten bearers

Some names with fewer than ten bearers will have been overlooked by not being included in the census due to the assumption that they are transcription errors; Hanks et al. (2016) have found that while some names with a low number of bearers in the census are due to transcription errors, most names with at least ten bearers in 1881 are genuine names.

v) Spelling variations

There are, no doubt, further unaccounted for spelling variations for many of the surnames in this study which could result in inaccuracy of both the parish and nationwide surname counts. It was not possible to anticipate every spelling variation of the names included, especially because many of the names could vary in their first letters, as Cornish-language words occasionally do (as demonstrated in section 3.4.6).

4.5.3 Surname Atlas software

The software is based on the 1881 census so would reflect any errors in the original document, any transcription errors, or any possible software errors.

4.6 Possible problems with surnames used

Selecting the surnames for the study required extensive research into the customs and conventions used in Cornwall during the surname stabilisation period, as well as during the time periods of the sources used. Many factors were uncovered which affected the spelling, pronunciation, and heredity of the surnames under consideration, and these left a large margin for possible error in terms of finding surnames unique to Bodmin Moor and in the final selection of names, both of which have the potential to affect the results of the study. These factors are listed below.

4.6.1 Accounting for all spelling variations

Many of the surnames found in the parish records had numerous variant spellings within the parishes themselves, as well as in the 1881 census; there are also probably many more variant spellings in the census which haven't been counted as they remain unknown. Both the number of bearers of a name and the question of surname continuity were crucial in determining if the name was specific to the Bodmin Moor area- yet both were highly affected by the possible existence of spelling variants. In order to determine if similar surnames were spelling variants of one another, Cornish place-name historian Oliver Padel was consulted and he advised on whether many of the names could have a common origin. Some pieces of advice he contributed were: that vowels in a name are more prone to variation than consonants, so are more easily interchangeable; that vowels in unstressed syllables can vary in the same name frequently; and that if a spelling variation is rare or occurs in the same parish as a similar name, the surnames should be considered the same (Padel, personal communication). This is because spelling variations differed among all classes and were still common until the 19th century, so the many variant spellings within one parish would reflect this. Therefore many names that were spelled slightly differently in the relatively small

population of Bodmin Moor, which in 1881 was 11,619 persons (Schurer & Woollard 2000), can be considered to be spelling variations of the same name.

An example of a name found extensively in Bodmin Moor that has multiple spellings is BARNICUTE. This name is spelled in seven different ways between the parish records and the census- BARNECUTT, BARNECCUT, BARNECUT, BARNICOATT, BARNICUT, BARNICUTT- and a brief foray into its derivation turned up even more additional spellings elsewhere: BARNACOTT, which is listed as a place-name in the Domesday Book (Morris et al., 1979) which still exists today just north of Bodmin Moor, and DE BERNICOTE, a topographical Saxon name from 1320 signifying a cottage ('cot') next to a stream ('bern') (Svensson 1987). But even after all the spellings of this name were counted, that number still did not reflect the actual number of bearers of the various forms of the name throughout the rest of Britain- there are at least seven more alternate spellings that were found using the *Surname Atlas* software (Archer 2015). This fact substantially lowered the frequency of many of the names in the parishes that at first appeared to be specific to the area, and therefore affected the terms of the criteria for the names being sampled.

4.6.2 Names ending in '-s'

Many of the surnames in the parish records appeared both with and without an '-s' as a suffix and this caused considerable question over whether they should be treated as the same name. A number of names ending in '-s' that appeared at first to be specific to Bodmin Moor were subsequently found in other areas of Britain without the terminal '-s' (example: CROWELLS vs. CROWELL). These were treated as the same name, based on the advice of Padel (personal communication), who considers names that end with an '-s' to be the same as those without. However, as discussed in section 3.2.2, the topographical name 'Rigg' has a different regional distribution than 'Riggs,' so it is therefore possible that some of the names in this study with the terminal '-s' should not have been combined.

4.6.3 Determining whether similar surnames have the same origin

Most of the surnames that appeared to be spelling variants differed by only a few letters, but in a few cases, it was more complicated to determine if similar-looking or similar-sounding names were derived from the same origin. One example of this is the name MENHENIT, which is found spelled at least nine different ways in the 18th century parish records (see below in table 4.1). The exact name is not found in the 1881 census but the similar-sounding surnames MENHENICK and MENHENIOT are:

Table 4.1 *Various spellings of the surname Menhenick, etc. The varied spellings of this name over many years makes it difficult to tell they are related*

Parish records (1702-1782) spelling	1881 census spelling
MENHENIT	MENHENIOT
MENHENITT	MENHENICK
MENHENNET	
MENHENNETT	
MENHENNIET	
MENHENNIT	
MENHINNET	
MENHINNETT	
MENHINNIOT	

At first glance these appear to be two or three different names which could all be misspellings of 'Menheniot,' a parish in southeast Cornwall. However, Padel (2012) has traced all of these spellings back to a 16th century farm called 'Mellionec' in mid-Cornwall; the name then made its way eastwards and was found in the Bodmin Moor parish records by the early 18th century. This was therefore treated as a 'continuous' name throughout the relevant time period in this study, despite the many different spellings.

The same situation was also encountered with the names BESWARRICK, BESWERICK, and BESWETHERICK. The first two spellings of the name appeared almost exclusively (88%) in the Bodmin Moor parishes in 1881 while BESWETHERICK had only a 5% frequency in the parishes. But according to Hanks et al. (2016), the variations of this name are based on a

Cornish locative name which originated from a place called Bosvathick in West Cornwall which then travelled eastwards to the Bodmin Moor parish of St. Neot by the 18th century. This is an example of a name that at first appeared to be 'Bodmin Moor-specific' but which instead actually comes from West Cornwall.

Despite having a common origin, names can become distinctive to one area as a result of variant spellings based on local pronunciations, and this can result in uniquely regional names. One example of this is the surname BERDINNER which was found at a frequency of 54% in the Moor parishes; it was then discovered that it derives from a regional pronunciation of the Cornish place-name BODINNAR/ BODONARD (White 1981) in West Cornwall. The alternate spellings BODINAR/BODENER have also been noted in various Cornish documents from the 18th century (Nance 1933). Only with this knowledge of its origins was it possible to deduce that it did not meet the criteria for the study.

An example of what may have begun as a very common name but became a regionally-specific one is the name BROAN: over half of the BROANs in Britain in 1881 were found in the Bodmin Moor parishes and so appeared to have a higher frequency there than elsewhere. But the name may have originally derived from the much more common BROWN, and then taken on a particular regional pronunciation and spelling; the same could be true for the similar-sounding BRAUND, also found in high numbers in the moor parishes. If it is assumed that this is the same ancestral line with differently-spelled names, and then the numbers of bearers of these names are combined, it affects the previous assumption that BROAN is one of the names that are concentrated primarily in the moor parishes and it therefore may not meet the sampling criteria.

4.6.4 Assuming that the same surname implies direct ancestry

Most of the sample population provided information about their paternal ancestry based on their personal genealogical records or family knowledge that explained their relationship to their paternal ancestors from at least the 18th century, and often much further back. But there are a few participants who did not provide any ancestry information beyond their paternal

grandfather (as per the sampling criterion), so there is no guarantee that they are related to the men bearing the same surname listed in the parish records from earlier years.

As discussed in section 3.4.8, most Cornish-language surnames share a limited number of prefixes so many locative surnames are repeated throughout Cornwall, and all bearers of these names certainly do not share a common ancestry. There are only two Cornish-language names in this study: TERNOUTH, which is a misspelling of TRENOWETH (meaning 'new farm') and has many other variant spellings (listed in section 4.8.2) - and TREHANE (which is 'farm' + a personal name) - but either of these names could belong to multiple locations and founders, so tracing ancestry through this type of common surname is very difficult.

Additional situations that must be accounted for are adoption, men using their mothers' surname, and extra-pair paternity (illegitimacy), which is approximated to be 1% per generation in Western populations (Larmuseau et al., 2013), although Deacon (2004) believes that in Cornwall illegitimacy rates were probably higher than in other English counties until the 1840s due to the many men working overseas in mines. However, the generally low number implies that legal genealogies rarely differ greatly from biological ones.

4.6.5 Cornish names not really Cornish

In selecting the names for the sample population, some of the most common surnames in the Bodmin Moor parishes (such as Williams, Thomas, and Jones) were excluded due to their high frequencies in the rest of England. Due to this restriction, some of the oldest surnames (and therefore Y chromosomes) found in Bodmin Moor may also have been excluded because, while many men of Cornish origin could share the same very common patronymic surnames as their English counterparts, this does not necessarily imply shared ancestry. As discussed in section 3.4.3, many of these seemingly 'English' surnames were found in 1881 at higher frequencies in Cornwall than anywhere else in England; in addition, many of the most common names found in Cornwall in 1881 overlapped with the most common names found in Devon at that time (Archer 2015), so cannot be considered regional names in keeping with the criteria for this study.

On the other hand, in some cases Oliver Padel's advice (personal communication) of not excluding names that are common elsewhere in England was followed. Padel cited the example of a family called MARTIN whose surname appears in the windows of the St. Neot church, which they had paid for in about 1520. So although the surname MARTIN is extremely common throughout the rest of England, the name ended up being used as one of the samples in the study because of its documented history in the parishes. This does not mean they are necessarily related to other 'English' MARTINs but instead could be a Cornish family who took on the patronymic surname; or it just as likely could have been from a MARTIN coming from elsewhere in England before 1702.

Alternatively, White (1981) also cautions that some of the names generally classified as of Cornish origin may be from any of the immigrant groups in Cornwall who became assimilated and whose names were changed in the successive spellings, or who may have adopted Cornish forms of their names.

4.6.6 Most of the names recruited are found all over Britain

The aim of finding surnames unique to Bodmin Moor was not achieved because most of the names were also found elsewhere in Britain in substantial numbers, although many of them were found mainly in Cornwall. In addition, some patronymic names that are among the most common throughout Britain were also included in the study due to the fact that exclusion of these common names would have reduced the already small sample population greatly. However, excluding a name that is also found elsewhere in high frequencies may have excluded some local Y chromosomes. For example, the surname COUMBE, which is used in this study, is a toponym meaning 'valley.' It is possible that the ancestral line in this study carrying this name got it from the local valley they lived in, so even if it is found at a high frequency elsewhere, it may still be a local name; alternatively, it is just as likely that they could be related to the many other COUMBEs in the rest of Britain, including those who use the spelling COOMBE or COMBE.

4.6.7 Using the oldest surnames in the parishes

Even names that have been in the Bodmin Moor parish records for hundreds of years are not necessarily indigenous to the area. Padel (2013a) cites an example of the surname DARITE which had been first mentioned in documents referring to the Bodmin Moor parish of St. Cleer in 1391 and later gave rise to the place-name in the same area by 1600. Padel believes the surname most likely originated with a French immigrant, so even the oldest of names in this area are not necessarily indicative of families native to the area, or even the country. Given the lack of complete historical records from earlier time periods, it should be assumed there were other instances of immigration into the area from even before records were being kept which may not be apparent from the surnames.

4.7 Surname selection

4.7.1 Methods

The criterion for including a surname in the study was that it should be found in one of the twelve parishes surrounding Bodmin Moor during the 80-year timespan (70 years for North Hill) from 1702-1782, and also in the 1881 census. The following were the steps taken to identify these names:

- i. Surnames from the online parish records on the FindMyPast website (FindMyPast 2016) for the years 1702-1782 were collated, resulting in 1,567 uniquely-spelled surnames throughout all twelve parishes.
- ii. Surnames from the 1881 census (Schurer & Woollard 2000) were collated, resulting in 1,051 uniquely-spelled surnames throughout all twelve parishes.
- iii. The 1,567 surnames from the parish records were compared with the 1,051 surnames from the 1881 census, resulting in 458 names that matched exactly in spelling (see Appendix 8.1.1), leaving 1,702 names that did not have an exact match between lists.

- iv. Many of these exact matches appeared to be slight spelling variations of each other (example: JASPER/JASPAR) and could reasonably be considered to be the same name; these presumed alternately-spelled names, or 'duplicates,' were counted as one name, using the 1881 spelling of the name (as this would be the spelling most likely to be in use today); this brought the number of names from the previous 458 down to 373 (these names are included in Appendix 8.1.1).
- v. The lists of 1,702 names without the exact same spellings between the two time periods were compared, resulting in 63 names (listed in Appendix 8.1.2) that were close enough to reasonably be considered the same name, despite their slight spelling variations that had occurred over the years. These names were added to the 'duplicates' list, using the 1881 spelling of these names, which brought the number of 'amended' duplicate names up to 436.
- vi. The remaining list of names from 1881 was compared to the 436 names on the 'amended duplicates' list and resulted in 111 names that consisted mainly of spelling variations of names on the 'amended duplicates' list. This did not add any new names, but this step was necessary in order to find the correct number of people bearing that name in the parishes in 1881, for use in estimating the name's frequency in the parishes as compared to the rest of Britain. The remaining names on the 1702-1782 list that lacked a close match in 1881 were permanently excluded because this would imply that there was no continuous male line carrying that name that could be used in the study. The final result was a list of 436 'final duplicate' names which appeared both in the 1702-1782 parish records as well as in the 1881 census.
- vii. Each of the 436 names on the 'final duplicates' name list was checked against the 1881 census in order to determine the total number of bearers of each surname within the twelve Bodmin Moor parishes in 1881. This 'parish surname count' was then divided by the total number of bearers of this surname throughout the

entirety of Britain to give a 'parish percentage' for that surname. The names with the highest percentages would imply names that were regionally-specific to Bodmin Moor and these would be the names that would be recruited for the study.

4.7.2 Problems with the methods used

The initial aim of identifying surnames that were specific to Bodmin Moor by using parish records and the census did not turn out to be a viable way of locating regionally-specific surnames. One major issue was determining if names that looked or sounded similar were actually derived from the same origin and therefore shared a common ancestor and could be considered the same name. There were many examples of this; one is the name RUNNALS, which is found at high frequencies in the moor parishes. Without deeply researching the origins of this name, there was no way to know if it is a name specific to Bodmin Moor or simply a regional pronunciation/spelling of the name RUNDLES (which it turned out to be), which is found in high frequencies elsewhere in Britain and therefore cannot be considered specific to Bodmin Moor.

The vagaries of the spellings of the surnames in this study has been mentioned in section 4.6 but an additional problem was discovered when the results of the most common names in the parishes were produced. The top five Bodmin Moor-specific names are listed in table 4.2 below in order of their frequency in the moor parishes as compared to the rest of Britain (see Appendix 8.1.3 for full list) and show that there were fewer than five surnames that were found in the Bodmin Moor parishes at a frequency of over 50% - all other names were found elsewhere in Britain at equally high frequencies.

Table 4.2 Top 5 Bodmin Moor-specific surnames in 1881

Surname	Parish surname count	1881 National surname count	Parish %
TAPRILL	5	5	100%
CAWRSE	47	56	84%
GOYENS, GOYINS	10	12	83%
TREGLOYNE, TREGLOIN	8	13	62%
SHILLABER	12	22	55%

However, even the few names that did appear to be regionally-specific turned out to be spelling variants of surnames that were more common elsewhere in Britain but had not been accounted for when consulting the census for surname counts, because these spelling variants were unknown. Two of these names (SHILLABER and TAPRILL) were both spelling variants of surnames found primarily in Devon (SHILLABEER and TAPERELL), as illustrated in figure 4.2 below; many of the names, including SHILLABER, had many additional variant spellings that were unaccounted for, as shown in figure 4.3 below, and on this basis had much greater frequencies elsewhere in Britain outside of Bodmin Moor.

These alternate spellings of the names were discovered through the use of the *British 19th Century Surname Atlas* (Archer 2015) which is software that maps the location and number of bearers of a surname throughout Britain based on the 1881 census, showing their distribution on the map according to regional boundaries. The names are also listed alphabetically, which allowed for the discovery of many additional spelling variants of the names on the list (see example in figure 4.3) and led to the conclusion that there were no surnames found at a very high frequency in the Bodmin Moor parishes as compared to other parts of Cornwall or the rest of Britain (Archer 2015).

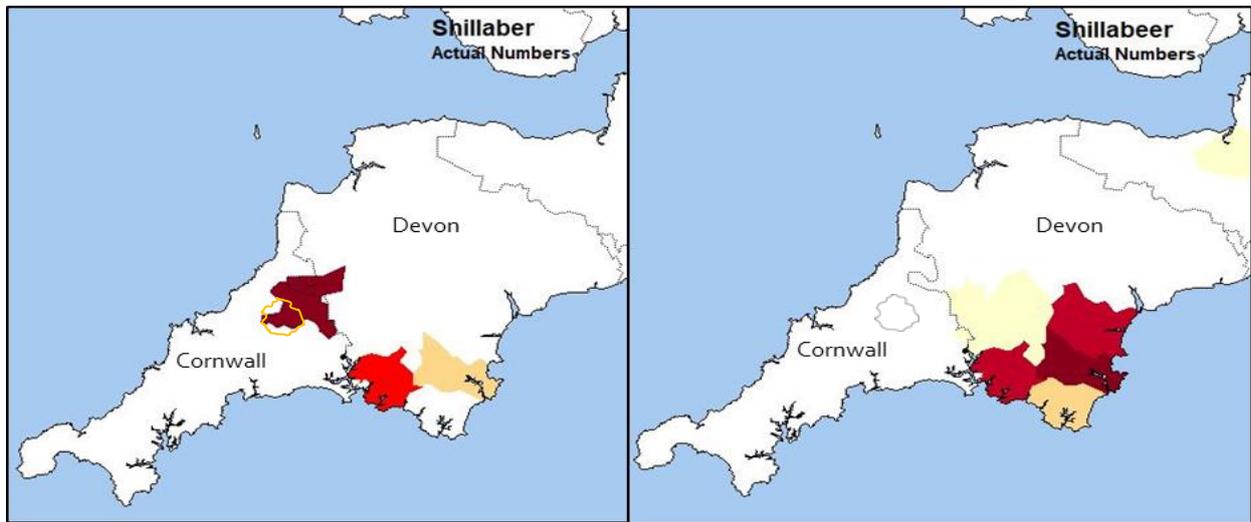


Figure 4.2 Geographic distribution of the surname 'SHILLABER' (Archer 2015). Bodmin Moor is shown outlined, close to the Devon border. The darker colour means a higher concentration of the surname is found in that area. a) In 1881 the surname SHILLABER was found in the greatest number in east Cornwall and Bodmin Moor b) With the addition of one letter, the name becomes SHILLABEER which is found only in Devon. The original name turned out to be SHOLBEARE which is a hamlet in south Devon (Postles 1995).

Enter Surname:

Rank	Name >>	Frequency	
202112	Shillabar	2	
60150	Shillabear	14	
13054	Shillabeer	197	
47717	Shillaber	21	
252517	Shillabere	1	
170961	Shillabier	3	
202112	Shillabur	2	

Figure 4.3 The many unanticipated spellings of 'SHILLABER' throughout the UK (Archer 2015). There are additional spellings in Appendix 8.1.2.

The allegedly Bodmin Moor-specific names GOYENS and TREGLOIN (shown in table 4.2) both had additional spelling variants found throughout Cornwall and therefore were not found at the high frequency in the moor parishes that they first appeared to be. Even the surname CAWRSE, which, with 47 out of 56 bearers appeared to be found exclusively in the Bodmin Moor parish of St. Neot in 1881, had the variant spelling CAWSE found primarily in

Devon (see figure 4.4 below), along with other spellings that were discovered at a later date (listed in section 4.8.2).

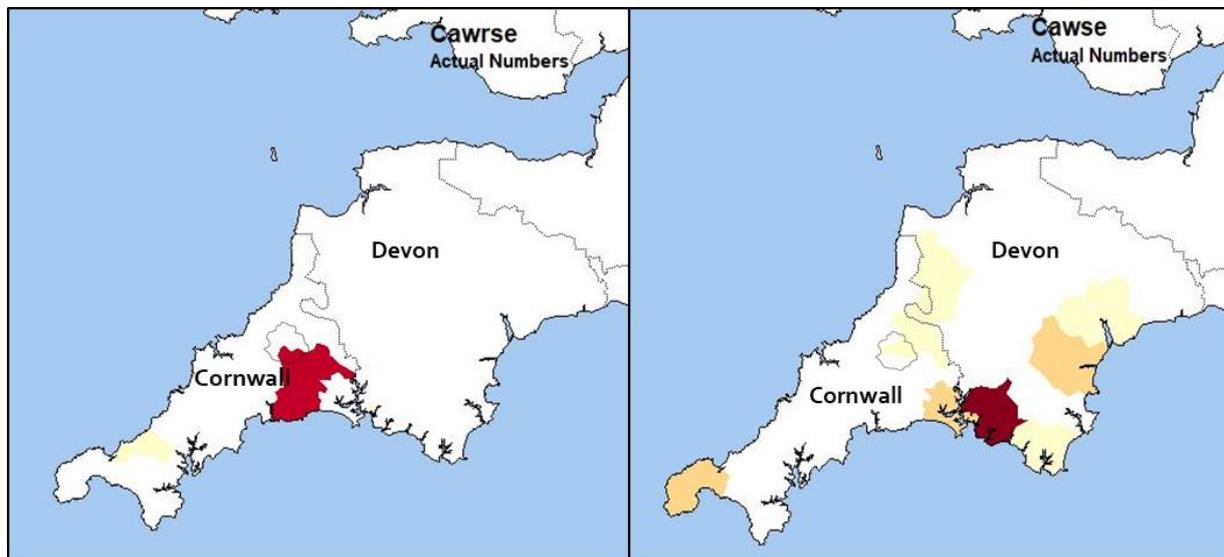


Figure 4.4 'CAWRSE' surname distribution (Archer 2015) a) 47 out of 56 CAWRSEs in Britain in 1881 resided in the southernmost Bodmin Moor parish of St. Neot b) An additional 196 'CAWSE's were residing throughout Britain, many in Devon, close to the Cornish border

Almost all of the Bodmin Moor surnames had spelling variants found outside the region; due to the relatively recent fixation of surname spellings, Y chromosome haplotype-sharing generally crosses spelling variants, meaning that all of the surname variants could derive from the same founder and share the same overall Y chromosome haplotype. Previous studies of surname-haplotype relationships support the idea that spelling variants often represent the same name shared by a group of men whose haplotypes are identical by descent: King & Jobling (2009b) found that a single 17-locus STR haplotype within haplogroup I is shared by 11 men with the surnames Grocott, Grocutt, Groucott and Groucutt; the same study contains several other examples. So if the Bodmin Moor names were considered in that light, the many name variants could imply a shared origin and thus negate the premise of unique spelling representing unique Y chromosomes.

4.7.3 Final surname selection

The conclusion was that there were no apparently regionally-distinctive Bodmin Moor surnames, but in order to have enough surnames to sample, it was decided that the top 100 names with the highest frequencies in the moor parishes (listed in Appendix 8.1.3) would be used to recruit volunteers, despite the fact that most of the names were found in substantial frequencies elsewhere in Britain. This was additionally justified by the fact that the appropriate individual genealogy supplied by each volunteer was also a crucial factor in selection and recruitment.

On the advice of Oliver Padel (personal communication), many of the oldest surnames which were found continuously in the Bodmin Moor parish records were also included in the study, despite their high frequencies elsewhere in Britain due to their being typically 'English' patronymic names (as discussed in section 4.6.5). This resulted in 125 additional names which were then added to the list of 100 names that had the highest frequencies in the moor parishes, resulting in a final number of 225 surnames that were used in recruitment (see Appendix 8.1.4).

4.7.4 Recruitment and selection of volunteers

The 225 surnames, along with details of the study and a request for volunteers, were advertised throughout Cornwall in various media, such as in the relevant parish newsletters, local organisations and community groups around Bodmin Moor, local parish councils, the Cornwall Online Parish Clerks, the Cornwall Council, the Cornwall Family History Society, the Cornwall Association of Local Historians, the Institute for Cornish Studies, the Royal Cornwall Museum, the Royal Institution of Cornwall, the Cornish Studies library, the county records office in Truro, local newspapers, and via BBC Radio Cornwall. Volunteers with applicable surnames contacted the study directly by email, with the details of their paternal-line ancestry, and if they fit the criteria an invitation was sent for them to attend a sampling session at one of three locations around Bodmin Moor. This resulted in a total of 47 samples from Bodmin Moor which were used in the study, the surnames of which are shown below in table 4.3.

Table 4.3 The 47 Bodmin Moor surnames used in this study 15 of the names (highlighted in blue) are on H.P. Guppy's list of "peculiar names" – those that in 1890 were found almost exclusively in Cornwall

BONEY	GRYLLS	MASTERS	STEPHENS
BUNT	HAM	MOYSE	STRIKE
BURNARD	HAMBLY	MUTTON	TAMBLIN
CAWRSE	HICKS	NOTTLE	TERNOUTH
COLE	HILL	OLIVER	TREHANE
CONGDON	HOSKEN	PETT	VENNING
COUCH	JASPER	ROWE	VERRAN
COUMBE	JOLL	RUNNALLS	WADGE
CROWLE	KEAST	SALTERN	WALKEY
DAVEY	KEAT	SANDERCOCK	WHERRY
DAWE	LANGDON	SHILLABER	WILLS
DONEY	MARTIN	SHOVELL	

4.8 Discussion of final surnames used

The surname results show that all of the surnames in the Bodmin Moor parishes in 1881 were also found elsewhere Britain, although many were found mainly in Cornwall and the southwest. The original premise of the study - that the upland landscape of Bodmin Moor prevented contact with populations outside the moor - is not supported by the surname data, which show a lack of Bodmin Moor-specific names, thus demonstrating that people did indeed move into and out of the area with regularity.

As shown in table 4.4 below, all 47 surnames had spelling variants, which caused problems in terms of estimating accurate percentages for each surname's locality throughout Britain. Most of the names were not specific to Cornwall and there is a lot of overlap with Devon names: almost half (21) of the names show their main location in 1881 as 'Devon and Cornwall.' While 18 names show Cornwall as their main location, this does not necessarily mean they originated there: many of the names were also common elsewhere in England,

and almost all of the names are classified as of English origin; only two are Cornish-language names. This does not mean that the ancestry attached to all these surnames is English, but it does show the influence of the English language and culture present in this part of Cornwall, even as far back as 700 years ago when surnames were forming.

This lack of unique surnames is an indication of the way in which Bodmin Moor has been exchanging migrants with the rest of Cornwall, England, and beyond, for many centuries (as discussed in Chapter 1). Reasons previously mentioned are the mining industry on the moor which encouraged immigration from all parts of Cornwall and elsewhere; the fact that the moor has never been self-contained economically, so people who lived there had to sell their tin and agricultural produce in the surrounding towns; that the southern parishes lay along a major historic and pilgrimage route to Bodmin, which was the main town in Cornwall and site of a monastery; and that the moor has been used for summering livestock for over 1,000 years, from English counties as far away as Somerset. Furthermore, the east side of the moor lies close to the Devon border, an area which experienced Anglo-Saxon influence and settlement from the late 7th century onwards. People also moved frequently in their lifetimes, often to nearby parishes, so influence from Devon is to be expected, and that is reflected in many of the surnames used in this study (see section 4.8.2).

4.8.1 Movement among parishes

Almost half of the surnames found in the Bodmin Moor parishes in 1881 were found in both Devon and Cornwall in high frequencies. While it is true that most people did not move far from their birthplace - Deacon (2004) notes that Cornish people usually relocated no further than to the next parish - the majority of people in the past did at some point in their lives move out of the parish in which they were born (Dark 1998). Rogers (1995) cites the pre-industrial parish turnover rate as one third per parish every 10 years and notes that frequent movement within a limited area was common until the Industrial Revolution. Crossley (2018) has found that while only 2.8% of the total heads of households in the Bodmin Moor parish of St. Neot in 1851 were born outside Cornwall, most of them were born in parishes adjacent to the River Tamar, which is within 10 miles of Bodmin Moor; indeed, almost all of the

volunteers in this study listed their earliest paternal ancestors as being born in different, but nearby, parishes to that of their paternal grandfather.

According to the parish records from the 18th century, most of the names in this study were found in more than one of the Bodmin Moor parishes, often adjacent ones- but many families also moved further away to a new area. McKinley (1990) states that it was unusual for families to remain in a parish for more than a few generations and this can be seen by comparing the surnames that were listed in the parish records in 1782 with those that were still in the parishes in 1881: out of the approximately 1,500 surnames found within the moor parishes in 1782, only 432 names- less than one third- remained 100 years later in the same twelve parishes. Many of the names would have disappeared due to the families moving away and many would have vanished from the parish records due to being carried only by daughters. But while this demonstrates that the majority of English people in the past moved out of the parish in which they were born, the surname results likewise confirm Hey's (1997) findings that there were also a small group of families which were rooted in the same area over the centuries who, despite the mobility of recent times, still remain to this day. These are the names that form the basis for this study.

4.8.2 Surname derivations and locations

Table 4.4 The 47 surnames used in this study, their spelling variants and derivations, and their primary locations in 1881 (Hanks 2016)

Name	Spelling variants	Derivation	Main location 1881
BONEY	Boni, Bonney	locative name (from Notts); nickname from Middle English 'big-boned'	Cornwall; Surrey
BUNT	Bunte, Bunce, Bant	nickname 'bunting' 'small bird'; relationship name from Middle English personal name *Bunt(e) - place-name Benton (Devon)	Cornwall; Shetland
BURNARD	Burnhard	Nickname 'hardy, brave'; relationship name	Cornwall and Devon; Bucks and Oxon
CAWRSE	Caws, Cawse, Caus, Cors	'reed, fen'; locative name from the Pays de Caux (Normandy)	Cornwall
COLE	Coles, Coll, Coal, Coul, Cowell, Coole, Coule, Coull	relationship name from Middle English and Old French personal name Col(e), a pet form of Nicholas	widespread in England
CONGDON	Congon	locative name from Congdon Shope in North Hill (Cornwall)	Cornwall and Devon
COUCH	Couche, Cooch, Gouge, Goudge, Goodge, Gudge, Gutch, Gooch	Nickname; Welsh: variant of Cough, from Welsh coch 'red(-haired)'; may have been taken by Welsh migrants to Devon and Cornwall, and confused with the English surname Couch	Cornwall and Devon
COUMBE	Coomb, Coombe, Coom, Combe, Comb, Coombes	locative name from Middle English coumb, 'valley, hollow, coomb'	Devon and Cornwall
CROWLE	Crowl, Crole, Kroll, Croule, Crowell, Crowells, Crowels, Crowls	locative name from either of two places named Crowle, (in Worcs and Lincs, 1201)	Cornwall
DAVEY	Davy, Davi, Davie	relationship name from Middle English	Devon and Cornwall; Middx and Surrey
DAWE	Daw, Dawes	relationship name from Middle English	Devon and Cornwall
DONEY	Dony	Norman, English: perhaps a variant of Dawnay	Cornwall

GRYLLS	Grills, Grill, Gryll	variant of Grill with post-medieval excrescent -s	Cornwall
HAM	Hamm, Hamme, Hams, Hame, Home, Sian	locative name for someone who lived at a place named from Middle English, which meant 'cultivated plot on the edge of woodland or moor'	Cornwall, Devon, and Somerset
HAMBLY	Hambley, Hamley	locative name from Sussex, though the surname is now associated mainly with Devon and Cornwall	Cornwall and Devon
HICKS	Hix, Hikes, Higgs, Hick	variant of Hick with genitival or post-medieval excrescent -s	widespread; esp. Cornwall
HILL	Hille, Hile, Hills, Hell	locative name from Middle English hill	widespread
HOSKEN	Hoskin, Hosking, Hoskins, Hoskyns, Hoskings, Haskin, Haskins, Hasking, Haskings	relationship name from the Middle English personal name Osekin	Cornwall
JASPER	Jesper	relationship name from the personal name Jasper	Cornwall and Devon; W Midlands
JOLL	Jolles	from the Middle English given name Julle	Cornwall and Devon
KEAST	Kest	nickname; Welsh 'cest' and Breton 'kest' but more likely to be English or Anglo-Norman	Cornwall and Devon
KEAT	Kyte, Keit, Keyte, Keet, Keat, Keate, Kett, Kight, Keates	nickname from Middle English kete, kyte 'kite' (the bird of prey), perhaps a nickname for a rapacious person	Cornwall
LANGDON	Langdown, Longden	locative name from Langdon (Devon, Dorset), Laidon (Essex), or Langdon (Kent)	widespread: esp. Somerset, Devon, and Cornwall
MARTIN	Martins, Martyn, Martyns, Marten, Martens, Martain, Matin, Martinet	relationship name from the Old French and Middle English personal name Martin	Middx, Kent, and Surrey; Lancs
MASTERS	Marsters	locative name, occupational name from Middle English '(at the) master's (house)', a name for someone who	widespread: esp. S England

		lived or worked there; with post-medieval excrement -s	
MOYSE	Moyes, Moyses, Moyce, Moys, Moise, Moist	relationship name from the Middle English personal name Moise, a vernacular form of Moses	Suffolk; Devon and Cornwall
MUTTON	Motton, Moden, Mouton	nickname from Middle English motoun 'sheep'	Cornwall; Northants
NOTTLE	Nattle, Natell, Nettell, Nottell	Cornish: possibly a locative name, from Nutwell (Devon), recorded as Nottewill in 1301	Cornwall
OLIVER	Olliver, Olver, Olphert, Olyver	English, Scottish: relationship name from the Old French personal name Oliver	widespread: esp. N England and S Scotland
PETT	Pitt, Pett, Putt, Pitts	variant of Pitt; locative name from one who lived in or by a pit or hollow	Kent and London; Devon; Lincs and Norfolk
ROWE	Rowes	locative name from Middle English 'row'. The surname may be for someone who lived by a hedgerow or in a row of houses in a street	Cornwall and Devon; Lancs
RUNNALLS	Runnells, Rundell, Rundall, Roundell, Roundhill, Runnalls	variant of Rundle with post-medieval excrement -s and loss of medial -d-	Cornwall and Devon
SALTERN	Saltren	locative name from Middle English 'building where salt is made, stored, or sold'	Devon and Cornwall
SANDERCOCK	Saundercock	relationship name from the personal name Sander + the Middle English diminutive suffix -co(c)k	Cornwall
SHILLABER	Sholbeare, Shillabearn, Shillibeer, Shellabear, etc	locative name from the lost place Shillibeer in Devon; hamlet in SW Devon	Devon
SHOVELL	Shovel	nickname from Middle English for someone who made or sold shovels, or for someone who used a shovel in his work	Devon; Lancs

STEPHENS	Stevens, Stephans, Steffens, Stivens, Stevans	variant of Stephen with genitival or post-medieval excrescent -s	Cornwall and Devon
STRIKE	Strick, Streek	nickname from Middle English 'a line or streak', perhaps with reference to a mark on the face, a differently coloured streak of hair	Cornwall
TAMBLIN	Tamlyn, Tamlin, Tamplin, Tamblyn, Tamblin, Tambling	relationship name from the Middle English, variant of Tomelin 'little Thomas'; by the post-medieval period, the surname was developing forms with intrusive -p- and -b-	Cornwall
TERNOUTH	Trenouth, Trenute , Trenuth Trenoweth, Trenewth, Trenwith, Trenowth ,etc	Cornish: locative name from tre - 'house, settlement' + nowyth 'new'	Cornwall
TREHANE	Trehan, Trehain	Cornish: locative name	Cornwall and Devon
VENNING	Fenning, Venning, Vening, Fennings	locative name from Middle English 'fen, marsh' + -ing , for someone who lived in or by a fen or marsh	Cornwall and Devon; Somerset
VERRAN	Verrant, Verren Verant, Verrand	Cornish, English: variant of Farrant	Cornwall
WADGE	Wadg, Wags	perhaps a variant of Watch	Devon and Cornwall; Durham
WALKEY	Walky	unexplained. Compare Walk	Cornwall and Devon
WHERRY	Werry, Weary	nickname from Middle English 'weary'. The name has in some areas, especially E England, been influenced by Middle English whery: 'wherry, rowing barge'	Cornwall; Lincs
WILLS	Willis, Will, Wells	variant of Will with genitival -s ; locative for someone who lived '(by the) spring or stream'	widespread in South England: esp. Devon, Cornwall, Somerset, and Dorset

Chapter 5 **Materials and Methods underlying molecular genetic study**

5.1 **Collection of samples**

In October 2016, 27 saliva samples were collected, with informed consent, from males in Bodmin Moor, east Cornwall. Ethical approval for the study was obtained on the condition that each sample was anonymised and stored under secure conditions (see Appendix section 8.1.5 for information/consent forms). The genealogical information provided by the volunteers was collected in hard copy or followed in a further email. Twenty additional samples were received at a later date through the post for those who could not attend the sampling sessions. This resulted in a total of 47 samples from Bodmin Moor which were used in the study.

The samples were collected using Forensix buccal swabs which were then stored in Eppendorf tubes in an NDS buffer solution (King et al., 2006), which is a basic solution that lyses cells with detergent (N-lauroylsarcosine) and preserves the DNA by chelating divalent metal ions through high EDTA concentration. The swabs were kept at room temperature for four days then stored at -20°C until DNA extraction approximately one month later. Twenty additional samples using Whatman buccal swabs were received at a later date through the post, put in NDS buffer, and stored at -20°C until DNA extraction.

An additional 57 extracted blood DNA samples from Cornwall and 49 extracted blood DNA samples from Devon, collected as part of the People of the British Isles study (Leslie et al., 2015), were received from Sir Walter Bodmer, University of Oxford. The PoBI samples had their paternal ancestry confirmed as local to their specified region, but surnames were not utilised. The final collection comprised 47 samples from Bodmin Moor, 57 general Cornish samples, and 49 samples from Devon, totalling 153 samples from the southwest of England.

5.2 DNA extraction and purification

The DNA from the 47 Bodmin Moor samples was extracted from the buccal swabs using the QiAmp DNA Mini kit on a QIAcube semi-automated workstation (Qiagen) following the manufacturer's instructions; this involves lysis of cells, adsorption of DNA onto a matrix under high salt conditions, sequential washes, DNA elution in low salt buffer, and finally storage in the AE buffer solution at -20°C.

5.3 DNA quantification

All DNA samples were measured for concentration using the Nanodrop 2000 Spectrophotometer (ThermoFisher Scientific). Concentration was measured based on the absorption of a 1 µl sample of DNA in solution at a wavelength of 260 nm. The concentrations of the samples from Bodmin Moor ranged from 2.2 ng/µl to 99 ng/µl. The concentrations of the PoBI samples ranged from 24.9 ng/µl to 500 ng/µl; they were then diluted with purified water down to 2 ng/µl for optimal use in the PCR. The Bodmin Moor samples were used without further dilution in the PCR. All samples were stored at -20°C.

5.4 PPY23 Y-STR multiplex typing

All 153 samples were tested for 23 Y-STRs in order to determine their haplotypes, using the PowerPlex Y23 kit (Promega). See table 5.1 below for the list of amplified loci. The primer mix included in the kit is tagged with four fluorescent dyes in order to distinguish the different loci when they are read on the electropherogram.

Table 5.1 PPY23 markers

STR	Repeat Sequence	Repeat Numbers included in Allelic Ladder
DYS576	AAAG	11-23
DYS389I	TCTG	9-17
DYS448	AGAGAT	14-24
DYS389II	TCTA	24-35
DYS19	TAGA	9-19
DYS391	TCTA	5-16
DYS481	CTT	17-32
DYS549	GATA	7-17
DYS533	ATCT	7-17
DYS438	TTTTC	6-16
DYS437	TCTA	11-18
DYS570	TTTC	10-25
DYS635	TSTA compound	15-28
DYS390	(TCTA) (TCTG)	17-29
DYS439	AGAT	6-17
DYS392	TAT	4-20
DYS643	CTTTT	6-17
DYS393	AGAT	7-18
DYS458	GAAA	10-24
DYS385a/b	GAAA	7-28
DYS456	AGAT	11-23
Y-GATA-H4	TAGA	8-18

5.4.1 PCR

The PPY₂₃ Master Mix consisted of *Taq* (a heat-stable DNA polymerase), dNTPs, and reaction buffers, plus a primer pair mix of forward and reverse primers included in the kit. A volume of 1 µl DNA per sample, at varying concentrations (see section 5.3), was added to 1/3 the manufacturer's recommended reagent reaction volumes (see table 5.2 below for reaction mix) equalling a total volume of 8 µl in the PCR. The samples were amplified in the Tetrad₂ Thermal Cycler (BioRad) using the following protocol: denaturation at 96°C for 2 minutes; then 30 cycles of the following steps: denaturation at 94°C for 10 seconds, annealing at 61°C for 1 minute, extension at 72°C for 30 seconds, then final extension at 60°C for 20 minutes; cooled to 4°C; then stored at -20°C in a light-protected box.

Table 5.2 PPY₂₃ reaction mix for a single 8-µl reaction

Reagent	Reaction volume
PPY ₂₃ 5x Master Mix	1.6 µl
10x Primer pair mix	0.8 µl
HPLC grade water (Fisher Chemicals)	4.6 µl
Template DNA	1 µl

5.4.2 Capillary electrophoresis fragment analysis

The denatured PCR products were run on an ABI 3130xl Genetic Analyzer (Applied Biosystems) using capillary electrophoresis (see Appendix 8.1.6). Each of the amplified fragments is assigned a size based on its relative mobility as it migrates through a polymer, compared to known in-capillary size standards. Preparation for the ABI consisted of adding each of the following components to a 96-well plate: 2 µl CC₅ internal lane size standard, 8 µl formamide, and 1 µl of DNA per sample, for a total reaction volume of 11 µl; one well contained 1 µl of the PPY₂₃ kit allelic ladder (representing fluorescently-labelled common

alleles) instead of DNA. The plate was denatured at 95°C for 3 minutes then cooled on ice for ~ 5 minutes before entering the ABI.

5.4.3 Analysis of electropherograms using GeneMapper software

Each sample was analysed using GeneMapper Software version 4.0 (Applied Biosystems) by observing the location of each peak displayed by each fluorescently-tagged allele. See Appendix 8.1.8 for GeneMapper settings. The location of the peak is based on the total length of the fragment, which includes the number of STR repeats plus the flanking DNA, including the primer sequences. Figure 5.1 shows all 23 variable loci as schematically represented by their sizes and dye colours.

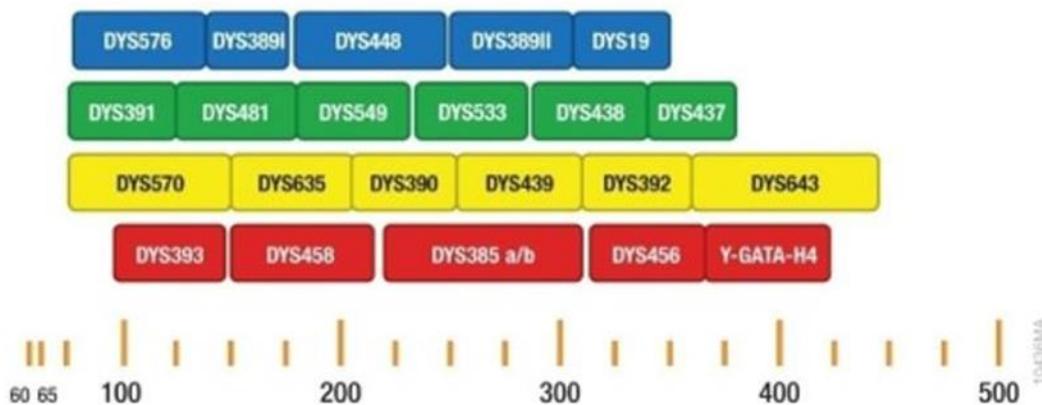


Figure 5.1 PPY23 markers Shown with their sizes in nucleotides and dye colours; the orange channel (bottom) represents the size standard

5.4.4 Haplogroup prediction

Haplotype data were exported from GeneMapper into NevGen software (NevGen 2017) to predict each sample's haplogroup, as validated by Khubrani et al. (2018). In the case of intermediate alleles, repeat numbers were rounded to the nearest integer. Missing alleles were coded '99' in input files, and thereby considered as missing data. Since marker *DYS389*

has two regions where the forward primer can bind due to the identical flanking regions, *DYS389I* was subtracted from *DYS389II* to get the correct allele configuration.

Based on the NevGen haplogroup predictor, the majority of the samples (120) belonged to haplogroup R1b and were SNP-typed for sub-SNPs of R1b using SNaPshot mini-sequencing.

5.5 SNaPshot Multiplex mini-sequencing

The SNaPshot Multiplex kit amplifies up to ten SNP-containing fragments simultaneously and anneals primers of different lengths to the sequence adjacent to each SNP site, followed by fluorescent single-base extension and capillary electrophoresis detection. The 120 samples belonging to haplogroup R1b were tested for the presence of specific sub-SNPs using a SNaPshot multiplex R1b assay, modified from a previously developed kit. The assay originally included ten primer pairs that had been tested to confirm amplicon size and specificity, however two of them (M269 and S145) did not work successfully in the multiplex, so were amplified in separate singleplexes.

Table 5.3 below shows the R1b sub-SNPs used in this study; justification for each marker is discussed in Chapter 6.

Table 5.3 R1b SNaPshot markers

Marker	ChrY coordinate, hg38	Base change	rs number
M269	20,577,481	T>C	rs9786153
L11	15,732,138	T>C	rs9786076
U106	8,928,037	C>T	rs16981293
U198	14,727,619	G>A	rs17222279
S116	19,995,425	C>A	rs34276300
U152	13,221,267	C>T	rs1236440
S145	13,542,548	C>G	rs11799226
M222	12,790,481	G>A	rs20321
Z253	7,253,034	G>A	none
DF27	21,380,150	G>A	rs577478344

5.5.1 SNaPshot PCR

All PoBI samples were used in the PCR at a concentration of 2 ng/ μ l while the Bodmin Moor (BM) samples were at a range of concentrations (see section 5.3). In the multiplex, varying volumes of DNA were used depending on the concentration and quality of each sample: the PoBI samples ranged from 1-6 μ l, while the BM samples were between 5-6 μ l each. The SNaPshot multimix was used at varying volumes ranging from 5-9 μ l depending on DNA volume, equalling a total reaction volume of 10 μ l in the PCR (see table 5.4). In the singleplex reactions, 1-2 μ l DNA was added to 9 μ l of the multimix, equalling a total reaction volume of 10- 11 μ l in the PCR. The amplification was carried out using the Tetrad Thermal Cycler using the following protocol: 94°C for 9 minutes; then 35 cycles of: 94°C for 30 seconds, 59°C for 30 seconds, 72°C for 1 minute; followed by a final extension stage at 72°C for 3 minutes.

Table 5.4 SNaPshot PCR components For a single x- μ l volume reaction

Reagent	Reaction volume
10 x PCR buffer	1 μ l
MgCl ₂ (25 mM)	1.6 μ l
dNTPs (25 mM)	0.16 μ l
AmpliTaq Gold polymerase (5 u/ μ l)	0.2 μ l
Primer mix (F + R)	Variable
Water	Variable
Template DNA	Variable

The primers and their amplicon sizes are listed below in table 5.5. All primers were diluted to 100 μ M from stock pellets (Sigma-Aldrich) and checked to see if they would interact with each other at their required annealing temperatures (<http://www.ncbi.nlm.nih.gov>) which ranged from 53.2°C- 61.3°C. All primer lengths were between 19-26 nucleotides. All primer

sequences had been previously designed for the existing R1b multiplex except for M269 which was from Busby et al. (2011) and Z253 which was from Rocca et al. (2012).

Table 5.5 SNaPshot PCR primers

SNaPshot PCR primers	Forward primer, 5'-3'	Reverse primer, 5'-3'	Amplicon Size (bp)
M269	AAGATCAGAGTATCTCCCTTTG	ATTTCTAGGAGTCTGTATTAC	760
L11	GGTTTTTTTATGCTGCTGCA	ACTCTTTTGCCTAAATTGCTTGT	310
U106	GCAAATCCCAAAGCTCCACG	TGTGTGTGCACACCTGTGG	374
U198	TAGGTTCTATGGTGATTTGAAC	CTTAATCAGAACAAGACATTCC	148
S116	AACCTGCAGCCATAAGTCTC	CAAGGGAGTGAGGCACTTAG	541
U152	CTTAGCTATACAGCCTCTTTTGG	AACATTCCACGCTTGAGGATAA	172
S145	CCAAGTCTTTGATGTGCTGTC	TCAAGGAGGTTCTTGATTTATGC	714
M222	CATTCAAGATCCCAGAAGTCTC	GGTGATGGATGAGGAGTAAAAA	264
Z253	CACTCACAGAGCAACACCAG	TGGGTGCAGACAGATACTACAAC	564
DF 27	GGGAATTTGATCCTGTCGTTG	GAACAAAGCCTCCAAGAAATATGAGG	673

5.5.2 PCR clean-up

Surplus primers and unincorporated dNTPs were removed from the resulting ~7 µl PCR product by adding 0.15 µl Exonuclease, which degrades excess single-stranded DNA, plus 1.5 µl recombinant Shrimp Alkaline Phosphatase (SAP) [1 U/µl], which dephosphorylates unincorporated dNTPs, plus 1.3 µl Exo1 10x buffer in a total reaction volume of 10 µl using the following Tetrad protocol: 37°C for 2 hours; 80°C for 15 minutes; 4°C for 15 minutes. All reagents were provided by New England Biolabs.

5.5.3 Allele-specific single base extension and chain termination

The amplified product is extended on the forward strand by a single base complementary to the SNP through the addition of one of four fluorescently-labelled dideoxynucleotide triphosphates, as shown in figure 5.2 below. The extension terminates at the added SNP

because the 3'- hydroxyl group at the 3rd Carbon which normally forms bonds with the phosphate on the DNA molecule has been removed, thus terminating chain elongation.

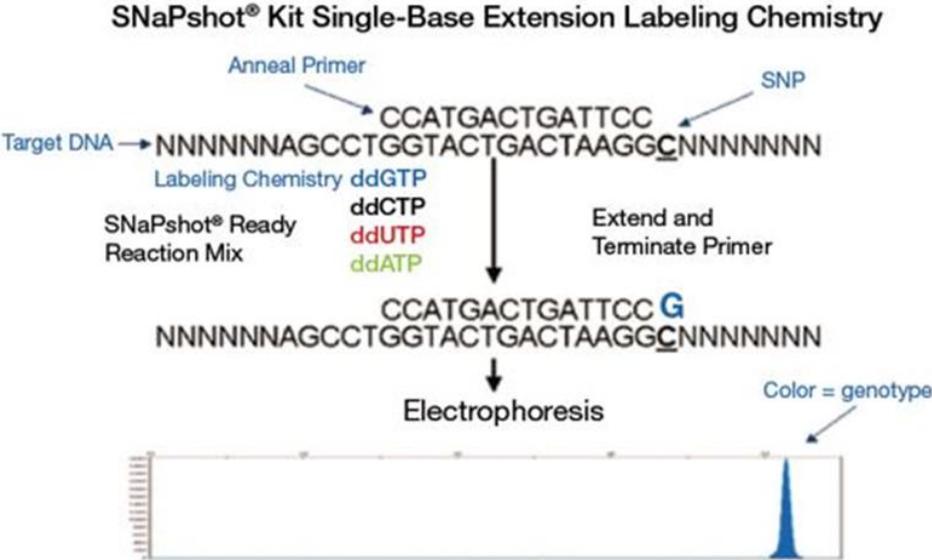


Figure 5.2 SNaPshot single-base extension reaction The ddUTP in the diagram is a ddTTP in the reaction

A non-annealing tail was added to each primer to make its length sufficiently different from other primers in order to prevent the SNP markers from overlapping in the electropherogram. Primer sequences are listed below in table 5.6.

Table 5.6 SNaPshot extension primers Z253 is on the reverse strand

SNaPshot extension primers	(Poly A tails) + sequence, 5' -3'	Extension product size (bp)	SNP state/colour
M269	(25) ATGATCAGGGTTTGGTTAAT	45	Ancestral/Derived
L11	(65) GACAGAACCAAAAGTTCTTC	85	Ancestral/Derived
U106	(12) GAAGAAGCAATTGAACCC	30	Ancestral/Derived
U198	(14) GTTCAAATGCATTCCATGTC	35	Ancestral/Derived
S116	(50) GGAGTTGGGGCTAAAGTAAAAG	72	Ancestral/Derived
U152	(13) CATTACTTTGAGAAGTATGG	33	Ancestral/Derived
S145	(34) CAACCGCTCTCTCAGACA	52	Ancestral/Derived
M222	(36) GGACTCATTCTAAGTACGCA	57	Ancestral/Derived
Z253	(60) TGTCTACATCCATATATAAC	80	Ancestral/Derived
DF27	(41) TGGCTTGAGAGTTTCTGCC	62	Ancestral/Derived

The reaction mix consisted of 1 µl of cleaned PCR product, 1.3 µl SNaPshot Multiplex Reaction mix (Applied Biosystems) which contains fluorescently-labelled ddNTPs, and varied amounts of primers and water, for a total volume of 6 µl in the Tetrad thermocycler. The extension reaction was carried out under the following conditions: 35 cycles of 96°C for 10 seconds, 50°C for 5 seconds, and 60°C for 30 seconds.

5.5.4 Post-extension treatment

After the extension phase, a purification step was performed to remove any unincorporated primers and ddNTPs which might interfere with fragment analysis. 1 µl of SAP [1 U/µl] was added directly to each extension product and incubated at 37°C for 60 minutes before being inactivated at 80°C for 15 minutes.

5.5.5 Capillary electrophoresis fragment analysis

For fragment length analysis, 8.76 µl HiDi formamide and 0.225 µl Genescan LIZ-120 size standard (Applied Biosystems) were added to 2 µl of the extension product. Genescan Liz-120 is an internal genetic size standard of labelled fragments of specific sizes which is included in every sample to create a reference ladder for size determination of the fragments. Samples were then denatured on the Tetrad at 96°C for 4 minutes and cooled on ice for 5 minutes before starting capillary electrophoresis.

5.5.6 GeneMapper analysis

SNaPshot results were displayed using GeneMapper Software v4.0 (see Appendix 8.1.6 for GeneMapper settings and allele calls) as peaks on an electropherogram, with allele sizes of varying lengths due to the primer length, the tail added to it, and slight differences in the molecular weight of the dyes, all of which affect the mobility of each product.

5.6 Analysis

5.6.1 R_{st}

Arlequin software version 3.5.2.2 (Excoffier & Lischer 2010) was used to calculate pairwise genetic distance between populations using Y-STR haplotype data and the statistical method R_{st} , which is a measure of population subdivision specifically for STRs. Because STRs differ from the SNP-based molecular evolution model, this can cause an underestimation of population differentiation when using F_{st} ; instead, R_{st} takes into account the different mutational properties of each marker, therefore accounting for the molecular distances between alleles. It does this by using a Stepwise Mutation Model:

$$R_{st} = \frac{S_t - S_w}{S_t}$$

where S = the average squared difference in allele size between all alleles in the total population; S_t = the variance in allele size of all the alleles in the total population; S_w = the variance in allele size within each subpopulation.

5.6.2 F_{st}

Using Arlequin software version 3.5.2.2, F_{st} was used to measure the genetic distance between sub-populations using their allele frequencies recorded from SNaPshot. F_{st} is a measure of the genetic distance between pairs of populations based on the proportion of allele frequencies between populations. F_{st} is calculated by using the formula:

$$F_{st} = \frac{H_t - H_s}{H_t}$$

where H = measure of the deviation of observed heterozygote frequencies from those expected under HW equilibrium; H_t = expected heterozygosity of the total population; H_s = average expected heterozygosity across sub-populations.

F_{st} has a value between 0 and 1. When there is little differentiation between subpopulations (as a result of high gene flow) F_{st} is close to 0. When sub-populations are highly structured (as a result of little gene flow), the F_{st} is closer to 1.

The significance of the R_{st} and F_{st} scores was measured by a p-value (based on permutation analysis in Arlequin) which was set at a threshold of $p < 0.05$.

5.6.3 Median-joining Networks

Weighted median-joining STR networks (Bandelt et al., 1999) were constructed using Network 5.0.0.3 and drawn with the aid of Network Publisher version 2.1.1.2 (Fluxus Engineering 2018). In order to reduce reticulations, the network was calculated using a variance-based weighting system where the more variable markers are given lower significance by giving them a weight of 1 and the less variable markers are given a weight of

5 (Qamar et al., 2002). Weights of each marker were applied according to their inverse population variance.

Networks included the bilocal STR DYS385, which exists within a palindromic repeated region, resulting in two separate alleles of different lengths. If they have the same repeat lengths, this appears as one peak of double height in Genemapper; if the alleles are different lengths, there are two peaks. This marker is often excluded from Network analysis because of the 'phasing' problem of the two copies among chromosomes, but was retained here because the recent radiation of haplogroup R1b (Larmuseau et al., 2014) supports an assumption that the commonest allele arrangement (11, 14) has not yet had time to greatly diversify.

DYS389I-allele lengths were subtracted from DYS389II-allele lengths prior to analysis, since the former is contained within the latter (Cooper et al., 1996).

5.6.4 MDS

Multidimensional scaling was used to display genetic distance between populations (as an R_{st} or F_{st} matrix) by reducing multidimensional data to two dimensions while minimising the loss of information. MDS plots were created with the R package isoMDS.

5.6.5 Exact tests of population differentiation

Tests, analogous to Fisher exact tests, were carried out in Arlequin.

Chapter 6 A comparison of the patrilineages of Cornwall and Devon

6.1 Introduction

The People of the British Isles project (Leslie et al., 2015) (see Introduction Chapter 1) showed a marked difference between the autosomal genomes of individuals with ancestry in Cornwall compared to those from Devon, based on analysis with the program fineSTRUCTURE (Lawson et al., 2012), which accounts for linkage disequilibrium between SNPs, as well as accounting for differences in SNP allele frequencies. Since Y chromosomes are generally more geographically differentiated than other parts of the genome (Seielstad et al., 1999) this led to the hypothesis that Y-based differentiation should also exist between the two populations, and might be even more distinct than the autosomal difference. It was therefore decided to recruit individuals with a minimum of three generations of local paternal ancestry from both Cornwall and Devon in order to analyse their Y chromosomes using STR and SNP analysis, and to undertake comparisons using standard population genetics measures.

STR analysis is useful because multiple STRs can be analysed easily in a single PCR and because the resulting haplotypes show variation in all populations, due to high STR mutation rates providing an absence of marker ascertainment bias compared to SNPs (Jobling & Tyler-Smith 2003). Furthermore, STR haplotypes can allow unbiased comparisons of populations using the R_{st} statistic (Slatkin 1995) which is analogous to F_{st} but accounts for inter-haplotype mutational distance.

STR haplotypes can also be used to predict haplogroups, using algorithms implemented in online tools such as NevGen (NevGen 2017), which provides a basis for the rational choice of markers for SNP typing. However, while this works well at a coarse level of resolution in which haplogroups are highly diverged from each other (Khubrani et al., 2018), it lacks power when haplogroups are closely related, since the STR haplotypes have not yet had time to develop sufficient mutations to diverge from one another (Larmuseau et al., 2014). This is especially true in the case of the sub-lineages of haplogroup R1b, which has undergone a very recent expansion (Batini et al., 2015), and is expected to be the predominant major lineage in

southwest England (in the only published study to date it represented 78% of a sample of 64 Cornish males) (Balaesque et al., 2010). Early studies had suggested a Palaeolithic origin for hg R1b in Europe (Rosser et al., 2000), but this was revised to a date associated with the development of farming in the Near East during the Neolithic age ~10,000 years ago (Balaesque et al., 2010) based on the geographical distribution of its STR haplotypes which imply a rapid expansion which cannot have begun before the Neolithic period. Balaesque et al. concluded that hg R1b was most likely spread from a single source in the Near East via Anatolia; along with evidence on the origins of other haplogroups, it was suggested that most European Y chromosomes originated in the Neolithic expansion.

Ideas about the ages and sources of European Y haplogroups have been recently revised due to the development of next-generation sequencing (NGS), which has allowed the megabase-scale sequencing of modern Y chromosomes and also the determination of Y haplogroups in ancient samples (Jobling & Tyler-Smith 2017). Several NGS-based studies have included some modern European samples (Poznik et al., 2016), but one focused more systematically on European populations (Batini et al., 2015). This study analysed 17 European and Middle Eastern populations, including samples from England, Ireland, and Orkney, determining variation in a 3.7-Mb segment of the Y chromosome which inferred a demographic expansion starting ~2.1–4.2 KYA – more recent than the Neolithic transition, and consistent with events in the European Bronze Age. The TMRCA (based on a Bayesian method) of the basal haplogroup R1b-M269 was estimated as 5,550YA (95%CI: 4,750–6,500 YA), while that of R1b-L11, predominant in Western Europe, was 4,510YA (95% CI: 3,920–5,160 YA).

The Bronze Age Yamnaya culture (dating to 5,300–4,600 YA) has been linked via genome-wide ancient DNA evidence to a large-scale migration from the Eurasian Steppe north of the Black Sea, which may have replaced much of the previous peoples of Europe (Haak et al., 2015); taken together with the evidence for a recent expansion within hg R1b, this suggests that this haplogroup may have originated with the Yamnaya. Indeed, Bronze Age burials as far west as Ireland show high autosomal Yamnaya ancestry and also examples of hg R1b Y chromosomes (Cassidy et al., 2016). However, the common Western European haplogroup

R1b-L11 has not been found thus far among Yamnaya Y chromosomes (Balanovsky et al., 2017), so understanding of the Bronze Age expansion and its role in the origin of hg R1b is incomplete. The most recent ancient DNA study (Olalde et al., 2018) analysed genome-wide data in 400 Neolithic, Copper Age, and Bronze Age Europeans, including 226 Beaker Culture-associated individuals, and traced the expansion of R1b in Western Europe, and particularly Britain, to the spread of the Beaker culture 5,000 years ago during the early Bronze Age. In particular, the sub-clade R1b-S116, predominant today in Western Europe, was found in the great majority of male ancient samples in Britain. Based on modern samples, this sub-lineage is dated to 4,210 YA (95% CI: 3700–4790YA) (Batini et al., 2015).

In summary, the expectation is that the majority of the Y chromosomes in southwest English samples will belong to haplogroup R1b which has undergone recent expansion in the Bronze Age, and therefore STR typing alone may not provide sufficient resolution to distinguish among the relevant populations. The haplotyping strategy was therefore to use an STR multiplex to provide initial diversity data and predict haplogroups, then to use a bespoke SNP-typing multiplex to analyse SNP sub-haplogroup diversity within haplogroup R1b. Intra- and inter-population comparisons could then be made on the basis of both STR haplotypes and SNP-defined haplogroups. Choice of SNPs to subdivide hg R1b is explained in section 6.2.4.

6.1.1 Placing the patrilineages of southwest England in a broader geographical context

As well as comparing Cornwall and Devon, it is important to look outward to the rest of England, to Wales and Ireland, and to the European continent to ask if there is genetic evidence for an influence from these sources on the patrilineages of the southwest.

In the PoBI study (Leslie et al., 2015), as well as comparing the regions of Britain to each other, an attempt was made to interpret the PoBI autosomal clusters in terms of likely contributions from Continental sources. Data were gathered from a large multiple sclerosis study, with geographical information coming from the hospital of treatment, and therefore not as precisely defined in terms of ancestry as the PoBI samples themselves. Using this approach,

a large number of differentiated European clusters (not including Ireland) were defined and the proportions of these contributing to the PoBI clusters was estimated. This is shown in figure 6.1 below.

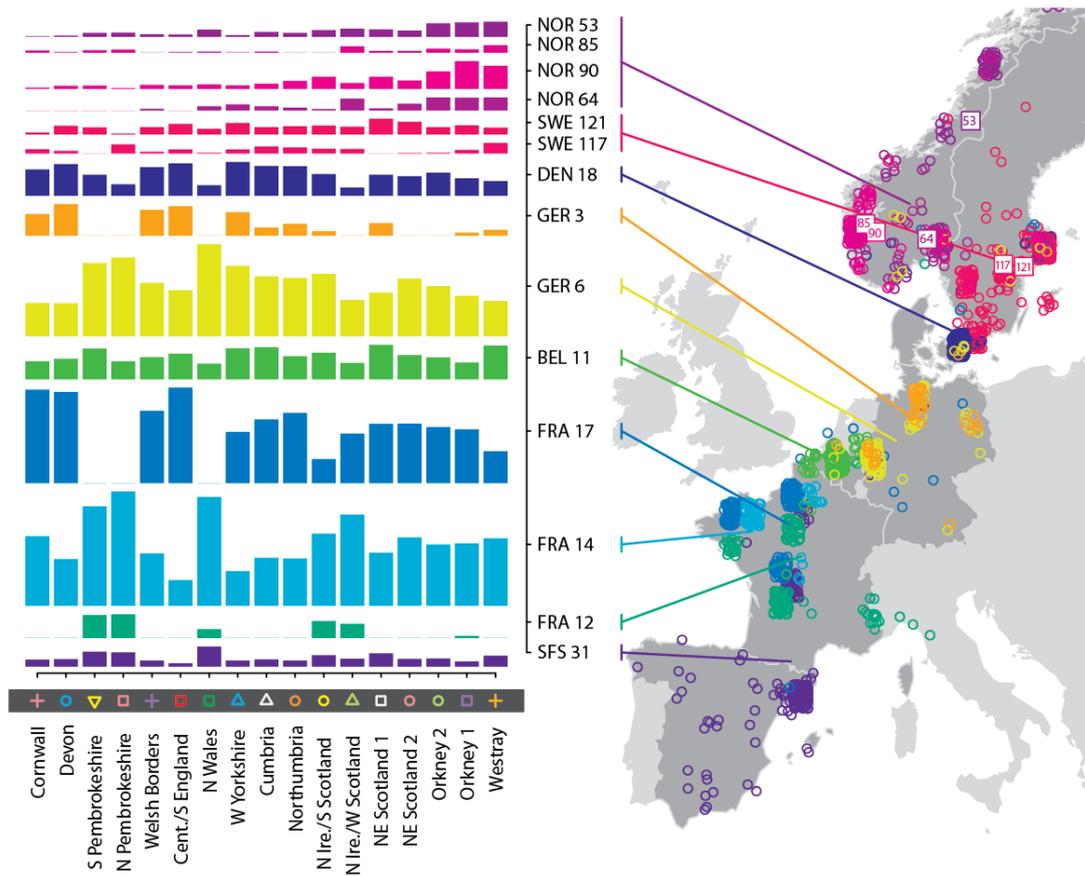


Figure 6.1 European group proportions in the 17 autosomal clusters identified in the PoBI study Each row represents one of the European groups (labels at right) that were inferred by clustering the 6,029 European samples using fineSTRUCTURE. Each column represents a UK cluster. Coloured bars have heights representing the proportion of the UK cluster's ancestry best represented by that of the European group labelled with that colour. The map shows the location (when known at regional level) of the samples assigned to each European group (Leslie et al., 2015).

The most notable feature of this analysis is the markedly higher Norwegian contribution to the Orkney clusters than to others, which is due to the association between Orkney and the kingdom of Norway in the Middle Ages. In the PoBI study and its supplemental materials, a narrative is given which explains the European contributions to clusters in terms of a simple historical model focused on migrations – the major Central/S England cluster is explained, for example, in terms of Anglo-Saxon mass migration. Dates (with large errors) are estimated for

these European contributions. Some authors have pointed to the dating uncertainty and challenged the PoBI project's interpretations, particularly in relation to Anglo-Saxon vs. Danish Viking contributions (Kershaw & Røyrvik 2016).

Focusing on Cornwall and Devon, figure 6.1 shows that the major differences between European contributions to the two are the elevated contribution of FRA 14 to Cornwall and the relatively elevated contributions of European groups SWE 121, DEN 18, and GER 3 to Devon. The PoBI study argues that DEN 18 and GER 3 reflect Anglo-Saxon migration, so their greater prominence in Devon could indicate higher levels of Anglo-Saxon ancestry there; FRA 14 is suggested to be a contribution of early post-Ice-Age migrants, so its higher Cornish frequency could be a reflection of relative Cornish isolation from the rest of England.

In this chapter, Y-STR data will be used to compare Cornwall and Devon to each other and then to other relevant populations in the British Isles and beyond, and to ask how this compares with the autosomal affiliations and evidence from other sources.

6.1.2 Data analysis

Y-STR haplotypes were analysed using NevGen software (NevGen 2017) to predict haplogroups by using a previously-devised Bayesian approach, but also considering the pairwise correlation of alleles among Y-STRs in calculating haplogroup probabilities. NevGen has been previously validated by analysing Saudi Arabian samples where SNP typing had also been carried out (Khubrani et al., 2018) to confirm the predictions, providing a >99% prediction accuracy. In addition, for a subset of the samples analysed here some Y-SNP data were available from SNP chip data provided by the PoBI project (Jon Wetton, personal communication); it was possible to use some of these data to validate the NevGen predictions, as described in section 6.2.3. NevGen predictions include: a percentage probability which reflects the confidence of the prediction based on how well the haplotype of the sample fits those found in the underlying STR/SNP database; a score of 'fitness' which is the closeness of the fit to the haplogroup's modal haplotype; and also a 'second-best'

fitness score. Actual haplogroup frequencies were compared between populations using pairwise population differentiation tests and F_{st} .

For comparisons of Cornwall and Devon to other European samples, Y-chromosome data were obtained from the literature and from unpublished studies from the Jobling laboratory (as described in section 6.3). To allow the maximum number of populations to be compared, some reduction in the number of Y-STRs considered was necessary. Pairwise R_{st} based on Y-STR haplotypes was calculated between populations and the relationships between populations (based on pairwise R_{st} matrices) were displayed graphically using multi-dimensional scaling (MDS), which represents in two dimensions an approximation to a multidimensional matrix; populations which lie closer to each other in the MDS plot are more closely related than those further apart.

6.2 Results

DNA samples from three populations from southwest England were assembled for analysis with Y-chromosomal markers, to allow a statistical comparison to be undertaken to assess differentiation between the populations. Two of the sample sets, respectively with ancestry from Cornwall and Devon, were chosen from the PoBI sample set because they had shown significant autosomal differentiation (Leslie et al., 2015). In addition, a sample set from Bodmin Moor in east Cornwall was also collected and analysed; this area lies on the border between Devon and Cornwall and, as suggested by Leslie et al., may have acted as part of a boundary separating the two populations, thus contributing to the genetic division seen in the autosomal data. The Bodmin Moor sample set was selected based on patrilineal surnames that had been found in that area continuously for several hundred years (see Chapter 4).

A current-generation Y-STR multiplex, PPY₂₃, was used to analyse the samples because of the high variability of STR haplotypes which are useful in discerning recent population and individual divergence, while also allowing the prediction of stable, less variable haplogroups which can be subdivided and confirmed using SNP-typing methods.

6.2.1 Y-STR haplotype diversity

Y-STR haplotypes based on the 23 STRs in the PPY23 multiplex were generated for all 153 samples (Cornwall, n = 57; Bodmin Moor, n = 47; Devon, n = 49) and are listed in Appendix section 8.1.9.

Figure 6.2 below shows an example of a PPY23 STR haplotype displayed as an electropherogram using GeneMapper 4.0 software. All 153 males analysed showed different Y-STR haplotypes. Given the large number of markers in the PPY23 multiplex, and the inclusion of two 'rapidly mutating' STRs (DYS570 and DYS576) (Ballantyne et al., 2010), this is not surprising, and high haplotype diversity has been observed previously (Purps et al., 2014) in all populations studied.

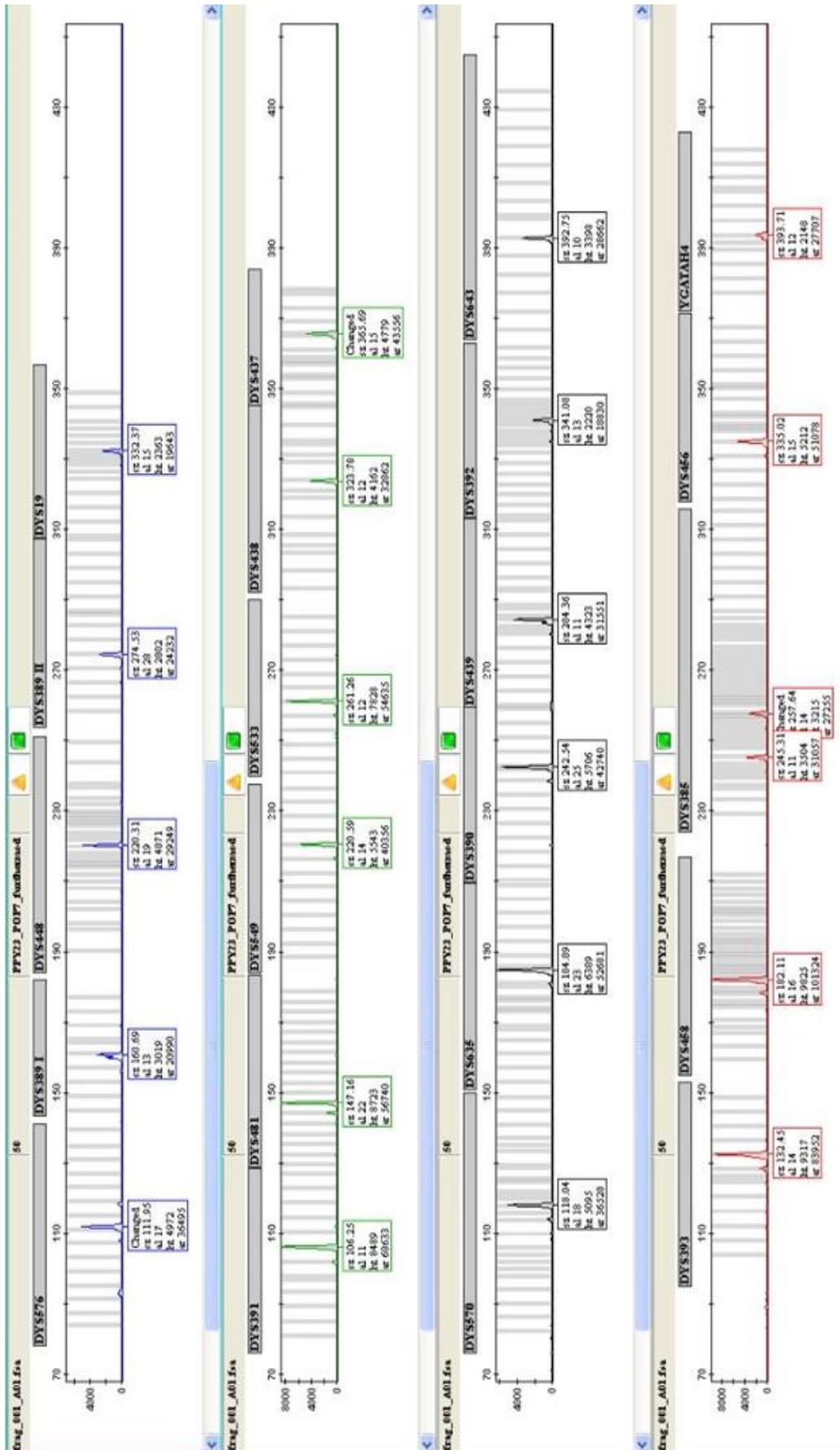


Figure 6.2 Example of an electropherogram showing a PPY23 haplotype Four dye channels are shown (from top to bottom: blue, green, yellow [displayed as black for clarity], and red); the fifth dye channel (orange) contains a size marker and is not shown. Above each channel the x-axis scale is in base-pairs; the y-axis represents arbitrary relative fluorescent units. Twenty-three major peaks are visible, representing the 23 STRs, and named above dye channels in grey boxes. Alleles are automatically determined by the GeneMapper software when they lie exactly within a bin (grey vertical stripes); most peaks show an exact allele size, while peaks marked "changed" have been manually adjusted to account for minor variation due to variables in the ABI matrix such as temperature or lane conditions, or due to the sequence of the actual allele.

6.2.2 Interpopulation comparisons based on Y-STR haplotypes using R_{st} and network analysis

All 153 haplotypes are displayed in figure 6.3, labelled according to population. The network shows that each haplotype is unique and there is no evidence of clustering by population.

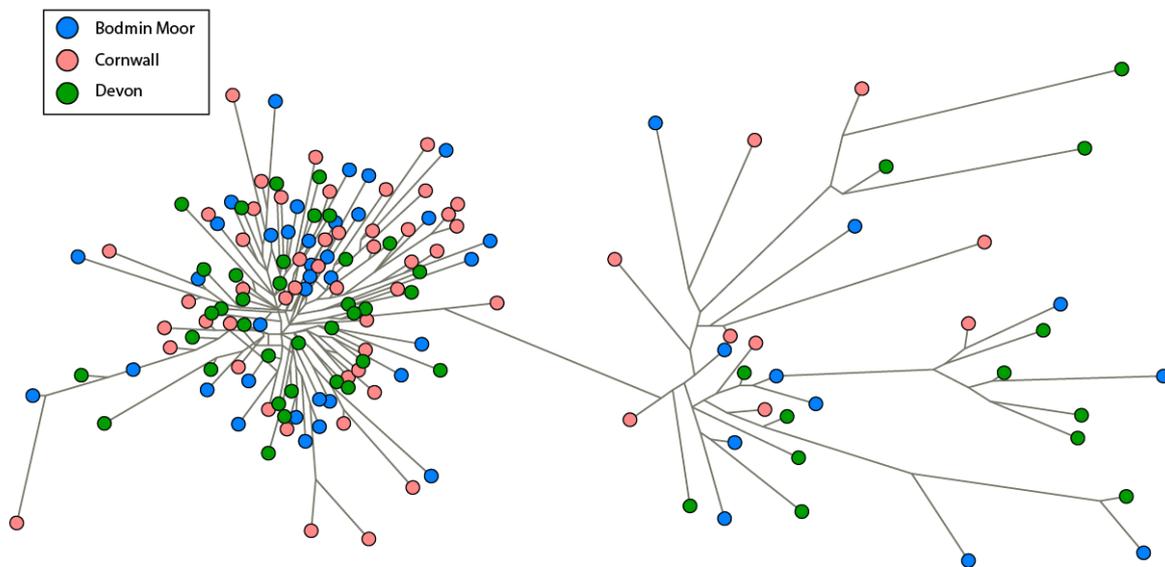


Figure 6.3 Median-joining network displaying relationships between 23-locus STR haplotypes in three SW English population samples. Circles represent individual haplotypes, with area proportional to sample size, and lines between them are proportional to the number of mutational steps. Colours represent the three populations, as given in the key, top left. Note the lack of clear clustering of any one population in the network.

Arlequin was used to calculate pairwise genetic distances between the three populations using STR haplotype data and the statistical method R_{st} (Slatkin 1995), which is a measure of population subdivision used specifically for STRs that takes into account the average of the mutational distances between haplotypes under a stepwise mutation model.

Table 6.1 Population pairwise R_{st} and p -values based on STR haplotype frequency comparisons between populations R_{st} is shown in the bottom diagonal, p -values are shown in the upper diagonal

	BM	COR	DEV
BM		0.31	0.92
COR	0.00090		0.21
DEV	0.00000	0.00701	

R_{st} values are very low and any differences between populations are non-significant. The value for Bodmin Moor lies between that of Cornwall and Devon, so Bodmin Moor could therefore be genetically affiliated with either area. It may be possible that by increasing the pooled sample size, R_{st} differences could emerge to suggest that Bodmin Moor is subtly more affiliated with either its eastern or western neighbours; to determine this, it was pooled with either Cornwall or Devon, and this pooled sample was tested against the remaining sample (i.e. [BM+COR] vs DEV, and COR vs [BM+DEV]). However, pairwise R_{st} values for these comparisons all remain very low and non-significant.

6.2.3 Haplogroup prediction from STR haplotypes

Since Y-STR haplotypes provide no evidence for population differentiation, it was decided to undertake analysis at the level of SNP-defined haplogroups. As a first step, NevGen software was used to predict the haplogroup of each sample based on its PPY₂₃ profile (see Appendix 8.1.10 for haplogroup predictions). Predicted haplogroups for all samples are displayed in the median-joining network in figure 6.4a. Forty-nine of the PoBI samples (13 COR and 36 DEV) have had their haplogroups directly confirmed by SNP-typing using Affymetrix SNP6.0 and Illumina 1.2M Duo SNP-chips (Jon Wetton, personal communication); these directly typed samples are highlighted in figure 6.4b, demonstrating that all predictions are consistent with known haplogroups, and supporting the use of the NevGen software for this purpose.

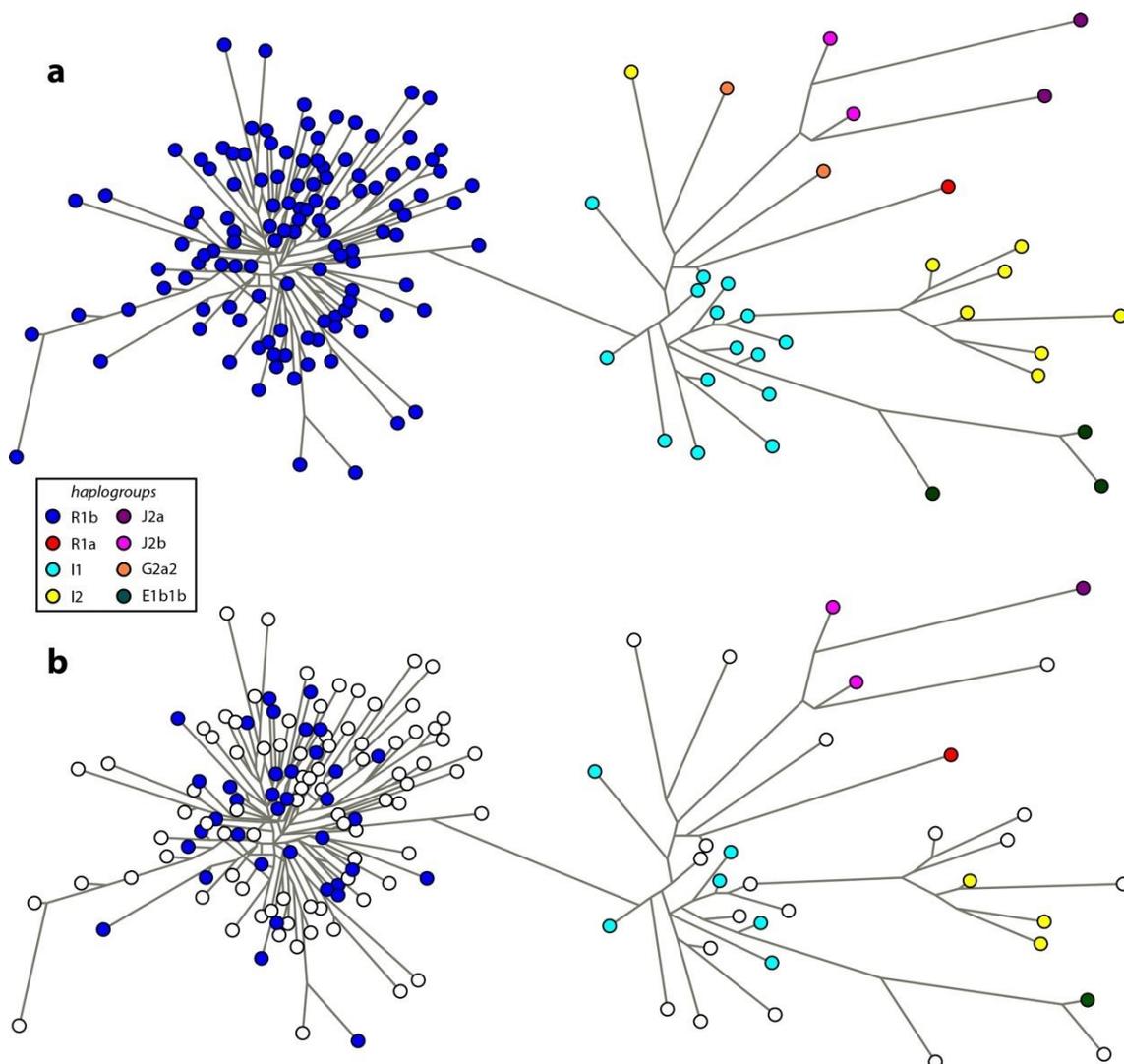


Figure 6.4 Predicted haplogroups in southwest English populations and comparison with known-haplogroup samples
 In these median-joining networks, circles represent haplotypes, with area proportional to sample size, and lines between them are proportional to the number of mutational steps. Colours represent predicted haplogroups, as given in the key. a) Predicted haplogroups in the Cornwall, Bodmin Moor, and Devon populations. The most common haplogroup predicted is R1b, which forms the major star-like cluster in the left part of the network. b) Here, 49 samples with known haplogroups from SNP-chip genotyping (Affymetrix SNP 6 and Illumina 1.2M Duo SNP-chips) in the PoBI sample set are highlighted with their haplogroup colours. All are consistent with the predicted haplogroups in part (a), supporting the haplogroup prediction approach.

As expected from prior data on southwest England (Balaesque et al., 2010), the majority of the samples in this study ($n = 120$, 78%) were predicted to belong to haplogroup R1b. In the median-joining network (figure 6.4), these R1b haplotypes occupy the major star-like expansion cluster, as expected from previous STR-based studies that include this lineage (Balaesque et al., 2010, Batini et al., 2015). The remaining 33 samples predict as haplogroups G, E1, R1a, J2, I1, and I2 (these are discussed further in section 6.3.1.); this spectrum of lineages is consistent with prior studies of Y haplogroup diversity in the British Isles (King &

Jobling 2009b). Haplotypes corresponding to these predicted haplogroups form small clusters outside of R1b or lie scattered in the network, as expected from published studies (Batini et al., 2015).

Figure 6.5 shows haplogroup frequencies as pie-charts on a map of southwest England. The similarity of the three populations is clear from visual inspection, but Cornwall has a slightly higher proportion of hg R1b.

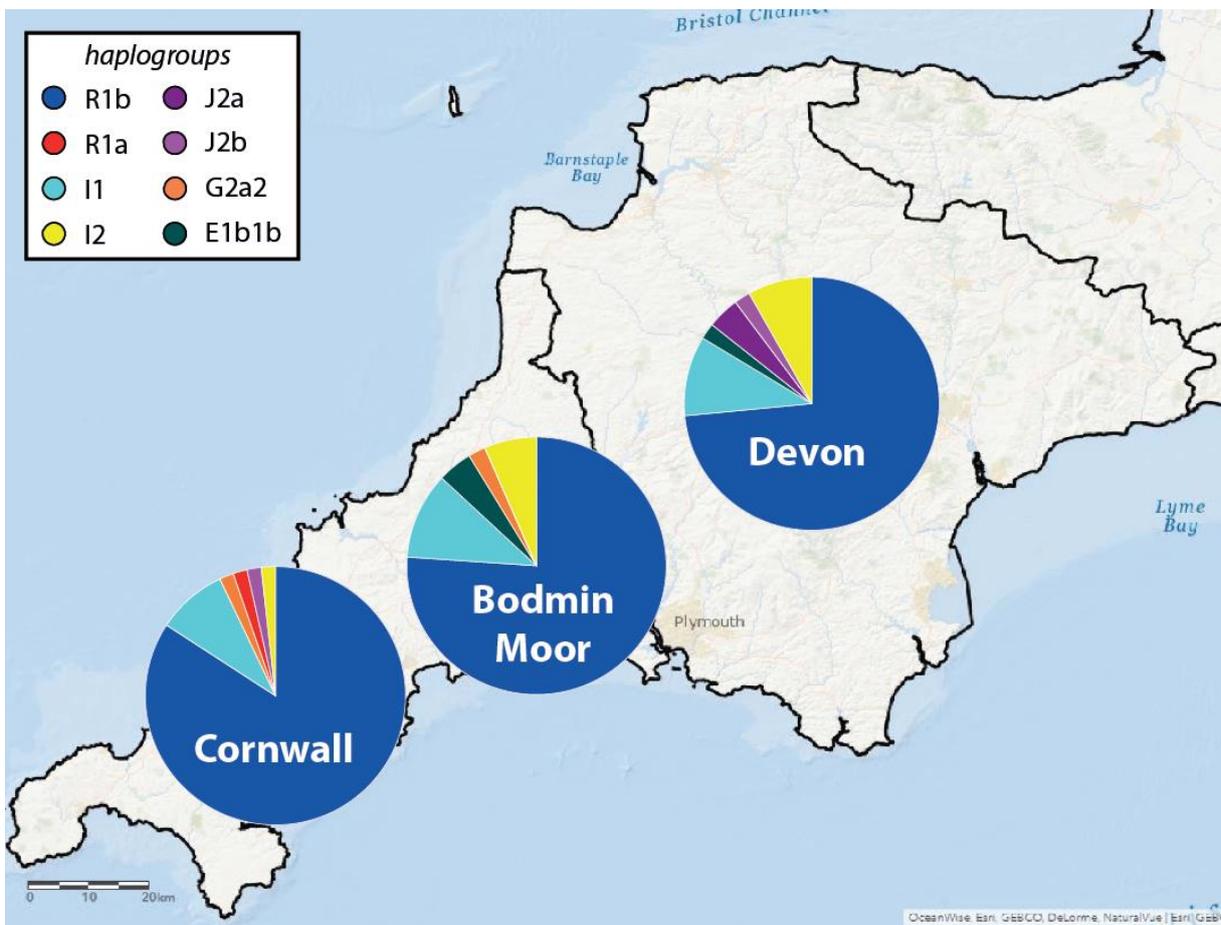


Figure 6.5 Haplogroup frequencies in the three populations Predicted haplogroups are denoted by colours as in the key top left. Sectors of pie charts are proportional to haplogroup frequency; pie-charts are not scaled to population size.

A pairwise comparison of the three populations based on these predicted haplogroup data was undertaken using Arlequin to estimate F_{st} , as shown in table 6.2 below. Unsurprisingly, given the very high frequency of hg R1b and consequent low discrimination between samples, F_{st} is very low, and differences are all non-significant.

Table 6.2 Population pairwise F_{st} and p -values based on haplogroup frequency comparisons between populations F_{st} is shown in the bottom diagonal, p -values are shown in the upper diagonal.

	BM	COR	DEV
BM		0.29	0.78
COR	0.00000		0.21
DEV	0.00000	0.01023	

As was done for Y-STR haplotypes, the Bodmin Moor sample was pooled with either Cornwall or Devon, then compared against the remaining singleton population. Again, F_{st} values were extremely low, and differences were non-significant. Pairwise F_{st} values for [BM+COR] vs DEV and COR vs [BM+DEV] are respectively 0.00000 and 0.00691, with p -values of 0.26 and 0.22 respectively.

6.2.4 Selection of SNPs for the subdivision of haplogroup R1b

Given that hg R1b expanded recently (Batini et al., 2015), Y-STR haplotypes have not yet had enough time to develop mutations to allow the distinction of R1b sub-lineages from one another (Larmuseau et al., 2014), unless very large numbers of markers (e.g. 67 STRs) are used. In effect, the recent expansion has caused some lineages of R1b to experience a convergence of STRs which can create highly similar or identical haplotypes within different sub-clades (Larmuseau et al., 2014). Therefore, because a large majority of the samples in this study belong to haplogroup R1b, in order to determine if there is any population sub-structure across the three populations, SNP-typing is required to subdivide this haplogroup. This necessitates a choice of which SNPs to type, which is complicated by the relative scarcity of academic studies that have attempted to define the fine geographical distribution of R1b sub-lineages. This contrasts with efforts made in the 'citizen scientist' community of genetic genealogists, who have gathered large amounts of data from individuals who have undertaken direct-to-consumer testing; however, online sources of information in this area are not systematic or peer-reviewed and are therefore difficult to validate.

In order to decide on the SNPs to be typed, a survey of the literature and of online forums was undertaken. Published material includes:

- (i) Studies of Irish populations, which identify a common founder lineage (Moore et al., 2006), subsequently shown to be defined by the SNP M222 (Sims et al., 2007).
- (ii) A community-led study (Rocca et al., 2012) of 1000 Genomes Project samples with Y chromosomes within hg R1b-L11, including populations from Great Britain, France, and Italy.
- (iii) A study of 2,043 M269-derived Y chromosomes from 118 West Asian and European populations (Myres et al., 2011), typing markers previously described (Karafet et al., 2008), including M412, M415, M478, M520, M529 (also known as S145 and L21), L11, L23, and S116 (P312), and supplemented in a later study (Busby et al., 2011).
- (iv) An NGS-based study (Batini et al., 2015), including English, Irish, and Orkney populations, that surveyed the distribution of the basal R1b-L11 lineage, and sub-lineages defined by S116 and M222.
- (v) Studies of variation in the Iberian Peninsula that identify lineages that appear to be common via expansion there, but limited elsewhere (Valverde et al., 2016).

Sub-clades defined by markers within these sets that show geographical differentiation within western Europe, and probable appreciable frequencies in England, were considered for inclusion in a multiplex assay. In addition, a survey of Cornwall and Devon online ancestry forums based on direct-to-consumer testing data suggested that the SNP Z253 (S218) might be informative, since a number of males with self-defined southwest English ancestry carried the derived allele (data not shown).

Consideration of this set of SNPs led to a list of ten (table 6.3) to be included in a SNaPshot multiplex. Figure 6.6 shows the phylogenetic relationships among the ten haplogroups defined by these SNPs; figure 6.7 shows all STR-predicted haplogroups in this study.

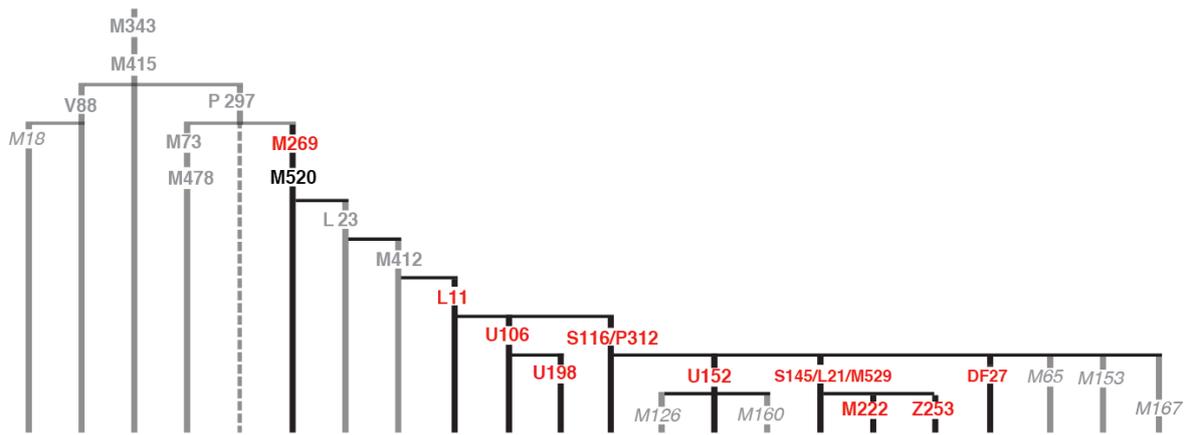


Figure 6.6 M269 phylogenetic tree The SNPs in red are included in the SNaPshot design used in this study; although DF27 was included in the design, it failed to yield reliable data and was eventually excluded

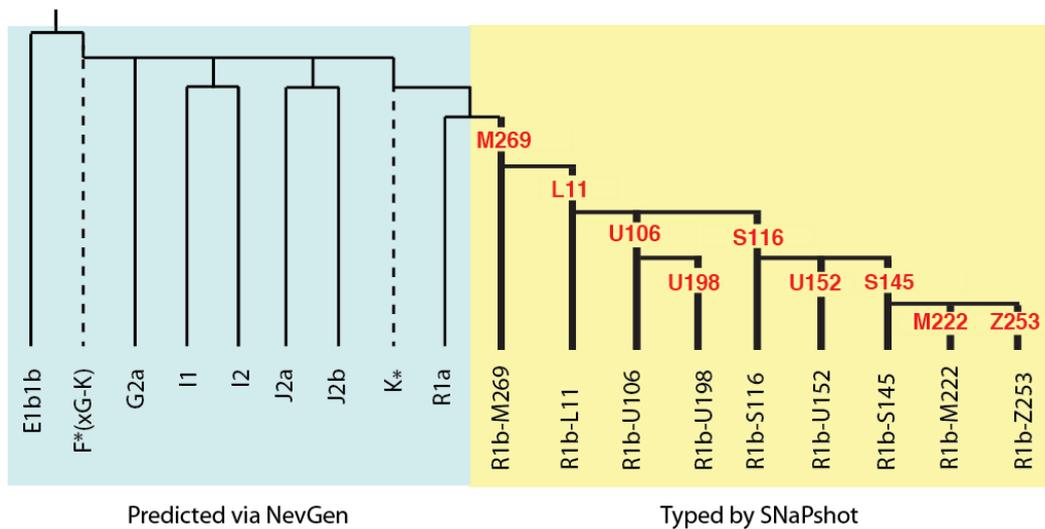


Figure 6.7 Phylogeny showing relationships among all haplogroups Haplogroups predicted from STR haplotypes in this study are shown with blue shading; the dashed lines indicate lineages located in the phylogeny but not found in this dataset. Haplogroups defined via SNP-typing within hg R1b are shown with yellow shading.

6.2.5 Relative frequencies of haplogroup R1b sub-lineages

The 120 samples belonging to haplogroup R1b were SNP-typed using SNaPshot multiplex mini-sequencing to determine the allelic states of the nine R1b sub-lineages described above. DF27 genotyping was not completed for all samples due to problems with amplification, so it was not included in the final results. M269 was not included in the SNaPshot multiplex as it was only required for two samples which were not derived for the downstream marker L11, so it was typed in a singleplex. S145 proved difficult to genotype reliably in the multiplex so

when other SNP calls did not exclude the lineage R1b-S145, it was typed in a separate singleplex. Figure 6.8 below shows examples of electropherograms (displayed by GeneMapper software) demonstrating the successful typing of seven sub-SNPs of R1b. See Appendix 8.1.11 for all SNaPshot allele calls.



Figure 6.8 Example of four electropherograms showing SNaPshot typing for seven SNPs within hg R1b Above each electropherogram the x-axis scale is in base-pairs; the y-axis represents arbitrary relative fluorescent units. SNPs, named above dye electropherograms in grey boxes, are distinguished by size of extension product. Alleles are distinguished by the fluorescent dye associated with the product, lie within bins (coloured vertical stripes), and are labelled below as 'o' (ancestral) or '1' (derived). Note that different dyes affect the mobility of products with the same lengths, and that some extraneous peaks are seen, but do not affect allele calling. Samples DEVo87 and BM24 are derived for U106, as designated by the green peak at ~33 bases. BM18 and COR266 are ancestral for U106, as shown by the blue peak at ~32 bases. COR266 is derived for S116, as designated by the red peak at ~69 bases, while the other three samples are ancestral as shown by the blue peaks. The two black peaks at 35-36 bases confirm the ancestral states of the U152 and U198 SNPs. All samples are derived for L11, shown by the blue peak at ~78 bases.

All 120 R1b samples were derived for M269, given the presence of the derived L11 allele in 118 of the samples and the confirmation of the M269 derived allele in the two samples that were ancestral for L11. Two SNPs, U198 and M222, were ancestral in all samples. Thus, of the nine possible haplogroups defined by the typed SNPs, seven were observed: R1b-M269* (n=2), R1b-L11* (n=3), R1b-U106* (n=38), R1b-S116* (n=30), R1b-U152 (n=7), R1b-S145* (n=33), R1b-Z253 (n=3). The * means the lineage is not derived for any further downstream SNPs in this study. Four of the samples contained at least one missing allele and were removed from the analysis.

Table 6.3 shows the distributions of these R1b haplogroups among the three southwest English populations, and figure 6.9 shows the frequencies of all haplogroups present in the entire sample set (including those predicted from STR haplotypes, combined as one category) on a map.

Table 6.3 Haplogroup R1b sub-lineage frequencies and distributions in the three populations

	BM	COR	DEV
M269*	1	1	0
L11*	2	0	1
U106*	11	11	16
S116*	10	9	11
U152	2	3	2
S145*	6	22	5
Z253	2	1	0

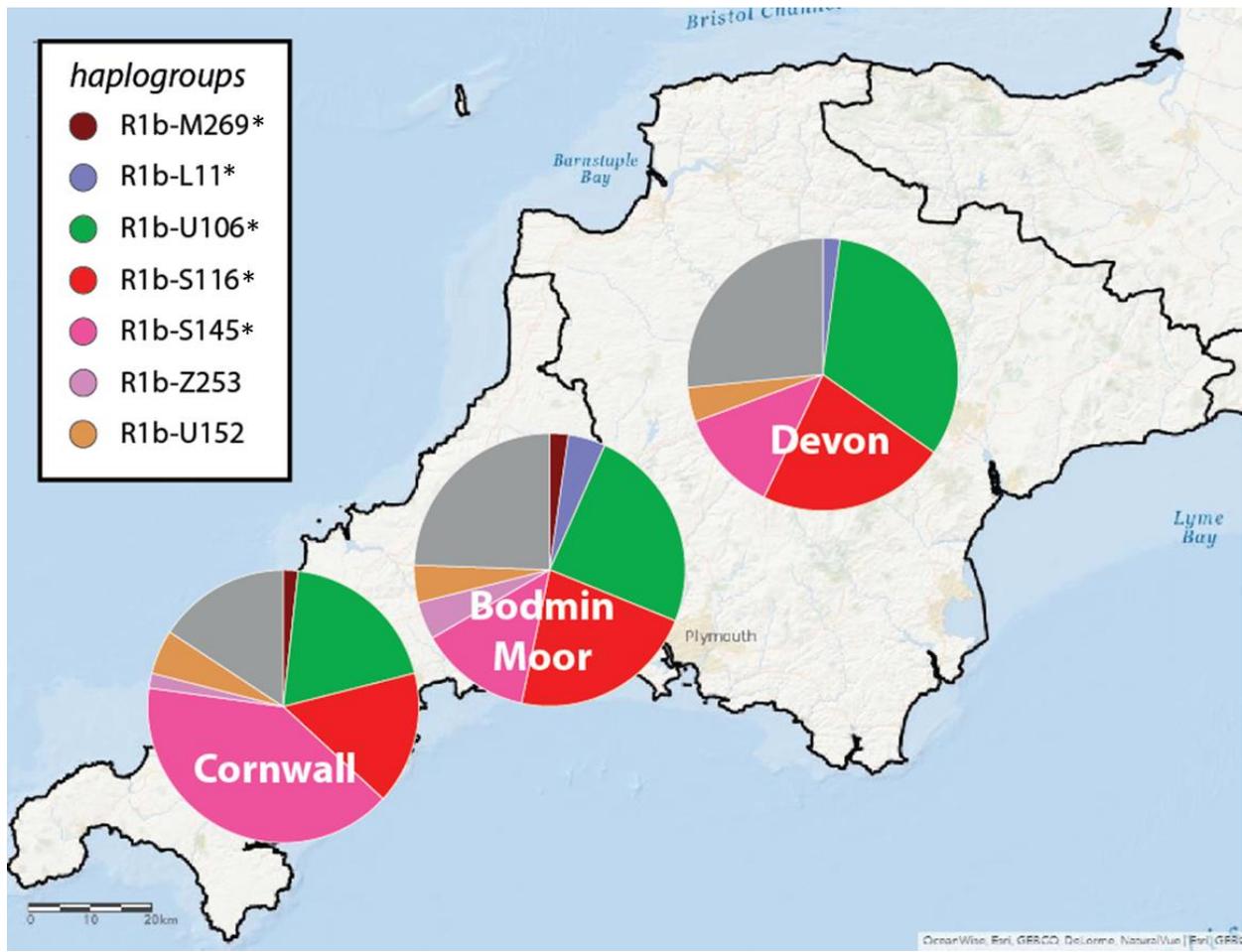


Figure 6.9 Haplogroup frequencies in the three populations including the hg R1b subdivision Haplogroups are denoted by colours as in the key top left; all other haplogroups besides R1b are shown in grey. Sectors of pie charts are proportional to haplogroup frequency; pie-charts are not scaled to population size.

As shown in figure 6.9, the three populations are relatively similar, but Cornwall has a higher proportion of hg R1b-S145. According to Rocca et al. (2012), S145 appears to be the most highly geographically localized of the major L11 sub-haplogroups, found primarily in Ireland, Brittany, and Britain (Myres et al., 2011, Rocca et al., 2012).

6.2.6 Interpopulation comparisons based on haplogroup frequencies

With haplogroups (both predicted and directly determined) for all samples, including the subdivision of hg R1b, F_{st} was calculated among the three populations using Arlequin. Table 6.4 shows that F_{st} between Devon and Bodmin Moor is extremely low while the highest value is observed between Devon and Cornwall, with a significant p-value of 0.02.

Table 6.4 Population pairwise F_{st} and p -values based on haplogroup frequency comparisons, including the R1b subdivision, between populations F_{st} is shown in the bottom diagonal, p -values are shown in the upper diagonal.

	BM	COR	DEV
BM		0.13	0.77
COR	0.01519		0.02
DEV	0.00000	0.04487	

As before, Bodmin Moor was pooled either with Cornwall or Devon, and another comparison undertaken. When pooled with Cornwall and compared to Devon, F_{st} is 0.01628, and non-significant ($p=0.09$); however, when pooled with Devon and compared with Cornwall, F_{st} increases to 0.03143, and is significant ($p=0.03$). Together, these results confirm an east-west differentiation of Y-chromosome lineages and indicate a stronger affiliation of Bodmin Moor with Devon than with Cornwall.

The two main subclades of R1b-L11 are defined by S116 and U106 (as shown in figure 6.7), and have been reported to show geographical differentiation: Villaescusa et al. (2017) have found R1b-S116 mainly in West and Southwest Europe, and R1b-U106 mainly in Central and Northern Europe. S116 shows greater diversity and appears to be about twice as frequent as U106 in the British Isles (Myres et al., 2011). In ancient DNA samples from Britain, S116 is prevalent (Olalde et al., 2018) and it has been claimed to be associated with Neolithic culture or possibly due to later trade networks. Given these suggestions, U106 might be more associated with Anglo-Saxon ancestry, and it seems reasonable to undertake population comparisons based on the three-way split of hg R1b as L11*, S116, and U106, with all other haplogroups pooled as a fourth category. Figure 6.10 shows frequencies of these haplogroup categories graphically on a map, and table 6.5 shows p -values associated with F_{st} .

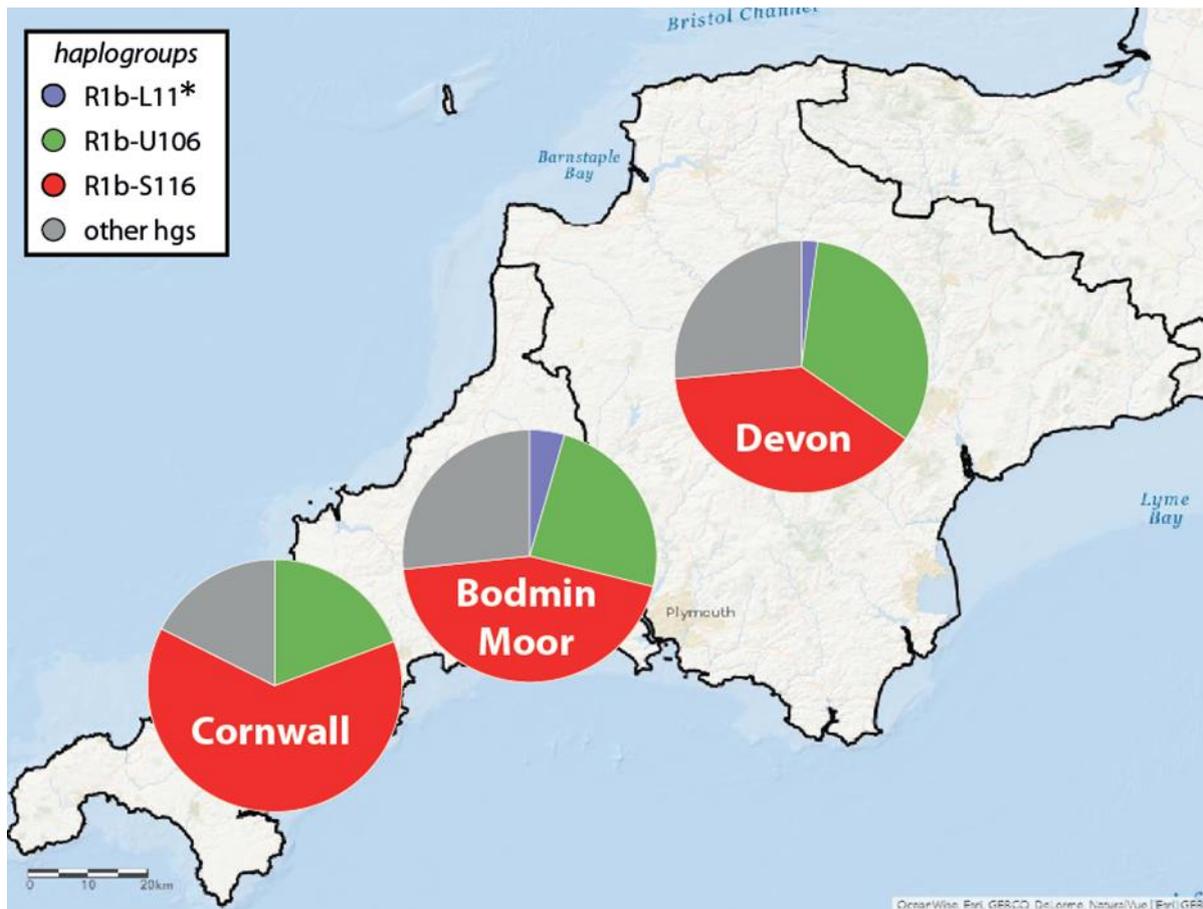


Figure 6.10 Haplogroup frequencies in the three populations, considering the major sub-divisions of hg R1b-L11. Haplogroups are denoted by colours as in the key top left. Sectors of pie charts are proportional to haplogroup frequency; pie-charts are not scaled to population size.

As shown in figure 6.10, all L-11 haplogroups are present in all three populations, but Cornwall has a higher proportion of S116.

Table 6.5 Population pairwise F_{st} and p -values based on haplogroup frequency comparisons of SNPs L11*, U106, S116, and all other hgs, between populations. F_{st} is shown in the bottom diagonal, p -values are shown in the upper diagonal

	BM	COR	DEV
BM		0.13	0.72
COR	0.01978		0.02
DEV	0.00000	0.05498	

The p -values associated with F_{st} show a significant difference between Cornwall and Devon. Bodmin Moor was then combined with either Cornwall or Devon and compared against the remaining singleton population: pooling Bodmin Moor with Cornwall gives a non-significant difference ($F_{st}= 0.02028$, p -value = 0.09), however, pooling it with Devon increases the

significance of the difference ($F_{st} = 0.07470$, $p\text{-value} = 0.002$). This underlines the closer affinity of Bodmin Moor to Devon, and possibly the difference between Cornwall and the rest of England overall.

6.2.7 STR haplotype relationships among R1b sublineages

In order to ask how the R1b sub-haplogroups were reflected in STR haplotypes, a weighted median-joining network was constructed for the R1b haplotypes. All sub-lineages of R1b are displayed in figure 6.11 below which shows (as expected) that the haplogroups show no evidence of structuring or clustering.

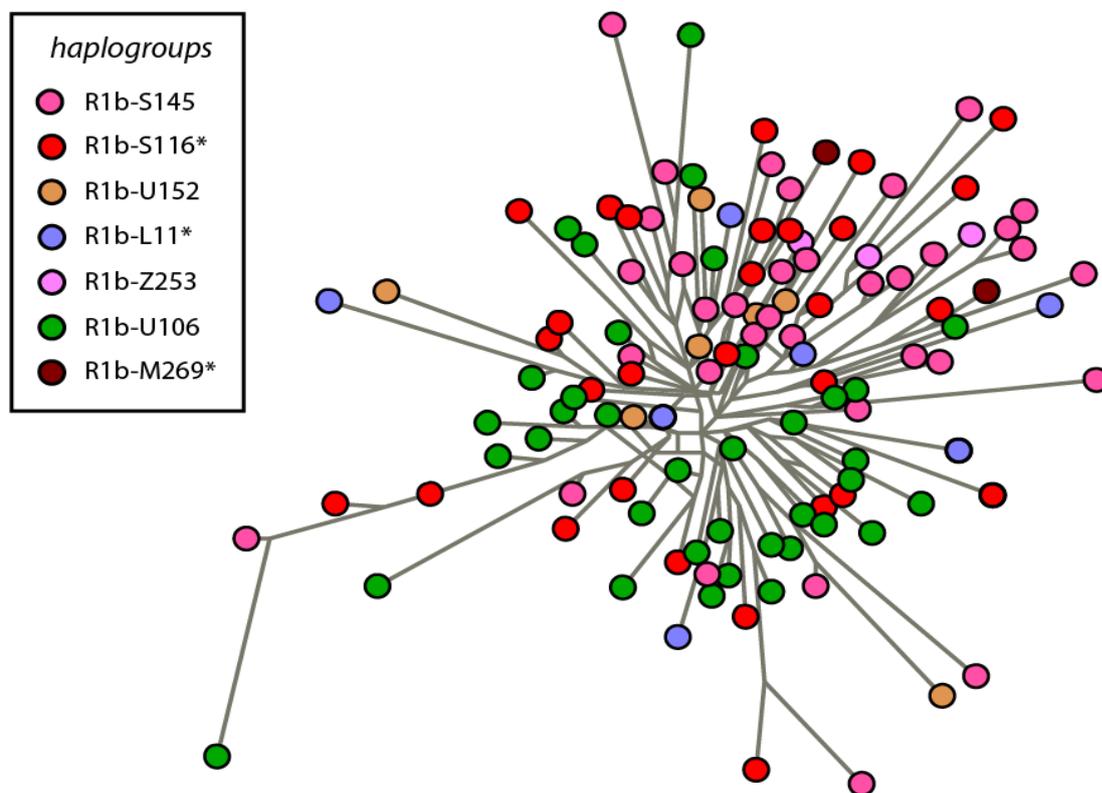


Figure 6.11 Y-STR haplotype relationships among hg R1b sub-lineages In this median-joining network, circles represent haplotypes, and lines between them are proportional to the number of mutational steps. Colours represent SNP-typed sub-haplogroups of hg R1b, as given in the key. STR haplotypes belonging to non-R1b haplogroups are not shown here.

6.2.8 Comparison of the matrilineages of Devon and Cornwall

The original hypothesis underlying this chapter was that the marked autosomal cluster membership differences between Cornwall and Devon might be reflected in a difference in Y lineages that could be even more pronounced. However, it is also of interest to know if matrilineal differentiation exists.

While there are no suitable published mitochondrial DNA (mtDNA) data to carry out a Devon/Cornwall comparison, it was possible to access data on mtDNA SNPs from the SNP chips used in the PoBI project. These data, as well as Y-SNP data, were kindly supplied to Mark Jobling's research group by Prof Sir Walter Bodmer. The data were cleaned and curated by Dr Jon Wetton. Table 6.6 below shows the frequencies of mtDNA haplogroups in the Devon (n=91) and Cornwall (n=114) PoBI samples.

Table 6.6 Occurrences of mtDNA haplogroups in Cornwall and Devon

hg	COR	DEV
F2e	1	0
H	33	25
H1	13	17
H2	2	2
H3	2	4
H4	2	4
H6	0	2
HV	4	5
J1	20	5
K	5	8
N	3	3
R	0	2
T	2	2
T2	7	5
U other	7	1
U5	9	4
U8a	1	0
X	3	2
Grand Total	114	91

Haplogroup frequencies were compared between the populations using a population differentiation test in Arlequin. This revealed no significant difference between the population samples ($p = 0.103$).

6.3 Setting the patrilineages of Cornwall and Devon in a broader geographical context

To place the Y diversity of the populations studied here in a broader context, relevant Y-STR data were gathered and pairwise R_{st} calculated among 22 populations including Cornwall, Bodmin Moor, and Devon (see table 6.7). In order to make all the datasets compatible, comparisons were done at the level of 12 Y-STRs only. Relationships between populations are represented in the MDS plot shown in figure 6.13. Six sub-populations from France were included, and the sampling locations of these are shown on the map in figure 6.12. Two are from the current region of Brittany.

Table 6.7 Populations used in pairwise R_{st} comparisons based on Y-STR haplotypes

Population	Sample size	Source/reference
Cornwall	57	This study
Bodmin Moor	47	This study
Devon	49	This study
Truro1	28	Balaresque et al. 2010
Truro2	34	Balaresque et al. 2010
Central England	127	Purps et al. 2014
Southern England	113	Purps et al. 2014
Wales	236	Purps et al. 2014
Ireland	124	Jobling lab data
Finistère, Brittany	73	Jobling lab data
Ile et Vilaine, Brittany	81	Jobling lab data
Loire Atlantique	47	Jobling lab data
Vendée	50	Jobling lab data
Baie de Somme	43	Jobling lab data
Normandy	87	Jobling lab data
Belgium	205	Purps et al. 2014
Netherlands	2075	Purps et al. 2014
Friesland	95	Purps et al. 2014
Sweden	167	Jobling lab data
Norway	375	Jobling lab data
Denmark1	184	Purps et al. 2014
Denmark2	106	Jobling lab data

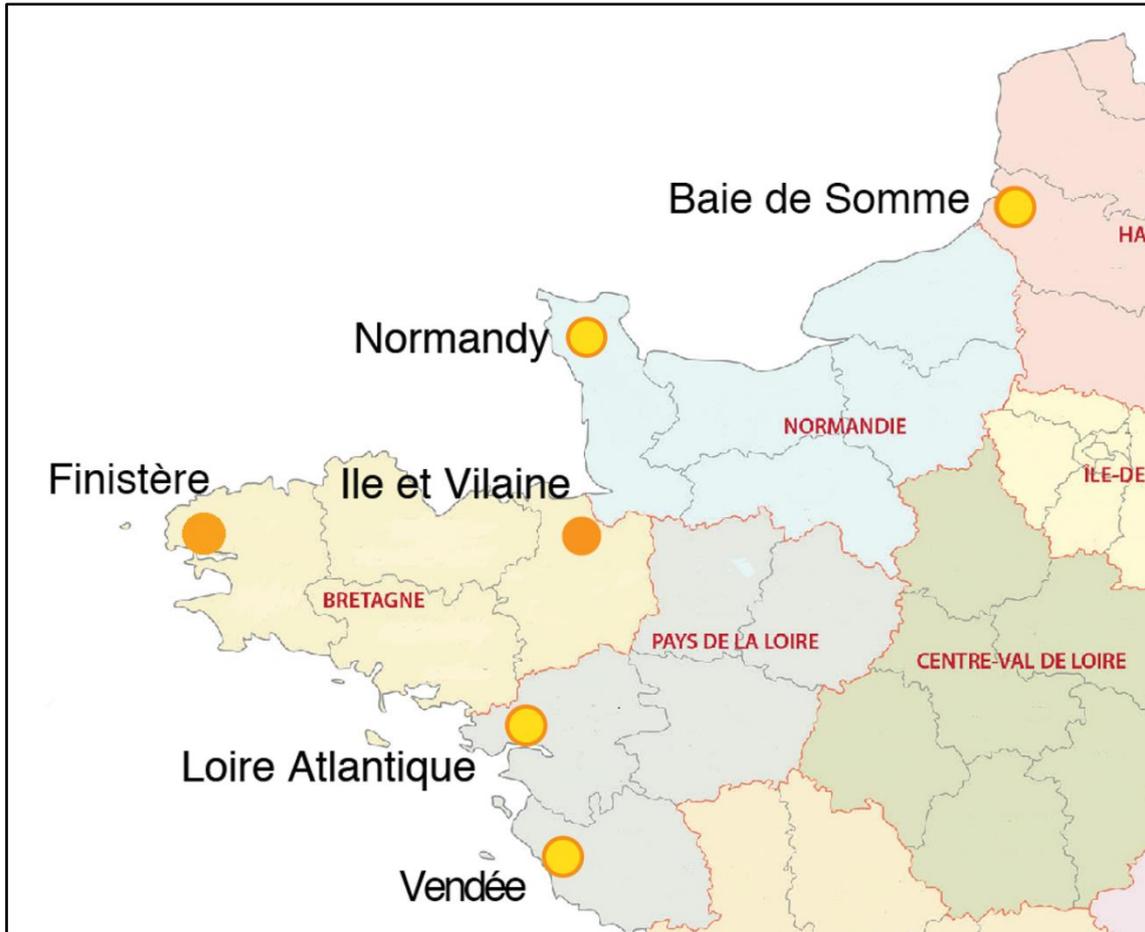


Figure 6.12 Map showing sampling locations for the six French sub-populations The solid orange dots represent the current region of Brittany

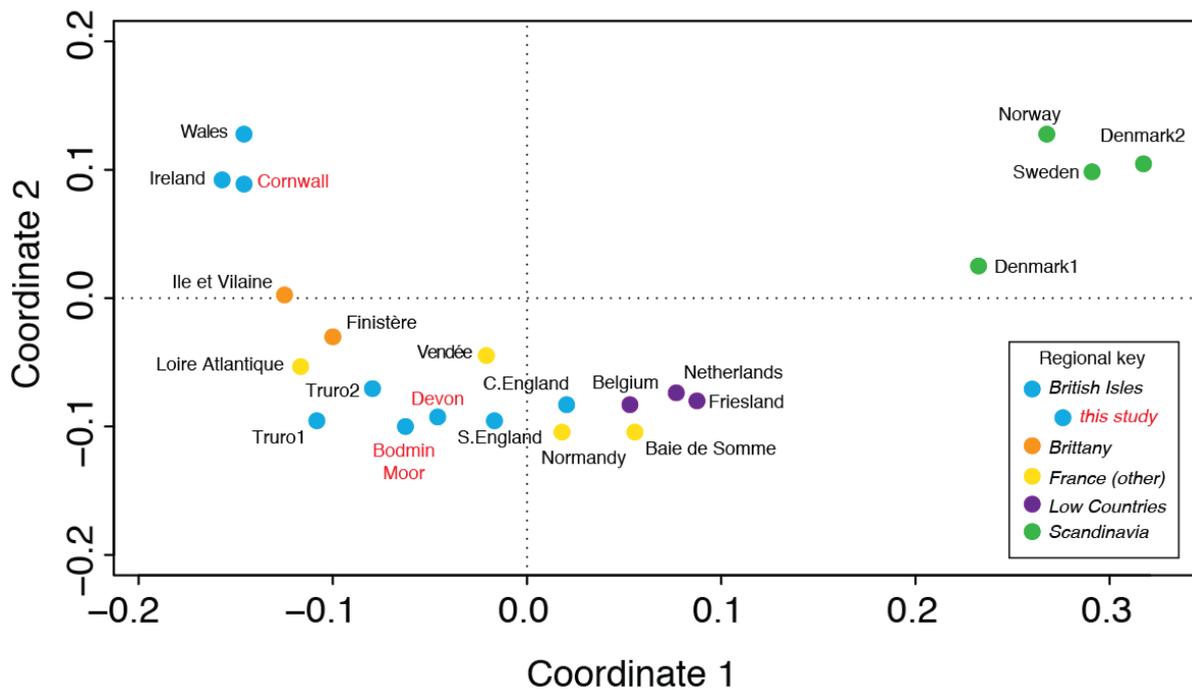


Figure 6.13 MDS plot based on R_{st} matrix showing relationships between populations of SW England and others within the British Isles and the Continent Pairwise R_{st} is based here on 12 Y-STR haplotypes to allow all populations to be compared. Populations are represented by circles coloured by region as shown in the key. Populations from this study are in red font

The extreme poles of this plot are occupied by Scandinavian populations on one side (which form a cluster) and the Celtic-speaking Atlantic Sea Zone populations of Wales and Ireland, together with the mid/west Cornwall sample from the present study, on the other. Samples from the Low Countries also form a cluster, closer to the Scandinavian samples than to the rest. Between the Low Countries cluster and the Wales/Ireland/Cornwall cluster are scattered the other British Isles populations, together with the six French populations. Devon and Bodmin Moor (from the present study) lie close together, distant from the Cornwall sample, emphasising the relationship between the two regions that has been demonstrated in the F_{st} values. Of the French samples, the two Brittany populations lie closest to the Cornwall sample; Loire Atlantique is also close and was historically part of the Duchy of Brittany. Notably, two other Cornish samples, labelled 'Truro1' and Truro2', are distinct from those sampled in this study and seem more affiliated with Devon and Bodmin Moor. These samples were collected at an agricultural show in Truro (mid-Cornwall) by Andy Demaine of Plymouth University in the 1990s (Mark Jobling, personal communication), and have been used in the Balaesque et al. (2010) study. No information is available about the surnames of these

individuals or about the histories of their individual paternal lines. This suggests that sampling criteria can have a marked effect on the results of an analysis such as this.

6.3.1 Investigating the origins of the non-R1b haplogroups

In addition to haplogroup R1b, there were 33 individuals whose Y chromosomes belonged to other NevGen-predicted haplogroups (listed in Appendix 8.1.10). It is of interest to ask if any possible source populations could be deduced for these 33 individuals: for example, if a substantial proportion matched one particular source, that might support the idea of contact with a particular region external to southwest England.

To address this, the PPY₂₃ Y-STR haplotypes of each of these samples was compared to a dataset consisting of over 16,000 PPY₂₃ haplotypes from Purps et al. (2014) which includes mostly European populations. A possible alternative was also considered in the Y Haplotype Reference Database (YHRD.org 2019) however, this was not used because it is limited to showing only exact haplotype matches whereas the Purps et al. dataset shows the closest matches from other populations.

In querying the Purps et al. dataset, the two most rapidly-mutating STRs, DYS570 and DYS576, were removed from the comparison as these would likely introduce recent mutational noise that might obscure connections reflecting contact in the more distant past. The dataset was arranged (by Dr Jon Wetton) from the paper's supplementary information to allow close matches to be detected for any input haplotype, and the number of steps' difference to be recorded.

Deciding on the appropriate number of haplotype mismatches that constitutes a meaningful connection is not straightforward. Bayesian modelling of Y-STR haplotype evolution (Walsh 2001) gives maximum-likelihood estimates for the number of generations separating two Y haplotypes that match by different numbers of mutational steps. This suggests that, for 20 Y-STRs, a perfect match corresponds to 0 ± 12.5 g (generations), a single mismatch to 12.8 ± 18.1 g, a double (two-step) mismatch to 26.3 ± 22.9 g, and a triple mismatch to 40.6 ± 27.2 g.

This illustrates the large uncertainty associated with pairwise comparisons. In practice, restriction to less than three steps' difference yields very few hits in the Purps et al. database, so a limit of three was chosen. Given a male generation time of 35 years (Fenner 2005) this corresponds to $1,421 \pm 952$ years ago, i.e. between 354 BCE and 1550 AD. This very large range suggests that interpreting any signal in terms of a specific historical connection is likely to be difficult or impossible.

Results

Table 6.8 shows the closest matches found for the 33 non-R1b Y-STR haplotypes from the Devon, Bodmin Moor, and Cornwall subsamples. Unsurprisingly, many matches are found in other British samples (shown in bold text) within the Purps et al. set: Devon and Bodmin Moor both had 12 close matches in Britain, while Cornwall had 8. Given the lack of fine-grained information about these British data, it is not possible to say whether these matches are geographically localised within Britain. For the non-British matches, no particular population emerges from a visual inspection of the data as contributing particularly large numbers of matches to any population. At a regional level, Eastern and Southern Europe are the least represented amongst the matches, followed by Northern Europe, with Central Europe being the most highly represented.

Table 6.8 Non- R1b haplotype closest matches British matches are shown in bold print; populations in capital letters are from this study

<u>Study population</u>	<u>Source pop. matches</u>	<u># of matches</u>	<u>mutational steps</u>
DEVON	Belgian	1	3
	BODMIN MOOR	1	3
	Dutch	6	3
	England	5	2,3
	Estonia	1	3
	Finland	1	1
	Frisia	1	3
	German	1	3
	Italian	1	3
	London	4	1,3
	PoBI	2	0,3

	Portuguese	1	3
	Sweden	2	2,3
	Swiss	2	3
BODMIN MOOR	Belgian	5	3
	Brit. African	1	3
	Serbia/Hungary/Croatia	1	2
	Danish/Italian/Lebanese	1	3
	DEVON	1	3
	Dutch	12	1
	England	5	2,3
	Finland	8	3
	Frisia	3	2
	German	16	2,3
	Greek	2	3
	London	4	3
	PoBI	1	2
	Sweden	6	2,3
	Swiss	6	2,3
	Tyrolean	2	2
	Wales	1	3
CORNWALL	Argentina	1	3
	Croatian	1	3
	Danish	1	3
	Dutch	4	3
	English/British	3	0,2,3
	Finland	1	3
	German	1	3
	Ireland	1	1
	Lithuanian	1	3
	London	4	3
	Peru	1	2
	PoBI	1	3
	Polish	1	3
	Spanish	1	3
	Sweden	1	2

This qualitative analysis does not support the idea that a particular source population outside Britain has contributed substantially to the non-R1b lineages within any of the three sub-populations analysed. However, the approach has limited power because (i) there is high uncertainty about the TMRCA of any pair of Y chromosomes and therefore corresponding

uncertainty about the significance of similar haplotypes, and (ii) population samples in the Purps et al. dataset are very variable in size (ranging from 30 for Calabria, to 2,085 for the Netherlands) and do not cover some regions of potential interest to this study, such as France.

6.3.2 Discussion

Y chromosomes from the three southwest populations were successfully analysed using STRs; R_{st} -based tests show no difference in populations, but supplied haplogroup predictions for further use in SNP-typing.

The haplogroup predictions give results that are expected considering the region and previous data: very high R1b frequencies and a selection of rarer haplogroups. Comparisons of all the predicted haplogroups show no significant differences between the three populations, and comparison of the non-R1b haplotypes displays no particular source population.

SNP-typing confirmed those samples belonging to hg R1b and revealed a range of different lineages, along with significant differences between Devon and Cornwall, and evidence of a closer affiliation of Bodmin Moor with Devon than with Cornwall. The deeper-rooting branches within R1b show patterns of differentiation and affiliation in the region which are compatible with greater Anglo-Saxon migration into Devon and Bodmin Moor, and stronger influence of earlier, possibly post-Ice Age or 'Celtic' substrates, in Cornwall. No signal of Irish migrants, in the form of haplogroup R1b-M222, is seen in any of the samples, but this is perhaps due to the fact that M-222 is found primarily in north-west Ireland (Moore et al., 2006), and Irish migration into southwest Britain probably came from the southeast coasts of Ireland, which are closer in proximity. However, an Irish (or Breton) presence in Cornwall could be implied by the slightly higher proportion of hg R1b-S145.

MDS analysis at the level of 12 STRs provides a geographically coherent picture of diversity with a clear clustering of Cornwall with the Atlantic Sea Zone countries of Wales, Ireland, and to a lesser extent, Brittany, which is compatible with the close relationship suggested by the historical record, as discussed in Chapter 1.

In terms of the PoBI autosomal cluster distinction, as hypothesised, the Y-chromosomal data also show evidence of a subtle but significant difference between Devon and the (mid/west) Cornish samples, but not between Devon and the (east- Cornish) Bodmin Moor samples. This suggests that any boundary is likely to lie west of Bodmin Moor. The lack of any significant mtDNA differentiation could support the idea that the processes responsible for the autosomal cluster differentiation may have been male-mediated; alternatively, this may reflect the greater female movement that results from long-term patrilocality.

Chapter 7 Discussion and Conclusion

7.1 Discussion

The aim of this thesis, inspired by the findings of the PoBI project, was to examine the basis of genetic differentiation between the people of Cornwall and Devon. What do historical sources have to say about their differences and their causes? Does Cornwall's reputation of isolation have any validity? What effect might Bodmin Moor have had on the contact and therefore genetics of its surrounding communities, as well as between Cornwall and Devon itself - did it act as a boundary, thus contributing to the genetic differentiation seen in the autosomal data? Given that the male-specific Y chromosome generally shows high geographical differentiation (Jobling & Tyler-Smith 2003), is there a clear Y-chromosomal genetic boundary between Cornwall and Devon? In order to determine if there are any significant differences between the populations of Devon, Bodmin Moor, and mid/western Cornwall, patrilineal surnames and/or local ancestry were used in Y-chromosome variation analysis; this project therefore also examined if local surnames were useful tools to represent deep, region-specific ancestry.

The results, limitations, and conclusions of the surname analysis of Bodmin Moor have been discussed fully in Chapter 4, with the conclusion that no surnames could be found that were indigenous to the Bodmin Moor parishes as a region. Most of the surnames were not unique to the area or even Cornwall, and many were found in high frequencies in Devon as well as in Bodmin Moor, which is consistent with the history of the area: the east side of the moor lies close to the Devon border and was under Anglo-Saxon influence from the 7th century. Devon and east Cornwall also had continual contact through trade, mining, and the constant movement of families to adjacent parishes, even across the county border of the River Tamar. There was also extensive immigration into the Bodmin Moor area due to the mining industry, and the moor's inhabitants had frequent contact with nearby market towns, thus exposing the area, and therefore genetics of the population, to many incomers. Thus, Bodmin Moor was not an isolated area but one open to outsiders, and consequently, using surnames was not a viable model for uncovering deeper ancestry in this region.

The surname-based results are also consistent with the analysis of the Y-chromosome lineages: distributions of Y-STR haplotypes showed no significant differences among populations, while Y haplogroups (when hg R1b is subdivided) showed significant differences between Cornwall and Devon, and demonstrated that Bodmin Moor is more closely affiliated with Devon. Taken together, the surname and genetic analyses carried out here do not support the idea of Bodmin Moor as a barrier to migration between Devon and Cornwall, as was suggested in the PoBI study, but rather an area that may be an intermediate between the two populations. The difference between Devon plus Bodmin Moor combined versus Cornwall is statistically significant, but small. At $F_{st} = 0.07$, this means that only 7% of the variation is found between the two populations, while the remaining 93% of the variation is found amongst the entire population (i.e. all three sub-populations) as a whole. To set this in some context, the range of F_{st} values for the 17 county-based PoBI clusters is from 0 to 0.14. This is based on haplogroups defined from Y-SNPs typed via a SNP-chip, so the haplogroup resolution is poorer than that achieved in this study (Mark Jobling, personal communication).

These observed Y-chromosomal differences between the populations could be due to a greater Anglo-Saxon contribution to Devon and Bodmin Moor, as is shown by the higher percentage of haplogroup R1b-U106 (which is found most frequently in Central and Northern Europe) which was imparted by the Anglo-Saxon immigration into that area. Haplogroup R1b-S116, which has a higher frequency in Cornwall and in the British Isles overall, may originate from the influence of an earlier 'Celtic' or pre-Celtic substrate in Cornwall, as well as reflect the lower amount of Anglo-Saxon input. This corresponds with the historical data which show that in most parts of Cornwall the Anglo-Saxon invasion consisted of only small numbers, leaving the native population substantially unchanged. This is in direct contrast to the Anglo-Saxon settlement of Devon and other parts of England where the linguistic and place-name evidence shows a substantial number of Anglo-Saxon settlers from at least the 7th century.

This interpretation matches with that of the European autosomal contributions made to the Devon and Cornwall autosomal clusters in the PoBI study (Leslie et al., 2015) which suggest that the Devon component is mostly from Denmark and Germany, which was interpreted to

reflect Anglo-Saxon migration. Cornwall was suggested to be mainly comprised of autosomal contributions from France, interpreted as input from post-Ice-Age migrants. This is consistent with the archaeological evidence which indicates two routes of settlement into Britain after the last Ice Age: one by land from Germany and Belgium, the region that once connected Britain to the Continent, and the other via sea from France, the area which has the highest genetic contributions into all the western British clusters (Cornwall, the three Welsh clusters, and the Northern Ireland/western Scotland cluster). This pattern of contact then continued and was magnified by migrations and influences from these same areas: 6,000 years of interaction with the Atlantic Sea Zone countries in western England, and later, Anglo-Saxon influence in eastern England.

The genetic evidence presented in this thesis, and the PoBI autosomal cluster findings, support the idea of Cornish distinctiveness. But while the results of the PoBI study are clear in as much as Cornwall and Devon are dominated by distinct clusters that are well separated in the cluster dendrogram (figure 2.5), the geographical position of the boundary between the two on the map is more open to doubt. Individual genomes are placed as a cluster-specific symbol on a point representing the centroid of the birthplace of the DNA donor's four grandparents. Aside from any uncertainty about these birthplaces, the centroid cannot be considered as a 'real' place- it just an average of four locations. Furthermore, examination of the birthplaces of the great-grandparents and ancestors even further back are likely to change the degree of indigeneity attached to an individual donor. The PoBI study authors chose Bodmin Moor and the River Tamar as candidate barriers responsible for the differentiation between the Cornwall and Devon clusters, but in reality the position of any such barrier cannot reliably be deduced from the study's own results- it could just as easily lie further east or further west.

In fact, both the Y chromosome and surname evidence from this study suggest that the source of this difference does lie further west of Bodmin Moor. As shown by the PoBI map (figure 2.6), the birthplaces of the volunteers' grandparents are mainly in mid- or west Cornwall, as opposed to east Cornwall where this study's Bodmin Moor dataset is located.

This implies that it is mid- and west Cornwall that are different, while east Cornwall (Bodmin Moor) is closer genetically to Devon than to the rest of Cornwall. In addition, the authors of the PoBI study mention in their supplementary materials that when the dataset is increased to 23 clusters, another distinct cluster appears at the western tip of Cornwall, also suggesting that this area is where a key difference lies.

The westerly shift of the boundary suggested by this study could be explained by Padel's (2009) hypothesis that until 1200AD, Wales, western Brittany, and much of Cornwall were effectively a single cultural and linguistic region, separate from that of the rest of England and east Cornwall as well, where the English language had been spoken from the beginning of the 12th century. Cooper's (2003) stance is that by the 16th century (and certainly much earlier, with respect to the timeframe of Anglo-Saxon migration), there was more to connect east Cornwall with Devon than with west Cornwall: their political and popular culture was the same, the tanners of the region shared a common identity which obscured any ethnic rivalries, and the Stannary laws created a strong link between the two regions. Meanwhile, west Cornwall had a different identity: it was more Celtic in language, in its method of assigning surnames, and in its retention of Cornish rather than English culture. Cooper (2003) notes that at this time Cornwall's different language, customs, and culture were acknowledged by both foreign and English travellers, while Griffiths (2003) concludes that Cornwall was still very much a county with a distinctive identity even into the late Middle Ages. Carew (1953, p.151) also observed that in the 16th century, in the "uttermost skirts of the shire"- meaning the remote areas west of the capital Truro- there were pockets of land that were isolated from the rest of the county, where the Cornish language remained and the people still clung to a Celtic rather than English identity. As late as the 18th century, Cornish was still spoken in the west, and in the 1980s, the dialect of east Cornwall was still more similar to that of Devon and western Somerset, as opposed to that of mid- and west Cornwall (Trudgill 1984). So, rather than seeing Bodmin Moor or the Tamar River as the cultural or physical dividing line between England and Cornwall, there appears to be a more westerly, presumably non-physical, boundary that has allowed part of Cornwall to remain a Celtic, or less "English," society- its separate language and culture.

Phythian-Adams (1993) identifies Devon and Cornwall as a 'cultural province' – a single cultural and political region which he defines as a section of country which share the same settlement patterns, farming, society, and culture. In addition, he states that they shared the same foreign outlook, to the south British sea, where much of their culture, material goods, and immigrants come from. As discussed in Chapter 1, Cunliffe (2012) agrees that Cornwall and all of the southwest peninsula's navigable waterways look outwards to the Atlantic Sea Zone countries which have been a major influence for over 6,000 years. Yet the genetic evidence (Y-STRs) in this study shows that Cornwall is closer to the Atlantic Sea Zone countries- Wales, Ireland, and Brittany- than is Devon. And both the surname and genetic results also imply that Devon and Bodmin Moor are more of a unified 'cultural province' than are Devon and the entirety of Cornwall. This is most likely because Bodmin Moor and Devon are separated from west Cornwall by distance, as well as by their different language and culture.

Along with the language difference, west Cornish distinctiveness could also have arisen from Cornwall's location on a peninsula which opened it up to sea-borne immigration, resulting in different patterns of maritime contact in relation to the rest of England. These trade networks were especially active during medieval times, and at this time, Cornish towns had a higher proportion of foreigners residing in them. This could have contributed to a more diverse, or at least different, genetic composition of the Cornish population. In order to address whether this could be an additional source of the Cornish 'difference' from England, an attempt was made to attribute source populations for the 33 non-R1b haplotypes found in this study; however, no convincing pattern emerged from this analysis, so the genetic data do not give insight into the idea of immigration to west Cornwall contributing to its distinctiveness.

Another factor that could have affected the difference between the west Cornish population and Devon is that there were different levels of incoming migrants into the two counties, as well as the fact that Devon has always been more populated than Cornwall. At the time of the Domesday Book in 1086AD, the population of Devon was estimated to be between 60-80,000 whereas Cornwall was less than 30,000, with most of the population concentrated in

the eastern part of the county, while the west remained sparsely populated - so the effects of genetic drift could have played a part in differentiating Cornwall's smaller, more westerly population from that of east Cornwall and Devon.

Any or all of these factors could have affected the genetics of the western Cornish population. But both the historical and genetic data imply that Bodmin Moor and the River Tamar were not major barriers to migration, as they were not boundaries between Devon and Cornwall for most of their known history. Pre-Roman archaeology shows no difference between Devon and Cornwall, and even during Roman and Anglo-Saxon rule, while the River Tamar and Bodmin Moor may have delayed overland immigration from England, the tribal lands of Dumnonia still stretched across most of the two counties. This only ceased in the 10th century when the Tamar was converted into a political and cultural border and the modern concept of "Cornwall" as a nation was created.

Perhaps the myth of Cornish "isolation" stems from this time: having less contact with the Anglo-Saxons may have resulted in Cornwall being perceived as marginal from the point of view of those in 'mainland' England and created a psychological division between the two areas. Ever since the Anglo-Saxon king Athelstan set the River Tamar as the border between England and Cornwall in 936AD, the river has been perceived as not only the border between two counties, but between 'Anglo-Saxon' Devon and 'Celtic' Cornwall. Borders can have emotional and psychological dimensions which have a strong effect on cultural identity (Tregidga 2012) and can play an even stronger role in keeping populations apart than physical barriers. For example, Phythian-Adams (1987) noted that as recently as 1861 there appeared to be what he considered a psychological barrier to geographic mobility between many adjacent English counties, which he attributes to either physical (geographical features) or cultural frontiers (county boundaries). And while historians Pooley & Turnbull (2005) believe that migration should be viewed as a basic human event, surnames show that most people did not move far from their birthplace and remained mainly within their county boundaries for many generations. Overall, proximity to one's home/neighbourhood appears to be a more important factor than nationality, as the Bodmin Moor data demonstrates.

Psychological boundaries can have an effect in more modern times as well. Some Cornish people have demanded devolution from the UK government, citing their distinct (albeit unused) language and unique cultural history to support their claim (Deacon et al., 2003), along with ancient boundary lines. In 2013, protests were held on both banks of the River Tamar due to a government proposal (Guardian 2013) to create a cross-border constituency between north Cornwall and Devon which would overlap the 1,000-year-old county line. Some residents on the Cornish side of the border felt that this is "England encroaching into Cornish territory," and that it shows a "lack of respect and understanding to Cornwall's cultural, political, and economic distinctiveness." They were also unhappy in the 1960s when a new bridge over the Tamar made transport between the two counties quicker, prompting one man to protest that Anglo-Saxon King Athelstan's 10th-century border means that Cornwall is technically "still part of West Wales" (Guardian 2013). Cornish identity played a major part in people's concern about the joining of constituencies: as one interviewee said "I think it's a great shame. Cornwall is not just any county. It has an identity of its own, a language, a culture." "We should be doing everything we can to preserve that."

While it is clear that Cornwall is anything rather than isolated, it may indeed be different from England. Throughout most of its known history, Cornwall's influences came primarily from overseas, probably because the overland routes from England were so difficult. Therefore it is possible that, although the internal landscape and topography of Cornwall were not a complete barrier, they could have played a part in delaying overland invaders from reaching the inner-most reaches of western Cornwall, thus protecting it from outside influence and preserving the Cornish language and culture. And while this may have led to the reputation of Cornwall being 'set apart' from the rest of England, it also has a long history as a flourishing and multi-cultural society, and is just as involved with the outside world as its neighbours to the east. As for landscape features such as Bodmin Moor, while it may have been seen as a hazardous terrain that deterred invaders from the outside, to the locals it had a different effect: from the tribes of Dumnonia to the medieval-era farmers who relied on it to make a living, the moor was not a marginalised area but a vital part of their culture and livelihood. In fact, rather than being barriers, both Bodmin Moor and the adjacent Tamar River Valley

region connecting Cornwall and Devon can be seen more as integrating areas rather than dividing ones: rather than separating Cornwall from Devon these areas have fostered trade, kinship, and cultural ties across them. The inhabitants of Bodmin Moor relied on interactions with the surrounding environment, towns, and economies of Devon, while the Tamar Valley area links the two counties through a similar landscape, shared employment through the natural resources of the area, and cross-border marriage and migration (Tregidga 2012). Due to these work, cultural, and kinship networks, it would seem that, through the centuries, this borderland region has produced as much unity as separation.

Both Bodmin Moor and Cornwall itself have been seen by outsiders as marginalised, isolated areas, but their reputations do not match their realities: to the people residing in these areas, they are just as involved and integrated with their surroundings as more central or populated regions. The results of this study are likely to contribute to the debate regarding Cornwall's 'separateness' as a distinct region from the rest of England, and to reignite discussion of the PoBI findings. The actual genetic difference between the two areas is low in comparison to other human populations, but even so, genetics has little to do with the cultural aspects that underlie Cornish identity, or lack of it. For every Cornishman who believes that England begins at the Tamar, there is another who shares the resources, opportunities, and connections the area offers to the lands to the east. As Fleure (1923, p.105) noted in his 1923 *Races of England and Wales*, "the distinction between English and Welsh or Cornish is hardly a racial one": "we are all mosaics of inheritance."

7.2 Limitations of this study and future work

This study used Y-chromosome analysis, an approach that has been popular in human genetics studies for many years (Jobling & Tyler-Smith 1995). However, it is important to remember that the male-specific region of the Y chromosome is a single genetic locus with a single evolutionary history and so it provides a limited picture of the past. It is susceptible to genetic drift, which could be responsible for some of the differences between populations observed in this study.

Although this study used Y-STRs, which are free of ascertainment bias, specific Y-SNPs were also chosen for typing, and this reintroduces such bias. Ideally, it would be better to determine Y-chromosome sequences, which has been done in a number of studies (Jobling & Tyler-Smith 2017). In order to address this, a project was begun as part of this thesis to collect many 10-Mb 'BigY' sequences from male volunteers from southwest England, focusing on Cornwall and Devon, who had undergone direct-to-consumer DNA testing from the companies FamilyTreeDNA and Full Genomes Corporation. Time was not available to include and analyse these data, but eventually they should provide an unbiased picture of the histories of lineages, and also allow dating of branch points in a highly resolved tree.

The sample sizes in this study were limited by the difficulty of finding volunteers from Bodmin Moor with the appropriate criteria, such as local paternal ancestry and surnames. Although the tests undertaken account for sample size, nonetheless larger and better-defined samples would be desirable. A primary flaw in the methods was assuming that the birthplace of the paternal grandfather was the same birthplace as that of any earlier paternal grandfathers- it turned out that many of the earlier paternal ancestors were from parishes outside the region. In addition, surnames were not a viable model for sampling the deep ancestry of the Bodmin Moor area- considering its history, the Bodmin Moor region turned out to not be an isolated area as first hypothesized. A more robust method for surveying local names would have been to focus on agricultural parishes rather than mining parishes, because it is likely that farming areas are generally made up of more local families who remained tied to the land for many generations (Guppy 1890).

Considering that the Cornish samples were most closely related to Wales, Ireland, and Brittany, it would be useful to do more comparisons with those populations. However, there is a lack of available Brittany data, but analysis of ancient DNA on burials in the Atlantic Sea Zone would be informative here, as it could show whether Y-chromosome types have shifted substantially through time in the regions studied, and also potentially provide reference DNAs for early Anglo-Saxons, Irish immigrants, or Breton traders, for example. In respect to

the absence of the Irish M-222 marker, sequence-based analysis may provide evidence of an Irish presence and would also help in identifying any specific links with Brittany, where further DNA analysis is also necessary.

Chapter 8 APPENDIX

8.1.1 The 458 exact matches found in both the parish records and the 1881 census

ABRAHAM	CROSS	JONAS	RESCORL
ADAMS	CROWELL, CROWELLS, CROWELS, CROWLE, CROWLS	JONES	RICH
ALLEN	CRUSE	JORDAN	RICHARD, RICHARDS
ANDREW, ANDREWS	CULLIS	JORY, JURY	RICKARD
ANGOVE, ANDGOVE	CURTIS	JOSE	RIDDLE
ARTHUR	DANIEL, DANIELS	JULIAN	ROBERTS
ASH	DAVEY, DAVY	KALLOW, KELLOW	ROBINS
AUGER	DAVIS	KEAST	RODD, RODDA
AUNGER	DAW, DAWE	KEAT	ROGERS
AXFORD	DEACON	KELLY	ROOSE, RUSE
AXWORTHY	DENNIS, DINNES	KEMP, KEMPE	ROSE, ROWSE
AYRES, EYRE	DINGLE	KENDALL	ROSEVEAR, ROSEVEARE
BALE	DINGLEY	KENT	ROW, ROWE
BALL	DOBB	KERNICK	RUBY
BARBER	DODGE, DOEDGE, DOIDGE	KINGDOM	RUNDALL, RUNDLE
BARNARD	DONEY, DONY	KINGDON	RUNNALLS, RUNNALS, RUNNELLS, RUNNELS
BARNECCUT, etc	DOWN	KITT	SALTERN
BARRET, BARRETT	DOWNING	KITTO, KITTOW	SAMBELLS
BARRIBAL, BARRIBALL	DRAKE	KNIGHT	SANDERCOCK, SAUNDERCOCK
BARTLETT	DRAYDON	LANDER	SANDERS, SAUNDERS
BASSETT	DUANCE, DUENCE, DUENS	LANDREY, LANDRY, LAUNDREY, LAUNDRY	SANDY
BASTARD	DUNN	LANE	SARGENT, SERJEANT
BATE	DUNSTAN	LANG	SCANTLEBURY
BATH	EAD, EDE	LANGDON	SCOTT
BATTEN, BATTON	EDWARDS	LANGFORD, LANGSFORD	SEARL, SEARLE
BAWDEN, BOWDEN	ELFORD	LANGMAID	SEYMOUR
BEER	ELIOTT, ELLIOTT	LANGSON, LANXON, LANSON	SHEAR, SHEARS, SHEER
BENNET, BENNETT, BENNE TTS	ELLICOTT	LARK	SHILLABER
BENNY	EVA	LAURANCE, LAWRENCE	SHORT
BERDINNER	EVANS	LAWREY, LAWRY, LOWREY	SHOVEL, SHOVELL
BERNARD	FARLEY	LEA, LEE, LEY	SIBLY
BEST	FERRIT, FERRITT	LEACH	SIMMENS, SYMONS
BESWARRICK, BESWERICK, BESWETHERICK	FOOT	LEAN	SKINNER, SCINER
BETTES	FORD	LEMIN	SLEEMAN, SLEMAN, SLIMAN
BICKFORD	FRENCH	LEWARNE	SLEEP, SLEAP
BILLING	FROST	LIBBY	SLOGGATT, SLOGGETT

BINNEY	FRY	LIGHT	SMALE, SMELE
BLAKE	FUDGE, FUGE	LOBB	SMETHERAM, SMITHERHAM
BLAMEY	GABREL, GABRIEL, GABRIL, GABRILL	LORD	SMITH, SMEETH
BLATCHFORD, Blichford	GARLAND	LUCAS	SNELL
BLEWETT, BLUETT	GEAKE	LYNE	SOWDEN
BLIGHT, BLOYE, BLYTH, BLYTHE	GEORGE	MACKIE	SPARE, SPEAR
BOND	GILBERT	MAGOR, MAKER, MEAGOR	SPARK, SPARKS
BONE	GILES	MALLET, MALLETT, MALLOTT	SPRY
BONEY	GILL	MANATON	STACEY
BONNAY, BONNEY, BUNNEY	GOODMAN	MANLEY	STANTAN, STANTON
BORROW	GOYENS, GOYINS	MARES	STEPHEN, STEPHENS, STEVENS
BOUNDAY, BOUNDY	GREEN	MARKS	STRIKE
BOWHAY	GREENWOOD	MARSHALL	STROUT
BRADFORD	GREET	MARTAIN, MARTEN, MARTIN, MARTYN	STURTRIDGE
BRAUND, BROAN	GREGORY	MASTERS	SWEET, SWEETT
BRAY	GRIGG	MATHEWS, MATTHEWS	TAMBLIN, TAMBLING, TAMBLYN, TAMLIN
BRENT	GROSE	MAUNDER, MONDER, MOUNDER	TAPRILL
BROAD	GRYLLS	MAY	TAYLOR
BROOKS	GUMB, GUMBE	MAYNE, MEYN	TERNOUTH, TRENOUTH
BROWN	GUNDRY	MELDERN, MILDREN	THOMAS
BRYANT	GYNN	MENHENICK, MENHENIOT	TINK
BUCKINGHAM, BUCKINHAM	HALLS	MICHELL, MITCHEL, MITCHELL	TOM, TOMS
BUCKLER	HAM	MINERS	TOOKER, TUCKER
BUDGE	HAMBLY, HAMBY, HAMLEY, HANLEY	MOYSE	TRAYES, TRAYS, TREAS, TREISE
BULLER	HAMMETT	MULLIS	TREGLOIN, TREGLOYNE
BULLOCK	HANCOCK, HANDCOCK	MUTTON	TREHANE
BUNT	HANN	NAIL, NILE, NILES	TRELEAVEN
BURNAFORD	HARFOOT	NATTLE, NOTTLE	TREHEWAY, TREHEWEY
BURNARD	HARPER	NICHOLAS, NICHOLLS, NICHOLS, NICOLLS, NICOOLS	TREVAIN, TREVAINS
BURNETT	HARRIS, HARRISS	NORTHCOTT	TREVATHAN
BURROWS	HARRY	NORTHEY, NORTHY	TREWEEK
BURT	HARVEY	ODGERS	TREWIN
BUTTON	HATCH	OKE	TRUSCOTT, TRUSTCOTT
CAUNTER	HAWK, HAWKE	OLIVER, OLLIVER	TURNER
CAWRSE	HAWKEN, HAWKIN, HAWKING, HAWKINS, HOCKING	OLPHERT	UREN
CHAMPIAN, CHAMPION	HAWKEY	OLVER	VEAL, VEALE, VEALL, VIAL
CHAPMAN	HAYNE	OUGH	VENNING
CHEESEWORTH, CHEESWORTH	HENDER, HENDRA	PALMER	VERRAN
CHUB, CHUBB	HENWOOD	PARKYN	VINCENT
CLEMANCE, CLEMENS, CLEMENTS	HERD, HEARD	PARNALL, PARNELL	VINE
CLEMING, CLEMINGS	HERRING	PARSON, PARSONS, PEARSON	VIVIAN

CLEMO, CLEMOW, CLYMO	HEYDON	PASCOE	WADGE, WEDGE
CLIFFE	HICK, HICKS	PAUL	WALKEY
COAD, COODE	HIGGS	PAULLEY	WALLIS, WALLACE
COBBLEDICK	HILL	PEARCE, PEARSE	WALSH, WELCH, WELSH
COCK, COCKS	HINGSTON	PEARN, PEARNE	WALTERS
COCKING	HOAR, HOARE, HORE	PEEK	WARD
COLE, COLES	HOBBS	PENBERTH	WARN, WARNE, WARREN, WARRING, WERREN, WERRIN
COLEMAN, COLMAN	HODGE	PENGELLEY, PENGELLY	WARRICK
COLLINGS, COLLINS	HOLMAN	PENNEY, PENNY	WATTS
COLMER	HONEY	PERKIN	WEARRY, WEARY, WHERRY
COLVILL, COLWILL	HONEYCOMBE	PERRY	WEBB
COMMINS, COMMONS	HOOPER	PETER, PETERS	WEBBER
CONDY, CUNDY, CUNDAY	HORNABROOK	PETHICK	WEEKS
CONGDON	HORRELL, HURRUL	PETT	WEST
COOK	HOSKEN, HOSKIN, HOSKING, HOSKINS	PHILIPPS, PHILLIPS, PHILLPS, PHILP	WESTLAKE
COOMBE, COOMBS, CUMBE	HURDON	PINCH	WHALE, WHELL
COPPIN	HUSBAND	POLARD, POLLARD	WHEELER, WEALER
CORNELIUS	HUTCHINGS	POLGLASE	WHITE
CORNISH	INCH	POLMEER	WHITEING, WHITTING
CORNOW	ISAAC	POMEROY, POMERY	WICKET, WICKETT
CORY, COREY	JAGO	POOLEY, POOLY	WILLCOCK, WILLCOCKS
COUCH	JAMES	POPELSTONE, POPPLESTONE	WILLIAMS, WILLYAMS
COURTIS	JANE	POTE	WILLS, WILCE
COURTS	JASPAR, JASPER, JESPER	PRIDEAUX	WILTON
COWLIN, COWLING	JAY	PROUT	WISE
COWLS	JEFFERY, JEFFRY	PRYNN	WOLRIDGE, WOOLDRIDGE
CRABB	JENKIN, JENKING, JENKINS	PRYOR	WOOD
CRADDOCK	JEWALS, JEWEL, JEWELL, JEWELLS, JEWELS, JOWEL	RAWLING, ROWLING	WOOLCOCK
CRAGO	JOHN, JOHNS	READ, REED	WORDEN
CRAPP	JOLL	REMFRY	WORTH
CREEPER	JOLLIFFE, JULIEFF	RENALS, RENNALS, REYNOLDS	YEO, YEWEE

8.1.2 The 63 names with spelling variations between the parish records and the 1881 census

Parish records spelling	1881 census spelling	Parish records spelling	1881 census spelling
AIR, ARE	AYRES, EYRE	LYTE	LIGHT
BALLAMY, BELLAMY	BLAMEY	MACEY, MACKIE	MACY
BARABEL, BARIBALL, BARRIBALL	BARRIBAL	MANLY	MANLEY
BARNACOT, BARNACOTT, BARNICOAT	BARNECCUT, BARNECUT, BARNECUTT, BARNICOATT, BARNICUT, BARNICUTT	MARE	MARES
BEDIMER, BEDINNER	BERDINNER	MAYN, MAIN, MEYN	MAYNE
BESWATHICK	BESWARRICK, BESWERICK, BESWETHERICK	MEAGER, MEAGRE	MEAGOR
BECFOR, BECKFORD	BICKFORD	MENHENIT, MENHENITT, MENHENNET, MENHENNETT, MENHENNIET, MENHENNIT, MENHINNET, MENHINNETT, MENHINNIOT, MENHINNIT, MENHINUTE, MINHINET, MINHINNET MINHINNETT, MINHINNIT	MENHENICK, MENHENIOT
BONNY	BONNAY, BONNEY	MOYES	MOYSE
BRAND	BRAUND, BROAN	NORTHCOAT, NORTHCOTE	NORTHCOTT
BUNNY	BUNNEY	OAK	OKE
BURROW	BURROWS	OLDFER	OLPHERT
CAUCE, CAWSE, CAUSE, CORSE	CAWRSE	PARKIN	PARKYN
CHEESSWORT	CHEESEWORTH, CHEESWORTH	PASCHO	PASCOE
CLEMENCE	CLEMANCE	PAULY, PAWLEY, PAWLY	PAULLEY
CLIFT	CLIFFE	PEAK, PEAKE	PEEK
COMMON	COMMINS, COMMONS	PENBERTHIE	PENBERTH
COWL	COWLS	PERKINS	PERKIN
CRADOCK	CRADDOCK	RENFREE	REMFRY
CROWL	CROWELL, CROWELL, CROWELS, CROWLE, CROWLS	RESCAUL, RESCORLA	RESCORL
CURNOW	CORNOW	ROBBINS	ROBINS
DAVIES	DAVIS	ROUS, ROUSE	ROWSE
DOWIDGE	DODGE, DOEDGE, DOIDGE	SALTREN, SALTERN	SALTURNE
DRAYDEN, DREADEN, DREADON, DREYDON	DRAYDON	SAMBELS	SAMBELLS
DUINS	DUANCE, DUENCE, DUENS	SHELIVER, SHELLAPER, SHELLEBAR, SHELLEVAR SHULLIVER	SHILLABER
DUNSTONE	DUNSTAN	SLYMAN	SLEEMAN, SLEMAN, SLIMAN
EADE, EADS	EAD	SMITHERAM	SMETHERAM, SMITHERHAM
GOYN, GOYNE, GOYNS, GOIN, GOINE, GOING	GOYENS, GOYINS	SMALEY	SMALE, SMELE
HANNE	HANN	TRETHEWY	TRETHEWAY, TRETHEWEY
JULEFF	JOLLIFFE, JULIEFF	TREVAYNES, TREVEANS	TREVAIN, TREVAINS
JULIANS	JULIAN	TREVETON	TREVATHAN
LEWARN	LEWARNE	URIN, URYN	UREN
LONGMAID	LANGMAID		

8.1.3 Top 100 names found in Bodmin Moor in 1881 and their frequencies

SURNAME	total number of name in parishes	Total number of name nationwide	parish %
TAPRILL	5	5	100%
CAWRSE	47	56	84%
GOYENS, GOYINS	10	12	83%
TREGLOIN, TREGLOYNE	8	13	62%
SHILLABER	12	22	55%
BERDINNER	7	13	54%
SMETHERAM, SMITHERHAM	13	29	45%
SHOVEL, SHOVELL	27	64	42%
FERRIT, FERRITT	6	16	38%
BARNECCUT, etc	25	68	37%
DUANCE, DUENCE, DUENS	11	31	35%
TREVAIN, TREVAINS	7	20	35%
CLEMING, CLEMINGS	5	16	31%
TREHANE	14	49	29%
BURNAFORD	6	22	27%
DONEY, DONY	163	610	27%
RUNNALLS, RUNNALS, RUNNELLS, RUNNELS	70	279	25%
NATTLE, NOTTLE	32	131	24%
POLMEER	3	13	23%
HONEYCOMBE	12	53	23%
CREEPER	12	65	18%
GUMB, GUMBE	7	42	17%
SALTERN	17	102	17%
WEARRY, WEARY, WHERRY	53	323	16%
CHEESEWORTH, CHEESWORTH	9	57	16%
CORNOW	2	13	15%
CRAPP	44	291	15%
HORNABROOK	6	41	15%
CRAGO	41	287	14%
SAMBELLS	11	80	14%
GYNN	17	127	13%
POTE	18	135	13%
HARFOOT	11	84	13%
TINK	13	101	13%
SLEEP, SLEAP	79	644	12%
LANDREY, LANDRY, LAUNDREY, LAUNDRY	27	235	11%
BUNT	59	521	11%
CROWELL, CROWELLS, CROWELS, CROWLE, CROWLS	41	365	11%
HURDON	3	28	11%
JASPAR, JASPER, JESPER	106	1050	10%

BESWARRICK, BESWERICK, BESWETHERICK	13	130	10%
PENBERTH	1	10	10%
AUNGER	7	72	10%
TREVATHAN	2	21	10%
COLMER	32	338	9%
STROUT	7	76	9%
PETHICK	39	427	9%
KEAST	78	870	9%
SANDERCOCK, SAUNDERCOCK	51	593	9%
BETTES	3	35	9%
JANE	73	862	8%
SIBLY	11	131	8%
COWLS	6	73	8%
VENNING	40	490	8%
DRAYDON	2	25	8%
BOUNDAY, BOUNDY	40	538	7%
BURNARD	36	502	7%
RESCORL	2	28	7%
LANGSON, LANXON, LANSON	9	129	7%
COURTS	20	289	7%
JOLL	10	149	7%
STRIKE	32	482	7%
AXWORTHY	14	214	7%
TRAYES, TRAYS, TREAS, TREISE	8	127	6%
NORTHEY, NORTHY	50	816	6%
REMFRY	3	49	6%
PEARN, PEARNE	31	513	6%
MANATON	6	100	6%
OLPHERT	2	34	6%
CONGDON	34	579	6%
TERNOUTH, TRENOUTH	7	120	6%
KEAT	15	271	6%
SLEEMAN, SLEMAN, SLIMAN	55	1032	5%
HAWK, HAWKE	95	1824	5%
VERRAN	9	178	5%
COUCH	87	1767	5%
MOYSE	34	694	5%
TRETHERWAY, TRETHERWEY	24	522	5%
MENHENICK, MENHENIOT	3	66	5%
GRYLLS	6	134	4%
LOBB	63	1472	4%
COPPIN	40	944	4%
HENDER, HENDRA	20	484	4%

HAYNE	29	721	4%
SLOGGATT, SLOGGETT	11	279	4%
MELDERN, MILDREN	7	178	4%
MUTTON	43	1108	4%
WADGE, WEDGE	44	1159	4%
BONEY	4	106	4%
WILTON	106	2839	4%
POLGLASE	9	242	4%
CLEMO, CLEMOW, CLYMO	18	489	4%
COAD, COODE	27	735	4%
BORROW	10	275	4%
RUBY	9	252	4%
TAMBLIN, TAMBLING, TAMBLYN, TAMLINE	21	594	4%
KITTO, KITTOW	19	560	3%
PARKYN	12	363	3%
BUDGE	29	881	3%

8.1.4 The 225 recruited surnames as listed on website

• Adams	• Allen	• Aunger	• Axworthy	• Barnecut
• Barret	• Barribal	• Bate	• Bawden	• Bennet
• Benney	• Berdinner	• Best	• Beswarrick, Beswerick	• Beswetherick
• Bettes	• Billing	• Bligh	• Bone	• Boney
• Borrow	• Bounday, Boundy	• Bray	• Broad	• Brown
• Buckler	• Budge	• Bunt	• Burnaford	• Burnard
• Caunter	• Cawrse	• Chapman	• Cheeseworth, Cheesworth	• Cleming, Clemings
• Clemo, Clemow, Clymo	• Coad, Coode	• Cock	• Cole	• Colling
• Colmer	• Congdon	• Coomb, Coombe	• Coppin	• Cornish
• Cornow	• Couch	• Courts, Courtes, Courtis, Cortis	• Cowling	• Cows
• Crabb	• Crago	• Crapp	• Creeper	• Crowell, Crowells, Crowels, Crowle, Crows
• Davy	• Dawe	• Deacon	• Dingle	• Dingley
• Doney, Dony	• Draydon	• Duance, Duence, Duens	• Elicot	• Elliott
• Even	• Ferritt	• Foote	• French	• Frost
• Fuidge	• Garland	• Geach	• Gill	• Goyens, Goyins
• Grylls	• Gumb, Gumbe	• Gynn	• Ham	• Hambley
• Hancocke	• Harfoot	• Harris	• Harvy	• Hatch
• Hawk, Hawke	• Hawken	• Hawkey	• Hayne	• Hender, Hendra
• Henwood	• Hicks	• Hill	• Hodge	• Honeycombe
• Hooper	• Hornabrook	• Hosken	• Hurdon	• Husband
• Isack	• Jane	• Jaspas, Jasper, Jesper	• Jeffery	• Jenkin
• Jewell	• John	• Joll	• Jory	• Keast
• Keat	• Kellow	• Kempe	• Kernicke	• Kitt
• Kitto, Kittow	• Knight	• Landrey, Landry, Laundry, Laundry	• Lang	• Langdon
• Langson, Lanxon, Lanson	• Lean	• Libby	• Lobb	• Lucas
• Lyne	• Manaton	• Marten	• Masters	• Mathew
• May	• Meldern, Mildren	• Menhenick, Menheniot	• Michell	• Moyse
• Mutton	• Nattle, Nottle	• Nichols	• Niles	• Northey, Northy
• Oliver, Olver, Olphert	• Parkin	• Parnall	• Paull	• Pawley
• Pearce	• Pearn, Pearne	• Penberth	• Penny	• Pethick
• Pett	• Philipps, Philp	• Polglase	• Polmeer	• Pomeroy
• Popplestone	• Pote	• Rawling	• Reed	• Remfry
• Rescorl	• Richards	• Rickard	• Roberts	• Robyns
• Rogers	• Roose	• Row	• Ruby	• Rundall, Rundle
• Runnalls, Runnells	• Saltern	• Sambells	• Sandercock, Saundercock	• Scott
• Sheer	• Shillaber	• Short	• Shovell	• Sibly
• Simons	• Skinnerd	• Sleeman, Sleman, Sliman	• Sleep, Sleap	• Sloggatt, Sloggett
• Smaley	• Smetheram, Smitherham	• Snell	• Speare	• Sprye
• Stanton	• Stephens	• Streeke, Strike	• Strout	• Sturtridge
• Sweet	• Tamblin, Tambling, Tamblyn, Tamline	• Taprill	• Taylor	• Ternouth, Trenouth
• Thomas	• Tink	• Tom	• Trayes, Trays, Treas, Treise	• Tregloin, Tregloyne
• Trehane	• Tretheway, Trethewey	• Trevain, Trevains	• Trevathan	• Truscott
• Venning	• Verran	• Vincent	• Vine	• Wadge, Wedge
• Walkey	• Warren	• Weary, Weary, Wherry	• Webb	• Whale
• White	• Wilcock	• Williams	• Wills	• Wilton



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Bodmin Moor - a cultural and genetic study

Researchers: Ms Jodie Lampert (email: jel27@le.ac.uk);
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Dr Richard Jones (School of History)

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Thank you for your interest in this research project. This information sheet provides an overview of the purpose of the research and details of what participation involves.

What is the purpose of this study?

Cornwall is a part of England whose location and landscape features may have contributed to its physical and cultural isolation from the rest of the country. It was originally home to the first inhabitants of Britain and due to the difficulty of accessing parts of the Southwest peninsula, may have experienced less occupation by invading groups into England, such as the Romans, the Anglo-Saxons, the Vikings, and the Normans. New techniques in DNA analysis have recently uncovered subtle genetic differences between the people of Cornwall and their neighbours in Devon. This study aims to follow up on these results by asking if the male Y-chromosome diversity also reflects these differences. We will look specifically at Bodmin Moor, a part of Cornwall that exhibits landscape features that may have isolated the communities surrounding it from each other or from the rest of Cornwall, and England.

Whilst there are no immediate benefits for those people participating in the project, it is hoped that this work will contribute to our understanding of the genetic makeup of Britain and the cultural history that underlies it, and also to illuminate the history of different parts of Cornwall and their genetic relationships to each other.

What does participation involve?

You will swab the inside of your mouth, using a brush supplied by us – full instructions are provided. You will also be asked to complete a consent form and a short questionnaire asking a few questions about your place of birth and your ancestry. From your saliva sample we will extract DNA and determine DNA profiles for your Y chromosome and possibly other parts of your genome. Both your DNA sample and the resulting data will be retained anonymously, and may be used in future studies by us, or by other scientists following publication.

Are there any risks to taking part?

No.

Will information obtained in the study be confidential?

The information you give us will be strictly confidential. Your sample and any resulting data will be referred to only by an ID number, so if information we gain about your DNA is published in scientific papers it will not be possible for any third party to identify you as the DNA donor. Information connecting you with the DNA extracted from your donated sample will be kept secure, and available only to the principal investigators.

How will the samples be used?

Samples collected from participants will be used for the following purposes:

- Extraction and storage of DNA





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Bodmin Moor - a cultural and genetic study

Researchers: Ms Jodie Lampert, and Prof Mark Jobling (Dept of Genetics); Dr Richard Jones (School of History)

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Participant questionnaire

Please help us by providing the following information:

	Place of birth (parish and county)	Surname
Me		
My father		
My mother		
My father's father		
My father's mother		
My mother's father		
My mother's mother		
Any further relevant ancestry information (write here or attach)		

Name of participant

Date

Signature



8.1.5 ABI run module settings- PPY23

Both analyses were done on a 36 cm capillary with POP7 polymer.

Name: PPY23_Fragment analysis36_POP7

Type: Regular

Template: Fragment analysis36_POP7

Name	Value	Range
Oven temperature	60	18...65 Deg. C
Poly Fill Vol	6500	6500...38000 steps
Current stability	5.0	0...2000 μ Amps
Pre Run voltage	15.0	0...15 kVolts
Pre Run time	180	1...1000 sec.
Injection voltage	1.2	1...15 kVolts
Injection time	23	1...600 sec.
Voltage number of steps	20	1...100 nk
Voltage step interval	15	1...60 sec.
Data delay time	60	1...3600 sec.
Run voltage	15.0	0...15 kVolts
Run time	1200	300...14000 sec.

8.1.6 ABI run module settings- SNaPshot

Name: Fragment analysis36_POP7_1

Type: Regular

Template: Fragment analysis36_POP7

Name	Value	Range
Oven temperature	60	18...65 Deg. C
Poly Fill Vol	6500	6500...38000 steps
Current stability	5.0	0...2000 μ Amps
Pre Run voltage	15.0	0...15 kVolts
Pre Run time	180	1...1000 sec.
Injection voltage	1.2	1...15 kVolts
Injection time	23	1...600 sec.
Voltage number of steps	20	1...100 nk
Voltage step interval	15	1...60 sec.
Data delay time	60	1...3600 sec.
run voltage	15.0	0...15 kVolts
Run time	1200	300...14000 sec.

8.1.7 GeneMapper 4.0 panel settings for POP7

PPY23- analysis method: all factory defaults were used, including bin settings

SNaPshot- analysis method: factory defaults were used. Bin settings are as follows:

SNP	Bin name	Bin min. (bp)	Bin max. (bp)	Bin colour
U106	0	30.5	32.7	blue
	1	32.0	33.7	green
U152	0	33.5	36.49	yellow
	1	35.5	38.49	red
U198	0	36.5	39.5	yellow
	1	38.5	39.5	red
M269	0	44.9	45.1	red
	1	46.8	47.2	yellow
S145	0	47.96	50.34	yellow
	1	48.14	52.39	blue
M222	0	54.0	58.27	yellow
	1	54.58	58.3	red
S116	0	67.7	69.2	blue
	1	69.2	70.1	red
L11	1	78.0	79.7	blue
	0	78.7	80.2	green
Z253	0	83.5	85.5	yellow
	1	83.5	85.5	red

8.1.8 PPY23 haplotypes

	DYS 19	DYS 389 I	DYS 389 II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 385a	DYS 385b	DYS 437	DYS 438	DYS 439	DYS 448	DYS 456	DYS 458	DYS 635	Y GATA H	DYS 481	DYS 533	DYS 549	DYS 570	DYS 576	DYS 643
BM1	14	13	16	24	10	13	13	11	14	15	12	12	19	15	18	23	12	22	14	13	17	19	10
BM10	14	13	16	24	10	13	13	11	14	15	12	12	17	15	19	*	12	21	12	12	16	19	10
BM11	15	13	17	23	11	13	13	12	14	15	12	12	19	16	17	23	12	22	12	13	17	18	10
BM12	13	12	16	22	10	11	13	13	13	15	10	12	20	14	16	23	11	26	11	12	21	17	12
BM14	13	13	16	24	11	13	13	11	14	15	12	12	19	15	18	23	13	23	12	13	17	18	10
BM15	14	13	16	24	10	13	13	11	15	15	13	13	19	16	18	23	12	23	12	11	17	17	9
BM16	14	13	16	24	11	13	13	12	14	15	12	12	19	15	17	23	12	22	12	13	17	16	10
BM17	16	13	16	22	10	12	14	15	15	16	8	11	20	17	15	21	11	26	13	13	19	18	13
BM18	14	12	16	24	11	15	13	11	14	15	12	11	19	15	16	24	12	22	12	15	16	18	10
BM2	14	12	17	24	11	13	13	11	14	15	12	12	19	16	19	23	13	25	14	13	18	18	10
BM21	14	13	16	25	10	13	13	11	14	15	12	12	19	15	16	23	12	23	13	12	18	17	10
BM22	14	13	17	23	10	13	13	11	14	14	12	13	19	17	19	24	12	22	12	12	17	18	*
BM23	14	13	16	23	10	13	13	12	13	15	12	12	19	15	17	24	12	22	12	13	17	18	10
BM24	14	14	16	23	12	13	13	11	14	15	12	12	19	15	18	23	11	22	12	14	16	18	10
BM3	14	13	16	24	11	13	13	11	15	14	12	11	18	15	17	23	12	22	12	13	17	17	10
BM31	14	13	16	24	10	13	13	10	14	15	12	11	19	16	13	23	12	22	12	14	17	18	10
BM32	14	14	16	23	11	13	13	11	15	15	12	12	19	17	16	23	12	22	12	12	17	18	11
BM33	15	12	16	22	10	11	13	14	14	16	10	10	20	14	14	21	11	25	11	12	19	16	12
BM34	15	14	17	24	10	13	13	11	15	15	12	13	19	17	18	23	11	22	12	13	18	17	9
BM35	16	13	16	23	11	13	13	11	14	15	12	11	18	16	18	24	12	22	12	12	17	18	10
BM36	14	13	16	24	11	13	12	11	14	16	12	13	19	15	16	23	12	23	12	12	18	19	11
BM37	14	12	16	24	11	13	13	11	13	15	12	11	19	16	18	23	12	22	12	14	17	17	10
BM4	14	13	16	24	11	13	14	11	14	15	12	12	19	15	18	23	12	23	12	13	18	17	10
BM40	14	13	16	23	11	13	13	11	14	14	13	12	19	17	16	23	11	21	12	13	18	17	10
BM41	15	12	16	23	10	13	13	11	14	16	12	12	19	16	18	23	12	22	11	13	21	16	10
BM42	14	13	16	24	11	13	13	11	14	15	12	12	18	16	17	23	12	22	12	13	17	19	11
BM43	14	14	16	23	11	13	13	11	14	16	12	12	19	17	17	23	12	22	12	14	17	18	10
BM44	14	13	16	24	11	13	13	10	14	15	12	13	19	16	18	23	12	22	12	13	17	17	10
BM45	15	13	16	23	11	13	13	11	15	15	12	12	19	15	17	25	12	23	12	13	17	17	10
BM46	14	12	16	23	10	11	13	13	14	16	10	11	20	14	16	21	11	25	11	12	21	18	13
BM5	15	13	18	24	10	13	14	11	14	15	12	11	19	16	18	23	12	23	14	12	17	18	10
BM50	15	13	15	25	11	13	14	11	14	15	12	11	19	15	16	23	12	22	12	14	18	17	10
BM51	14	14	16	23	11	13	13	11	15	15	12	11	19	16	17	24	12	23	12	12	18	16	10

BM52	13	14	16	24	11	13	13	11	14	15	12	11	19	16	17	23	11	22	12	12	17	18	10
BM53	15	13	17	23	10	11	14	13	15	16	10	12	20	15	16	21	11	21	9	12	18	16	11
BM54	14	13	16	23	11	13	13	12	14	15	12	11	19	18	19	23	12	22	12	12	17	18	10
BM55	14	13	16	24	10	13	13	12	14	14	12	12	18	15	17	23	11	22	12	12	17	19	10
BM56	15	13	16	24	11	13	13	11	14	14	12	*	19	18	17	23	*	24	13	12	18	18	*
BM57	16	12	16	25	10	11	13	13	17	15	10	11	21	14	18	20	10	23	11	12	18	16	13
BM61	15	13	16	22	10	11	13	13	15	16	10	11	20	14	15	22	*	25	12	13	23	18	12
BM62	14	13	17	24	10	11	13	17	18	14	10	12	20	17	15	22	12	22	12	12	20	17	12
BM7	14	12	16	22	10	12	13	14	15	16	10	11	20	14	15	21	11	25	12	13	22	17	12
BM71	13	12	18	24	10	10	13	16	17	14	10	11	20	16	19	21	9	26	10	11	21	20	12
BM72	15	14	16	24	10	11	14	16	16	15	10	12	20	14	17	21	12	26	12	11	18	17	14
BM73	14	13	16	25	11	13	13	11	14	15	12	11	19	17	17	23	12	22	12	13	16	17	10
BM8	14	13	16	24	11	13	12	14	14	15	12	14	19	15	17	23	12	23	12	12	18	18	10
BM9	14	13	16	23	11	13	13	10	14	15	12	12	19	15	19	23	12	22	13	14	18	19	10
COR005	14	13	17	24	10	13	14	11	14	15	12	11	19	15	18	23	12	22	12	13	17	17	10
COR012	14	12	16	23	11	13	14	11	13	15	12	12	18	17	17	23	12	22	13	12	17	18	10
COR 017	14	13	16	25	11	13	13	11	15	15	12	11	19	15	16	23	12	23	14	13	17	17	10
COR019	16	13	17	25	10	11	13	11	14	14	11	11	20	15	15	23	12	22	12	11	19	19	10
COR025	14	14	16	23	10	13	13	11	15	15	12	12	19	15	16	23	12	22	12	13	17	17	11
COR035	15	12	17	22	10	11	13	13	15	16	10	11	20	13	15	22	10	24	11	9	17	16	12
COR038	14	13	16	24	11	13	13	11	13	15	13	12	19	16	16	23	11	22	12	13	17	19	10
COR040	14	13	17	24	10	13	14	12	14	15	12	13	19	16	17	23	12	22	14	14	16	16	10
COR042	14	13	16	25	11	13	13	11	15	15	12	12	19	15	16	23	12	23	14	13	17	17	10
COR043	14	14	16	24	10	13	13	11	14	15	12	12	19	15	15	23	12	22	13	13	18	17	10
COR048	14	13	16	23	10	13	13	11	14	15	12	12	19	16	17	23	12	22	12	13	17	19	10
COR049	14	13	16	23	11	13	13	11	14	15	12	12	19	17	18	23	11	22	12	13	17	16	10
COR051	14	13	16	24	11	13	13	11	14	15	12	13	19	16	18	24	12	24	13	12	17	18	10
COR055	14	13	17	24	11	13	13	11	14	15	12	11	19	16	17	23	12	22	13	11	17	18	10
COR 057	14	13	16	23	11	13	13	11	14	15	12	11	19	17	16	23	12	22	12	13	16	17	11
COR058	14	13	16	25	10	13	13	11	13	15	12	11	19	15	17	23	12	22	13	13	17	18	10
COR061	14	13	16	24	11	14	13	11	14	14	12	12	19	15	17	23	11	22	13	13	18	18	10
COR093	14	13	16	24	11	13	13	11	13	14	12	12	20	16	18	23	12	22	12	12	17	18	10
COR096	14	13	16	25	11	13	13	11	14	15	12	12	19	16	18	23	12	22	12	12	17	17	10
COR097	14	13	16	24	11	13	13	11	15	15	12	12	19	16	18	23	12	23	12	13	18	17	11
COR201	14	13	16	24	11	13	13	11	14	15	12	12	17	16	17	23	12	22	12	13	17	19	11
COR202	14	13	16	23	11	13	13	11	14	15	12	11	19	16	17	24	10	22	12	13	17	17	10
COR203	14	13	16	23	11	13	13	11	14	14	12	11	19	17	16	23	12	22	12	12	16	17	11
COR208	15	12	16	22	10	11	14	12	14	16	10	13	22	16	17	22	11	23	9	12	18	19	12

COR209	14	14	16	25	11	13	13	11	15	14	12	12	19	15	16	23	11	23	12	13	19	18	10
COR211	14	13	16	24	11	13	14	12	12	15	12	11	19	15	17	23	12	23	13	13	17	18	10
COR212	14	13	16	23	11	13	13	12	16	15	13	11	19	17	17	23	11	22	12	13	18	19	10
COR214	14	13	16	24	11	13	12	12	14	15	12	13	19	16	15	23	12	24	12	13	18	16	10
COR215	15	13	16	24	10	13	13	11	14	14	12	11	19	16	17	23	11	22	12	13	16	17	10
COR217	15	12	16	24	11	11	12	14	17	16	9	13	19	13	16	21	11	24	12	14	17	16	9
COR223	14	12	17	22	10	11	13	13	14	16	10	12	19	14	14	21	11	25	11	12	19	16	11
COR224	14	13	17	23	11	13	15	10	14	15	12	12	19	16	16	23	12	22	12	13	16	17	10
COR227	14	13	16	23	11	11	13	13	15	16	10	12	20	14	15	21	11	25	12	12	21	16	13
COR232	14	13	16	23	11	13	13	11	14	15	12	13	19	17	18	23	12	22	11	12	17	17	10
COR233	14	13	16	24	10	13	13	10	14	15	12	11	19	16	13	23	12	22	12	14	16	18	10
COR235	14	13	16	24	11	13	13	11	14	14	12	14	19	16	15	23	12	22	12	11	17	17	11
COR238	14	14	15	23	10	13	13	11	14	17	13	12	19	15	18	23	13	21	13	12	17	19	11
COR239	14	13	16	25	11	13	13	11	14	15	12	12	19	15	16	23	12	24	14	14	17	18	10
COR240	14	12	16	22	10	11	13	13	15	16	10	11	20	14	15	24	11	25	11	12	20	16	11
COR241	14	13	16	22	11	13	13	11	14	16	10	12	19	15	17	23	12	22	13	12	17	18	13
COR242	15	12	16	22	10	11	13	13	14	16	10	11	20	14	16	22	12	22	11	12	19	16	13
COR243	14	13	16	25	10	13	13	11	14	15	12	11	19	16	18	24	12	24	12	13	17	18	10
COR248	16	13	16	23	10	12	14	15	15	15	10	11	20	17	16	21	11	25	12	12	20	17	13
COR251	15	14	16	24	10	13	13	11	14	15	12	12	19	15	18	23	12	22	12	12	17	18	10
COR252	14	13	18	24	11	13	13	11	14	15	12	12	19	15	18	23	11	23	12	13	20	17	10
COR256	14	13	16	24	11	13	14	12	14	15	12	8	19	16	16	23	12	22	12	14	17	18	10
COR257	14	13	16	24	11	13	13	11	15	15	12	12	19	16	18	23	12	24	14	13	18	21	11
COR258	14	14	16	26	11	13	12	11	15	15	12	12	19	15	18	23	12	22	12	14	19	17	9
COR259	14	13	16	23	11	13	13	11	14	15	12	14	19	16	16	23	12	22	12	14	16	18	10
COR260	14	13	15	25	11	13	13	11	14	15	12	12	19	16	17	23	13	22	12	13	17	19	10
COR261	16	13	16	24	11	13	13	11	13	15	12	13	18	17	17	23	11	22	12	12	17	17	10
COR262	14	13	16	25	11	13	13	11	14	16	12	12	19	15	17	23	12	23	12	12	20	20	10
COR263	14	13	16	24	11	13	13	12	15	15	12	13	19	16	17	23	12	24	12	12	19	18	10
COR266	14	14	16	23	11	13	13	11	14	15	12	12	18	16	17	23	12	22	13	13	18	19	10
COR267	14	13	16	23	11	13	13	11	14	15	12	12	19	18	17	23	11	22	12	12	18	18	11
COR273	15	13	17	23	12	13	13	11	14	15	12	14	19	17	17	23	11	23	12	13	20	17	10
COR276	15	13	16	23	11	13	13	11	14	15	12	12	19	16	18	24	11	22	12	12	18	17	10
DEV001	14	13	16	26	11	12	12	10	14	15	12	12	19	15	17	23	11	22	12	12	17	18	10
DEV005	14	12	16	24	11	13	13	11	14	15	12	11	19	17	18	24	12	22	12	13	16	19	10
DEV008	14	12	17	22	10	11	12	14	14	16	10	11	21	13	14	23	11	25	11	13	21	16	12
DEV011	15	14	17	23	10	12	14	14	15	14	10	11	19	14	15	21	10	26	11	12	21	17	12
DEV012	14	13	16	24	10	13	13	11	14	15	12	12	19	16	18	23	12	23	12	14	19	17	11

DEV013	14	13	17	24	11	13	13	11	14	15	11	12	19	16	17	25	12	22	12	13	18	16	10
DEV014	14	13	16	24	10	13	14	11	13	15	12	12	19	19	16	23	13	22	12	14	16	17	10
DEV022	14	13	16	24	11	14	13	11	13	15	12	12	19	16	18	23	11	22	12	13	17	18	10
DEV024	14	13	16	24	11	13	13	11	15	15	12	11	19	16	17	23	12	22	13	13	16	15	10
DEV025	14	13	16	23	11	13	14	11	15	15	12	11	19	17	18	23	12	21	12	13	17	17	10
DEV027	13	12	16	22	11	11	13	13	13	16	10	11	19	15	15	22	11	25	10	11	20	15	12
DEV032	15	12	16	23	11	11	12	10	17	16	9	12	20	13	16	23	11	23	12	12	17	17	9
DEV033	14	12	16	22	10	11	13	13	15	16	10	11	20	14	14	21	11	25	12	13	22	16	12
DEV035A	14	13	16	23	12	13	13	11	13	15	12	11	19	16	17	23	12	22	12	13	17	17	10
DEV037	14	13	16	23	11	13	13	11	15	15	12	12	19	16	17	23	13	22	12	13	16	16	11
DEV038	14	13	16	23	11	13	13	11	14	14	12	12	19	13	17	23	11	22	12	13	17	18	10
DEV043	14	13	16	24	11	13	13	12	15	15	12	11	19	16	17	23	11	22	13	13	17	17	10
DEV045	14	13	16	23	10	13	13	11	14	15	12	13	19	18	17	23	12	22	12	13	17	18	11
DEV054	14	13	16	24	11	13	13	11	14	15	11	12	19	15	17	24	11	22	12	13	18	17	10
DEV055	14	12	17	22	10	11	13	13	15	15	10	11	20	14	16	22	11	24	11	11	20	16	12
DEV056	14	13	16	23	11	13	13	11	14	14	12	13	19	17	17	23	11	22	12	12	17	15	10
DEV059	13	12	18	24	10	10	13	16	17	14	10	13	20	15	18	21	9	26	10	12	20	19	12
DEV060	14	12	15	23	11	13	13	11	14	15	12	11	19	15	16	23	13	22	12	12	18	*	10
DEV061	15	12	17	24	11	13	13	11	14	13	12	11	19	16	17	24	12	23	13	14	17	18	9
DEV062	14	13	18	24	11	13	13	11	14	15	12	12	19	15	18	23	12	22	12	13	20	18	10
DEV066	15	13	16	24	11	13	13	11	14	14	12	12	19	16	17	24	12	22	12	13	17	17	10
DEV079	14	13	17	24	10	11	12	15	15	16	9	13	19	17	19	22	12	22	11	12	15	19	9
DEV084	14	13	16	24	11	13	13	12	14	15	12	11	19	15	16	23	12	22	12	12	14	17	10
DEV087	14	13	16	23	11	13	14	11	14	14	12	12	19	16	17	23	11	24	11	13	17	18	10
DEV088	14	13	16	25	11	13	13	11	14	15	12	13	19	17	17	23	11	22	12	14	18	17	10
DEV091	14	13	16	24	10	13	13	11	14	15	12	12	19	16	18	24	12	22	12	13	17	19	10
DEV093	14	13	16	23	11	13	13	11	14	14	12	12	19	16	16	23	12	22	12	13	17	17	10
DEV094	14	13	16	24	10	13	13	12	14	15	12	12	19	16	17	23	12	22	12	13	17	18	10
DEV095	15	14	17	23	10	12	14	15	16	14	10	11	20	15	16	21	11	26	12	13	19	16	13
DEV201	14	12	18	23	10	11	14	14	14	16	10	11	20	15	15	23	11	24	11	12	21	17	12
DEV202	15	13	16	23	11	12	13	15	15	15	11	11	20	16	16	20	11	26	14	13	19	16	13
DEV203	14	13	17	23	11	13	13	12	14	15	12	11	19	17	19	23	12	22	12	12	16	18	11
DEV208	14	13	16	23	10	13	13	11	14	15	12	12	19	15	17	23	13	23	11	13	18	17	10
DEV219	14	13	16	24	11	14	13	11	14	15	12	12	19	16	20	23	12	22	13	11	17	18	10
DEV223	14	13	16	24	10	14	13	11	14	15	12	12	19	16	17	23	11	23	12	12	16	16	12
DEV224	14	13	17	24	10	13	13	11	15	15	12	12	19	15	17	23	13	22	13	14	17	17	10
DEV501	14	13	16	24	11	13	13	12	14	15	12	13	20	16	17	23	12	22	12	13	17	17	10
DEV504	14	13	16	23	11	13	13	11	14	15	12	12	19	16	17	23	12	22	12	14	16	16	10

DEV508	14	13	16	24	11	13	14	11	13	15	12	12	19	15	19	23	12	23	12	13	18	17	10
DEV510	14	13	17	23	11	13	13	11	14	15	12	12	19	18	17	23	11	22	11	13	17	17	10
DEV512	16	14	18	23	10	12	14	15	15	14	10	12	20	17	15	21	11	27	13	13	20	17	12
DEV513	15	13	16	23	12	13	13	11	14	15	12	12	18	16	18	23	12	23	12	12	18	20	10
DEV517	14	13	15	23	10	11	12	13	17	15	9	11	21	15	14	21	12	22	12	13	14	17	10
DEV560	14	13	15	23	11	13	13	11	14	15	12	13	18	15	17	23	12	22	12	13	18	18	10

8.1.9 Haplogroup predictions

Sample	Illumina confirmed hg	<u>NevGen prediction</u>
BM1	n/a	R1b
BM2	n/a	R1b
BM3	n/a	R1b
BM4	n/a	R1b
BM5	n/a	R1b
BM7	n/a	I1
BM8	n/a	R1b
BM9	n/a	R1b
BM10	n/a	R1b
BM11	n/a	R1b
BM12	n/a	I1
BM14	n/a	R1b
BM15	n/a	R1b
BM16	n/a	R1b
BM17	n/a	I2a2a
BM18	n/a	R1b
BM21	n/a	R1b
BM22	n/a	R1b
BM23	n/a	R1b
BM24	n/a	R1b
BM31	n/a	R1b
BM32	n/a	R1b
BM33	n/a	I1
BM34	n/a	R1b
BM35	n/a	R1b
BM36	n/a	R1b
BM37	n/a	R1b
BM40	n/a	R1b
BM41	n/a	R1b
BM42	n/a	R1b
BM43	n/a	R1b
BM44	n/a	R1b
BM45	n/a	R1b
BM46	n/a	I1
BM50	n/a	R1b
BM51	n/a	R1b
BM52	n/a	R1b
BM53	n/a	G2a2
BM54	n/a	R1b
BM55	n/a	R1b

BM56	n/a	R1b
BM57	n/a	I2a2b
BM61	n/a	I1
BM62	n/a	E1b1b
BM71	n/a	E1b1b
BM72	n/a	I2a2a
BM73	n/a	R1b
COR005		R1b
COR012	R1b1a2a1a1	R1b
COR017		R1b
COR019	R1a1a1	R1a
COR025		R1b
COR035	I1	I1
COR038	R1b1a2a1a1	R1b
COR040	R1b1a2a1a1	R1b
COR042		R1b
COR043	R1b1a2a1a1	R1b
COR048	R1b1a2a1a1	R1b
COR049	R1b1a2a1a1a	R1b
COR051	R1b1a2a1a1	R1b
COR055	R1b1a2a1a1 (rs3860001)	R1b
COR057	R1b1a2a1a1	R1b
COR058		R1b
COR061	R1b1a2a1a1	R1b
COR093	R1b1a2a1a1	R1b
COR096	R1b1a2a1a1	R1b
COR097	R1b1a2a1a1a	R1b
COR201		R1b
COR202		R1b
COR203		R1b
COR208		G2a2
COR209		R1b
COR211		R1b
COR212		R1b
COR214		R1b
COR215		R1b
COR217	J2b2	J2b2a
COR223	I1	I1
COR224		R1b
COR227	I1	I1
COR232		R1b
COR233		R1b
COR235		R1b
COR238		R1b
COR239		R1b

COR240		l1
COR241		R1b
COR242		l2a2a
COR243	R1b1a2a1a1b3	R1b
COR248		l2a2a
COR251		R1b
COR252		R1b
COR256		R1b
COR257		R1b
COR258	R1b1a2a1a1	R1b
COR259		R1b
COR260	R1b1a2a1a1	R1b
COR261		R1b
COR262		R1b
COR263		R1b
COR266	R1b1a2a1a1	R1b
COR267		R1b
COR273		R1b
COR276		R1b
DEV001	R1b1a2a1a1	R1b
DEV005	R1b1a2a1a1b	R1b
DEV008	l1	l1
DEV011	l2a2a	l2a2a
DEV012	R1b1a2a1a1a	R1b
DEV013	R1b1a2a1a1a	R1b
DEV014	R1b1a2a1a1	R1b
DEV022		R1b
DEV024	R1b1a2a1a1	R1b
DEV025	R1b1a2a1a1a	R1b
DEV027	l1	l1
DEV032	J2b2	J2b2a
DEV033	l1	l1
DEV035A	R1b1a2a1a1b3	R1b
DEV037	R1b1a2a1a1a	R1b
DEV038	R1b1a2a1a1a (rs2574024)	R1b
DEV043	R1b1a2a1a1	R1b
DEV045	R1b1a2a1a1a	R1b
DEV054		R1b
DEV055	l1	l1
DEV056	R1b1a2a1a1a	R1b
DEV059	E1b1b1b2a	E1b1b
DEV060	R1b1a2a1a1a5c1	R1b
DEV061	R1b1a2a1a1	R1b
DEV062	R1b1a2a1a1	R1b
DEV066	R1b1a2a1a1a	R1b

DEV079	J2	J2a1
DEV084	R1b1a2a1a1	R1b
DEV087	R1b1a2a1a1a	R1b
DEV088	R1b1a2a1a1	R1b
DEV091	R1b1a2a1a1	R1b
DEV093	R1b1a2a1a1a	R1b
DEV094	R1b1a2a1a1b3 (rs7067370)	R1b
DEV095	l2a2a	l2a2a
DEV201		l1
DEV202		l2a2a
DEV203	R1b	R1b
DEV208		R1b
DEV219		R1b
DEV223		R1b
DEV224		R1b
DEV501	R1b1a2a1a1	R1b
DEV504	R1b1a2a1a1a	R1b
DEV508	R1b1a2a1a1	R1b
DEV510	R1b1a2a1a1a	R1b
DEV512	l2a2a	l2a2a
DEV513	R1b1a2a1a1	R1b
DEV517		J2a1
DEV560		R1b

8.1.10 SNaPshot allele calls

0 = ancestral allele 1 = derived allele x = missing allele call
 Calls listed in **bold** were inferred using upstream markers

	U106	U152	U198	S145	M222	S116	L11	Z253	M269	hg
BM1	0	0	0	1	0	1	1	0	1	R1b-S145*
BM10	0	0	0	0	0	1	1	0	1	R1b-S116*
BM11	0	0	0	1	0	1	1	0	1	R1b-S145*
BM14	0	1	0	0	0	1	1	0	1	R1b-U152
BM15	0	0	0	1	0	1	1	0	1	R1b-S145*
BM16	0	0	0	0	0	1	1	0	1	R1b-S116*
BM18	0	0	0	0	0	0	1	0	1	R1b-L11*
BM2	0	0	0	1	0	1	1	1	1	R1b-Z253
BM21	0	0	0	0	0	1	1	0	1	R1b-S116*
BM22	1	0	0	0	0	0	1	0	1	R1b-U106*
BM23	1	0	0	0	0	0	1	0	1	R1b-U106*
BM24	1	0	0	0	0	0	1	0	1	R1b-U106*
BM3	0	1	0	0	0	1	1	0	1	R1b-U152
BM31	1	0	0	0	0	0	1	0	1	R1b-U106*
BM32	1	0	0	0	0	0	1	0	1	R1b-U106*
BM34	1	0	0	0	0	0	1	0	1	R1b-U106*
BM35	0	0	0	0	0	1	1	0	1	R1b-S116*
BM36	0	0	0	0	0	0	0	0	1	R1b-M269 [xL11]
BM37	0	0	0	0	0	1	1	0	1	R1b-S116*
BM4	0	0	0	1	0	1	1	0	1	R1b-S145*
BM40	1	0	0	0	0	0	1	0	1	R1b-U106*
BM41	0	0	0	0	0	0	1	0	1	R1b-L11*
BM42	0	0	0	1	0	1	1	0	1	R1b-S145*
BM43	1	0	0	0	0	0	1	0	1	R1b-U106*
BM44	1	0	0	0	0	0	1	0	1	R1b-U106*
BM45	1	0	0	0	0	0	1	0	1	R1b-U106*
BM5	0	0	0	0	0	1	1	0	1	R1b-S116*
BM50	0	0	0	1	0	1	1	1	1	R1b-Z253
BM51	1	0	0	0	0	0	1	0	1	R1b-U106*
BM52	0	0	0	0	0	1	1	0	1	R1b-S116*
BM54	0	0	0	0	0	1	1	0	1	R1b-S116*
BM55	0	0	0	x	x	x	1	0	1	R1b-L11 (partial)
BM56	0	0	0	x	x	x	1	x	1	R1b-L11 (partial)
BM73	0	0	0	0	0	1	1	0	1	R1b-S116*
BM8	0	0	0	1	0	1	1	0	1	R1b-S145*
BM9	0	0	0	0	0	1	1	0	1	R1b-S116*
COR005	0	0	0	1	0	1	1	1	1	R1b-Z253
COR012	0	0	0	1	0	1	1	0	1	R1b-S145*
COR017	0	0	0	1	0	1	1	0	1	R1b-S145*

COR025	1	0	0	0	0	0	1	0	1	R1b-U106*
COR038	0	0	0	1	0	1	1	0	1	R1b-S145*
COR040	0	0	0	1	0	1	1	0	1	R1b-S145*
COR042	0	0	0	1	0	1	1	0	1	R1b-S145*
COR043	0	0	0	1	0	1	1	0	1	R1b-S145*
COR048	0	0	0	1	0	1	1	0	1	R1b-S145*
COR049	1	0	0	0	0	0	1	0	1	R1b-U106*
COR051	0	0	0	1	0	1	1	0	1	R1b-S145*
COR055	0	0	0	1	0	1	1	0	1	R1b-S145*
COR057	0	0	0	0	0	1	1	0	1	R1b-S116*
COR058	0	0	0	1	0	1	1	x	1	R1b-S145 (partial)
COR061	0	0	0	1	0	1	1	0	1	R1b-S145*
COR093	0	0	0	0	0	1	1	0	1	R1b-S116*
COR096	0	0	0	0	0	1	1	0	1	R1b-S116*
COR097	1	0	0	0	0	0	1	0	1	R1b-U106*
COR201	0	0	0	1	0	1	1	0	1	R1b-S145*
COR202	1	0	0	0	0	0	1	0	1	R1b-U106*
COR203	0	0	0	0	0	1	1	0	1	R1b-S116*
COR209	0	0	0	0	0	1	1	0	1	R1b-S116*
COR211	0	0	0	1	0	1	1	0	1	R1b-S145*
COR212	0	1	0	0	0	1	1	0	1	R1b-U152
COR214	0	0	0	0	0	0	0	0	1	R1b-M269 [XL11]
COR215	1	0	0	0	0	0	1	0	1	R1b-U106*
COR224	0	0	0	0	0	1	1	0	1	R1b-S116*
COR232	1	0	0	0	0	0	1	0	1	R1b-U106*
COR233	1	0	0	0	0	0	1	0	1	R1b-U106*
COR235	1	0	0	0	0	0	1	0	1	R1b-U106*
COR238	0	0	0	1	0	1	1	0	1	R1b-S145*
COR239	0	0	0	1	0	1	1	0	1	R1b-S145*
COR241	0	0	0	1	0	1	1	0	1	R1b-S145*
COR243	0	1	0	0	0	1	1	0	1	R1b-U152
COR251	0	0	0	1	0	1	1	0	1	R1b-S145*
COR252	0	0	0	1	0	1	1	0	1	R1b-S145*
COR256	0	0	0	0	0	1	1	0	1	R1b-S116*
COR257	0	0	0	1	0	1	1	0	1	R1b-S145*
COR258	0	0	0	1	0	1	1	0	1	R1b-S145*
COR259	0	0	0	0	0	1	1	0	1	R1b-S116*
COR260	0	0	0	1	0	1	1	0	1	R1b-S145*
COR261	0	1	0	0	0	1	1	0	1	R1b-U152
COR262	0	0	0	1	0	1	1	0	1	R1b-S145*
COR263	0	0	0	0	0	1	1	0	1	R1b-S116*
COR266	0	0	0	1	0	1	1	0	1	R1b-S145*
COR267	1	0	0	0	0	0	1	0	1	R1b-U106*
COR273	1	0	0	0	0	0	1	0	1	R1b-U106*
COR276	1	0	0	0	0	0	1	0	1	R1b-U106*

DEV001	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV005	0	0	0	1	0	1	1	0	1	R1b-S145*
DEV012	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV013	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV014	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV022	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV024	0	0	0	1	0	1	1	0	1	R1b-S145*
DEV025	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV 035A	0	1	0	0	0	1	1	0	1	R1b-U152
DEV037	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV038	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV043	0	0	0	0	0	0	1	0	1	R1b-L11*
DEV045	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV054	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV056	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV060	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV061	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV062	0	0	0	1	0	1	1	0	1	R1b-S145*
DEV066	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV084	0	0	0	1	0	1	1	0	1	R1b-S145*
DEV087	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV088	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV091	0	0	0	1	0	1	1	0	1	R1b-S145*
DEV093	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV094	0	1	0	0	0	1	1	0	1	R1b-U152
DEV203	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV208	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV219	0	0	0	1	0	1	1	x	1	R1b-S145 (partial)
DEV223	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV224	0	0	0	0	0	1	1	x	1	R1b-S116*
DEV501	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV504	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV508	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV510	1	0	0	0	0	0	1	0	1	R1b-U106*
DEV513	0	0	0	0	0	1	1	0	1	R1b-S116*
DEV560	0	0	0	0	0	1	1	0	1	R1b-S116*

Chapter 9 BIBLIOGRAPHY

1000 GENOMES PROJECT CONSORTIUM, 2012. An Integrated Map of Genetic Variation from 1,092 Human Genomes. *Nature*, **491**(7422), pp. 56.

ALEXANDER, D.H., NOVEMBRE, J. and LANGE, K., 2009. Fast Model-Based Estimation of Ancestry in Unrelated Individuals. *Genome Research*, **19**, pp. 1655-1664.

ALTENBERG, K., 2003. *Experiencing Landscapes : A Study of Space and Identity in Three Marginal Areas of Medieval Britain and Scandinavia*. Stockholm: Almqvist and Wiksell International.

ARCHER, S., 2015. *The British 19th Century Surname Atlas*. Ver 1.20 edn. Dartford: Archer Software.

AXFORD, E.C., 1975. *Bodmin Moor*. Newton Abbot Eng.; North Pomfret, Vt: David & Charles.

BALANOVSKY, O., CHUKHRYAEVA, M., ZAPOROZHCHENKO, V., URASIN, V., ZHABAGIN, M., HOVHANNISYAN, A., AGDZHOYAN, A., DIBIROVA, K., KUZNETSOVA, M. and KOSHEL, S., 2017. Genetic Differentiation between Upland and Lowland Populations Shapes the Y-Chromosomal Landscape of West Asia. *Human Genetics*, **136**(4), pp. 437-450.

BALARESQUE, P., BOWDEN, G.R., ADAMS, S.M., LEUNG, H., KING, T.E., ROSSER, Z.H., GOODWIN, J., MOISAN, J., RICHARD, C. and MILLWARD, A., 2010. A Predominantly Neolithic Origin for European Paternal Lineages. *PLoS Biol*, **8**(1), pp. e1000285.

BALCHIN, W.G.V., 1983. *The Cornish Landscape*. Rev. edn. London: Hodder and Stoughton.

BALLANTYNE, K.N., GOEDBLOED, M., FANG, R., SCHAAP, O., LAO, O., WOLLSTEIN, A., CHOI, Y., VAN DUIJN, K., VERMEULEN, M. and BRAUER, S., 2010. Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications. *The American Journal of Human Genetics*, **87**(3), pp. 341-353.

BALLANTYNE, K.N., RALF, A., ABOUKHALID, R., ACHAKZAI, N.M., ANJOS, M.J., AYUB, Q., BALAŽIĆ, J., BALLANTYNE, J., BALLARD, D.J. and BERGER, B., 2014. Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. *Human Mutation*, **35**(8), pp. 1021-1032.

BANDELT, H., FORSTER, P. and RHL, A., 1999. Median-Joining Networks for Inferring Intraspecific Phylogenies. *Molecular Biology and Evolution*, **16**(1), pp. 37-48.

BATINI, C., HALLAST, P., ZADIK, D., DELSER, P.M., BENAZZO, A., GHIROTTI, S., ARROYO-PARDO, E., CAVALLERI, G.L., DE KNIJFF, P. and DUPUY, B.M., 2015.

Large-Scale Recent Expansion of European Patrilineages shown by Population Resequencing. *Nature Communications*, **6**.

BEDDOE, J., 1971. *The Races of Britain : A Contribution to the Anthropology of Western Europe*. [1st ed. reprinted]. London: Hutchinson.

BESNIER, M., 1924. *The Victoria History of the Counties of England. A History of the County of Cornwall, Edited by W. Page. Part 5: Romano-British Remains, by the Late F. Haverfield*. London: The St. Catherine Press.

BOWDEN, G.R., BALARESQUE, P., KING, T.E., HANSEN, Z., LEE, A.C., PERGL-WILSON, G., HURLEY, E., ROBERTS, S.J., WAITE, P. and JESCH, J., 2008. Excavating Past Population Structures by Surname-Based Sampling: The Genetic Legacy of the Vikings in Northwest England. *Molecular Biology and Evolution*, **25**(2), pp. 301-309.

BRAYSHAY, M., 1996. John Leland in the West Country. In: M. BRAYSHAY, ed, *Topographical Writers in South-west England*. Exeter: University of Exeter Press, pp. 34-49.

BURTON, M.L., MOORE, C.C., WHITING, J.W., ROMNEY, A.K., ABERLE, D.F., BARCELO, J.A., DOW, M.M., GUYER, J.I., KRONENFELD, D.B. and LEVY, J.E., 1996. Regions Based on Social Structure. *Current Anthropology*, **37**(1), pp. 87-123.

BUSBY, G.B., BRISIGHELLI, F., SÁNCHEZ-DIZ, P., RAMOS-LUIS, E., MARTINEZ-CADENAS, C., THOMAS, M.G., BRADLEY, D.G., GUSMÃO, L., WINNEY, B. and BODMER, W., 2011. The Peopling of Europe and the Cautionary Tale of Y Chromosome Lineage R-M269. *Proceedings of the Royal Society B: Biological Sciences*, **279**(1730), pp. 884-892.

CALAFELL, F. and LARMUSEAU, M., 2017. The Y Chromosome as the most Popular Marker in Genetic Genealogy Benefits Interdisciplinary Research. *Human Genetics*, **136**(5), pp. 559-573.

CANN, R.L., STONEKING, M. and WILSON, A.C., 1987. Mitochondrial DNA and Human Evolution. *Nature*, **325**(6099), pp. 31.

CAPELLI, C., REDHEAD, N., ABERNETHY, J.K., GRATRICK, F., WILSON, J.F., MOEN, T., HERVIG, T., RICHARDS, M., STUMPF, M.P.H., UNDERHILL, P.A., BRADSHAW, P., SHAHA, A., THOMAS, M.G., BRADMAN, N. and GOLDSTEIN, D.B., 2003. A Y Chromosome Census of the British Isles. *Current Biology*, **13**(11), pp. 979-984.

CAREW, R., 1953. *Richard Carew of Antony; the Survey of Cornwall*. reprint of 1603 edn. London: Andrew Melrose.

CASSIDY, L.M., MARTINIANO, R., MURPHY, E.M., TEASDALE, M.D., MALLORY, J., HARTWELL, B. and BRADLEY, D.G., 2016. Neolithic and Bronze Age Migration to Ireland and Establishment of the Insular Atlantic Genome. *Proceedings of the National Academy of Sciences*, **113**(2), pp. 368-373.

- CAVALLI-SFORZA, L.L., MENOZZI, P. and PIAZZA, A., 1993. Demic Expansions and Human Evolution. *Science*, **259**(5095), pp. 639-646.
- CHARNOCK, R., 2015. *Patronymica Cornu-Britannica*. Available: (www.archive.org) 2015.
- COOPER, G., AMOS, W., HOFFMAN, D. and RUBINSZTEIN, D.C., 1996. Network Analysis of Human Y Microsatellite Haplotypes. *Human Molecular Genetics*, **5**(11), pp. 1759-1766.
- COOPER, J.P.D., 2003. *Propaganda and the Tudor State : Political Culture in the Westcountry*. Oxford: Clarendon.
- CORNWALL COUNCIL, 2019. *Cornwall Council*. Available: <https://www.cornwall.gov.uk/> [January 2019].
- CORNWALL GUIDE, 2019. *Cornwalls.co.uk*. Available: <https://www.cornwalls.co.uk/Warleggan2018>.
- CORNWALL PARISH REGISTER INDEX, 2016. *Historical Cornwall Population Statistics*. Available: <https://www.cornwalleng.com/statistics.html> [January 2019].
- COWLES, F.I., 1934. *The Magic of Cornwall*. London: Heath Cranton.
- CROSSLEY, G., 2018. *Kinship and strategies for family survival on Bodmin Moor during the long nineteenth century (1793 – 1911)*, Oxford University thesis.
- CROW, J.F., 2000. The Origins, Patterns and Implications of Human Spontaneous Mutation. *Nature Reviews Genetics*, **1**(1), pp. 40.
- CUNLIFFE, B.W., 2012. *Britain Begins*. Oxford: Oxford University Press.
- DARK, A., 1998. Surnames and One-Name Studies. In: A. DARK, ed, *Beginning Genealogy*. Gerrards Cross: Hillingdon Family History Society, pp. 5-7.
- DAVIES, N., 2000. *The Isles: A History*. London: Macmillan.
- DEACON, B., 2015. *Bernard Deacon's Cornish Studies Resources*. Available: <https://bernarddeacon.wordpress.com/> [September, 2016].
- DEACON, B., 2009. Cornishness and Englishness: Nested Identities Or Incompatible Ideologies? *International Journal of Regional and Local Studies*, **5**(2), pp. 9-29.
- DEACON, B., 2007. *A Concise History of Cornwall*. Cardiff: University of Wales Press.
- DEACON, B., 2004. *The Cornish Family: The Roots of our Future*. Fowey: Cornwall Editions.

- DEACON, B., COLE, D. and TREGIDGA, G., 2003. *Mebyon Kernow and Cornish Nationalism*. Cardiff: Welsh Academic Press.
- DEANE, T. and SHAW, T., 1975. *The Folklore of Cornwall*. London: Batsford.
- DEFOE, D., 1927. *A tour through the whole island of Great Britain Letter VIII*. Available: <https://ebooks.adelaide.edu.au/d/defoe/daniel/britain/letter8.html> [March 2017].
- DEVON COUNTY COUNCIL, 2016. *Devon Parish Registers Online*. Available: <http://www.devon.gov.uk/pronline> [January 2016].
- DITMAS, E., 1973. A Reappraisal of Geoffrey of Monmouth's Allusions to Cornwall. *Speculum*, **48**(3), pp. 510-524.
- DOYLE, A.C., 1902. *The Hound of the Baskervilles*. London: Grosset and Dunlap.
- DRUMMOND, A.J. and RAMBAUT, A., 2007. BEAST: Bayesian Evolutionary Analysis by Sampling Trees. *BMC Evolutionary Biology*, **7**(1), pp. 214.
- DU MAURIER, D., 2007. *Vanishing Cornwall*. London: Virago.
- DU MAURIER, D., 1936. *Jamaica Inn*. London: Pocket Books.
- DUDLEY, D. and MINTER, E.M., 1962. The Medieval Village at Garrow Tor, Bodmin Moor, Cornwall. *Medieval Archaeology*, **6**(1), pp. 272-294.
- EXCOFFIER, L. and LISCHER, H.E., 2010. Arlequin Suite Ver 3.5: A New Series of Programs to Perform Population Genetics Analyses Under Linux and Windows. *Molecular Ecology Resources*, **10**(3), pp. 564-567.
- FAITH, R., 2011. Some Devon Farms before the Norman Conquest. In: S. TURNER and B. SYLVESTER, eds, *Life in medieval landscapes: people and places in the Middle Ages*. Bollington: Windgather, pp. 73-88.
- FENNER, J.N., 2005. Cross-cultural Estimation of the Human Generation Interval for use in Genetics-based Population Divergence Studies. *American Journal of Physical Anthropology: The Official Publication of the American Association of Physical Anthropologists*, **128**(2), pp. 415-423.
- FINDMYPAST, 2016. *FindMyPast*. Available: <http://www.findmypast.co.uk/>.
- FLETCHER, D., 2003. The Parish Boundary: A Social Phenomenon in Hanoverian England. *Rural History*, **14**(2), pp. 177-196.
- FLEURE, H.J., 1923. *The Races of England and Wales : A Survey of Recent Research*. London: Benn.

FLUXUS ENGINEERING, 2018. *Fluxus Engineering*. Available: <http://www.fluxus-engineering.com/sharenet.htm>2018.

FOLLIOTT-STOKES, A.G., 1912. *The Cornish Coast and Moors*. New edn. London: Greening.

FORSTER, P., RÖHL, A., LÜNNEMANN, P., BRINKMANN, C., ZERJAL, T., TYLER-SMITH, C. and BRINKMANN, B., 2000. A Short Tandem Repeat-based Phylogeny for the Human Y Chromosome. *The American Journal of Human Genetics*, **67**(1), pp. 182-196.

FOX, H.S.A., 2012. *Dartmoor's Alluring Uplands: Transhumance and Pastoral Management in the Middle Ages*. Exeter: University of Exeter Press.

FRANKLIN, L., 2006. Imagined Landscapes. In: S. TURNER, ed, *Medieval Devon and Cornwall: shaping an ancient countryside*. Bollington, Macclesfield: Windgather Press, pp. 96-99.

GEAREY, B.R., CHARMAN, D.J. and KENT, M., 2000. Palaeoecological Evidence for the Prehistoric Settlement of Bodmin Moor, Cornwall, Southwest England. Part II: Land use Changes from the Neolithic to the Present. *Journal of Archaeological Science*, **27**(6), pp. 493-508.

GRIFFITHS, R., 2003. The Island of England in the Fifteenth Century: Perceptions of the Peoples of the British Isles. *Journal of Medieval History*, **29**(3), pp. 177-200.

GUARDIAN, 2013. *Cornwall-Devon boundary may change*. Available: <https://www.theguardian.com/uk/2011/sep/13/cornwall-devon-boundary-change> [September 2013].

GUPPY, H.B., 1890. *Homes of Family Names in Great Britain*. London: Harrison and Sons.

HAAK, W., LAZARIDIS, I., PATTERSON, N., ROHLAND, N., MALLICK, S., LLAMAS, B., BRANDT, G., NORDENFELT, S., HARNEY, E. and STEWARDSON, K., 2015. Massive Migration from the Steppe was a Source for Indo-European Languages in Europe. *Nature*, **522**(7555), pp. 207.

HALLAST, P., BATINI, C., ZADIK, D., MAISANO DELSER, P., WETTON, J.H., ARROYO-PARDO, E., CAVALLERI, G.L., DE KNIJFF, P., DESTRO BISOL, G., DUPUY, B.M., ERIKSEN, H.A., JORDE, L.B., KING, T.E., LARMUSEAU, M.H., LOPEZ DE MUNAIN, A., LOPEZ-PARRA, A.M., LOUSTRADIS, A., MILASIN, J., NOVELLETTO, A., PAMJAV, H., SAJANTILA, A., SCHEMPP, W., SEARS, M., TOLUN, A., TYLER-SMITH, C., VAN GEYSTELEN, A., WATKINS, S., WINNEY, B. and JOBLING, M.A., 2015. The Y-Chromosome Tree Bursts into Leaf: 13,000 High-Confidence SNPs Covering the Majority of Known Clades. *Molecular Biology and Evolution*, **32**(3), pp. 661-673.

- HALLIDAY, F.E., 2001. *A History of Cornwall*. [2nd, revised] edn. London: House of Stratus.
- HAMMOND, R., ed., 1967. *North Cornwall : Newquay, Perranporth, Padstow, Tintagel, Bude, Etc.* 18th edn. London: Ward Lock.
- HANKS, P., COATES, R. and MCCLURE, P., 2016. *The Oxford Dictionary of Family Names in Britain and Ireland*. Oxford: Oxford University Press.
- HARVEY, R.G., SMITH, M.T., SHERREN, S., BAILEY, L. and HYNDMAN, S.J., 1986. How Celtic are the Cornish?: A Study of Biological Affinities. *Man*, , pp. 177-201.
- HELGASON, A., EINARSSON, A.W., GUÐMUNDSDÓTTIR, V.B., SIGURÐSSON, Á, GUNNARSDÓTTIR, E.D., JAGAÐEESAN, A., EBENESERSDÓTTIR, S.S., KONG, A. and STEFÁNSSON, K., 2015. The Y-Chromosome Point Mutation Rate in Humans. *Nature Genetics*, **47**(5), pp. 453-457.
- HERRING, P., 2011. Shadows of Ghosts: Early Medieval Transhumants in Cornwall. In: S. TURNER and B. SYLVESTER, eds, *Life in Medieval Landscapes*. Bollington: Windgather, pp. 89-105.
- HERRING, P., 2008. *Bodmin Moor: Vol. 2, an Archaeological Survey*. Swindon: English Heritage.
- HEY, D., 2000a. *Family Names and Family History*. London: Hambledon and London.
- HEY, D., 2000b. Moorlands. In: J. THIRSK, ed, *The English Rural Landscape*. Oxford: Oxford University Press, pp. 188-209.
- HEY, D., 1997. The Local History of Family Names. *Local Historian*, **27**(4), pp. xx.
- HICKS, N., 1982. Make Grandma Spell it Out. *Cornwall Family History Society*, **24**, pp. 13.
- HIGHAM, N., 2007. Britons in Anglo-Saxon England: An Introduction. In: N. HIGHAM, ed, *Britons in Anglo-Saxon England*. Woodbridge, Suffolk: Boydell Press, pp. 1-15.
- HOSKINS, W.G., 1959. *Devon and its People*. Exeter: Wheaton.
- HUGHES, J.F., SKALETSKY, H., PYNTIKOVA, T., GRAVES, T.A., VAN DAALEN, S.K., MINX, P.J., FULTON, R.S., MCGRATH, S.D., LOCKE, D.P. and FRIEDMAN, C., 2010. Chimpanzee and Human Y Chromosomes are Remarkably Divergent in Structure and Gene Content. *Nature*, **463**(7280), pp. 536.
- JACKSON, K.H., 1953. *Language and History in Early Britain : A Chronological Survey of the Brittonic Languages, 1st to 12th Century A.D.* Edinburgh: Edinburgh University Press.

- JAMES, S., 1999. *The Atlantic Celts : Ancient People Or Modern Invention?* London: British Museum Press.
- JEFFREYS, A.J., WILSON, V. and THEIN, S.L., 1985. Individual-Specific 'fingerprints' of Human DNA. *Nature*, **316**(6023), pp. 76.
- JOBLING, M.A., 2001. In the Name of the Father: Surnames and Genetics. *TRENDS in Genetics*, **17**(6), pp. 353-357.
- JOBLING, M.A. and TYLER-SMITH, C., 2017. Human Y-Chromosome Variation in the Genome-Sequencing Era. *Nature Reviews Genetics*, **18**(8), pp. 485.
- JOBLING, M.A. and TYLER-SMITH, C., 2003. The Human Y Chromosome: An Evolutionary Marker Comes of Age. *Nature Reviews Genetics*, **4**(8), pp. 598-612.
- JOBLING, M.A. and TYLER-SMITH, C., 1995. Fathers and Sons: The Y Chromosome and Human Evolution. *Trends in Genetics*, **11**(11), pp. 449-456.
- JOHNSON, N., 1990. *Cornwall's Archaeological Heritage: From Prehistory to the Tudors: 8000 BC-AD 1540*. Truro: Twelveheads Press.
- JOHNSON, N., ROSE, P., BONNEY, D., CARTER, A. and ENGLISH HERITAGE, 1994. *Bodmin Moor: Vol.1, an Archaeological Survey*. Swindon: English Heritage.
- JONES, D. and ESSEX, S., 1999. Land use Change in the British Uplands: A Case Study of Bodmin Moor, Cornwall. *Geography*, **84**(1), pp. 11-23.
- KANDT, J., CHESHIRE, J.A. and LONGLEY, P.A., 2016. Regional Surnames and Genetic Structure in Great Britain. *Transactions of the Institute of British Geographers*, **41**(4), pp. 554-569.
- KARAFET, T.M., MENDEZ, F.L., MEILERMAN, M.B., UNDERHILL, P.A., ZEGURA, S.L. and HAMMER, M.F., 2008. New Binary Polymorphisms Reshape and Increase Resolution of the Human Y Chromosomal Haplogroup Tree. *Genome Research*, **18**, pp. 830-838.
- KARMIN, M., SAAG, L., VICENTE, M., SAYRES, M.A.W., JÄRVE, M., TALAS, U.G., ROOTSI, S., ILUMÄE, A., MÄGI, R. and MITT, M., 2015. A Recent Bottleneck of Y Chromosome Diversity Coincides with a Global Change in Culture. *Genome Research*, **25**, pp. 459-466.
- KAYSER, M., 2017. Forensic use of Y-Chromosome DNA: A General Overview. *Human Genetics*, **136**(5), pp. 621-635.
- KAYSER, M., CAGLIÀ, A., CORACH, D., FRETWELL, N., GEHRIG, C., GRAZIOSI, G., HEIDORN, F., HERRMANN, S., HERZOG, B. and HIDDING, M., 1997. Evaluation of Y-Chromosomal STRs: A Multicenter Study. *International Journal of Legal Medicine*, **110**(3), pp. 125-133.

KELLY, T., 1934. *The History of Devon and Cornwall, from the Earliest Times to 1714*. London: Murray.

KERSHAW, J. and RØYRVIK, E.C., 2016. The 'People of the British Isles' Project and Viking Settlement in England. *Antiquity*, **90**(354), pp. 1670-1680.

KHUBRANI, Y.M., WETTON, J.H. and JOBLING, M.A., 2018. Extensive Geographical and Social Structure in the Paternal Lineages of Saudi Arabia Revealed by Analysis of 27 Y-STRs. *Forensic Science International: Genetics*, **33**, pp. 98-105.

KIMURA, M. and OHTA, T., 1973. Mutation and Evolution at the Molecular Level. *Genetics*, **73**, pp. Suppl 73: 1-35.

KING, T.E., BALLEREAU, S.J., SCHÜRER, K.S. and JOBLING, M.A., 2006. Genetic Signatures of Coancestry within Surnames. *Current Biology*, **16**(4), pp. 384-388.

KING, T.E. and JOBLING, M.A., 2009a. Founders, Drift, and Infidelity: The Relationship between Y Chromosome Diversity and Patrilineal Surnames. *Molecular Biology and Evolution*, **26**(5), pp. 1093-1102.

KING, T.E. and JOBLING, M.A., 2009b. What's in a Name? Y Chromosomes, Surnames and the Genetic Genealogy Revolution. *Trends in Genetics*, **25**(8), pp. 351-360.

KITSON, P.M., 2009. Religious Change and the Timing of Baptism in England, 1538-1750. *The Historical Journal*, **52**(2), pp. 269-294.

KIVISILD, T., 2015. Maternal Ancestry and Population History from Whole Mitochondrial Genomes. *Investigative Genetics*, **6**(1), pp. 3.

LARMUSEAU, M.H., VANDERHEYDEN, N., VAN GEYSTELEN, A., OVEN, M., KNIJFF, P. and DECORTE, R., 2014. Recent Radiation within Y-chromosomal Haplogroup R-M269 Resulted in High Y-STR Haplotype Resemblance. *Annals of Human Genetics*, **78**(2), pp. 92-103.

LARMUSEAU, M., VANDERHEYDEN, N., VAN GEYSTELEN, A., VAN OVEN, M., KAYSER, M. and DECORTE, R., 2014. Increasing Phylogenetic Resolution Still Informative for Y Chromosomal Studies on West-European Populations. *Forensic Science International: Genetics*, **9**, pp. 179-185.

LARMUSEAU, M., VANOVERBEKE, J., VAN GEYSTELEN, A., DEFRAENE, G., VANDERHEYDEN, N., MATTHYS, K., WENSELEERS, T. and DECORTE, R., 2013. Low Historical Rates of Cuckoldry in a Western European Human Population Traced by Y-Chromosome and Genealogical Data. *Proceedings of the Royal Society of London B: Biological Sciences*, **280**(1772), pp. 20132400.

LASKER, G.W., BOYCE, A.J., BRUSH, G. and MASCIE-TAYLOR, C.G.N., 1985. *Surnames and Genetic Structure*. Cambridge: Cambridge University Press.

- LAWSON, D.J., HELLENTHAL, G., MYERS, S. and FALUSH, D., 2012. Inference of Population Structure using Dense Haplotype Data. *PLoS Genetics*, **8**(1), pp. e1002453.
- LESLIE, S., WINNEY, B., HELLENTHAL, G., DAVISON, D., BOUMERTIT, A., DAY, T., HUTNIK, K., ROYRVIK, E.C., CUNLIFFE, B. and LAWSON, D.J., 2015. The Fine-Scale Genetic Structure of the British Population. *Nature*, **519**(7543), pp. 309-314.
- LIPPOLD, S., XU, H., KO, A., LI, M., RENAUD, G., BUTTHOF, A., SCHRÖDER, R. and STONEKING, M., 2014. Human Paternal and Maternal Demographic Histories: Insights from High-Resolution Y Chromosome and mtDNA Sequences. *Investigative Genetics*, **5**(1), pp. 13.
- MARSDEN, P., 2014. Cornish Identity: Why Cornwall has always been a Separate Place. *The Guardian, Apr*, **26**, pp. 2014.
- MARTINEZ-CADENAS, C., BLANCO-VEREA, A., HERNANDO, B., BUSBY, G.B., BRION, M., CARRACEDO, A., SALAS, A. and CAPELLI, C., 2016. The Relationship between Surname Frequency and Y Chromosome Variation in Spain. *European Journal of Human Genetics*, **24**(1), pp. 120.
- MATEOS, P., 2014. *Names, Ethnicity and Populations : Tracing Identity in Space*. Heidelberg; New York: Springer.
- MATTHEWS, C.M., 1966. *English Surnames*. London: Weidenfeld & Nicolson.
- MCCLURE, P., 2014. Explaining English Surnames: Linguistic Ambiguity and the Importance of Context. Part Two—interpreting the Modern Data. *Nomina*, **37**, pp. 109-141.
- MCCLURE, P., 1981. Nicknames and Petnames: Linguistic Forms and Social Contexts. *Nomina*, **5**, pp. 63-76.
- MCCLURE, P., 1979. Patterns of Migration in the Late Middle Ages: The Evidence of English Place-Name Surnames. *The Economic History Review*, **32**(2), pp. 167-182.
- MCKINLEY, R., 1990. *A History of British Surnames*. London: Longman.
- MENOZZI, P., PIAZZA, A. and CAVALLI-SFORZA, L., 1978. Synthetic Maps of Human Gene Frequencies in Europeans. *Science*, **201**(4358), pp. 786-792.
- MOORE, L.T., MCEVOY, B., CAPE, E., SIMMS, K. and BRADLEY, D.G., 2006. A Y-Chromosome Signature of Hegemony in Gaelic Ireland. *The American Journal of Human Genetics*, **78**(2), pp. 334-338.
- MORRIS, J., THORN CAROLINE, THORN FRANK and PADEL, O.J., 1979. *Domesday Book / 10, Cornwall*. Chichester: Phillimore.
- MUNN, P., 1976. *The Story of Cornwall's Bodmin Moor*. Bodmin: Bodmin Books.

- MYRES, N.M., ROOTSI, S., LIN, A.A., JÄRVE, M., KING, R.J., KUTUEV, I., CABRERA, V.M., KHUSNUTDINOVA, E.K., PSHENICHNOV, A. and YUNUSBAYEV, B., 2011. A Major Y-Chromosome Haplogroup R1b Holocene Era Founder Effect in Central and Western Europe. *European Journal of Human Genetics*, **19**(1), pp. 95.
- NANCE, R.M., 1973. When was Cornish Last Spoken Traditionally? *Cornwall Family History Society*, **7.1**, pp. 76-82.
- NCBI.NLM.NIH.GOV, *National Centre for Biotechnology*. Available: www.ncbi.nlm.nih.gov/tools/primer-blast/ [April 2016].
- NEVGEN, 2017. *NevGen*. Available: http://www.nevgen.org/NevGenGenealogyTools_v1_o.html 2017.
- NORTH, C., 1995. Fustian, Figs, and Frankincense: Jacobean Shop Inventories for Cornwall. *Journal of the Royal Institution of Cornwall*, **2**(2), pp. 32-77.
- NORTH, D.J., SHARPE, A. and INSTITUTE OF CORNISH STUDIES, 1980. *A Word-Geography of Cornwall*. Redruth: Institute of Cornish Studies.
- NOVEMBRE, J., JOHNSON, T., BRYC, K., KUTALIK, Z., BOYKO, A.R., AUTON, A., INDAP, A., KING, K.S., BERGMANN, S. and NELSON, M.R., 2008. Genes Mirror Geography within Europe. *Nature*, **456**(7218), pp. 98.
- OLALDE, I., BRACE, S., ALLENTOFT, M.E., ARMIT, I., KRISTIANSEN, K., BOOTH, T., ROHLAND, N., MALLICK, S., SZÉCSÉNYI-NAGY, A. and MITTNIK, A., 2018. The Beaker Phenomenon and the Genomic Transformation of Northwest Europe. *Nature*, **555**(7695), pp. 190.
- PADEL, O.J., 2013a. Five Cornish Toponyms Revisited: Crim, Darite, Uthnoe, Port Isaac, Treverva. *Studia Celtica*, **47**(1), pp. 69-111.
- PADEL, O.J., 2013b. Historical Background to the Sculpture. In: A. PRESTON-JONES, ed, *Corpus of Anglo-Saxon stone sculpture. Vol.11, Early Cornish sculpture*. Oxford: Oxford University Press, pp. 21-33.
- PADEL, O.J., 2012. Origin of the Surname Menhinick, Menhenitt. *Journal of the Royal Institution of Cornwall*, **1**, pp. 89-100.
- PADEL, O.J., 2009. *Slavery in Saxon Cornwall: The Bodmin Manumissions*. Cambridge: Hughes Hall & Department of Anglo-Saxon, Norse and Celtic, University of Cambridge.
- PADEL, O.J., 2007. Place-Names and the Saxon Conquest of Devon and Cornwall. In: N. HIGHAM, ed, *Britons in Anglo-Saxon England*. Suffolk: The Boydell Press Woodbridge, pp. 215-230.
- PADEL, O.J., 1988. *A Popular Dictionary of Cornish Place-Names*. Penzance: A. Hodge.

- PADEL, O.J., 1985a. Cornish Surnames in 1327. *Nomina*, 9(1), pp. 81-87.
- PADEL, O.J., 1985b. *Cornish Place-Name Elements*. Nottingham: English Place-Name Society.
- PATTISON, J.E., 2008. Is it Necessary to Assume an Apartheid-Like Social Structure in Early Anglo-Saxon England? *Proceedings of the Royal Society of London B: Biological Sciences*, 275(1650), pp. 2423-2429.
- PAYTON, P., 1996. *Cornwall*. Fowey: Alexander Associates.
- PAYTON, P., 1992. *The Making of Modern Cornwall : Historical Experience and the Persistence of "Difference"*. Redruth: Dyllansow Truran.
- PEARSE, R., 1983. *The Land Beside the Celtic Sea : Some Aspects of Ancient, Medieval and Victorian Cornwall*. Redruth: Truran.
- PHYTHIAN-ADAMS, C., 1993. Introduction: An Agenda for English Local History. In: C. PHYTHIAN-ADAMS, ed, *Societies, cultures and kinship 1580-1850: Cultural provinces and English local history*. London: Leicester University Press, pp. 1-23.
- PHYTHIAN-ADAMS, C., 1987. *Re-Thinking English Local History*. Leicester: Leicester University Press.
- POOLEY, C. and TURNBULL, J., 2005. *Migration and Mobility in Britain since the Eighteenth Century*. London: Routledge.
- POSTLES, D., 1995. *The Surnames of Devon*. Oxford: Leopard's Head Press.
- POUNDS, N.J., 1973. Barton Farming in Eighteenth-Century Cornwall. *Journal of the Royal Institution of Cornwall*, 7, pp. 55.
- POZNIK, G.D., XUE, Y., MENDEZ, F.L., WILLEMS, T.F., MASSAIA, A., SAYRES, M.A.W., AYUB, Q., MCCARTHY, S.A., NARECHANIA, A. and KASHIN, S., 2016. Punctuated Bursts in Human Male Demography Inferred from 1,244 Worldwide Y-Chromosome Sequences. *Nature Genetics*, 48(6), pp. 593.
- PRICE, G., 1984. *The Languages of Britain*. London: Edward Arnold.
- PURPS, J., SIEGERT, S., WILLUWEIT, S., NAGY, M., ALVES, C., SALAZAR, R., ANGUSTIA, S.M., SANTOS, L.H., ANSLINGER, K. and BAYER, B., 2014. A Global Analysis of Y-Chromosomal Haplotype Diversity for 23 STR Loci. *Forensic Science International: Genetics*, 12, pp. 12-23.
- QAMAR, R., AYUB, Q., MOHYUDDIN, A., HELGASON, A., MAZHAR, K., MANSOOR, A., ZERJAL, T., TYLER-SMITH, C. and MEHDI, S.Q., 2002. Y-Chromosomal DNA Variation in Pakistan. *The American Journal of Human Genetics*, 70(5), pp. 1107-1124.

- REANEY, P.H., 1967. *The Origin of English Surnames*. London: Routledge and Kegan Paul.
- REANEY, P.H. and WILSON, R.M., 1995. *A Dictionary of English Surnames*. 3rd with corrections and additions edn. Oxford: Oxford University Press.
- REDMONDS, G., 2004. *Names and History: People, Places, and Things*. London: A&C Black.
- REDMONDS, G., 1972. Surname Heredity in Yorkshire. *Local Historian*, **10**(4), pp. 171-177.
- REDMONDS, G., KING, T.E. and HEY, D., 2011. *Surnames, DNA, and Family History*. Oxford: Oxford University Press.
- RIPPON, S., 2012. *Making Sense of an Historic Landscape*. Oxford: Oxford University Press.
- ROCCA, R.A., MAGOON, G., REYNOLDS, D.F., KRAHN, T., TILROE, V.O., DEN VELDE BOOTS, PETER M OP and GRIERSON, A.J., 2012. Discovery of Western European R1b1a2 Y Chromosome Variants in 1000 Genomes Project Data: An Online Community Approach. *PLoS One*, **7**(7), pp. e41634.
- ROEWER, L. and EPPLIN, J.T., 1992. Rapid and Sensitive Typing of Forensic Stains by PCR Amplification of Polymorphic Simple Repeat Sequences in Case Work. *Forensic Science International*, **53**(2), pp. 163-171.
- ROGERS, C.D., 1995. *The Surname Detective: Investigating Surname Distribution in England, 1086-Present Day*. Manchester: Manchester University Press.
- ROSE, P. and PRESTON-JONES, A., 1995. Changes in the Cornish Countryside. In: D. HOOKE and S. BURNELL, eds, *Landscape and settlement in Britain, AD 400-1066*. Exeter: University of Exeter Press, pp. 51-68.
- ROSENBERG, N.A., PRITCHARD, J.K., WEBER, J.L., CANN, H.M., KIDD, K.K., ZHIVOTOVSKY, L.A. and FELDMAN, M.W., 2002. Genetic Structure of Human Populations. *Science*, **298**(5602), pp. 2381-2385.
- ROSSER, Z.H., ZERJAL, T., HURLES, M.E., ADOJAAN, M., ALAVANTIC, D., AMORIM, A., AMOS, W., ARMENTEROS, M., ARROYO, E. and BARBUJANI, G., 2000. Y-Chromosomal Diversity in Europe is Clinal and Influenced Primarily by Geography, rather than by Language. *The American Journal of Human Genetics*, **67**(6), pp. 1526-1543.
- ROWSE, A.L., 1969. *Tudor Cornwall : Portrait of a Society*. London: Macmillan.

SCHURER, K., and WOOLLARD, M., 2000. *1881 Census for England and Wales, the Channel Islands and the Isle of Man (Enhanced Version)*. Available: <http://doi.org/10.5255/UKDA-SN-4177-1> [October 2015].

SEIELSTAD, M., BEKELE, E., IBRAHIM, M., TOURÉ, A. and TRAORÉ, M., 1999. A View of Modern Human Origins from Y Chromosome Microsatellite Variation. *Genome Research*, **9**(6), pp. 558-567.

SIMS, L.M., GARVEY, D. and BALLANTYNE, J., 2007. Sub-populations within the Major European and African Derived Haplogroups R1b3 and E3a are Differentiated by Previously Phylogenetically Undefined Y-SNPs. *Human Mutation*, **28**(1), pp. 97.

SLATKIN, M., 1995. A Measure of Population Subdivision Based on Microsatellite Allele Frequencies. *Genetics*, **139**(1), pp. 457-462.

SNELL, K.D.M., 2006. *Parish and Belonging : Community, Identity and Welfare in England and Wales, 1700–1950*. Cambridge: Cambridge University Press.

SOARES, P., ERMINI, L., THOMSON, N., MORMINA, M., RITO, T., RÖHL, A., SALAS, A., OPPENHEIMER, S., MACAULAY, V. and RICHARDS, M.B., 2009. Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock. *The American Journal of Human Genetics*, **84**(6), pp. 740-759.

STANES, R., 2000. *A History of Devon*. 2nd edn. Chichester: Phillimore.

STOYLE, M., 2002. *West Britons : Cornish Identities and the Early Modern British State*. Exeter: University of Exeter Press.

STOYLE, M., 1997. Cornish Rebellions, 1497-1648. *History Today*, **47**(5), pp. 22-28.

SUN, J.X., HELGASON, A., MASSON, G., EBENESERSDOTTIR, S.S., LI, H., MALLICK, S., GNERRE, S., PATTERSON, N., KONG, A. and REICH, D., 2012. A Direct Characterization of Human Mutation Based on Microsatellites. *Nature Genetics*, **44**(10), pp. 1161.

SVENSSON, Ö, 1987. *Saxon Place-Names in East Cornwall*. Lund: Lund University Press.

SYKES, B. and IRVEN, C., 2000. Surnames and the Y Chromosome. *The American Journal of Human Genetics*, **66**(4), pp. 1417-1419.

THOMAS, C., 1973. *The Importance of being Cornish*. Exeter: University of Exeter.

THOMAS, J., 2007. *Lost Cornwall*. Edinburgh: Birlinn.

THOMSON, R., PRITCHARD, J.K., SHEN, P., OEFNER, P.J. and FELDMAN, M.W., 2000. Recent Common Ancestry of Human Y Chromosomes: Evidence from DNA

Sequence Data. *Proceedings of the National Academy of Sciences*, **97**(13), pp. 7360-7365.

TILLEY, C., 2010. *Interpreting Landscapes : Geologies, Topographies, Identities*. Walnut Creek, Calif.: Left Coast Press.

TILLEY, C., 1996. The Powers of Rocks: Topography and Monument Construction on Bodmin Moor. *World Archaeology*, **28**(2), pp. 161-176.

TODD, M. and FLEMING, A., 1987. *The South West to AD 1000*. London: Longman.

TREGIDGA, G., 2012. *Memory, Place and Identity : The Cultural Landscapes of Cornwall*. London: Francis Boutle Publishers.

TRUDGILL, P., 1984. *Language in the British Isles*. Cambridge: Cambridge University Press.

TURNER, S., 2006. *Making a Christian Landscape: The Countryside in Early Medieval Cornwall, Devon and Wessex*. Exeter: University of Exeter Press.

UK GOV, 2014. *Cornish granted minority status within the UK*. Available: <https://www.gov.uk/government/announcements> [April 2014].

URQUHART, A., OLDROYD, N.J., KIMPTON, C.P. and GILL, P., 1995. Highly Discriminating Heptaplex Short Tandem Repeat PCR System for Forensic Identification. *BioTechniques*, **18**(1), pp. 11-1.

VALVERDE, L., ILLESCAS, M.J., VILLAESCUSA, P., GOTOR, A.M., GARCÍA, A., CARDOSO, S., ALGORTA, J., CATARINO, S., ROUAULT, K. and FÉREC, C., 2016. New Clues to the Evolutionary History of the Main European Paternal Lineage M269: Dissection of the Y-SNP S116 in Atlantic Europe and Iberia. *European Journal of Human Genetics*, **24**(3), pp. 437-441.

VICTORIA HISTORY OF THE COUNTIES OF ENGLAND, 1924. *The Victoria History of the Counties of England. A History of the County of Cornwall / Part 8, the Domesday Survey for Cornwall, Introduction by L.F. Salzman and Others, Translation of the Text by Thomas Taylor*. London: St. Catherine Press.

VILLAESCUSA, P., ILLESCAS, M.J., VALVERDE, L., BAETA, M., NUÑEZ, C., MARTÍNEZ-JARRETA, B., ZARRABEITIA, M.T., CALAFELL, F. and DE PANCORBO, M.M., 2017. Characterization of the Iberian Y Chromosome Haplogroup R-DF27 in Northern Spain. *Forensic Science International: Genetics*, **27**, pp. 142-148.

WADE, J.H., 1928. *Rambles in Cornwall*. London: Methuen.

WALSH, B., 2001. Estimating the Time to the most Recent Common Ancestor for the Y Chromosome Or Mitochondrial DNA for a Pair of Individuals. *Genetics*, **158**(2), pp. 897-912.

WEALE, M.E., WEISS, D.A., JAGER, R.F., BRADMAN, N. and THOMAS, M.G., 2002. Y Chromosome Evidence for Anglo-Saxon Mass Migration. *Molecular Biology and Evolution*, **19**(7), pp. 1008-1021.

WHITE, G.P., 1981. *A Handbook of Cornish Surnames*. 2nd edn. Redruth: Dyllansow Truran.

WHYTE, I.D., WINCHESTER, A.J.L., HOOKE, D. and SOCIETY FOR LANDSCAPE STUDIES, 2004. *Society, Landscape and Environment in Upland Britain*. Great Britain: Society for Landscape Studies.

WILCOX, A., 1999. *National Index of Parish Registers. Vol.8, Part 4, Cornwall*. London: Society of Genealogists.

WILDER, J.A., KINGAN, S.B., MOBASHER, Z., PILKINGTON, M.M. and HAMMER, M.F., 2004. Global Patterns of Human Mitochondrial DNA and Y-Chromosome Structure are Not Influenced by Higher Migration Rates of Females Versus Males. *Nature Genetics*, **36**(10), pp. 1122.

WILKINS, J.F. and MARLOWE, F.W., 2006. Sex-biased Migration in Humans: What should we Expect from Genetic Data? *Bioessays*, **28**(3), pp. 290-300.

WINNEY, B., BOUMERTIT, A., DAY, T., DAVISON, D., ECHETA, C., EVSEEVA, I., HUTNIK, K., LESLIE, S., NICODEMUS, K. and ROYRVIK, E.C., 2012. People of the British Isles: Preliminary Analysis of Genotypes and Surnames in a UK-Control Population. *European Journal of Human Genetics*, **20**(2), pp. 203.

WRIGLEY, E.A., 2007. English County Populations in the Later Eighteenth Century. *The Economic History Review*, **60**(1), pp. 35-69.

Y CHROMOSOME CONSORTIUM, 2002. A Nomenclature System for the Tree of Human Y-Chromosomal Binary Haplogroups. *Genome Research*, **12**(2), pp. 339-348.

YHRD.ORG, 2019. *Y Haplotype Reference Database*. Available: <https://yhrd.org/> [January 2019].

YU, N., CHEN, F., OTA, S., JORDE, L.B., PAMILO, P., PATTHY, L., RAMSAY, M., JENKINS, T., SHYUE, S. and LI, W., 2002. Larger Genetic Differences within Africans than between Africans and Eurasians. *Genetics*, **161**(1), pp. 269-274.

ZHIVOTOVSKY, L.A., UNDERHILL, P.A., CINNIOĞLU, C., KAYSER, M., MORAR, B., KIVISILD, T., SCOZZARI, R., CRUCIANI, F., DESTRO-BISOL, G. and SPEDINI, G., 2004. The Effective Mutation Rate at Y Chromosome Short Tandem Repeats, with Application to Human Population-Divergence Time. *The American Journal of Human Genetics*, **74**(1), pp. 50-61.

