



**Post-glacial colonisation of Europe by the wood mouse,  
*Apodemus sylvaticus*: evidence of a northern refugium and  
dispersal with humans**

Journal:	<i>Biological Journal of the Linnean Society</i>
Manuscript ID	BJLS-4586.R1
Manuscript Type:	Research Article
Date Submitted by the Author:	10-Jul-2016
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Keywords:	Cytochrome <i>b</i> , Demography, Human introduction, Mitochondrial DNA, Molecular clock, Phylogeography

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47 **Running title:** Phylogeography of the wood mouse  
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## ABSTRACT

The wood mouse *Apodemus sylvaticus* is an opportunistic rodent that is found throughout most of the European mainland. It is present on many islands around the margins of the continent and in northern Africa. The species has been the subject of previous phylogeographic studies but these have focussed on the more southerly part of its range. A substantial number of new samples, many of them from the periphery of the species' range, contribute to an exceptional dataset comprising 981 mitochondrial cytochrome *b* sequences. These new data provide sufficient resolution to transform our understanding of the species' survival through the last glaciation and its subsequent re-colonisation of the continent. The deepest genetic split we found is in agreement with previous studies and runs from the Alps to central Ukraine, but we further distinguish two separate lineages in wood mice to the north and west of this line. It is likely that this part of Europe was colonised from two refugia, putatively located in the Iberian peninsula and the Dordogne or Carpathian region. The wood mouse therefore joins the growing number of species with extant populations that appear to have survived the Last Glacial Maximum in northern refugia, rather than solely in traditionally recognised refugial locations in the southern European peninsulas. Furthermore, the existence of a northern refugium for the species was predicted in a study of mitochondrial variation in a specific parasite of the wood mouse, demonstrating the potential value of data from parasites to phylogeographic studies. Lastly, the presence of related haplotypes in widely disparate locations, often on islands or separated by substantial bodies of water, demonstrates the propensity of the wood mouse for accidental human-mediated transport.

## ADDITIONAL KEY WORDS

Cytochrome *b*  
Demography  
Human introduction  
Mitochondrial DNA  
Molecular clock  
Phylogeography

## INTRODUCTION

The wood (or field) mouse *Apodemus sylvaticus* (Linnaeus, 1758) is one of several European representatives from a genus that is distributed across the Palaearctic region (Musser & Carleton, 2005). The wood mouse shares much of its range with the closely-related yellow-necked mouse *A. flavicollis* (Melchior, 1834), but it is found in many locations around the western margins of the continent and in North Africa, while the yellow-necked mouse reaches further east into western Asia (Montgomery, 1999a,b; Amori *et al.*, 2008; Schlitter *et al.*, 2008). Although the wood mouse is often associated with temperate woodland, it is highly adaptable and opportunistic, and is found in a wide range of habitats including forests, hedgerows, fields, grassland, gardens and dunes (Flowerdew & Tattersall, 2008).

The phylogeography of this very numerous and widely distributed European species has previously been studied by a number of authors (Michaux *et al.*, 2003; Michaux, Libois & Filippucci, 2005; Hoofer *et al.*, 2007; Lalíš *et al.*, 2016), based on various series of mitochondrial cytochrome *b* (cyt *b*) gene sequences. Unsurprisingly, given the emphasis at that time on Mediterranean peninsulas as glacial refugia and as the source of populations that colonised northern Europe in the Holocene (Taberlet *et al.*, 1998; Hewitt, 1999), the earlier work was focused on the southern part of the continent and few data *were* related to the northern and more peripheral parts of the species' range (Michaux *et al.*, 2003). Since then, more northerly glacial refugia have been identified as the source of contemporary populations in several temperate European mammal species (Deffontaine *et al.*, 2005; Kotlík *et al.*, 2006; Vega *et al.*, 2010; Wójcik *et al.*, 2010; McDevitt *et al.*, 2012), and it is now widely accepted that the Mediterranean peninsulas were often harbours of endemic diversity, rather than sources for subsequent population expansion (Bilton *et al.*, 1998). In the present study, we have 454 new cyt *b* sequences from these more northerly and peripheral locations, while another recent study provides a large volume of data from North Africa (Lalíš *et al.* 2016), so that sampling now covers most of the species' range. This impressive dataset now includes 981 wood mouse cyt *b* sequences and 543 haplotypes.

In addition, the field of phylogeography has developed considerably since the time of these earlier studies, and we have applied modern techniques and assumptions to the analysis of the data. In particular, there is now a radically altered understanding of the timing of phylogeographic events, following the realisation that molecular clock rates are time dependent (Ho *et al.*, 2005), when measured over the recent timescales that apply to studies of intraspecific genetic variation. This has led to an appreciation of the need for calibrations that are directly based on the data themselves, or at least on equivalent data from other species, rather than deep interspecific splits that are associated with fossils of known age (Ho *et al.*, 2005, 2011; Ho & Larson, 2006). Here we have used a mitochondrial cyt *b* clock rate that was directly estimated from 23 radiocarbon dated sub-fossil samples of another rodent, the common vole *Microtus arvalis* (Martíková *et al.*, 2013). These remains were obtained from archaeological sites in Orkney and were therefore deposited over a timescale similar to that which is likely to operate here and under the specific climatic background of the later Pleistocene and Holocene in Europe.

The wood mouse is present on numerous islands around the Atlantic coasts of Europe, including those of the British Isles, and of the Mediterranean Sea (Corbet, 1978; Montgomery, 1999b). In contrast, the closely related yellow-necked mouse is found in much of the wood mouse mainland European range, but is recorded from far fewer island locations (Montgomery, 1999a). The prevalence of the wood mouse on islands, and its close association with human activities, led to the realisation that it had been introduced, presumably by accident, to the islands around Britain during the Holocene (Corbet, 1961; Berry, 1969). Following this realisation, the frequency of non-metrical skeletal characters in island and mainland populations were used as a proxy for genetic variation, to infer the source of the introductions of wood mice and other island mammals (Berry, Evans & Sennett, 1967; Berry, 1969, 1973). The results of these studies appeared to implicate Viking settlers from Scandinavia in the introduction of these species to the islands around Britain,

a conclusion that has been confirmed more recently with molecular data from the western house mouse *Mus musculus domesticus* Schwarz and Schwarz, 1943 (Searle *et al.*, 2009a; Jones *et al.*, 2012, 2013). These analyses of phenotypic characters share a common goal with many of the phylogeographic analyses that have subsequently been developed, to place genetic variation in its historical and geographic context.

Given the number of these island wood mouse populations, accidental human introductions may have played an important role in dispersal of the species at the margins and, by implication, elsewhere in its range. Despite the earlier studies using non-metrical characters, this aspect of post-glacial colonisation received little attention in previous phylogeographic studies of the wood mouse, other than a recent paper which focused on the North African range of the species (Lalis *et al.*, 2016). This may be due to their bias towards the Mediterranean peninsulas and the more central European mainland (Michaux *et al.*, 2003; Michaux, Libois & Filippucci 2005; Hoofer *et al.*, 2007). In addition to range-wide European phylogeographic reconstruction, the present study therefore seeks to examine the role of human introductions in the post-glacial spread of the wood mouse.

## MATERIAL AND METHODS

Genomic DNA was extracted from 407 frozen or ethanol preserved tissue samples and from 47 preserved skins or dried soft tissue adhering to skulls, using commercially available extraction kits (QIAGEN DNeasy®). In the case of frozen or ethanol preserved tissues, the entire 1140 base-pair cyt b gene was generally amplified in a single polymerase chain reaction (PCR) using standard protocols and primers originally adapted for *Microtus* voles (Jaarola & Searle, 2002) but also effective for other mammals including *Apodemus*. In a limited number of cases, a shorter segment of the cyt b gene (usually trimmed to 818 base-pairs) was amplified using primers developed for *Apodemus* (Michaux *et al.*, 2003). For museum skins and other dried tissue, the cyt b gene was amplified using a protocol designed for this type of material, along with a suite of new or previously published primers (Table S.1; Conroy & Cook, 1999; Michaux *et al.*, 2001; Jaarola & Searle, 2002; Wójcik *et al.*, 2010). Museum skins yield reduced amounts of DNA, which is also more fragmented, therefore the gene was amplified in five overlapping fragments of about 230 to 360 base-pairs. Negative controls, with no tissue in the DNA extraction and no template DNA in the PCR, were included in each procedure.

Sequencing was carried out in commercial facilities, using primers listed in Table S.1. For DNA amplified from frozen or ethanol preserved tissue samples, the two PCR primers and two newly designed internal primers were initially used, but only the two internal primers were used latterly. For DNA amplified from skins or other dried tissue, the PCR primers were used. Sequences for all new haplotypes reported in this paper have been deposited in the GenBank database (KX159497 – KX159717) and, where available, voucher specimens are preserved in either the National Museums of Scotland or the Mammal Research Institute, Polish Academy of Sciences.

An alignment was prepared from the 454 new sequences that were generated in the course of this study, together with 527 previously published sequences from the species, using Seaview 4.5.4 (Gouy, Guindon & Gascuel, 2010). Details for all sequences, including source, sample material, geographical locality, GenBank and voucher reference numbers are provided in Table S.2. Most of the previously published sequences are considerably shorter than the complete 1140 base-pair cyt b gene amplified here, therefore lengths of sequences are also included in this table. There has been some confusion in earlier literature (Michaux *et al.*, 2003, 2005; Lalis *et al.*, 2016) regarding data for some of the published sequences. The anomalies have been corrected in the course of the present study and the list of data in Table S.2 may be taken as definitive for all *A. sylvaticus* cyt b sequences that are available in the GenBank database at the time of writing.

Haplotypes were determined using the program Arlequin 3.5 (Excoffier & Lischer, 2010) and subsequent visual checking of alignments with Seaview 4.5.4. Sequences differing only by missing calls were initially defined as separate haplotypes, which were used in phylogenetic reconstruction. These haplotypes are shown in the complete list of specimens (Table S.2). For geographic analysis (see below), sequences differing only by missing nucleotide data were defined as the same haplotype.

The program jModeltest 2.1.7 (Darriba *et al.*, 2012) was used to compare a range of GTR-nested nucleotide substitution models, with or without unequal base frequencies and gamma distribution of rates across sites. The best model was selected and used in subsequent phylogenetic and population genetic analyses, based on Decision Theory (DT) or Bayesian Information Criterion (BIC), depending on the particular method employed in these analyses.

A maximum likelihood (ML) tree was inferred from the 543 haplotypes with PhyML 3.0 (Guindon *et al.*, 2010). The substitution model was Tamura-Nei+G (Tamura & Nei, 1993), a single transition and two transversion rates with gamma distribution across sites and unequal base frequencies, selected according to the DT (above). The outgroup used was *A. flavicollis*, which is included within the same subgenus *Sylvaemus* as *A. sylvaticus* (Michaux *et al.*, 2002; Suzuki *et al.*, 2008).

Branch support was quantified by the Shimodaira-Hasegawa-like test (SH-aLRT) implemented in PhyML 3.0 (Guindon *et al.*, 2010), a non-parametric version of the approximate likelihood ratio test (aLRT; Anisimova & Gascuel, 2006). The SH-aLRT is based on the Shimodaira-Hasegawa multiple tree comparison procedure (Shimodaira & Hasegawa, 1999). It makes use of intermediate likelihood values from the original ML tree search and consequently offers a fast alternative to bootstrap support values, which require the inference of many replicate ML trees (Anisimova *et al.*, 2011). The SH-aLRT has slightly more power and is almost as conservative as the standard non-parametric bootstrap procedure, at least for support thresholds down to 0.8 (Anisimova *et al.*, 2011), therefore the interpretation of support values from the two methods will be similar.

Nuclear mitochondrial translocations (numts) were unwittingly included in previous phylogenetic analyses of *Apodemus cyt b* gene sequences (Martin *et al.*, 2000; Reutter *et al.*, 2003; Suzuki *et al.*, 2008), however their presence and characteristics have subsequently been established (Dubey *et al.*, 2009). The newly prepared alignment was therefore checked for anomalous sequences, containing nonsense codons, stop codons or shifts of the reading frame, as these might represent numts. In addition, another ML tree was inferred, using the whole *A. sylvaticus* cyt *b* alignment together with outgroup sequences from four other members of the subgenus *Sylvaemus* and four *A. sylvaticus* numt sequences available from GenBank, to check that our cyt *b* alignment did not contain any sequences that were similar to these previously identified numts.

Reticulating networks may be more effective than bifurcating trees in recovering intraspecific patterns of genetic variation (Posada & Crandall, 2001). Minimum Spanning and Median Joining algorithms (Bandelt, Forster & Röhl, 1999), both implemented in the program PopART 1.7 (Leigh J, <http://popart.otago.ac.nz>), were therefore used to infer networks from all of the 981 cyt *b* sequences (Table S.2). The reticulating network was then compared with the ML tree, to confirm the structure and to identify any additional information about the relationships among lineages.

The genetic structure, as identified in the ML tree, was tested by Analysis of Molecular Variance (AMOVA), based on genetic distances within and among the mitochondrial lineages, using Arlequin 3.5. Percentages of variation and  $\Phi_{ST}$  were calculated and their significance tested with 10,000 permutations of individuals among lineage populations. In addition,  $\Phi_{ST}$  was calculated for each pairwise comparison of lineage populations, with significance again tested using 10,000 permutations.

Genetic variation in lineage populations was examined using a range of analyses available in DnaSP 5.10.01 (Librado & Rozas, 2009). Nucleotide diversity ( $\pi$ ), the average number of pairwise differences (per site) between sequences, was calculated for each lineage and its standard deviation was computed as the root of the variance. Two test statistics,  $D$  (Tajima, 1989) and  $F_S$  (Fu, 1997) were also calculated for each lineage, to identify episodes of possible recent demographic expansion in them. Significance of Tajima's  $D$  statistic was determined from published confidence limits with a beta distribution (Tajima, 1989), while significance of Fu's  $F_S$  was determined using null distributions obtained from 1,000 coalescent simulations.

The frequency distributions of pairwise nucleotide site differences (mismatches) were obtained for each lineage using Arlequin v.3.5, to determine whether the population had passed through a recent demographic expansion. A sudden demographic expansion leads to a unimodal mismatch distribution that can be described by a model with three parameters, which are composed of the mutation rate together with the time since expansion ( $r$ ), the population size before ( $\theta_0$ ) and after ( $\theta_1$ ) the event (Rogers & Harpending, 1992). These were calculated using a generalized least-square approach (Schneider & Excoffier, 1999) and the expected distribution compared with the observed one graphically and by computing the sum of squared deviations (SSD) between the two distributions and the raggedness index ( $r$ ). Significance of the SSD and  $r$ , together with confidence intervals for the  $r$  parameter, were obtained by re-calculating them for each distribution obtained from 10,000 coalescent simulations that used the original estimated

parameters of the demographic expansion. An indication of the relative time of expansion was obtained for each lineage, by comparing the values of nucleotide diversity ( $\pi$ ) and the mismatch  $\tau$  parameter from each of them.

More sophisticated demographic analyses were carried out using Bayesian Markov chain Monte Carlo (MCMC) simulations in *Beast 2.3.1* (Bouckaert *et al.*, 2014). Individual coalescent genealogies and skyline models (Drummond *et al.*, 2005) of the effective population size for female voles belonging to each of the six identified mitochondrial lineages were co-estimated using a shared model of sequence evolution. Separate genealogies and demographic models are appropriate for these distinct female lineage populations, which are presumed to be independent and the result of distinct population expansions, as this takes account of genetic structure within the overall population of the species. The number of groups in the skyline model for each lineage was based on the (unequal) number of sequences within them. The shared substitution model used was the Tamura-Nei+G (Tamura & Nei, 1993), as selected using the BIC in *jModeltest* 2.1.7. Base frequencies, kappa values for transition/transversion rates and the alpha parameter of the gamma distribution of rates were all estimated along with the other parameters of the model. The molecular clock rate was fixed at  $3.27 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ , which was previously estimated from radiocarbon dated sequences of another rodent, the common vole *Microtus arvalis* (Martíková *et al.*, 2013). A strict molecular clock was used, given that the sequences are from a single species and there should be little variation in branch rates. Prior parameter distributions are shown in Table S.3 and all simulations were repeated without sequence data, in order to test the joint distributions of parameters obtained with the priors alone and ensure that the results were not unduly influenced by these.

Posterior parameter distributions were obtained from eight separate MCMC chains that were each run for 100 million generations, using different random seeds, with the first 10 million generations removed as burnin. Log files from these eight simulations were examined using *Tracer 1.6* (Rambaut *et al.*, 2014), to check for convergence, based on the posterior distributions and the traces of the values for each parameter. The effective sample size (ESS) for each parameter was at least 200, which is generally considered to be a sufficient sample of the posterior distribution. The log files were combined using the *LogCombiner* program from the *Beast 2.3.1* package. The posterior distribution, value trace and ESS for each parameter was then examined in the combined file using *Tracer 1.6* (Rambaut *et al.*, 2014). This program was also used to derive the Bayesian Skyline Plot (BSP), effective female population size over time, for each lineage.

For haplotypes found in more than one geographical location, pairwise geodesic distances (World Geodetic System: WGS84) were calculated between each of these locations. Locations within a single land mass or island archipelago were collapsed to their mean (for two locations) or centroid coordinates. Connections between locations with identical haplotypes were mapped, where these involved sea crossings. Calculations were carried out with *R* 3.2.2 (Hijmans, 2015; R Core Team, 2015) and mapping with *QGIS v2.0.1* (QGIS Development Team 2004-2014), using *OpenStreetMap* coastline data (<http://www.openstreetmap.org>).

## RESULTS

The alignment contained 981 *cyt b* sequences (Table S.2) comprising 543 haplotypes, as defined above. There were 521 haplotypes, after collapsing those distinguished only by missing nucleotide data. Most of the species' mainland European range (Montgomery, 1999b) has now been sampled, with substantial coverage of peripheral regions to the west, north and east, including Iberia, France, Britain, Scandinavia and Poland. Many of the islands on the Atlantic are now included, with samples from Iceland, Ireland and 45 of the islands around Britain. In addition, many sequences from North Africa have recently become available (Lalis *et al.*, 2016). Remaining shortcomings in the coverage are largely confined to the south-eastern part of the wood mouse range and the Mediterranean islands.

There was no evidence for any *numts* among the sequences studied here. None of them contained any nonsense codons, nucleotide insertions or deletions that would shift the reading frame, and there were no internal stop codons. All of the wood mouse sequences clustered together in a highly supported (SH-aLRT 1.00) clade within the ML tree that was inferred for the whole alignment together with four *Sylvaemus* outgroup and four wood mouse *numt* sequences from GenBank (Fig. S.1). Furthermore, the wood mouse clade was less closely associated with the *numt* sequences than with the outgroup sequences, both of which also clustered into monophyletic groups.

The 543 haplotypes clustered into six distinct lineages within the ML tree (Fig. 1) and these have been named here according to the geographical distributions of the sampled sequences (Fig. 2). The *south-eastern*, *Sicilian* and *African* lineages were previously identified in other studies (Michaux *et al.* 2003, 2005; Lalis *et al.* 2016). The *central* and *peripheral* lineages are newly identified here, having previously been considered a single homogeneous group (subclade 2b of Michaux *et al.*, 2003). The *Channel Island* lineage comprises only two new haplotypes (based on five sequences) from the islands of Sark and Guernsey, off the northern coast of France. A well-supported (SH-aLRT 0.97) node connects the *Channel Island* and *African* lineages. Five of the six lineages had strong SH-aLRT support (0.86 – 0.97) in the ML tree (Fig. 1). The central lineage was less well-supported, with SH-aLRT of 0.78, which is just below the threshold where the SH-aLRT begins to diverge and become less conservative, albeit remaining substantially more powerful, than the standard bootstrap (Anisimova *et al.*, 2011).

The 543 haplotypes clustered into five distinct haplogroups in the Minimum Spanning and Median Joining Networks, which were very similar to each other (Fig. 3). The *central* and *peripheral* haplogroups were very closely related to each other, as were the *south-eastern* and *Sicilian* haplogroups. Of the *central* and *peripheral* haplogroups, the former was more closely related to the *south-eastern* and *Sicilian* haplogroups. The *African* haplogroup was clearly associated with the *central* haplogroup and included the two haplotypes from the geographically distant *Channel Islands* of Sark and Guernsey.

An AMOVA, using genetic distances within and among the six lineage populations, showed that most of the variation was attributable to the divergence between the lineages ( $\Phi_{ST} = 0.770$ , bootstrap 0.05/99.95 percentile range 0.643 – 0.846). Pairwise fixation indices for combinations of the six lineages also lend support to the identified genetic structure (Table 1). These ranged from 0.603 – 0.894 and all of them were significant based on 10,000 permutations of individuals among groups.

There is a clear genetic split in the data, which in mainland Europe is geographically aligned from the Alps to central Ukraine (Fig. 2). This genetic split is apparent in both the ML tree, where it is represented by a deep node within the genealogy (Fig. 1) and in the network, where the split is represented by a branch with multiple mutational steps (Fig. 3). The split is also apparent from the higher fixation indices for pairs that include either the *south-eastern* or *Sicilian* lineage, along with one of the other lineages. The continent to the south of this geographical divide, from the

Italian and Balkan peninsulas to Ukraine, is occupied by the *south-eastern* lineage, together with the more closely related and endemic *Sicilian* lineage, while to the north and west, the remainder of Europe is occupied by the *central* and *peripheral* lineages, together with the *Channel Island* lineage (Fig. 2). The *central* lineage reaches from the Iberian peninsula in the west to the southern part of the Fennoscandian peninsula in the north. The *peripheral* lineage is found in predominantly more peripheral locations that extend from Ukraine and Poland in the east to the western European mainland, Scandinavia, the British Isles and Iceland. There is also one more lineage, the *African*, found only in the North African part of the species' range.

Nucleotide diversity ( $\pi$ ), an indicator of the relative age of the clade in question, is shown for each lineage in Table 2. The nucleotide diversity is higher in the *Sicilian* lineage (0.01295) than in the *south-eastern*, *central* or *peripheral* ones (0.00468 – 0.00597), whereas the *African* and the *Channel Island* lineages both have lower diversity (0.00366, 0.00263).

The graphs of mismatch distributions for the *central*, *peripheral*, *African*, *south-eastern* and *Sicilian* lineages all show the characteristic unimodal pattern that is indicative of a recent demographic expansion. However, the observed distributions of the latter two, and especially the *Sicilian* lineage, are not so close to the expected sudden expansion distributions with the model parameters (Fig. S.2). The mismatch distribution for the *Channel Island* lineage is bimodal, but the sample size for this group ( $n = 5$ ) is very small. The sum of squared deviations (SSD) from the model distributions are low (0.001 – 0.014) for all of the lineages other than the *Channel Island* one (0.365), as expected after a recent demographic expansion, and none of their  $p$ -values indicate a significant departure from the model of recent expansion (Table 2). Similarly, the low values (0.005 – 0.028) of the raggedness indices ( $r_i$ ) for all but the *Channel Island* lineage (0.880) are concomitant with recent expansions. The associated  $p$ -value for the *African* lineage shows a significant departure from the expansion model.

The mismatch Tau parameter ( $\tau$ ), representing time since the onset of expansion, was similar for the *central*, *peripheral* and *south-eastern* lineages (4.000 – 5.395), but somewhat higher (8.000) in the *Sicilian* lineage and lower (2.875) in the *African* lineage (Table 2). This is broadly in accord with the relative ages of the lineages from nucleotide diversity. The Tau parameter for the *Channel Island* lineage is high (6.068), despite its relatively low nucleotide diversity, but the sample size is very small ( $n = 5$ ). In general, the widths of the 95% confidence intervals for the Tau parameter appear to reflect the sample size (Table 2). Tajima's  $D$  and Fu's  $F_s$  statistics were negative for all lineages other than the *Channel Island* one (Table 2). These tests are more sensitive to demographic expansion than the mismatch  $p$ -values and all of the negative test statistics were significant, other than Tajima's  $D$  for the *Sicilian* lineage, which is of earlier origin according to the nucleotide diversity ( $\pi$ ). There was no signal of recent expansion for the *Channel Island* lineage, but the sample size was very small.

With the previously estimated rodent cyt *b* clock rate ( $3.27 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ; Martínková *et al.*, 2013), the tMRCA of the *central*, *peripheral* and *south-eastern* lineages (estimated with Beast) are quite similar, with medians ranging from 16.4 to 22.3 Kya (Table 3), as for their Tau parameter values (Table 2). This time span is broadly coincident with the cold period around the Last Glacial Maximum (LGM; ca. 21.0 Kya; Mix, Bard & Schneider, 2001) of the most recent (Weichselian) glaciation of Europe, just before the rapid increase in temperature that marked the beginning of the Bølling-Allerød interstadial (ca. 14.7 Kya; Steffensen *et al.*, 2008). This is consistent with expansion of the three lineages out of three separate late glacial refugia. The tMRCA for the *African* lineage (median 7.4 Kya) and *Channel Island* lineage (median 5.6 Kya) are much more recent. The *African* lineage has a low value for the Tau parameter, in line with the more recent tMRCA, but the *Channel Island* lineage does not. Finally, the tMRCA for the *Sicilian* lineage is much earlier than the others (median 29.0 Kya), reflected in the higher value of its Tau parameter, indicating that its most recent population expansion was initiated prior to the LGM.

The Bayesian skyline models, derived from the individual coalescent genealogies for each lineage, show the effective female population size ( $N_{ef}$ ) from the median tMRCA of the respective lineage to the present (Fig. 4). Although the *south-eastern*, *central* and *peripheral* lineages appear to have originated during the cold stage towards the end of the Weichselian glaciation, the demographic expansion of the *south-eastern* lineage was earlier than that of the other two lineages, around 14–15 Kya, which coincides with the sudden and rapid warming of the climate about 14.7 Kya (Steffensen *et al.*, 2008). However, the *central* and *peripheral* lineage populations did not expand until about 8 to 9 Kya, following the establishment of the Holocene interglacial, around 10.7 Kya (Steffensen *et al.*, 2008). Demographic expansion of the *African* lineage closely followed its time of origin, beginning about 7 Kya, as expected for an introduction to a new location. There is no signal of demographic expansion in the *Channel Island* lineage population, but the sample size was very small ( $n = 5$ ). The population of the *Sicilian* lineage underwent a relatively gradual expansion, beginning sometime after its estimated time of origin, and coinciding with the period when the climate changed from its LGM minimum (around 21 Kya) to its Holocene maximum (after 10 Kya).

Although the overall genetic structure was clearly defined (Fig. 1; Fig. 3), and most of the variation was partitioned between the six lineages (Table 1), there was no discernible geographic structure within them. However, 68 different haplotypes were found in more than one geographical location (Table S.2) and pairwise geodesic distances between locations with the same haplotype ranged up to 2,331 km. Of the 68 shared haplotypes, 14 were present on more than one land mass (Table S.4). Three of these haplotypes, all of them from the *central* lineage, were present on both the European mainland and the Fennoscandian peninsula, which were connected by land bridges between 13.1 and 12.7 Kya and from 12.1 to 10.3 Kya, prior to the formation of the Baltic Sea (Herman *et al.*, 2014; based on Björck, 1995a, b). Another two of the shared haplotypes were found on closely adjacent islands that might have been united with each other at some point after the last glaciation: Westray with mainland Orkney, Walney with Piel and Sheep Islands off north-western England. However, for the 12 remaining shared haplotypes, connections between their current locations would have required sea crossings, given the consistently high post-glacial sea levels around north-western Europe and the British Isles (Sturt, Garrow & Bradley, 2013). All of these potential overseas connections are between the British Isles, Iceland and the southern part of the Fennoscandian peninsula (Fig. S.3).

## DISCUSSION

Our new phylogeographic data confirm the earlier finding (Michaux *et al.*, 2003) that the main genetic split in the wood mouse runs from the Alps to central Ukraine (Fig. 2). However, the higher resolution of the larger dataset, especially in the northern and marginal parts of the range, demonstrates that the main genetic group to the north and west of the split (subclade 2b of Michaux *et al.*, 2003) comprises two distinct and well-supported lineages, named here as the *central* and the *peripheral*, which have clearly different but overlapping distributions.

The identification of these two lineages gives rise to the most important new insight of the current study: that the mainland European population of the wood mouse has emerged from a combination of three glacial refugia, two of them somewhere in south-eastern and south-western Europe, and the third in a more northerly location. This interpretation is based on the present distributions of the *south-eastern* lineage, the *central* lineage that ranges from the Iberian peninsula north to Scandinavia, and the *peripheral* lineage that is confined to more northerly parts of the continent (Fig. 2). Unfortunately, the data are insufficient to give any indication of the precise locations of these putative glacial refugia. The existence of two southern refugia, in Iberia and south-eastern Europe, was inferred in earlier studies of the wood mouse (Michaux *et al.*, 2003, 2005), but the presence of a northern refugium was not established. However, as stated earlier, the prevalence of northerly refugia was not generally recognised until relatively recently, and the phylogeographic pattern inferred here, with survival of lineages in a combination of southern and northern refugia, has now been found in a number of Eurasian rodents and other small mammals (Deffontaine *et al.*, 2005; Vega *et al.*, 2010; McDevitt *et al.*, 2012).

Although the presence of a northerly refugium has not previously been identified from genetic variation in the wood mouse itself, the existence of this refugium was predicted in a comparative phylogeographic study of the wood mouse and one of its parasites (Nieberding *et al.*, 2004, 2005). The nematode *Heligmosomoides polygyrus* (Dujardin, 1845) is a direct (without intermediate host) and specific endoparasite of the wood mouse, and it is therefore expected that genetic variation in their naturally occurring populations would be closely aligned. Refugia for both species were initially thought to be located in southern European peninsulas (Nieberding *et al.*, 2004). However, additional genetic structure was subsequently identified in populations of *H. polygyrus* *cyt b*, based on samples from Ireland and Denmark, and this was attributed to the presence of an unidentified refugium in a more northerly location (Nieberding *et al.*, 2005). This highlights the potential value of genetic data from parasites, particularly when data from the host is lacking or variation is limited by some factor such as introgression or selection.

The presence of northern and southern refugia may contribute to a general phylogeographic process that has been proposed, whereby northern or outlying locations are now occupied by the first lineages to colonise the continent, while more southern or central parts of the range are occupied by other lineages that have subsequently replaced them (Searle and Wilkinson, 1987; Piertney *et al.*, 2005; Searle *et al.*, 2009b). This process, and the resulting pattern of central and peripheral lineages, may be attributed to specific adaptive features of the lineages (McDevitt *et al.*, 2012; Kotlik *et al.*, 2014). Such a model might apply to the wood mouse, given the distributions of the *peripheral* and *central* lineages, which we have therefore named accordingly. If this were the case, the *peripheral* lineage may have been first to colonise central and northern Europe, but has subsequently been replaced by the *central* lineage in much of north-western and central Europe, although some "relict" individuals remain scattered there. The median tMRCAAs of the *peripheral* and *central* lineages (16.363 and 22.254 Kya respectively; Table 3) appear to conflict with this interpretation, but these dates reflect the coalescence of each lineage whereas their demographic expansions were more closely aligned (beginning after 10 Kya; Fig. 4). If the *central* lineage began to expand contemporaneously from a more southerly location than the *peripheral* lineage, then it is conceivable that it would follow in the wake of latter and only partially replace it.

It has been demonstrated consistently, using directly and indirectly dated molecular data, that molecular clock rates are time dependent, over the timescales that apply to studies of intraspecific genetic variation like the present one (Ho *et al.*, 2005, 2011, 2015; Ho & Larson, 2006). In the absence of dated ancient DNA from the wood mouse itself, the need for calibration from contemporaneous events was met here by the application of a *cyt b* clock rate that was estimated using directly radiocarbon dated post-glacial remains from another rodent (Martíková *et al.*, 2013). Similar clock rates to the one used here ( $3.27 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ) have been inferred for another species of rodent in Europe, *Microtus agrestis* (Linnaeus, 1761), by comparing mitochondrial genetic variation with external events (Herman & Searle, 2011; Herman *et al.*, 2014), and such clock rates have also been applied to house mouse colonisation (Rajabi-Maham, Orth & Bonhomme, 2008; Macholán *et al.*, 2012). Notably, similar clock rates have been obtained with dated ancient DNA from a wide range of mammals and birds (Ho, Kolokotonis & Allaby, 2007).

That rate is between two and three times higher than the rates ( $0.9 - 1.2 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ) that were estimated for *A. sylvaticus* *cyt b* in the most recent phylogeographic study of the species (Lalis *et al.*, 2016). However, these were estimated from inferred splits between *A. sylvaticus*, *A. flavicollis* and *A. mystacinus*. Although those estimates were obtained from variation at third codon positions alone, this may not have been sufficient to account for all of the rate decay. The rate used here is also two times higher than recently estimated *cyt b* clock rates for *A. argenteus* ( $1.1 - 1.6 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ) and *A. speciosus* ( $1.2 - 1.7 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ), obtained by relating the timing of demographic expansions in the Japanese archipelago to post-glacial climate (Suzuki *et al.*, 2015). This approach of calibration to external events has been applied elsewhere, for example with river catchments (Burridge *et al.*, 2008) and land bridges (Herman and Searle 2011; Herman *et al.*, 2014), and therefore, as an *Apodemus* rate, may be more reliable than the *Microtus* rate that we used. We have therefore considered the effect on our results, had we applied a clock rate ( $1.4 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ) based on that obtained by external calibration of genetic variation in *Apodemus* (Suzuki *et al.*, 2015).

The directly dated *Microtus* molecular clock calibration leads to the following scenario:

The three mainland European lineages of wood mouse all originated around the time of the LGM (ca. 21.0 Kya), presumably within bottlenecked populations that survived the LGM in three separate refugia. The subsequent demographic expansions of these three lineages are evident from the mismatch distributions (Fig. S.2), neutrality statistics (Table 2) and the skyline plots of population size (Fig. 4). Such expansions are, of course, expected in populations that must have occupied their present ranges in response to the climatic changes after the last glaciation. The demographic expansion of the south-eastern lineage began when the climate rapidly warmed at the beginning of the Bølling-Allerød interstadial (ca. 12.9 to 14.7 Kya), which marked the end of the Weichselian glaciation. Presumably this lineage was soon able to occupy most of its present range (Fig. 2), because it is confined to the southern part of eastern Europe, from Italy to Ukraine.

However, the populations of the central and peripheral lineages did not expand until about five thousand years later, after the beginning of the Holocene interglacial. A similar situation has previously been found in the field vole *M. agrestis* (Linnaeus, 1761), another Eurasian rodent, where the six extant *cyt b* lineages appear to have expanded at the beginning of the Holocene (Herman & Searle, 2011). These field vole lineages are thought to have originated within geographically dispersed refugia at the time of the Younger Dryas (Herman & Searle, 2011), the cold period which separated the Bølling-Allerød from the Holocene (ca. 11.7 to 12.9 Kya; Steffensen *et al.*, 2008). Although the central and peripheral lineages of the wood mouse originated at an earlier time, around the LGM (ca. 21.0 Kya), their populations may also have gone through bottlenecks at the Younger Dryas climatic minimum, in which case these single locus skyline plots would only recover the most recent expansion subsequent to this event. The

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5 partial replacement of the *peripheral* lineage by the *central* lineage would then have occurred  
6 during the Holocene expansion of the two lineages after the Younger Dryas.  
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8 This scenario can be contrasted with that based on the *Apodemus* clock rate:  
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10 The *Apodemus* clock rate (Suzuki *et al.*, 2015) is about 2.3 times lower than the *Microtus* rate that  
11 we used, and would have led to time estimates increased by that factor. The resulting tMRCAAs for  
12 the three mainland European lineages (ca. 38 to 52 Kya) might conceivably relate to population  
13 bottlenecks at earlier temperature minima within the Weichselian glacial period (Johnsen *et al.*,  
14 2001). Although the subsequent demographic expansions of the *central* and *peripheral* lineages  
15 would then broadly coincide with the post-glacial climatic warming after the LGM, the somewhat  
16 earlier expansion of the *south-eastern* lineage would be aligned with the coldest period towards  
17 the end of the Weichselian (Johnsen *et al.*, 2001) and there would be no post-glacial signal of  
18 expansion in this lineage. The scenario based on the *Apodemus* clock rate fits poorly with  
19 expectations in terms of population expansions, and we believe that the scenario based on the  
20 *Microtus* rate is much more realistic and therefore we continue to follow that here.  
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22 While the overall phylogeographic pattern suggests that the mainland European wood mouse  
23 population is composed of three maternal lineages that colonised the continent from separate  
24 glacial refugia, it is nevertheless difficult to associate these putative refugia with any specific  
25 locations. Fossil remains of the wood mouse have been recorded from LGM sites in the eastern  
26 Pyrenees, northern Spain, the Dordogne region of southern central France and from north-  
27 eastern Italy, to the south-east of the Alps (Sommer & Nadachowski, 2006). In addition, there are  
28 sporadic records of wood mouse from the Carpathian basin around the time of the LGM, although  
29 the species does not make a substantial contribution to the fauna there until the Holocene  
30 (Pazonyi, 2004). Only one of these refugia, in north-eastern Italy, can be placed within the  
31 exclusive range of a lineage, the *south-eastern*. The eastern Pyrenees are a possible source of  
32 the *central* lineage, given their location on the edge of the Iberian peninsula, while the Dordogne  
33 or the Carpathians might be the source of the *peripheral* lineage. Nevertheless, it is interesting  
34 that the wood mouse has only rarely been found in Carpathian sites from the LGM, from where  
35 other temperate species have been inferred to have colonised Europe after the last glaciation  
36 (Kotlik *et al.*, 2006; Wójcik *et al.*, 2010; McDevitt *et al.*, 2012; Stojak *et al.*, 2015). Tentative  
37 support for the Dordogne as the refugium for the *peripheral* (*PER*) lineage is provided by species  
38 distributional modelling (Fløjgaard *et al.*, 2009), as their reconstruction of suitable LGM habitat for  
39 the wood mouse included the Mediterranean coast of France, which is quite close to the  
40 Dordogne, but did not include the Carpathian basin. According to the species distribution model,  
41 potentially suitable LGM habitat was also present in the Iberian peninsula, now occupied only by  
42 animals from the *central* lineage, and in the current exclusive range of the *south-eastern* lineage.  
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44 The genetic divergence of wood mice from Sicily has previously been noted (Michaux *et al.*,  
45 1998, 2003) and the *Sicilian* lineage does indeed appear to be older than the others, based on  
46 both its mitochondrial genetic diversity and time of coalescence (ca. 29 Kya). The delay in the  
47 onset of its demographic expansion, until about eight thousand years later, might conceivably be  
48 due to a limited availability of suitable habitat on the island before the climate began to warm after  
49 the LGM. It is much earlier than the expansions of the other lineages, but this is not surprising,  
50 given its Mediterranean location, whereas the expansion of the other lineages would have been  
51 constrained until later by the climatic conditions further north in the continent. Application of the  
52 clock rate inferred for *Apodemus* (Suzuki *et al.*, 2015) would place the tMRCA of the *Sicilian*  
53 lineage around 68 Kya, which coincides with temperature minima around Marine Isotope Stage  
54 (MIS) 4 (Johnsen *et al.*, 2001) and is therefore plausible. However, the gradual rise in the  
55 population size (Fig. 4) would have lasted from about 50 to 25 Kya, within the Weichselian glacial  
56 period.  
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58 The timescale for closure of the Messina Strait, based on sophisticated geophysical models,  
59 demonstrates the existence of a land-bridge between Sicily and the Italian mainland from around  
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6 27 to 17 Kya (Antonioli *et al.*, 2012; 2014), With the radiocarbon dated *Microtus* clock rate, the  
7 median tMRCA of the *Sicilian* lineage is about two thousand years earlier than the appearance of  
8 the land-bridge, although the connection was present within the 95% HPD interval of the tMRCA  
9 (19.6 to 40.5 Kya). With the clock rate derived from *Apodemus*, the most recent 95% confidence  
10 limit for the tMRCA of the Sicilian lineage was around 46 Kya, well before the time of the land  
11 bridge. However, there is fossil evidence of wood mice from Sicily that has been dated around  
12 32+/-4 Kya (Bonfiglio *et al.*, 2008), prior to the presence of the land-bridge, and it therefore seems  
13 that wood mice, although not a part of the original endemic island fauna, were able to reach the  
14 island with the early influx of mainland species in the late glacial (Bonfiglio *et al.*, 2001, 2002,  
15 2008).

16 While the isolated wood mouse population of Sicily appears to have arrived by some other  
17 means, the *African* and *Channel Island* lineages were most likely introduced accidentally to these  
18 outlying locations by human agents, following their original overland colonisation of mainland  
19 Europe. These two lineages are much more recent in origin than the mainland or *Sicilian* ones,  
20 with median tMRCA estimate of about 7.4 Kya and 5.6 Kya respectively (Table 3), based on the  
21 radiocarbon dated *Microtus* molecular clock rate (Martínková *et al.*, 2013). The *African* lineage is  
22 closely related to the central lineage (Fig. 3), the only one found in the Iberian peninsula (Fig. 2),  
23 suggesting that the wood mouse reached North Africa from there, rather than elsewhere in  
24 southern Europe. The demographic expansion of the *African* lineage followed closely after its  
25 origin (Fig. 4). Furthermore, the relative timing of expansions in different North African locations,  
26 inferred from mismatch analyses of cyt b sequences, provide evidence of earlier introduction to  
27 Morocco than Algeria, suggest that the wood mouse colonised the continent via the Strait of  
28 Gibraltar (Lalis *et al.*, 2016). The dates of the earliest wood mouse fossils from the Maghreb,  
29 recovered in the Tingitana Peninsula of Morocco (6 to 7.5 Kya) and in Algeria (2.5 to 4 Kya), fit  
30 well with these relative times of expansion (Lalis *et al.*, 2016; following Stoetzel, 2009, 2013).  
31 However, with the clock rate inferred for *Apodemus* (Suzuki *et al.*, 2015), the tMRCA of the  
32 *African* lineage would be around 17 Kya, indicating that the species colonised the continent  
33 immediately after the last glaciation, and pre-dating the fossil evidence.  
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35 The close relationship between the *African* and *Channel Island* lineages can most reasonably be  
36 explained by an introduction from one location to the other, most likely from Africa to the Channel  
37 Islands, or introduction to their present locations from a common source. If the latter, there is no  
38 precise indication of where this might be, although it would most likely be located within the  
39 Iberian peninsula. With the radiocarbon dated clock rate, the inferred timing of the introductions to  
40 the Channel Islands (ca. 5.6 Kya; median tMRCA) suggests that the mice may have been  
41 translocated by Neolithic people, but given the 95% HPD interval of the tMRCA (1.3 to 11.5 Kya),  
42 later introductions are also possible. Interestingly, ca. 3 Kya introductions between the  
43 Mediterranean and north-western Europe (Britain, northern France and nearby areas) have been  
44 suggested for the house mouse (Jones *et al.*, 2013). Using the *Apodemus* clock rate (Suzuki *et*  
45 *al.*, 2015), the wood mouse would have been introduced to the Channel Islands around 11.5 Kya,  
46 before the Neolithic.  
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48 While most of the genetic variation was partitioned among the six lineages, a substantial  
49 proportion (23%) was due to the differences among the sequences within them. However, in spite  
50 of their overall variability, little geographical structure was discernible within the lineages and  
51 closely related sequences were frequently obtained from widely separated localities, sometimes  
52 at opposite ends of the species' range. This pattern is remarkable for a small mammal, once  
53 again suggesting that wood mice have a high capacity for dispersal. Despite the lack of  
54 geographical structure within lineages, it is possible to gain some information about the pattern of  
55 colonisation from the presence of specific haplotypes at more than one location. In most cases,  
56 this could be attributed to natural overland colonisation, although this might (in some cases) have  
57 been mediated by humans. The movement of animals between some shared locations would  
58 involve water crossings (Fig. S.3), sometimes between islands that have been separated  
59 throughout the post-glacial period (Sturt, Garrow & Bradley, 2013). Dispersal to or from these  
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5 islands must surely be due to human activity, so sharing of haplotypes between these locations  
6 provides a means to examine the effect of human influence, overlaid upon the otherwise natural  
7 distribution of the species.  
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9 All of the inferred translocations relating to presence of specific haplotypes in more than one  
10 location and definitively involving water crossings were between the British Isles, Iceland and the  
11 southern part of the Fennoscandian Peninsula (Fig. S.3), which might implicate Norse Viking  
12 settlers in the process. This has previously been proposed for the wood mouse (Berry, Evans &  
13 Sennitt, 1967; Berry, 1969; 1973) and for the house mouse (Searle *et al.*, 2009a; Jones *et al.*,  
14 2012; 2013). A similar hypothesis has also been put forward to explain the presence of  
15 Scandinavian mtDNA haplotypes in Irish badgers *Meles meles* (Frantz *et al.*, 2014). Wood mice  
16 probably reached Iceland with Norse people, as historical documentation indicates that they were  
17 the first people to colonise the island, around 1100 years BP (Smith, 1995; Price & Gestsdóttir,  
18 2006). However, as the islands around Britain have been occupied since the Mesolithic (Corbet,  
19 1961), animals could have been translocated at any time since then, and this is reflected in the  
20 presence of the *peripheral* lineage throughout the British Isles. The lack of observed  
21 mitochondrial genetic structure across the wide ranges of the *central* and *peripheral* lineages, and  
22 the presence of the wood mouse on so many islands (Montgomery, 1999b), together show that  
23 the species has a high capacity for dispersal by human agency. It therefore seems likely that  
24 wood mice have been transferred repeatedly between locations throughout the Holocene, in what  
25 is probably an ongoing process. Interestingly, it is the subsequent translocations between the  
26 British Isles and Scandinavia, identified here through mitochondrial haplotype sharing, rather than  
27 the background of common ancestry between all of the *peripheral* lineage, that was identified in  
28 the earlier work based on non-metrical skeletal characters (Berry, Evans & Sennitt, 1967; Berry,  
29 1969, 1973).  
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31 The phylogeography of the wood mouse provides an interesting contrast with that of the house  
32 mouse. It appears to have survived the LGM in three mainland European locations, together with  
33 another population on the island of Sicily. The initial colonisation of the mainland European  
34 continent by the wood mouse was apparently the result of a natural post-glacial expansion into  
35 newly available habitat and this was followed by a phase of further, human-mediated,  
36 introductions to numerous islands and otherwise inaccessible locations around the western and  
37 southern margins of the continent. The house mouse was a later arrival in Europe, introduced  
38 from its natural range in the east in conjunction with the gradual spread of human agriculture,  
39 conurbations and trade (Bonhomme *et al.*, 2010). Although it too has been introduced to many  
40 islands on the margins of Europe, originally by Norse or Danish Vikings in the case of those  
41 around the Atlantic coasts, it has subsequently been carried all over the world as a true  
42 commensal (Jones *et al.*, 2013). The wood mouse, in spite of its capacity for human dispersal,  
43 has got little further than the margins of its natural range, presumably because it is anthropophilic,  
44 rather than a true commensal like the house mouse (Hulme-Beaman *et al.*, 2016).  
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## ACKNOWLEDGEMENTS

We thank the three anonymous reviewers for their helpful comments.

We thank the following individuals and organisations who provided samples or advice: Paulo Alves, J Ballantyne, David Bates, Sam Berry, Tom Black, Bristol City Museum and Art Gallery, Joan Carter, Norma Chapman, John Chester, Mike Cockram, Countryside Council for Wales, Shirley Cross, Charles David, Tim Deans, Fraser Dodds, Tim Dodman, K Fairclough, Clem Fisher, Alain Frantz, Nick Gould, Great North Museum: Hancock, İslam Gündüz, Hampshire Museums, Gemma Harding, Mary Harman, Dawn Hayden, Alice Helyar, Herbert Art Gallery and Museum (Coventry), Martin Heubeck, Stephen Hewitt, Lister Hogarth, Phil Howard, Hugh Insley, Inverness Museum and Art Gallery, Maarit Jaarola, Jóhannes B. Jóhannsson, Gareth Jones, Andrew Kitchener, Guðmundur Ó. Kristjánsson, Steve Lane, Linley C Lewis, Ian Linn, Liverpool Museum, Patrick Lowe, Herbert Mackenzie, Anne MacLellan, John Allan MacLellan, Natalia Martíková, Peter Mayhew, Damien McDevitt, Bob McGowan, Yvonne Meyer-Lucht, Alina Mishta, Eric Morton, Museum nationale d'Histoire naturelle (Paris), National Trust for Scotland, North Lincolnshire Museum, Alan Ogden, Geoff Oxford, Helga Óskarsdóttir, Marine Pascal, Michel Pascal, Abbie Patterson, Joana Paupério, Les Pearce, Josephine Pemberton, Brian Rabbits, Ramugondo V Rambau, F Ratter, Ian Ross, Royal Society for the Protection of Birds, Hazel Ryan, Mike Ryan, Kate Sampson, R Sandling, Sue Scoggins, Scottish Natural Heritage, Mark Shaw, Ingibjörg Sigurjónsdóttir, Karl Skirnisson, R Swann, Christine Taylor, Sandra Telfer, Nina Thomson, Steve Thomson, George Trafford, Sam Trebilcock, Tullie House Museum, R Tulloch, Karen Varnham, Rodrigo Vega, Phil Wheeler, Sian Whitehead, Derek Yalden, Grace Yoxon.

We thank Barbara Marczuk and Iwona Ruczyńska for their help in the laboratory.

Fieldwork in Iceland was supported by the Genetics Society Heredity Grant.

## REFERENCES

- Amori G, Hutterer R, Kryštufek B, Yigit N, Mitsain G, Palomo LJ. 2008. *Apodemus flavicollis*. The IUCN Red List of Threatened Species 2008: e.T1892A8699693.
- Anisimova M, Gascuel O. 2006. Approximate Likelihood-Ratio Test for branches: a fast, accurate, and powerful alternative. *Systematic Biology* **55**: 539-552.
- Anisimova M, Gil M, Dufayard J-F, Dessimoz C, Gascuel O. 2011. Survey of branch support methods demonstrates accuracy, power, and robustness of fast likelihood-based approximation schemes. *Systematic Biology* **60**: 685-699.
- Antonioli F, Presti VL, Morticelli MG, Mannino MA, Lambeck K, Ferranti L, Bonfiglio L, Mangano G, Sannino GM, Furlani S, Sulli A, Palombo MR, Canese SP. 2012. The land bridge between Europe and Sicily over the past 40 kyr: timing of emersion and implications for the migration of *Homo sapiens*. *Rendiconti Online della Società Geologica Italiana* **21**:1167-1169.
- Antonioli F, Presti VL, Morticelli MG, Bonfiglio L, Mannino MA, Palombo MR, Sannino G, Ferranti L, Furlani S, Lambeck K, Canese S, Catalano R, Chiocci FL, Mangano G, Scicchitano G, Tonielli R. 2014. Timing of the emergence of the Europe-Sicily bridge (40-17 cal ka BP) and its implications for the spread of modern humans. In: Harff J, Bailey G, Lüth F, eds. *Geology and archaeology: submerged landscapes of the continental shelf*. Geological Society, London, Special Publications **411**: 111-144.
- Bandelt H, Forster P, Röhl A. 1999. Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution* **16**: 37-48.
- Berry RJ, Evans IM, Sennitt BFC. 1967. The relationships and ecology of *Apodemus sylvaticus* from the Small Isles of the Inner Hebrides, Scotland. *Journal of Zoology* **152**: 333-346.
- Berry RJ. 1969. History in the evolution of *Apodemus sylvaticus* (Mammalia) at one edge of its range. *Journal of Zoology* **159**: 311-328.
- Berry RJ. 1973. Chance and change in British long-tailed field mice (*Apodemus sylvaticus*). *Journal of Zoology* **170**: 351-366.
- Bilton DT, Mirol PM, Mascheretti S, Fredga K, Zima J, Searle JB. 1998. Mediterranean Europe as an area of endemism for small mammals rather than a source for northwards postglacial colonization. *Proceedings of the Royal Society of London. Series B. Biological Sciences* **265**: 1219-1226.
- Björck S. 1995a. A review of the history of the Baltic Sea, 13.0-8.0 ka BP. *Quaternary International* **27**: 19-40.
- Björck S. 1995b. Late Weichselian to early Holocene development of the Baltic Sea - with implications for coastal settlements in the southern Baltic region. In: Fischer A, ed. *Man and sea in the Mesolithic. Coastal settlement above and below present sea level*. Proceedings of the International Symposium, Kalundborg, Denmark, 1993. Oxbow Monograph **53**. Oxford: Oxbow Books, 23-34.
- Bonfiglio L, Mangano G, Marra AC, Masini F. 2001. A new late Pleistocene vertebrate faunal complex from Sicily (S. Teodoro Cave, North-Eastern Sicily, Italy). *Bollettino della Società Paleontologica Italiana* **40**: 149-158.

- 1  
2  
3  
4  
5 **Bonfiglio L, Mangano G, Marra AC, Masini F, Pavia M, Petruso D.** 2002. Pleistocene  
6 Calabrian and Sicilian bioprovinces. *Geobios* **35**: 29-39.  
7  
8 **Bonfiglio L, Esu D, Mangano G, Masini F, Petruso D, Soligo M, Tuccimei P.** 2008. Late  
9 Pleistocene vertebrate-bearing deposits at San Teodoro Cave (North-Eastern Sicily): preliminary  
10 data on faunal diversification and chronology. *Quaternary International* **190**: 26-37.  
11  
12 **Bonhomme F, Orth A, Cucchi T, Rajabi-Maham H, Catalan J, Boursot P, Auffray J-C,  
13 Britton-Davidian J.** 2010. Genetic differentiation of the house mouse around the Mediterranean  
14 basin: matrilineal footprints of early and late colonization. *Proceedings of the Royal Society.  
15 Series B. Biological Sciences* **278**: 1034-1043.  
16  
17 **Bouckaert R, Heled J, Kühnert D, Vaughan T, Wu C-H, Xie D, Suchard MA, Rambaut A,  
18 Drummond AJ.** 2014. BEAST 2: A software platform for Bayesian evolutionary analysis. *PLoS  
19 Computational Biology* **10**: e1003537.  
20  
21 **Burridge, CP, Craw D, Fletcher D, Waters JM.** 2008. Geological dates and molecular rates: fish  
22 DNA sheds light on time dependency. *Molecular Biology and Evolution* **25**: 624-633.  
23  
24 **Conroy CJ, Cook JA.** 1999. MtDNA evidence for repeated pulses of speciation within arvicoline  
25 and murid rodents. *Journal of Mammalian Evolution* **6**: 221-245.  
26  
27 **Corbet GB.** 1961. Origin of the British insular races of small mammals and of the 'Lusitanian'  
28 fauna. *Nature* **191**: 1037-1040.  
29  
30 **Corbet GB.** 1978. *The mammals of the Palaearctic region: a taxonomic review*. London: British  
31 Museum (Natural History).  
32  
33 **Darriba D, Taboada GL, Doallo R and Posada D.** 2012. jModelTest 2: more models, new  
34 heuristics and parallel computing. *Nature Methods* **9**: 772.  
35  
36 **Deffontaine V, Libois R, Kotlik P, Sommer R, Nieberding C, Paradis E, Searle JB, Michaux  
37 JR.** 2005. Beyond the Mediterranean peninsulas: evidence of central European glacial refugia for  
38 a temperate forest mammal species, the bank vole (*Clethrionomys glareolus*). *Molecular Ecology*  
39 **14**: 1727-1739.  
40  
41 **Drummond AJ, Rambaut A, Shapiro B, Pybus OG.** 2005. Bayesian coalescent inference of  
42 past population dynamics from molecular sequences. *Molecular Biology and Evolution* **22**: 1185-  
43 1192.  
44  
45 **Dubey S, Michaux J, Brünnler H, Hutterer R, Vogel P.** 2009. False phylogenies on wood mice  
46 due to cryptic cytochrome-*b* pseudogene. *Molecular Phylogenetics and Evolution* **50**: 633-641.  
47  
48 **Excoffier L, Lischer HE.** 2010. Arlequin suite ver 3.5: a new series of programs to perform  
49 population genetics analyses under Linux and Windows. *Molecular Ecology Resources* **10**: 564-  
50 567.  
51  
52 **Fløjgaard C, Normand S, Skov F, Svenning J-C.** 2009. Ice age distributions of European small  
53 mammals: insights from species distribution modelling. *Journal of Biogeography* **36**: 1152-1163.  
54  
55 **Flowerdew JR, Tattersall FH.** 2008. Wood mouse *Apodemus sylvaticus*. In: Harris S, Yalden  
56 DW, eds. *Mammals of the British Isles: Handbook, 4<sup>th</sup> edition*. Southampton: The Mammal  
57 Society, 125-137.  
58  
59  
60

- 1  
2  
3  
4  
5     **Frantz AC, McDevitt AD, Pope LC, Kochan J, Davison J, Clements CF, Elmeros M, Molina-**  
6     **Vacas G, Ruiz-Gonzalez A, Balestrieri A, Van Den Berge K, Breyne P, Do Linh San E, Argen**  
7     **EO, Suchentrunk F, Schley L, Kowalczyk R, Kostka BI, Cirovic D, Sprem N, Colyn M,**  
8     **Ghirardi M, Racheva V, Braun C, Oliveira R, Lanszki J, Stubbe A, Stubbe M, Stier N, Burke**  
9     **T. 2014. Revisiting the phylogeography and demography of European badgers (*Meles meles*)**  
10    **based on broad sampling, multiple markers and simulations. *Heredity* 113: 443-453.**
- 11  
12    **Fu Y-X. 1997. Statistical tests of neutrality of mutations against population growth, hitchhiking**  
13    **and background selection. *Genetics* 147: 915– 925.**
- 14  
15    **Gouy M, Guindon S, Gascuel O. 2010. SeaView version 4: a multiplatform graphical user**  
16    **interface for sequence alignment and phylogenetic tree building. *Molecular Biology and Evolution***  
17    **27: 221-224.**
- 18  
19    **Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New**  
20    **algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance**  
21    **of PhyML 3.0. *Systematic Biology* 59: 307-21.**
- 22  
23    **Herman JS, Searle JB. 2011. Post-glacial partitioning of mitochondrial genetic variation in the**  
24    **field vole. *Proceedings of the Royal Society. Series B. Biological Sciences* 278: 3601-3607.**
- 25  
26    **Herman JS, McDevitt AD, Kawałko A, Jaarola M, Wójcik JM, Searle JB. 2014. Land-bridge**  
27    **calibration of molecular clocks and the post-glacial colonization of Scandinavia by the Eurasian**  
28    **field vole *Microtus agrestis*. *PLoS ONE* 9: e103949.**
- 29  
30    **Hewitt GM. 1999. Post-glacial re-colonization of European biota. *Biological Journal of the***  
31    ***Linnean Society* 68: 87-112.**
- 32  
33    **Hijmans RJ. 2015. geosphere: Spherical Trigonometry. R package version 1.4-3. <http://CRAN.R-project.org/package=geosphere>.**
- 34  
35  
36    **Ho SYW, Phillips MJ, Cooper A, Drummond AJ. 2005. Time dependency of molecular rate**  
37    **estimates and systematic overestimation of recent divergence times. *Molecular Biology and***  
38    ***Evolution* 22:1561-1568.**
- 39  
40    **Ho SYW, Larson G. 2006. Molecular clocks: when times are a-changin'. *Trends in Genetics* 22:**  
41    **79-83.**
- 42  
43    **Ho SYW, Kolokotronis S-O, Allaby RG. 2007. Elevated substitution rates estimated from**  
44    **ancient DNA sequences. *Biology Letters* 3: 702-705.**
- 45  
46    **Ho SYW, Lanfear R, Bromham L, Phillips MJ, Soubrier J, Rodrigo AG, Cooper A. 2011.**  
47    **Time-dependent rates of molecular evolution. *Molecular Ecology* 20:3087-3101.**
- 48  
49    **Ho SYW, Duchene S, Molak M, Shapiro B. 2015. Time-dependent estimates of molecular**  
50    **evolutionary rates: evidence and causes. *Molecular Ecology* 24: 6007-6012.**
- 51  
52    **Hoofer SR, Gaschak S, Dunina-Barkovskaya Y, Makluk J, Meeks HN, Wickliffe JK, Baker**  
53    **RJ. 2007. New information for systematics, taxonomy, and phylogeography of the rodent genus**  
54    ***Apodemus* (*Sylvaemus*) in Ukraine. *Journal of Mammalogy* 88: 330-342.**
- 55  
56    **Hulme-Beaman A, Dobney K, Cucci T, Searle JB. 2016. An ecological and evolutionary**  
57    **framework for commensalism in anthropogenic environments. *Trends in Ecology and Evolution***  
58    **<http://dx.doi.org/10.1016/j.tree.2016.05.001>.**
- 59  
60

Jaarola M, Searle JB. 2002. Phylogeography of field voles (*Microtus agrestis*) in Eurasia inferred from mitochondrial DNA sequences. *Molecular Ecology* **11**: 2613–2621.

Johnsen SJ, Dahl-Jensen D, Gundestrup N, Steffensen JP, Clausen HB, Miller H, Masson-Delmotte V, Sveinbjörnsdóttir AE, White J. 2001. Oxygen isotope and palaeotemperature records from six Greenland ice-core stations: Camp Century, Dye-3, GRIP, GISP2, Renland and NorthGRIP. *Journal of Quaternary Science* **16**: 299–307.

Jones EP, Skirnisson K, McGovern TH, Gilbert MTP, Willerslev E, Searle JB. 2012. Fellow travellers: a concordance of colonization patterns between mice and men in the North Atlantic region. *BMC Evolutionary Biology* **12**: 35.

Jones, EP, Eager HM, Gabriel SI, Jóhannesdóttir F, Searle JB. 2013. Genetic tracking of mice and other bioproxies to infer human history. *Trends in Genetics* **29**: 298-308.

Kotlík P, Deffontaine V, Mascheretti S, Zima J, Michaux JR, Searle JB. 2006. A northern glacial refugium for bank voles *Clethrionomys glareolus*. *Proceedings of the National Academy of Sciences of the United States of America* **103**: 14860–14864.

Kotlík P, Marková S, Vojtek L, Stratil A, Šlechta V, Hyršl P, Searle JB. 2014. Adaptive phylogeography: functional divergence between haemoglobins derived from different glacial refugia in the bank vole. *Proceedings of the Royal Society. Series B. Biological Sciences* **281**: 20140021.

Lalis A, Leblois R, Liefried S, Ouarour A, Beeravolu CR, Michaux J, Hamani A, Denys C, Nicolas V. 2016. New molecular data favour an anthropogenic introduction of the wood mouse (*Apodemus sylvaticus*) in North Africa. *Journal of Zoological Systematics and Evolutionary Research*. **54**: 1-12.

Librado P, Rozas J. 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* **25**: 1451-1452.

McDevitt AD, Zub K, Kawalko A, Oliver MK, Herman JS, Wójcik JM. 2012. Climate and refugial origin influence the mitochondrial lineage distribution of weasels *Mustela nivalis* in a phylogeographic suture zone. *Biological Journal of the Linnean Society* **106**: 57-69.

Macholán M, Mrkvicová Vyskočilová M, Bejček V, Štastný K. 2012. Mitochondrial DNA sequence variation and evolution of Old World house mice (*Mus musculus*). *Folia Zoologica* **61**: 284-307.

Martin Y, Gerlach G, Schlotterer C, Meyer A. 2000. Molecular phylogeny of European muroid rodents based on complete cytochrome *b* sequences. *Molecular Phylogenetics and Evolution* **16**: 37–47.

Martíková N, Barnett R, Cucchi T, Struchen R, Pascal M, Pascal M, Fischer MC, Higham T, Brace S, Ho SYW, Quéré J-P, O'Higgins P, Excoffier L, Heckel G, Hoelzel AR, Dobney KM, Searle JB. 2013. Divergent evolutionary processes associated with colonization of offshore islands. *Molecular Ecology* **22**: 5205-5220.

Michaux JR, Sara M, Libois R, Matagne R. 1998. Is the woodmouse (*Apodemus sylvaticus*) of Sicily a distinct species? *Belgian Journal of Zoology* **128**: 211-214.

Michaux JR, Kinet S, Filippucci MG, Libois R, Besnard A, Catzeffis F. 2001. Molecular identification of three sympatric species of wood mice (*Apodemus sylvaticus*, *A. flavicollis*, *A. alpicola*) in western Europe (Muridae: Rodentia). *Molecular Ecology Notes* **1**: 260–263.

- 1  
2  
3  
4  
5  
6 **Michaux JR, Chevret P, Filippucci M-G, Macholan M.** 2002. Phylogeny of the genus  
7 *Apodemus* with a special emphasis on the subgenus *Sylvaemus* using the nuclear IRBP gene  
8 and two mitochondrial markers: cytochrome *b* and 12S rRNA. *Molecular Phylogenetics and*  
9 *Evolution* **23**: 123–136.  
10  
11 **Michaux JR, Magnanou E, Paradis E, Nieberding C, Libois R.** 2003. Mitochondrial  
12 phylogeography of the woodmouse (*Apodemus sylvaticus*) in the Western Palearctic region.  
13 *Molecular Ecology* **12**: 685–697.  
14  
15 **Michaux JR, Libois R, Filippucci M-G.** 2005. So close and so different: comparative  
16 phylogeography of two small mammal species, the yellow-necked fieldmouse (*Apodemus*  
17 *flaviventer*) and the woodmouse (*Apodemus sylvaticus*) in the Western Palearctic region. *Heredity*  
18 **94**: 52–63.  
19  
20 **Mix AC, Bard E, Schneider R.** 2001. Environmental processes of the ice age: land, oceans,  
21 glaciers (EPILOG). *Quaternary Science Reviews* **20**: 627–657.  
22  
23 **Montgomery WI.** 1999a. *Apodemus flaviventer* (Melchior, 1834). In: Mitchell-Jones AJ, Amori G,  
24 Bogdanowicz W, Kryštufek B, Reijnders PJH, Spitzenberger F, Stubbe M, Thissen JBM, Vohralík  
25 V, Zima J, eds. *The atlas of European mammals*. London: T & AD Poyser, 270–1.  
26  
27 **Montgomery WI.** 1999b. *Apodemus sylvaticus* (Linnaeus, 1758). In: Mitchell-Jones AJ, Amori G,  
28 Bogdanowicz W, Kryštufek B, Reijnders PJH, Spitzenberger F, Stubbe M, Thissen JBM, Vohralík  
29 V, Zima J, eds. *The atlas of European mammals*. London: T & AD Poyser, 274–5.  
30  
31 **Musser GG, Carleton MD.** 2005. Superfamily Muroidea. In: Wilson DE, Reeder DM, eds.  
32 *Mammal species of the world. A taxonomic and geographic reference*. 3<sup>rd</sup> edition. Baltimore: John  
33 Hopkins University Press, 894–1531.  
34  
35 **Nieberding C, Morand S, Libois R, Michaux JR.** 2004. A parasite reveals cryptic  
36 phylogeographic history of its host. *Proceedings of the Royal Society. Series B. Biological*  
37 *Sciences* **271**: 2559–2568.  
38  
39 **Nieberding C, Libois R, Douady CJ, Morand S, Michaux JR.** 2005. Phylogeography of a  
40 nematode (*Heligmosomoides polygyrus*) in the western Palearctic region: persistence of northern  
41 cryptic populations during ice ages? *Molecular Ecology* **14**: 765–779.  
42  
43 **Pazonyi P.** 2004. Mammalian ecosystem dynamics in the Carpathian Basin during the last  
44 27,000 years. *Palaeogeography, Palaeoclimatology, Palaeoecology* **212**: 295 – 314.  
45  
46 **Piertney SB, Stewart WA, Lambin X, Telfer S, Aars J, Dallas JF.** 2005. Phylogeographic  
47 structure and postglacial evolutionary history of water voles (*Arvicola terrestris*) in the United  
48 Kingdom. *Molecular Ecology* **14**: 1435–1444.  
49  
50 **Posada D, Crandall KA.** 2001. Intraspecific gene genealogies: trees grafting into networks.  
51 *TRENDS in Ecology & Evolution* **16**: 37–45.  
52  
53 **Price TD & Gestsdóttir H.** 2006. The first settlers of Iceland: an isotopic approach to  
54 colonisation. *Antiquity* **80**: 130–144.  
55  
56 **R Core Team.** 2015. R: A language and environment for statistical computing. R Foundation for  
57 Statistical Computing, Vienna, Austria. <https://www.R-project.org/>  
58  
59  
60

- 1  
2  
3  
4  
5 **Rajabi-Maham H, Orth A, Bonhomme F.** 2008. Phylogeography and postglacial expansion of  
6 *Mus musculus domesticus* inferred from mitochondrial DNA coalescent, from Iran to Europe.  
7 *Molecular Ecology* **17**: 627-641.
- 8  
9 **Rambaut A, Suchard MA, Xie D, Drummond AJ.** 2014. *Tracer v1.6*. Available from  
10 <http://beast.bio.ed.ac.uk/Tracer>
- 11 **Reutter BA, Petit E, Brünner H, Vogel P.** 2003. Cytochrome *b* haplotype divergences in West  
12 European *Apodemus*. *Mammalian Biology* **68**: 153-164.
- 13  
14 **Rogers AR, Harpending H.** 1992. Population growth makes waves in the distribution of pairwise  
15 genetic differences. *Molecular Biology and Evolution* **9**: 552-569.
- 16  
17 **Schlitter D, van der Straeten E, Amori G, Hutterer R, Kryštufek B, Yigit N, Mitsain G.** 2008.  
18 *Apodemus sylvaticus*. *The IUCN Red List of Threatened Species 2008*: e.T1904A8791394.
- 19  
20 **Schneider S, Excoffier L.** 1999. Estimation of demographic parameters from the distribution of  
21 pairwise differences when the mutation rates vary among sites: application to human  
22 mitochondrial DNA. *Genetics* **152**: 1079-1089.
- 23  
24 **Searle JB, Wilkinson PJ.** 1987. Karyotypic variation in the common shrew (*Sorex araneus*) in  
25 Britain - a 'Celtic Fringe'. *Heredity* **59**: 345-351.
- 26  
27 **Searle JB, Jones CS, Gündüz İ, Scascitelli M, Jones EP, Herman JS, Rambau RV, Noble**  
28 **LR, Berry RJ, Giménez MD, Jóhannesdóttir, F.** 2009a. Of mice and (Viking?) men:  
29 phylogeography of British and Irish house mice. *Proceedings of the Royal Society. Series B.*  
30 *Biological Sciences* **276**: 201-207.
- 31  
32 **Searle JB, Kotlík P, Rambau RV, Marková S, Herman JS, McDevitt AD.** 2009b. The Celtic  
33 fringe of Britain: insights from small mammal phylogeography. *Proceedings of the Royal Society.*  
34 *Series B. Biological Sciences* **276**: 4287-4294.
- 35  
36 **Shimodaira H, Hasegawa M.** 1999. Multiple comparisons of log-likelihoods with applications to  
37 phylogenetic inference. *Molecular Biology and Evolution* **16**: 1114-1116.
- 38  
39 **Smith KP.** 1995. Landnám: the settlement of Iceland in archaeological and historical perspective.  
40 *World Archaeology* **26**: 319-347.
- 41  
42 **Sommer RS, Nadachowski A.** 2006. Glacial refugia of mammals in Europe: evidence from fossil  
43 records. *Mammal Review* **36**: 251-265.
- 44  
45 **Steffensen JP, Andersen KK, Bigler M, Clausen HB, Dahl-Jensen D, Fischer H, Goto-**  
46 **Azuma K, Hansson M, Johnsen SJ, Jouzel J, Masson-Delmotte V, Popp T, Rasmussen SO,**  
47 **Röhlisberger R, Ruth U, Stauffer B, Siggaard-Andersen M-L, Sveinbjörnsdóttir AE,**  
48 **Svensson A, White JWC.** 2008. High-resolution Greenland ice core data show abrupt climate  
49 change happens in few years. *Science* **321**: 680-684.
- 50  
51 **Stoetzel E.** 2009. *Les Microvertébrés du site d'occupation humaine d'El Harhoura 2 (Pléistocène*  
52 *Supérieur-Holocène, Maroc): Systématique, Évolution, Taphonomie et Paléoécologie*. Paris:  
53 Muséum national d'Histoire naturelle. PhD Thesis.
- 54  
55 **Stoetzel E.** 2013. Late Cenozoic micromammal biochronology of northwestern Africa.  
56 *Palaeogeography, Palaeoclimatology, Palaeoecology* **392**: 359-381.
- 57  
58  
59  
60

1  
2  
3  
4  
5  
6 **Stojak J, McDevitt AD, Herman JS, Searle JB, Wójcik JM.** 2015. Post-glacial colonization of  
7 eastern Europe from the Carpathian refugium: evidence from mitochondrial DNA of the common  
8 vole *Microtus arvalis*. *Biological Journal of the Linnean Society* **115**: 927-939.

9  
10 **Sturt F, Garrow D, Bradley S.** 2013. New models of North West European Holocene  
11 palaeogeography and inundation. *Journal of Archaeological Science* **40**: 3963-3976.

12  
13 **Suzuki H, Filippucci MG, Chelomina GN, Sato JJ, Serizawa K, Nevo E.** 2008. A  
14 biogeographic view of *Apodemus* in Asia and Europe inferred from nuclear and mitochondrial  
15 gene sequences. *Biochemical Genetics* **46**: 329-346.

16  
17 **Suzuki Y, Tomozawa M, Koizumi Y, Tsuchiya K, Suzuki H.** 2015. Estimating the molecular  
18 evolutionary rates of mitochondrial genes referring to Quaternary ice age events with inferred  
19 population expansions and dispersals in Japanese *Apodemus*. *BMC Evolutionary Biology* **15**:  
20 187.

21  
22 **Taberlet P, Fumagalli L, Wust-Saucy A-G, Cosson J-F.** 1998. Comparative phylogeography  
23 and postglacial colonization routes in Europe. *Molecular Ecology* **7**: 453-464.

24  
25 **Tajima F.** 1989. Statistical method for testing the neutral mutation hypothesis by DNA  
26 polymorphism. *Genetics* **123**: 585-595.

27  
28 **Tamura K, Nei M.** 1993. Estimation of the number of nucleotide substitutions in the control region  
29 of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* **10**: 512-526.

30  
31 **Vega R, Fløjgaard C, Lira-Noriega A, Nakazawa Y, Svenning JC, Searle JB.** 2010. Northern  
32 glacial refugia for the pygmy shrew *Sorex minutus* in Europe revealed by phylogeographic  
33 analyses and species distribution modelling. *Ecography* **33**: 260-271.

34  
35 **Wójcik JM, Kawałko A, Marková S, Searle JB, Kotlík P.** 2010. Phylogeographic signatures of  
36 northward post-glacial colonization from high-latitude refugia: a case study of bank voles using  
museum specimens. *Journal of Zoology* **281**: 249-262.  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
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49  
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## FIGURES

**Fig. 1** Maximum likelihood (ML) tree for 543 wood mouse *cyt b* haplotypes. Tree inferred with *PhyML 3.0*, support (SH-aLRT) only shown for identified lineages and deeper splits.

**Fig. 2** Locations of samples from the six wood mouse *cyt b* lineages. Colours refer to lineages identified by ML tree inference and other analyses. Coastline data from *OpenStreetMap* (<http://www.openstreetmap.org>). Limits of species range (dashed line) following Schlitter *et al.* (2008).

**Fig. 3** Median Joining Network for 981 wood mouse sequences, obtained with *PopART 1.7*. Area of circle represents frequency of haplotype and mutational steps are indicated by hatch marks across branches. Black dots indicate inferred intermediate haplotypes.

**Fig. 4** Bayesian skyline plots showing effective female population size with time, for each lineage. Effective female population size ( $N_{ef}$ ), multiplied by mean generation time ( $T$ ), in years. Solid line is median and dashed lines are 95% highest posterior density (HPD) limits.  $N_{ef} \times T$  plotted on log scale for clarity and truncated to median estimate of tMRCA.

## TABLES

**Table 1** Fixation indices ( $\phi_{ST}$ ) calculated from genetic distance in all pairwise combinations of lineages. All indices were significant ( $p < 0.05$ ), based on 10,000 permutations of individuals among lineage populations.

	African	central	Channel Is	peripheral	south-eastern
<i>central</i>	0.68884				
<i>Channel Is</i>	0.71494	0.71941			
<i>peripheral</i>	0.72329	0.60346	0.76854		
<i>south-eastern</i>	0.89389	0.85019	0.84730	0.86032	
<i>Sicilian</i>	0.89367	0.84557	0.78516	0.86087	0.67214

**Table 2** Genetic variation within the six wood mouse cyt *b* lineages. Nucleotide diversity ( $\pi$ ), with standard deviation in italics below; Tajima's *D*, with significance *p* from beta distribution; Fu's  $F_S$ , with significance *p* from 1,000 coalescent simulations; mismatch Tau ( $\tau$ ) with 95% confidence interval, sum of squared deviations from model distribution (SSD) and Harpending's raggedness index (*ri*), with associated *p*-values derived from 10,000 coalescent simulations.

		<i>n</i>	$\pi$	<i>D</i>	<i>p</i>	$F_S$	<i>p</i>	Tau ( $\tau$ )	95% CI ( $\tau$ )	SSD	<i>p</i>	<i>ri</i>	<i>p</i>
14	African	298	0.00366 0.00015	-2.635	<0.001	-232.616	0.000	2.875	2.191 - 5.168	0.001	0.090	0.028	0.016
15	central	274	0.00597 0.00031	-2.350	<0.01	-148.553	0.000	5.395	2.977 - 7.139	0.001	0.549	0.010	0.567
16	Channel Is	5	0.00263 0.00077	1.686	>0.10	3.526	0.970	6.068	0.000 - 77.737	0.365	0.037	0.880	0.092
17	peripheral	342	0.00468 0.00023	-2.525	<0.001	-207.570	0.000	4.000	3.275 - 6.621	0.002	0.102	0.013	0.343
18	south-eastern	47	0.00506 0.00046	-2.330	<0.01	-34.059	0.000	5.000	3.637 - 17.842	0.006	0.211	0.005	0.497
19	Sicilian	15	0.01295 0.00116	-1.135	>0.10	-6.577	0.004	8.000	5.562 - 20.121	0.014	0.160	0.015	0.755

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**Table 3** Time to most recent common ancestor (tMRCA) for each mitochondrial lineage  
6 population. Median and 95% highest posterior density (HPD) range of times, obtained from 540  
7 million post-burnin genealogy samples in *Beast 2.3.1*. Trees calibrated with intraspecific rodent  
8 cyt *b* clock rate ( $3.27 \times 10^{-7}$  substitutions site $^{-1}$  year $^{-1}$ ) estimated from radiocarbon dated samples  
9 of *Microtus arvalis* (Martíková *et al.*, 2013).  
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Lineage	95% HPD lower (Kya)	Median (Kya)	95% HPD upper (Kya)
African	5.137	7.430	11.376
central	9.404	22.254	37.355
Channel Is	1.339	5.591	11.543
peripheral	8.689	16.363	32.252
south-eastern	13.779	19.868	29.079
Sicilian	19.628	29.018	40.483

**SUPPLEMENTARY FIGURES**

**Fig. S.1** Maximum likelihood (ML) tree for wood mouse sequences (monophyletic clade collapsed), together with four *Apodemus* outgroup and four wood mouse *numt* sequences (GenBank reference numbers shown). Branch supports are SH-aLRT obtained with *PhyML 3.0*.

**Fig. S.2** Mismatch distributions for six wood mouse *cyt b* lineages. Observed (solid line) and expected (dashed line) distributions of pairwise differences between sequences within lineages.

**Fig. S.3** Connections between locations with the same haplotype. Lines represent connections between all pairs of locations with the same haplotype, where movements between such locations would involve a sea crossing, given the present location of coastlines. Lines coloured according to lineage (Fig. 2). Locations are collapsed to mean or centroid coordinates within each land mass or archipelago. Coordinates of locations and geodesic distances between them in supplementary information (Table S.4) and coastline data from *OpenStreetMap* (<http://www.openstreetmap.org>).

**SUPPLEMENTARY TABLES**

**Table S.1** PCR (P) and sequencing (S) primers used to obtain the new *cyt b* sequences reported in this study, from frozen or ethanol (EtOH) preserved tissues and from dry tissues or museum skins.

**Table S.2** Details of 981 *cyt b* sequences from *A. sylvaticus*. Lineage, GenBank number, voucher (where available) or sample number, haplotype name, *cyt b* sequence length, locality, WGS84 coordinates and source of material. Sequences differing only by missing base calls treated as distinct haplotypes. Voucher codes refer to collections of the Mammal Research Institute, Polish Academy of Sciences, Białowieża (MRI.PAS) and National Museums of Scotland, Edinburgh (NMS.Z). \* indicates new sequences from this study.

**Table S.3** Prior parameter distributions from coalescent genealogy sampling with *Beast 2.3.1*. Linked substitution and clock model parameters, unlinked tree parameters.

**Table S.4** Locations with the same haplotype. Geographical coordinates for locations and pairwise geodesic distances between them, where movements between such locations would involve a sea crossing, given the present location of coastlines. Locations collapsed to mean or centroid coordinates within each land mass or archipelago.

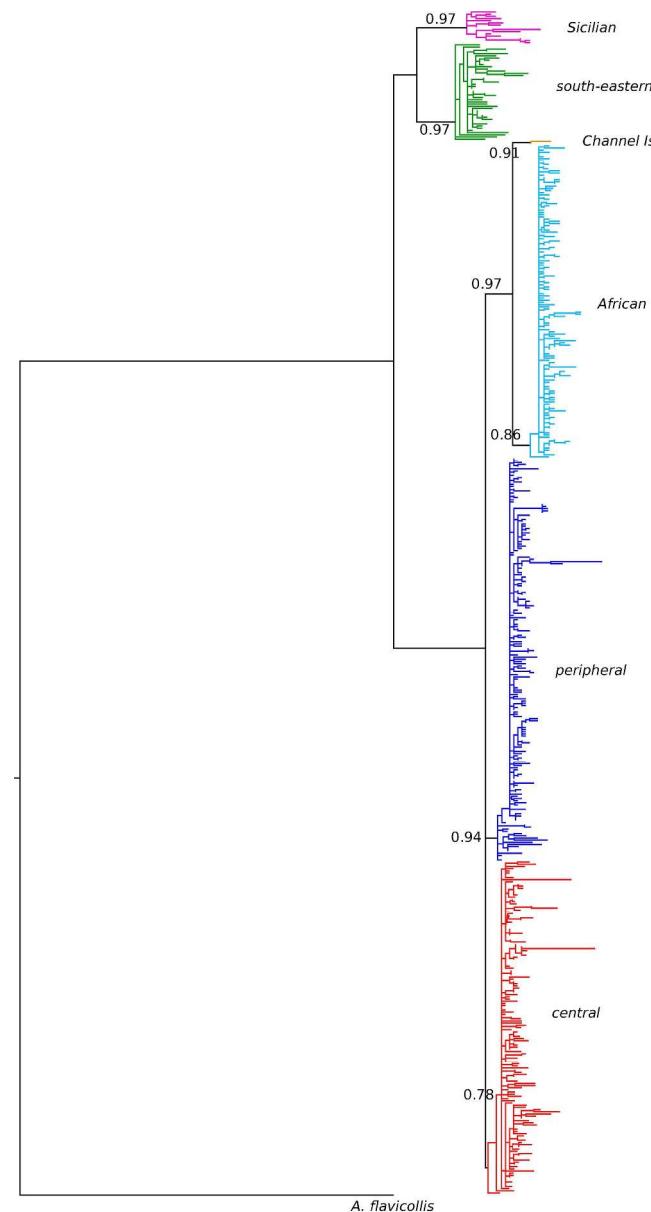
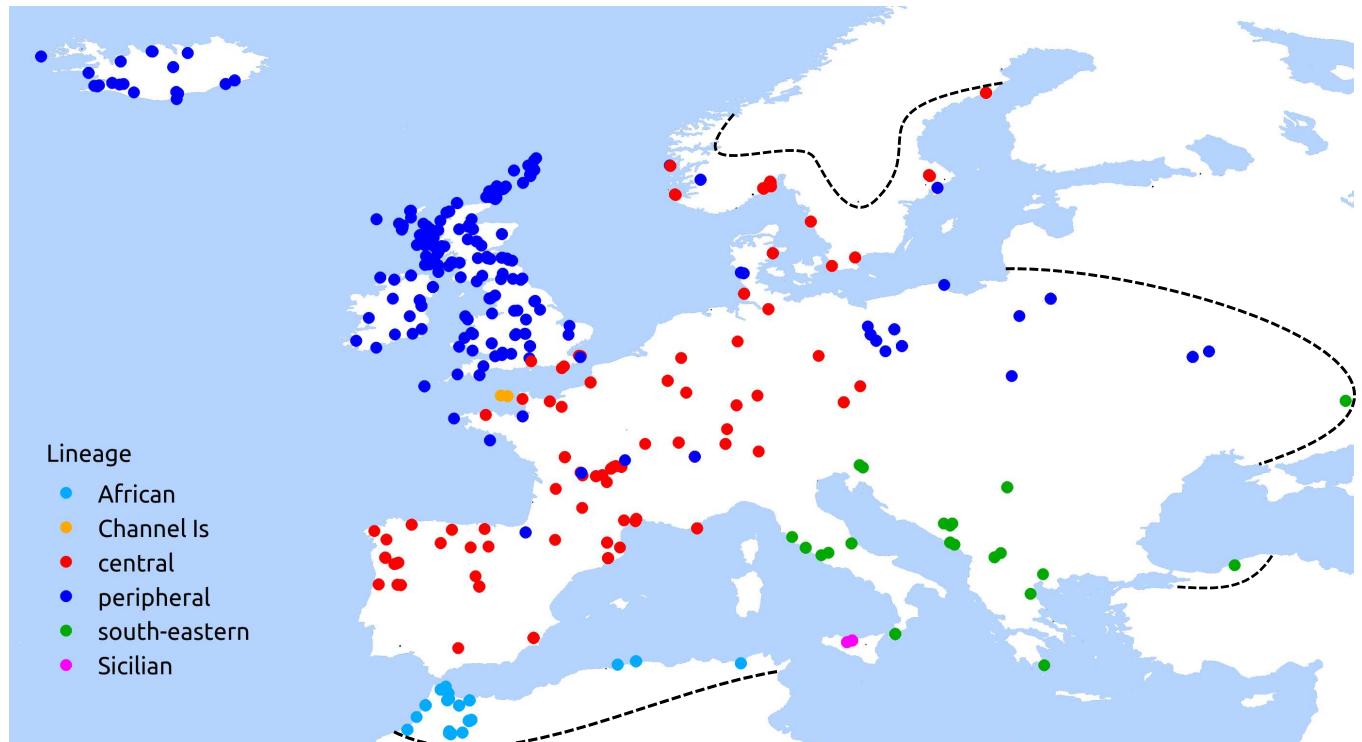


Fig. 1 Maximum likelihood (ML) tree for 543 wood mouse cyt b haplotypes. Tree inferred with PhyML 3.0, support (SH-aLRT) only shown for identified lineages and deeper splits.

244x457mm (300 x 300 DPI)



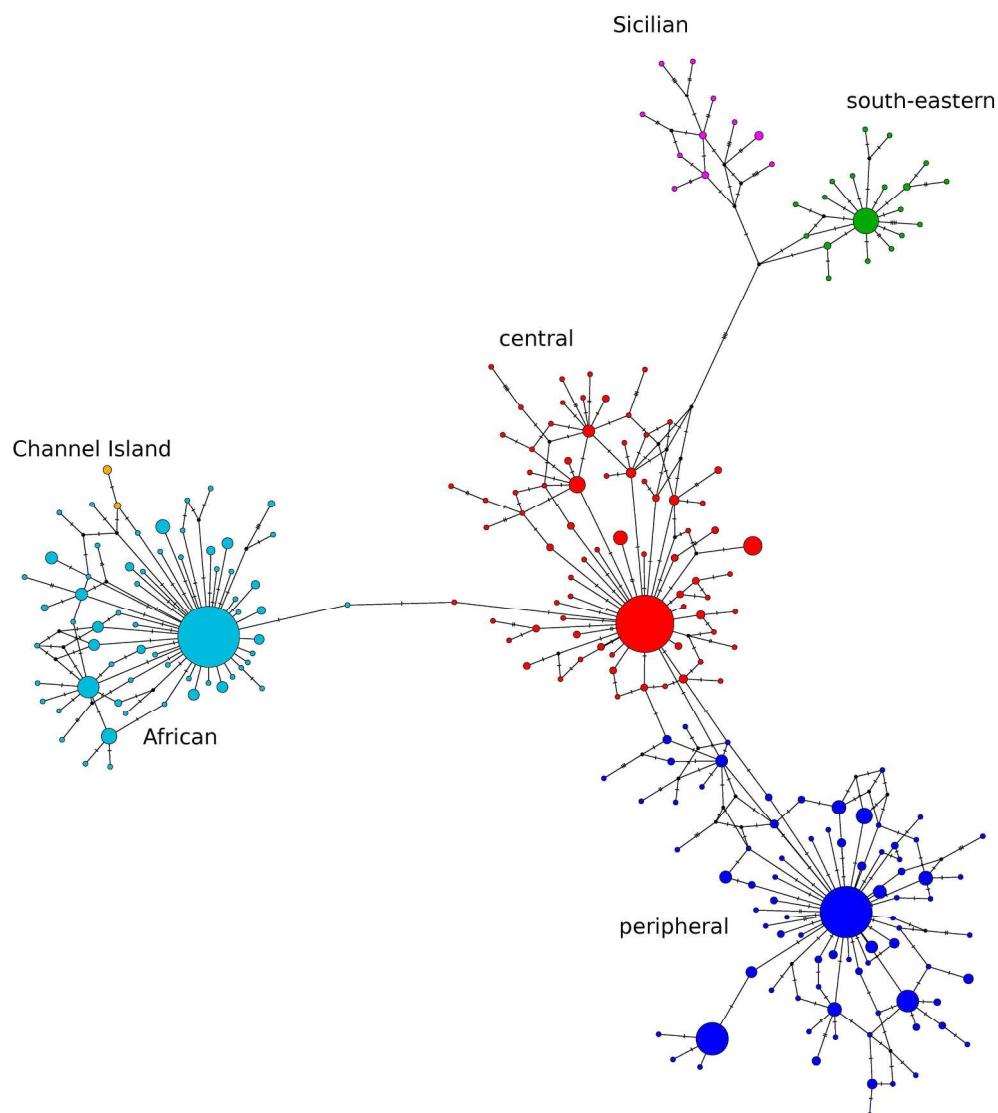


Fig. 3 Median Joining Network for 981 wood mouse sequences, obtained with PopART 1.7. Area of circle represents frequency of haplotype and mutational steps are indicated by hatch marks across branches.  
Black dots indicate inferred intermediate haplotypes.

207x234mm (300 x 300 DPI)

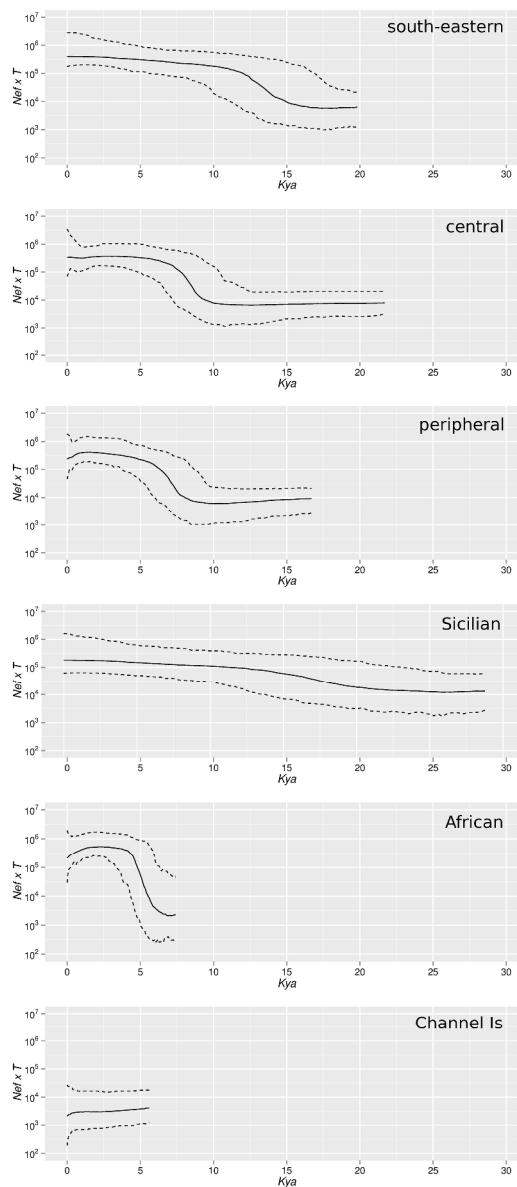


Fig. 4 Bayesian skyline plots showing effective female population size with time, for each lineage. Effective female population size ( $Nef$ ), multiplied by mean generation time ( $T$ ), in years. Solid line is median and dashed lines are 95% highest posterior density (HPD) limits.  $Nef \times T$  plotted on log scale for clarity and truncated to median estimate of tMRCA.

282x628mm (300 x 300 DPI)

Fig. S.1 Maximum likelihood (ML) tree for wood mouse sequences (monophyletic clade collapsed), together with four *Apodemus* outgroup and four wood mouse numt sequences (GenBank reference numbers shown). Branch supports are SH-aLRT obtained with PhyML 3.0.

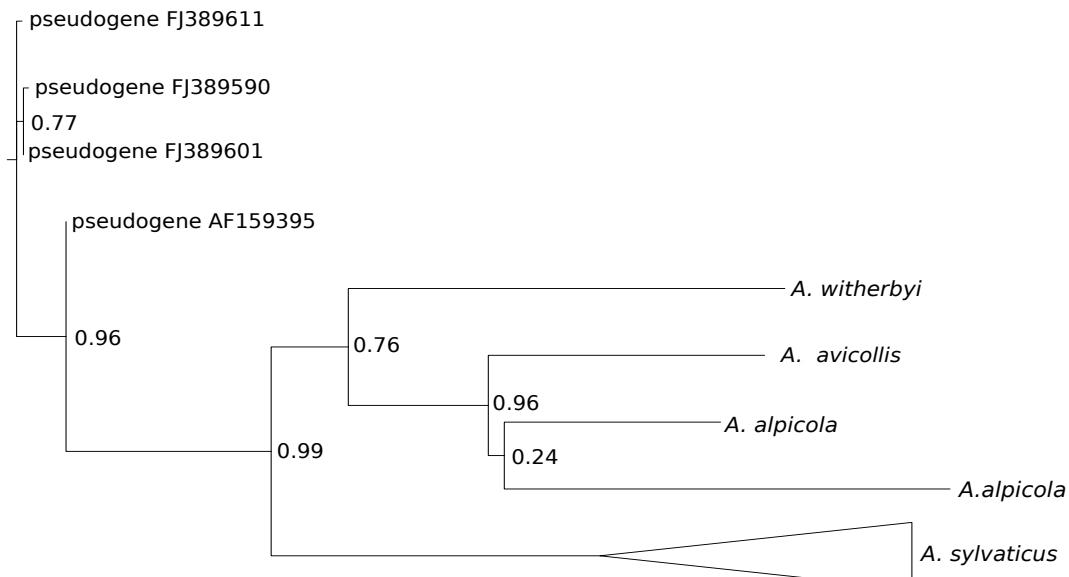


Fig. S.2 Mismatch distributions for six wood mouse cyt b lineages.  
Observed (solid line) and expected (dashed line) distributions of pairwise differences between sequences within lineages.

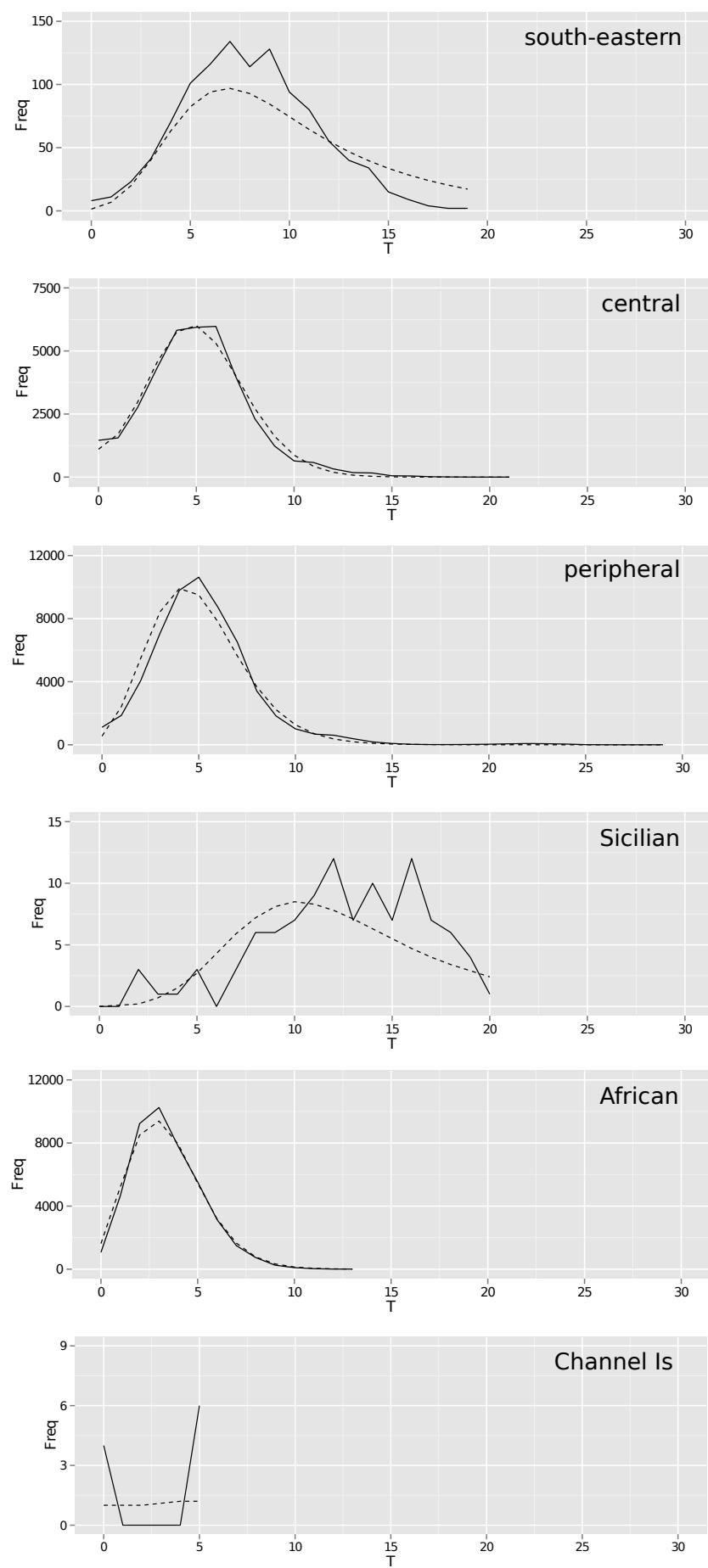
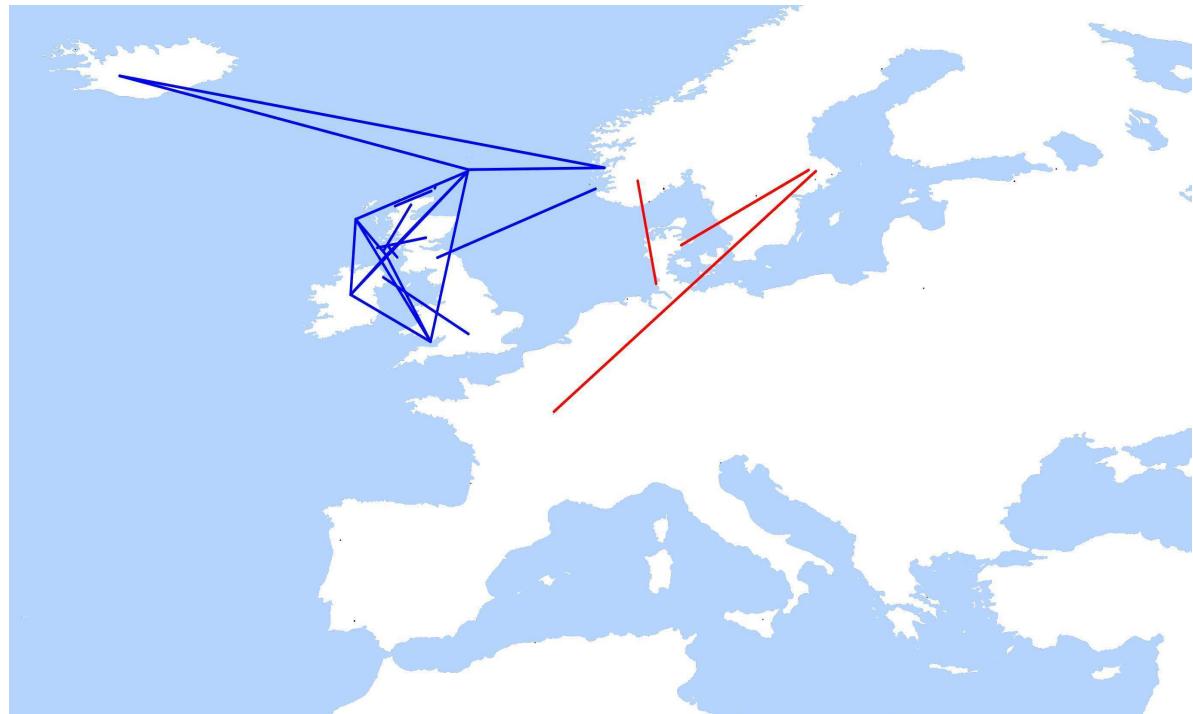


Fig. S.3 Connections between locations with the same haplotype. Lines represent connections between all pairs of locations with the same haplotype, where movements between such locations would involve a sea crossing, given the present location of coastlines. Lines coloured according to lineage (Fig. 2). Locations are collapsed to mean or centroid coordinates within each land mass or archipelago. Coordinates of locations and geodesic distances between them in supplementary information (Table S.4) and coastline data from OpenStreetMap (<http://www.openstreetmap.org>).



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3 **Table S.1** PCR (P) and sequencing (S) primers used to obtain the new cyt b sequences reported  
4 in this study, from frozen or ethanol (EtOH) preserved tissues and from dry tissues or museum  
5 skins.

Primer	Oligonucleotide sequence 5'-3'	Material	Use	Source
L14727-SP	GACAGGAAAAATCATCGTTG	Frozen/EtOH/dry	P S	Jaarola & Searle, 2002
H15915-SP	TTCATTACTGGTTTACAAGAC	Frozen/EtOH	P S	Jaarola & Searle, 2002
LasI	TGAATCTGAGGAGGATTCTCAGTA	Frozen/EtOH	S	This study
HasI	GGGTTATTAGATCCAGTTTC	Frozen/EtOH	S	This study
L7	ACCAATGACATGAAAAATCATCGTT	Frozen/EtOH	P S	Michaux <i>et al.</i> , 2003
H16	ACATGAATYGGAGGYCAACCWG	Frozen/EtOH	P S	Michaux <i>et al.</i> , 2003
Syl1R	CATTCCCTCGTCCTACGTGAA	Dry	P S	This study
Syl2F	CCCATATCTGTCGAGACGTAAA	Dry	P S	This study
Syl2R	TGGAGAAAACAAGAGGTGAACAA	Dry	P S	This study
SylUP	GAGGAGGGATTCTCAGTAGAC	EtOH/dry	P S	Michaux <i>et al.</i> , 2001
SylDN	TTAATATGGGTGGGTGTTA	EtOH/dry	P S	Michaux <i>et al.</i> , 2001
Syl4Fn	CCCATTCACCCATACTATACTATCAA	Dry	P S	This study
Syl4Rn	AATTGAAGCTAGTTGTCCGATG	Dry	P S	This study
Syl5F	ATATTCCGCCAACACTCA	Dry	P S	This study
VOLE-14	TTTCATTACTGGTTACAAGAC	EtOH/dry	P S	Conroy & Cook (1999)

30 **Conroy CJ, Cook JA.** 1999. MtDNA evidence for repeated pulses of speciation within arvicoline  
31 and murid rodents. *Journal of Mammalian Evolution* 6: 221–245.

33 **Jaarola M, Searle JB.** 2002. Phylogeography of field voles (*Microtus agrestis*) in Eurasia inferred  
34 from mitochondrial DNA sequences. *Molecular Ecology* 11: 2613–2621.

36 **Michaux JR, Kinet S, Filippucci MG, Libois R, Besnard A, Catzeffis F.** 2001. Molecular  
37 identification of three sympatric species of wood mice (*Apodemus sylvaticus*, *A. flavicollis*, *A.  
38 alpicola*) in western Europe (Muridae: Rodentia). *Molecular Ecology Notes* 1: 260–263.

**Table S.2** Details of 981 cyt b sequences from *A. sylvaticus*. Lineage, GenBank number, voucher (where available) or sample number, haplotype name, cyt b sequence length, locality, WGS84 coordinates and source of material. Sequences differing only by missing base calls treated as distinct haplotypes. Voucher codes refer to collections of the Mammal Research Institute, Polish Academy of Sciences, Białowieża (MRI.PAS) and National Museums of Scotland, Edinburgh (NMS.Z). \* indicates new sequences from this study.

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM582033	TA104	Algeria_1_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582034	TA105	Algeria_2_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582035	TA52	Algeria_3_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582036	TA56	Algeria_4_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582037	TA57	Algeria_5_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582038	TA67	Algeria_6_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582039	TA75	Algeria_7_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582040	TA76	Algeria_8_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582041	TA85	Algeria_9_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582042	TA86	Algeria_10_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582043	TA87	Algeria_10_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582044	TA89	Algeria_10_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582045	TA91	Algeria_10_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582046	TA95	Algeria_11_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM581763	C2	Algeria_12_s	864	Algeria, Zeralda	36.7170	2.8500	Lalis <i>et al.</i> 2016
African	KM582047	TA98	Algeria_Morocco_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM582048	TA99	Algeria_Morocco_s	864	Algeria, Cap Djinet	36.8780	3.7210	Lalis <i>et al.</i> 2016
African	KM581760	A4	Algeria_Morocco_s	864	Algeria, Zeralda	36.7170	2.8500	Lalis <i>et al.</i> 2016
African	KM581770	C7	Algeria_Morocco_s	864	Algeria, Zeralda	36.7170	2.8500	Lalis <i>et al.</i> 2016
African	KM581938	MA563	Algeria_Morocco_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581942	MA572	Algeria_Morocco_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581944	MA576	Algeria_Morocco_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581946	MA584	Algeria_Morocco_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581950	MA592	Algeria_Morocco_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581762	C102	Algeria_Morocco_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581967	MA644	Algeria_Morocco_s	864	Morocco, Chrouda	35.3660	-5.1710	Lalis <i>et al.</i> 2016
African	KM581978	MA665	Algeria_Morocco_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581985	MA674	Algeria_Morocco_s	864	Morocco, Chrouda	35.3660	-5.1710	Lalis <i>et al.</i> 2016
African	KM581897	MA503	Algeria_Morocco_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581901	MA510	Algeria_Morocco_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581895	MA474	Algeria_Morocco_s	864	Morocco, Esperada	35.5340	-5.5340	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581864	MA384	Algeria_Morocco_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581866	MA389	Algeria_Morocco_s	864	Morocco, Ifrane	33.4940	-5.0570	Lalis <i>et al.</i> 2016
African	KM581869	MA400	Algeria_Morocco_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581871	MA411	Algeria_Morocco_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581877	MA421	Algeria_Morocco_s	864	Morocco, Ifrane	33.5000	-5.1130	Lalis <i>et al.</i> 2016
African	KM582014	MA937	Algeria_Morocco_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582016	MA939	Algeria_Morocco_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582024	MA950	Algeria_Morocco_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582030	RE3	Algeria_Morocco_s	864	Morocco, Ifrane	33.4720	-5.1390	Lalis <i>et al.</i> 2016
African	KM581780	JM1	Algeria_Morocco_s	864	Morocco, Moyen-Atlas ISR	33.5000	-4.5000	Lalis <i>et al.</i> 2016
African	KM581915	MA533	Algeria_Morocco_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581918	MA536	Algeria_Morocco_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581921	MA540	Algeria_Morocco_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581926	MA547	Algeria_Morocco_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581934	MA556	Algeria_Morocco_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581803	MA270	Algeria_Morocco_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581804	MA273	Algeria_Morocco_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581820	MA295	Algeria_Morocco_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581828	MA313	Algeria_Morocco_s	864	Morocco, Taza	34.1040	-4.0730	Lalis <i>et al.</i> 2016
African	KM581841	MA339	Algeria_Morocco_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581842	MA340	Algeria_Morocco_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581843	MA341	Algeria_Morocco_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
central	AJ511879	JRM-107	Belgium_1_s	965	Belgium, Ardennes, Rochefort	50.1600	5.2200	Dubey <i>et al.</i> 2009
central	AJ511906	JRM-102	Belgium_2_s	963	Belgium, Ardennes, Rochefort	50.1600	5.2200	Michaux <i>et al.</i> 2003
central	AJ511877	JRM-104	Belgium_3_s	963	Belgium, Ardennes, Rochefort	50.1600	5.2200	Michaux <i>et al.</i> 2003
central	AJ511878	JRM-105	Belgium_4_s	965	Belgium, Ardennes, Rochefort	50.1600	5.2200	Dubey <i>et al.</i> 2009
central	AJ298605	JRM-101	Belgium_5	1040	Belgium, Ardennes, Rochefort	50.1600	5.2200	Michaux <i>et al.</i> 2001
central	AJ298598	JRM-103	Belgium_6_s	980	Belgium, Ardennes, Rochefort	50.1600	5.2200	Michaux <i>et al.</i> 2001
south-eastern	JF819976	BK_S6	BosniaHerzegovina_1	1140	Bosnia Herzegovina, Mt Zelengora	43.4000	18.7000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819977	BK_S7	BosniaHerzegovina_2	1140	Bosnia Herzegovina, Mt Zelengora	43.4000	18.7000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819981	BK_S11	BosniaHerzegovina_3	1140	Bosnia Herzegovina, Morine	43.4000	18.3000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819978	BK_S8	BosniaHerzegovina_4	1140	Bosnia Herzegovina, Gacko	43.3000	18.6000	Kryštufek <i>et al.</i> 2012
central	AJ511889	JRM-373	Czech_Rep_1_s	963	Czech Republic, Pilsen, Kašperské	49.1439	13.5594	Michaux <i>et al.</i> 2003
central	AJ511890	JRM-374	Czech_Rep_2_s	958	Czech Republic, Pilsen, Kašperské	49.1439	13.5594	Michaux <i>et al.</i> 2003
central	AJ511907	JRM-375	Czech_Rep_3_s	964	Czech Republic, Bohemia, Klíneč	49.9026	14.3426	Michaux <i>et al.</i> 2003

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Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
central	AJ511908	JRM-372	Czech_Rep_4_s	965	Czech Republic, Pilsen, Kašperské	49.1439	13.5594	Michaux <i>et al.</i> 2003
peripheral	KX159510	JSH_DK12	Denmark_1	1140	Denmark, Ribe, Roager	55.2517	8.8222	*
peripheral	KX159510	JSH_DK19	Denmark_1	1140	Denmark, Ribe, Vester Vedsted	55.2850	8.6856	*
peripheral	KX159511	JSH_DK18	Denmark_2	1140	Denmark, Ribe, Vester Vedsted	55.2850	8.6856	*
central	FJ389639	JM-1193	Denmark_3_s	818	Denmark, Aarhus area	56.2000	10.2000	Dubey <i>et al.</i> 2009
peripheral	FJ389640	JM-1201	Denmark_4_s	818	Denmark, Aarhus area	56.2000	10.2000	Dubey <i>et al.</i> 2009
peripheral	FJ389664	JM-1196	Denmark_5_s	818	Denmark, Aarhus area	56.2000	10.2000	Dubey <i>et al.</i> 2009
peripheral	KX159512	D1192	Denmark_6_s	818	Denmark, Aarhus area	56.2000	10.2000	*
central	FJ389622	JM-1195	Denmark_Sweden_s	818	Denmark, Aarhus area	56.2000	10.2000	Dubey <i>et al.</i> 2009
central	FJ389621	JM-1200	Denmark_Sweden_s	818	Denmark, Aarhus area	56.2000	10.2000	Dubey <i>et al.</i> 2009
central	KX159514	S4599	Denmark_Sweden_s	818	Sweden, Goteborg	57.7000	12.0000	*
central	KX159514	S4609	Denmark_Sweden_s	818	Sweden, southern Sweden	NA	NA	*
central	FJ389626	JM-4661	Denmark_Sweden_s	818	Sweden, Uppsala area	59.9000	17.6000	Dubey <i>et al.</i> 2009
central	FJ389624	JM-4676	Denmark_Sweden_s	818	Sweden, Uppsala area	59.9000	17.6000	Dubey <i>et al.</i> 2009
central	KX159514	C4714	Denmark_Sweden_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159514	C4717	Denmark_Sweden_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	FJ389623	JM-4775	Denmark_Sweden_s	818	Sweden, Uppsala area	59.9000	17.6000	Dubey <i>et al.</i> 2009
central	KX159514	C4797	Denmark_Sweden_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159514	C4806	Denmark_Sweden_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	FJ389625	JM-4854	Denmark_Sweden_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
peripheral	KX159513	JSH_D39	Denmark_Germany	1140	Germany, Nordfriesland, Kattinger Watt	54.2831	8.8403	*
peripheral	KX159513	JSH_DK11	Denmark_Germany	1140	Denmark, Ribe, Roager	55.2517	8.8222	*
central	KX159518	NMS.Z.2009.101.3P	France_1	1140	France, Côtes d'Armor, Belle-Isle-en-Terre	48.5452	-3.3963	*
central	KX159519	NMS.Z.2009.101.4P	France_2	1140	France, Puy-de-Dôme, Bussières	46.0697	2.6325	*
central	KX159520	NMS.Z.2009.101.6P	France_3	1140	France, Creuse, Villemaloux	45.9995	2.5384	*
central	KX159521	NMS.Z.2009.101.7P	France_4	1140	France, Creuse, Villemaloux	45.9995	2.5384	*
central	KX159522	NMS.Z.2009.101.9P	France_5	1140	France, Puy-de-Dôme, le Quartier	46.1212	2.7626	*
central	KX159523	NMS.Z.2009.101.10P	France_6	1140	France, Puy-de-Dôme, le Quartier	46.1212	2.7626	*
central	KX159524	NMS.Z.2009.101.12P	France_7	1140	France, Puy-de-Dôme, Marcillat	46.0811	3.0321	*
central	KX159525	NMS.Z.2009.101.13P	France_8	1140	France, Puy-de-Dôme, Marcillat	46.0811	3.0321	*
central	KX159526	JSH_Ca2	France_9	1140	France, Hérault, Caussiniojouls	43.5506	3.1528	*
central	KX159527	JSH_F34A2	France_10	1140	France, Calvados, Caen	49.1848	-0.3602	*
central	KX159528	JSH_F35A2	France_11	1140	France, Calvados, Caen	49.1848	-0.3602	*
central	KX159529	JSH_F144C3	France_12	1140	France, Somme, Abbeville	50.0833	1.5667	*
central	KX159530	JSH_F178C7	France_13	1140	France, Somme, Abbeville	50.0833	1.5667	*

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
central	KX159531	JSH_LN7	France_14	1140	France, Tarn-et-Garonne, Saint-Amans	44.1410	1.1715	*
central	KX159532	JSH_MN574	France_15	1140	France, Franch-Comté, Etrabonne	47.2335	5.7423	*
central	KX159533	JSH_MN572	France_16	1140	France, Franch-Comté, Etrabonne	47.2335	5.7423	*
central	KX159533	JSH_MN575	France_16	1140	France, Franch-Comté, Etrabonne	47.2335	5.7423	*
central	KX159534	JSH_NX2	France_17	1140	France, Haute-Vienne, Naxon	45.6770	1.1889	*
peripheral	KX159535	JSH_WM1	France_18	1140	France, Corrèze, Lacelle	45.6415	1.8248	*
central	KX159536	JSH_WM15	France_19	1140	France, Haute-Vienne, Aixe-sur-Vienne	45.7959	1.1346	*
central	KX159536	JSH_WM3	France_19	1140	France, Corrèze, Lacelle	45.6415	1.8248	*
central	KX159537	JSH_WM4	France_20	1140	France, Corrèze, Lacelle	45.6415	1.8248	*
central	KX159538	JSH_WM10	France_21	1140	France, Haute-Vienne, Aixe-sur-Vienne	45.7959	1.1346	*
peripheral	KX159539	JSH_WM14	France_22	1140	France, Haute-Vienne, Aixe-sur-Vienne	45.7959	1.1346	*
peripheral	KX159540	JSH_WM16	France_23	1140	France, Haute-Vienne, Aixe-sur-Vienne	45.7959	1.1346	*
central	KX159541	JSH_WM19	France_24	1140	France, Ille-et-Vilaine, Broualan	48.4743	-1.6500	*
central	KX159542	JSH_WM20	France_25	1140	France, Ille-et-Vilaine, Broualan	48.4743	-1.6500	*
peripheral	KX159543	JSH_WM21	France_26	1140	France, Ille-et-Vilaine, Broualan	48.4743	-1.6500	*
central	KX159544	JSH_WM22	France_27	1140	France, Manche, Saint-Rémy-des-Landes	49.3004	-1.6563	*
peripheral	AJ511935	JRM-575	France_28_s	965	France, Hérault, Murviel	43.6167	3.7333	Michaux <i>et al.</i> 2003
central	AJ511883	JRM-144	France_29_s	963	France, Var, Cap Lardier	43.1715	6.6139	Michaux <i>et al.</i> 2003
central	AJ511884	JRM-145	France_30_s	964	France, Var, Cap Lardier	43.1715	6.6139	Michaux <i>et al.</i> 2003
peripheral	AJ511885	JRM-270	France_31_s	965	France, Pyrénées-Orientales, Py Mantet	42.4970	2.3518	Michaux <i>et al.</i> 2003
central	AJ511887	JRM-272	France_32_s	951	France, Pyrenees Orientales, Py Mantet	42.4970	2.3518	Michaux <i>et al.</i> 2003
central	AJ511896	JRM-577	France_33_s	963	France, Hérault, Murviel	43.6167	3.7333	Michaux <i>et al.</i> 2003
central	AJ511898	JRM-589	France_34_s	919	France, Nièvre, Morvan	47.1712	4.1534	Michaux <i>et al.</i> 2003
central	AJ511899	JRM-396	France_35_s	962	France, Corrèze, Sérandon	45.3606	2.3374	Michaux <i>et al.</i> 2003
central	AJ511900	JRM-143	France_36_s	932	France, Var, Cap Lardier	43.1715	6.6139	Michaux <i>et al.</i> 2003
peripheral	AJ511901	JRM-345	France_37_s	965	France, Allier	46.4000	3.2000	Michaux <i>et al.</i> 2003
central	AJ511904	JRM-142	France_38_s	965	France, Var, Cap Lardier	43.1715	6.6139	Michaux <i>et al.</i> 2003
central	AJ511910	JRM-714	France_39_s	965	France, Hérault, Murviel	43.6167	3.7333	Michaux <i>et al.</i> 2003
central	AJ298599	JRM-269	France_40_s	925	France, Pyrénées-Orientales, Py Mantet	42.4970	2.3518	Michaux <i>et al.</i> 2001
central	AJ511974	JRM-271	France_41_s	709	France, Pyrenees Orientales, Py Mantet	42.4970	2.3518	Michaux <i>et al.</i> 2003
central	KM581746	VN1731	France_42_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581745	VN1730	France_43_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581751	VN1736	France_43_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581753	VN1738	France_43_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581698	21004	France_44_s	701	France, Hérault, Montbazin	43.5160	3.6930	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
central	KM581701	VV1997117	France_45_s	701	France, Gironde, Forêt de Moulis	45.0400	-0.0800	Lalis <i>et al.</i> 2016
central	KM581696	VV199990	France_46_s	701	France, Franch-Comté, Etrabonne	47.2335	5.7423	Lalis <i>et al.</i> 2016
central	KM581744	VN1729	France_46_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581747	VN1732	France_46_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581754	VN1739	France_46_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581748	VN1733	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581749	VN1734	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581750	VN1735	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581755	VN1740	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581756	VN1742	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581758	VN1745	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581759	VN1767	France_47_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581697	20989	France_48_s	701	France, Hérault, Montbazin	43.5160	3.6930	Lalis <i>et al.</i> 2016
central	KM581699	21007	France_49_s	701	France, Hérault, Montbazin	43.5160	3.6930	Lalis <i>et al.</i> 2016
central	KM581695	VV199784	France_50_s	701	France, Orne, Vimoutiers	48.9280	0.1990	Lalis <i>et al.</i> 2016
central	KX159545	NMS.Z.2009.101.5P	France_Luxembourg_Portugal	1140	France, Puy-de-Dôme, Bussières	46.0697	2.6325	*
central	KX159545	NMS.Z.2009.101.881	France_Luxembourg_Portugal	1140	Luxembourg	49.6000	6.1000	*
central	KX159545	JSH_F140C3	France_Luxembourg_Portugal	1140	France, Somme, Abbeville	50.0833	1.5667	*
central	KX159545	JSH_F159C7	France_Luxembourg_Portugal	1140	France, Somme, Abbeville	50.0833	1.5667	*
central	KX159545	JSH_GV1	France_Luxembourg_Portugal	1140	Portugal, Vila Real, Gouvães da Serra	41.4798	-7.7267	*
central	KM581742	VE42	France_Spain_1_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581752	VN1737	France_Spain_1_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581757	VN1743	France_Spain_1_s	701	France, Vienne, Saint Benoît	46.5460	0.3480	Lalis <i>et al.</i> 2016
central	KM581680	785	France_Spain_2_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581700	VV1997112	France_Spain_2_s	701	France, Franch-Comté, Etrabonne	47.2335	5.7423	Lalis <i>et al.</i> 2016
central	KX159546	NMS.Z.2009.101.2P	France_Sweden	1140	France, Côtes d'Armor, Belle-Isle-en-Terre	48.5452	-3.3963	*
central	KX159546	NMS.Z.2009.101.6S	France_Sweden	1140	Sweden, Skåne Län, SW of Kristianstad	56.0000	14.1000	*
central	KX159546	JSH_WM18	France_Sweden	1140	France, Corrèze, Saint-Setiers	45.6953	2.1284	*
central	KX159546	JSH_WM7	France_Sweden	1140	France, Haute-Vienne, Moulin de Vienne	45.8167	1.0917	*
peripheral	KX159515	JSH_BI1	FR_Belle_Ile_1	1140	France, Morbihan, Belle Ile	47.3375	-3.1958	*
peripheral	KX159516	JSH_BI3	FR_Belle_Ile_2	1140	France, Morbihan, Belle Ile	47.3375	-3.1958	*
peripheral	KX159517	JSH_MPAs43	FR_Ile_de_Quemenez	1140	France, Finistère, Ile de Quemenez	48.3736	-4.9000	*
peripheral	KX159547	NMS.Z.2009.101.162M	GB_Aberdeen_1	1140	Scotland, Aberdeenshire, Torphins	57.1074	-2.6290	*
peripheral	KX159548	NMS.Z.2009.101.164M	GB_Aberdeen_2	1140	Scotland, Aberdeenshire, Torphins	57.1074	-2.6290	*
peripheral	KX159549	NMS.Z.2009.101.1294M	GB_Anglesey	1140	Wales, Anglesey, Capel Mawr	53.2143	-4.3661	*

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159549	NMS.Z.2009.101.1297M	GB_Anglesey	1140	Wales, Anglesey, Capel Mawr	53.2143	-4.3661	*
peripheral	KX159550	NMS.Z.2009.101.587M	GB_Argyll	1140	Scotland, Kintyre, Southend	55.3117	-5.6417	*
peripheral	KX159550	NMS.Z.2009.101.588M	GB_Argyll	1140	Scotland, Argyll, Cruachan	55.6438	-5.6630	*
peripheral	KX159551	NMS.Z.2009.101.568	GB_Argyll_Lothian	1140	Scotland, Argyll, North Shian	56.5263	-5.3590	*
peripheral	KX159551	NMS.Z.2009.101.1926M	GB_Argyll_Lothian	1140	Scotland, W. Lothian, Shieldhill	55.9714	-3.7721	*
peripheral	KX159552	NMS.Z.2009.101.347	GB_Arran_Scarba	1140	Scotland, Arran, Brodick	55.5924	-5.1501	*
peripheral	KX159552	NMS.Z.2009.101.841	GB_Arran_Scarba	1140	Scotland, Scarba	56.1873	-5.6792	*
peripheral	KX159553	NMS.Z.2009.101.65	GB_Benbecula	1140	Scotland, Benbecula, Torlum	57.4351	-7.3814	*
peripheral	KX159554	NMS.Z.2009.101.77M	GB_Berwick	1140	Scotland, Berwickshire, Grantshouse	55.8903	-2.3245	*
peripheral	KX159555	NMS.Z.2009.101.852	GB_Bute_1	1140	Scotland, Bute, Kingarth	55.7694	-5.0097	*
peripheral	KX159556	NMS.Z.2009.101.853	GB_Bute_2	1140	Scotland, Bute, Kingarth	55.7694	-5.0097	*
peripheral	KX159557	NMS.Z.2009.101.1138M	GB_Caernarvon_1	1140	Wales, Caernarvon, Carmel	53.0691	-4.2507	*
peripheral	KX159558	NMS.Z.2009.101.1238M	GB_Caernarvon_2	1140	Wales, Caernarvon, Carmel	53.0691	-4.2507	*
peripheral	KX159559	NMS.Z.2009.101.233	GB_Canna	1140	Scotland, Canna, Cuil a' Bhainne	57.0571	-6.5174	*
peripheral	KX159559	NMS.Z.2009.101.234	GB_Canna	1140	Scotland, Canna, A'Chill lower wood	57.0584	-6.5060	*
peripheral	KX159559	NMS.Z.2009.101.888	GB_Canna	1140	Scotland, Canna	57.0591	-6.5127	*
peripheral	KX159560	NMS.Z.2009.101.1103M	GB_Cardigan	1140	Wales, Cardigan, Clarach	52.4268	-4.0751	*
peripheral	KX159561	NMS.Z.2009.101.627M	GB_Cheshire	1140	England, Cheshire, Thingwall	53.3478	-3.0980	*
peripheral	KX159562	NMS.Z.2009.101.434	GB_Coll	1140	Scotland, Coll, Feall Bay	56.5951	-6.6544	*
peripheral	KX159562	NMS.Z.2009.101.439	GB_Coll	1140	Scotland, Coll, Feall Bay	56.5914	-6.6572	*
peripheral	KX159563	NMS.Z.2009.101.844	GB_Cumbrae	1140	Scotland, Great Cumbrae, Millport	55.7529	-4.9494	*
peripheral	KX159563	NMS.Z.2009.101.845	GB_Cumbrae	1140	Scotland, Great Cumbrae, Millport	55.7529	-4.9494	*
peripheral	KX159564	NMS.Z.2009.101.1145M	GB_Cumbria	1140	England, Cumbria, Cartmel	54.2030	-2.9520	*
peripheral	KX159565	NMS.Z.2009.101.955M	GB_Derby	1140	England, Derbyshire, Ambergate	53.0615	-1.4896	*
peripheral	KX159566	JSH_SD7	GB_Devon	1140	England, Devon	50.4276	-3.6908	*
peripheral	KX159566	JSH_SD9	GB_Devon	1140	England, Devon	50.4276	-3.6908	*
peripheral	KX159567	NMS.Z.2009.101.33M	GB_Dumfries_Cumbria	1140	Scotland, Dumfries, Amisfield	55.1376	-3.5608	*
peripheral	KX159567	NMS.Z.2009.101.685M	GB_Dumfries_Cumbria	1140	England, Cumbria, Brampton	54.9723	-2.6764	*
peripheral	KX159568	NMS.Z.2009.101.484M	GB_Durham_Northumberland	1140	England, Durham, Gateshead	54.9389	-1.7409	*
peripheral	KX159568	JSH_D32	GB_Durham_Northumberland	1140	England, Northumberland, Kielder	55.2331	-2.5919	*
peripheral	KX159569	NMS.Z.2009.101.525M	GB_Durness	1140	Scotland, Durness, Balnakeil	58.5845	-4.7677	*
peripheral	KX159570	NMS.Z.2009.101.1920M	GB_Dyfed	1140	Wales, Dyfed, Cwmytydu	52.1912	-4.4051	*
peripheral	KX159571	NMS.Z.2009.101.627	GB_Eday	1140	Scotland, Eday, Skaill	59.1779	-2.7593	*
peripheral	KX159571	NMS.Z.2009.101.628	GB_Eday	1140	Scotland, Eday, Skaill	59.1779	-2.7593	*
peripheral	KX159572	NMS.Z.2009.101.443	GB_Eigg	1140	Scotland, Eigg, Kildonan	56.8899	-6.1259	*

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Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159572	NMS.Z.2009.101.462	GB_Eigg	1140	Scotland, Eigg, Manse Wood	56.8868	-6.1370	*
peripheral	KX159572	NMS.Z.2009.101.467	GB_Eigg	1140	Scotland, Eigg, Allt Eas Chuthain	56.8902	-6.1440	*
peripheral	KX159573	NMS.Z.2009.101.14M	GB_Fife	1140	Scotland, Fife, Dalgety Bay	56.0380	-3.3433	*
peripheral	KX159574	NMS.Z.2009.101.236	GB_Foula	1140	Scotland, Foula, Punds	60.1194	-2.0594	*
peripheral	KX159574	NMS.Z.2009.101.238	GB_Foula	1140	Scotland, Foula, Punds	60.1194	-2.0594	*
peripheral	KX159574	NMS.Z.2009.101.242	GB_Foula	1140	Scotland, Foula, Punds	60.1194	-2.0594	*
peripheral	KX159575	NMS.Z.2009.101.644	GB_Foulney	1140	England, Foulney	54.0664	-3.1536	*
peripheral	KX159576	NMS.Z.2009.101.1234M	GB_Glamorgan	1140	Wales, Glamorgan, Swansouth-eastern	51.5914	-4.0224	*
peripheral	KX159577	NMS.Z.2009.101.452M	GB_Glocs	1140	England, Gloucestershire, Bristol	51.4940	-2.6049	*
Channel Island	KX159578	NMS.Z.2009.101.1061	GB_Guernsey	1140	Guernsey	49.4616	-2.6837	*
Channel Island	KX159578	NMS.Z.2009.101.1062	GB_Guernsey	1140	Guernsey	49.4616	-2.6837	*
peripheral	KX159579	NMS.Z.2009.101.435M	GB_Hampshire	1140	England, Hampshire, Whitchurch	51.2293	-1.3283	*
peripheral	KX159580	NMS.Z.2009.101.958	GB_Harris	1140	Scotland, Harris, Luskentyre	57.8887	-6.9373	*
peripheral	KX159581	NMS.Z.2009.101.159M	GB_Inverness_1	1140	Scotland, Inverness, Drummond	57.4574	-4.2351	*
peripheral	KX159582	NMS.Z.2009.101.222M	GB_Inverness_2	1140	Scotland, Inverness, Tomatin	57.3357	-3.9951	*
peripheral	KX159583	NMS.Z.2009.101.270M	GB_Inverness_3	1140	Scotland, Inverness-shire, Arisaig	56.9343	-5.8610	*
peripheral	KX159584	NMS.Z.2009.101.479	GB_Islay_1	1140	Scotland, Islay, Cnoc Mor Ghrosdeil	55.6491	-6.2757	*
peripheral	KX159584	NMS.Z.2009.101.488	GB_Islay_1	1140	Scotland, Islay, Machrie	55.6587	-6.2593	*
peripheral	KX159585	NMS.Z.2009.101.598	GB_Islay_2	1140	Scotland, Islay, Ardilistry	55.6677	-6.0741	*
peripheral	KX159586	NMS.Z.2009.101.835	GB_Jura_N_Scotland	1140	Scotland, Jura, Craighouse	55.8527	-5.9432	*
peripheral	KX159586	NMS.Z.2009.101.837	GB_Jura_N_Scotland	1140	Scotland, Jura, Lagg	55.9391	-5.8542	*
peripheral	KX159586	NMS.Z.2009.101.220M	GB_Jura_N_Scotland	1140	Scotland, Easter Ross, Tain	57.8144	-4.0636	*
peripheral	KX159586	NMS.Z.2009.101.519M	GB_Jura_N_Scotland	1140	Scotland, Durness, Sangomore	58.5689	-4.7407	*
central	KX159587	NMS.Z.2009.101.976M	GB_Kent	1140	England, Kent, Whitstable	51.3514	1.0187	*
central	KX159587	NMS.Z.2009.101.977M	GB_Kent	1140	England, Kent, Herne Common	51.3319	1.1122	*
peripheral	KX159588	NMS.Z.2009.101.964M	GB_Kirkcudbright_1	1140	Scotland, Kirkcudbright, Glen Trool	55.0645	-4.5822	*
peripheral	KX159589	NMS.Z.2009.101.1255M	GB_Kirkcudbright_2	1140	Scotland, Kirkcudbright, Kippford	54.8670	-3.8246	*
peripheral	KX159590	NMS.Z.2009.101.1022M	GB_Lancashire	1140	England, Lancashire, Stalybridge	53.4769	-2.0527	*
peripheral	KX159591	NMS.Z.2009.101.84	GB_Lewis	1140	Scotland, Lewis, Bhalto	58.2011	-6.9789	*
peripheral	KX159591	NMS.Z.2009.101.88	GB_Lewis	1140	Scotland, Lewis, Bhalto	58.2011	-6.9789	*
peripheral	KX159591	NMS.Z.2009.101.90	GB_Lewis	1140	Scotland, Lewis, Cnip	58.2153	-6.9383	*
peripheral	KX159591	NMS.Z.2009.101.93	GB_Lewis	1140	Scotland, Lewis, Cnip	58.2153	-6.9383	*
peripheral	KX159592	NMS.Z.2009.101.667M	GB_Lincoln	1140	England, Lincolnshire, Epworth	53.5269	-0.8248	*
peripheral	KX159593	NMS.Z.2009.101.580	GB_Lismore_1	1140	Scotland, Lismore, Clachan	56.5363	-5.4852	*
peripheral	KX159593	NMS.Z.2009.101.586	GB_Lismore_1	1140	Scotland, Lismore, Clachan	56.5367	-5.4738	*

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159594	NMS.Z.2009.101.583	GB_Lismore_2	1140	Scotland, Lismore, Achnacroish	56.5165	-5.4882	*
peripheral	KX159595	NMS.Z.2009.101.83M	GB_Lothian_1	1140	Scotland, East Lothian, Thorntonloch	55.9530	-2.3923	*
peripheral	KX159596	NMS.Z.2009.101.700M	GB_Lothian_2	1140	Scotland, Edinburgh, Cammo	55.9592	-3.3166	*
peripheral	KX159597	NMS.Z.2009.101.552	GB_Muck	1140	Scotland, Muck, Carn Mhic Asgaill	56.8377	-6.2333	*
peripheral	KX159597	NMS.Z.2009.101.555	GB_Muck	1140	Scotland, Muck, Carn Mhic Asgaill	56.8377	-6.2333	*
peripheral	KX159598	NMS.Z.2009.101.243	GB_Muckle_Roe	1140	Scotland, Muckle Roe, Scarvataing	60.3568	-1.3856	*
peripheral	KX159599	NMS.Z.2009.101.846	GB_Mull_1	1140	Scotland, Mull, Tobermory	56.6229	-6.0966	*
peripheral	KX159599	NMS.Z.2009.101.880	GB_Mull_1	1140	Scotland, Mull, Calgary	56.5818	-6.2763	*
peripheral	KX159600	NMS.Z.2009.101.848	GB_Mull_2	1140	Scotland, Mull, Fishnish	56.5097	-5.8388	*
peripheral	KX159601	NMS.Z.2009.101.719M	GB_Norfolk	1140	England, Norfolk, Gayton	52.7623	0.5699	*
peripheral	KX159602	NMS.Z.2009.101.245	GB_North_Ronaldsay	1140	Scotland, North Ronaldsay, Twyness	59.3598	-2.4468	*
peripheral	KX159602	NMS.Z.2009.101.247	GB_North_Ronaldsay	1140	Scotland, North Ronaldsay, Twyness	59.3598	-2.4468	*
peripheral	KX159602	NMS.Z.2009.101.248	GB_North_Ronaldsay	1140	Scotland, North Ronaldsay, Twyness	59.3598	-2.4468	*
peripheral	KX159603	NMS.Z.2009.101.485M	GB_Northumberland	1140	England, Northumberland, Hexham	54.9885	-2.1109	*
peripheral	KX159604	NMS.Z.2009.101.269	GB_Orkney_mainland	1140	Scotland, Orkney Mainland, Hundland	59.1114	-3.2293	*
peripheral	KX159604	NMS.Z.2009.101.270	GB_Orkney_mainland	1140	Scotland, Orkney Mainland, Hyval	59.0593	-3.2292	*
peripheral	KX159605	NMS.Z.2009.101.453	GB_Orkney_mainland_Rousay	1140	Scotland, Orkney Mainland, Birsay	59.1374	-3.2355	*
peripheral	KX159605	NMS.Z.2009.101.983	GB_Orkney_mainland_Rousay	1140	Scotland, Rousay, Wasbister	59.1758	-3.0584	*
peripheral	KX159605	NMS.Z.2009.101.998	GB_Orkney_mainland_Rousay	1140	Scotland, Rousay, Wasbister	59.1758	-3.0584	*
peripheral	KX159605	JSH_NM16	GB_Orkney_mainland_Rousay	1140	Scotland, Orkney Mainland, Orphir	58.9241	-3.1494	*
peripheral	KX159605	JSH_NM219	GB_Orkney_mainland_Rousay	1140	Scotland, Orkney Mainland, St Ola	58.9691	-2.9669	*
peripheral	KX159605	JSH_NM285	GB_Orkney_mainland_Rousay	1140	Scotland, Orkney Mainland, St Ola	58.9691	-2.9669	*
peripheral	KX159606	NMS.Z.2009.101.712	GB_Papa_Westray	1140	Scotland, Papa Westray, Hundland	59.3739	-2.8728	*
peripheral	KX159606	NMS.Z.2009.101.713	GB_Papa_Westray	1140	Scotland, Papa Westray, Hundland	59.3739	-2.8728	*
peripheral	KX159607	NMS.Z.2009.101.753M	GB_Pembroke	1140	Wales, Pembrokeshire, Tavernspite	51.7721	-4.6581	*
peripheral	KX159608	NMS.Z.2009.101.52M	GB_Perth_1	1140	Scotland, Perthshire, Aldclune	56.7546	-3.8006	*
peripheral	KX159609	NMS.Z.2009.101.60M	GB_Perth_2	1140	Scotland, Perthshire, Blair Atholl	56.7602	-3.8451	*
peripheral	KX159610	NMS.Z.2009.101.637	GB_Perth_Colonsay	1140	Scotland, Colonsay	56.0663	-6.2270	*
peripheral	KX159610	NMS.Z.2009.101.65M	GB_Perth_Colonsay	1140	Scotland, Perthshire, Dunkeld	56.5623	-3.6011	*
peripheral	KX159611	NMS.Z.2009.101.55M	GB_Perth_Inverness	1140	Scotland, Perthshire, Drumochter	56.8596	-4.2502	*
peripheral	KX159611	NMS.Z.2009.101.233M	GB_Perth_Inverness	1140	Scotland, Inverness-shire, Buntait	57.3378	-4.6566	*
peripheral	KX159612	NMS.Z.2009.101.2012M	GB_Powys_1	1140	Wales, Powys, Abergavenny	51.9344	-3.1127	*
peripheral	KX159613	NMS.Z.2009.101.2013M	GB_Powys_2	1140	Wales, Powys, Abergavenny	51.9344	-3.1127	*
peripheral	KX159614	NMS.Z.2009.101.964	GB_Raasay	1140	Scotland, Raasay, North Fearn	57.3491	-6.0243	*
peripheral	KX159615	NMS.Z.2009.101.226M	GB_Ross	1140	Scotland, Easter Ross, Avoch	57.5682	-4.1683	*

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159615	NMS.Z.2009.101.607M	GB_Ross	1140	Scotland, Wester Ross, Ardlair	57.7330	-5.5458	*
peripheral	KX159615	NMS.Z.2009.101.1159M	GB_Ross	1140	Scotland, Wester Ross, Balmacara	57.2951	-5.6447	*
peripheral	KX159616	NMS.Z.2009.101.97	GB_Rum_1	1140	Scotland, Rum, Kinloch	57.0098	-6.2776	*
peripheral	KX159616	NMS.Z.2009.101.140	GB_Rum_1	1140	Scotland, Rum, Kinloch	57.0098	-6.2776	*
peripheral	KX159617	NMS.Z.2009.101.114	GB_Rum_2	1140	Scotland, Rum, Kinloch	57.0098	-6.2776	*
peripheral	KX159618	NMS.Z.2009.101.918	GB_Sanday	1140	Scotland, Sanday, Lady	59.2589	-2.5366	*
peripheral	KX159618	JSH_NM280	GB_Sanday	1140	Scotland, Sanday, Little south-eastern	59.2421	-2.5654	*
Channel Island	KX159619	JSH_ILS31	GB_Sark	1140	Britain, Channel Islands, Sark	49.4323	-2.3594	*
Channel Island	KX159619	JSH_ILS50	GB_Sark	1140	Britain, Channel Islands, Sark	49.4323	-2.3594	*
Channel Island	KX159619	JSH_ILS56	GB_Sark	1140	Britain, Channel Islands, Sark	49.4323	-2.3594	*
peripheral	KX159620	JSH_ILSC4	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC14	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC16	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC22	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC40	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC42	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159620	JSH_ILSC62	GB_Scilly	1140	England, Scilly Isles	49.9000	-6.3000	*
peripheral	KX159621	NMS.Z.2009.101.838	GB_Seil	1140	Scotland, Seil	56.2715	-5.6275	*
peripheral	KX159622	NMS.Z.2009.101.648	GB_Sheep	1140	England, Sheep Island	54.0641	-3.2024	*
peripheral	KX159623	NMS.Z.2009.101.777	GB_Shetland_mainland	1140	Scotland, Shetland Mnld, Cunningsburgh	60.0478	-1.2028	*
peripheral	KX159624	NMS.Z.2009.101.354	GB_Skye_1	1140	Scotland, Skye, Uig	57.6027	-6.3505	*
peripheral	KX159625	NMS.Z.2009.101.361	GB_Skye_2	1140	Scotland, Skye, Loch Leathan	57.4798	-6.1822	*
peripheral	KX159626	NMS.Z.2009.101.455M	GB_Somerset	1140	England, Somerset, Dundry	51.3760	-2.6321	*
peripheral	KX159627	NMS.Z.2009.101.422	GB_South_Ronaldsay_1	1140	Scotland, South Ronaldsay, Herston	58.8098	-3.0023	*
peripheral	KX159627	JSH_NM146	GB_South_Ronaldsay_1	1140	Scotland, South Ronaldsay, Grimness	58.8278	-2.8896	*
peripheral	KX159627	JSH_NM160	GB_South_Ronaldsay_1	1140	Scotland, South Ronaldsay, Windwick	58.7627	-2.9439	*
peripheral	KX159628	NMS.Z.2009.101.618	GB_South_Ronaldsay_2	1140	Scotland, South Ronaldsay, Hoxa	58.8204	-3.0233	*
peripheral	KX159628	NMS.Z.2009.101.719	GB_South_Ronaldsay_2	1140	Scotland, South Ronaldsay, Hoxa	58.8204	-3.0233	*
peripheral	KX159629	NMS.Z.2009.101.715	GB_South_Ronaldsay_3	1140	Scotland, South Ronaldsay, Quendrie	58.8163	-2.9834	*
peripheral	KX159630	NMS.Z.2009.101.975	GB_St_Kilda	1140	Scotland, St Kilda	57.8099	-8.5706	*
peripheral	KX159630	NMS.Z.2009.101.976	GB_St_Kilda	1140	Scotland, St Kilda	57.8099	-8.5706	*
peripheral	KX159631	NMS.Z.2009.101.1965M	GB_Suffolk	1140	England, Suffolk, Mildenhall	52.3362	0.5246	*
central	KX159632	NMS.Z.2009.101.434M	GB_Sussex_Hampshire	1140	England, Hampshire, Avington	51.0849	-1.2447	*
central	KX159632	NMS.Z.2009.101.744M	GB_Sussex_Hampshire	1140	England, East Sussex, Hailsham	50.8442	0.3068	*
central	KX159632	NMS.Z.2009.101.2014M	GB_Sussex_Hampshire	1140	England, East Sussex, East Dean	50.7580	0.2061	*

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peripheral	KX159633	NMS.Z.2009.101.89M	GB_Sutherland	1140	Scotland, Sutherland, Loch Assynt	58.1811	-5.1191	*
peripheral	KX159634	NMS.Z.2009.101.1208M	GB_Sutherland_Hoy	1140	Scotland, Sutherland, Lochinver	58.1299	-5.2607	*
peripheral	KX159634	NMS.Z.2009.101.865	GB_Sutherland_Hoy	1140	Scotland, Hoy, Rackwick	58.8648	-3.3766	*
peripheral	KX159634	NMS.Z.2009.101.866	GB_Sutherland_Hoy	1140	Scotland, Hoy, Pegal	58.8591	-3.2273	*
peripheral	KX159634	NMS.Z.2009.101.867	GB_Sutherland_Hoy	1140	Scotland, Hoy, White Glen	58.8950	-3.3154	*
peripheral	KX159636	NMS.Z.2009.101.645	GB_Walney_Sheep_Piel	1140	England, Walney	54.0569	-3.2083	*
peripheral	KX159636	NMS.Z.2009.101.649	GB_Walney_Sheep_Piel	1140	England, Sheep Island	54.0641	-3.2024	*
peripheral	KX159636	NMS.Z.2009.101.676	GB_Walney_Sheep_Piel	1140	England, Walney, Wylock	54.0657	-3.2239	*
peripheral	KX159636	NMS.Z.2009.101.678	GB_Walney_Sheep_Piel	1140	England, Piel Island	54.0626	-3.1733	*
peripheral	KX159638	NMS.Z.2009.101.445M	GB_Warwick_Derby	1140	England, Warwickshire, Coventry	52.3810	-1.5166	*
peripheral	KX159638	NMS.Z.2009.101.1042M	GB_Warwick_Derby	1140	England, Derbyshire, Crowden	53.4877	-1.8960	*
peripheral	KX159637	NMS.Z.2009.101.446M	GB_Warwick	1140	England, Warwickshire, Coventry	52.3902	-1.5459	*
peripheral	KX159635	NMS.Z.2009.101.453M	GB_Wales_SW_England	1140	England, Somerset, Weston-super-mare	51.3208	-2.9514	*
peripheral	KX159635	NMS.Z.2009.101.760M	GB_Wales_SW_England	1140	England, Devon, Bickleigh	50.8555	-3.5059	*
peripheral	KX159635	NMS.Z.2009.101.1106M	GB_Wales_SW_England	1140	Wales, Cardigan, New Cross	52.3741	-3.9992	*
peripheral	KX159639	JSH_NM18	GB_Westray	1140	Scotland, Westray, Swartmill	59.2968	-2.9141	*
peripheral	KX159639	JSH_NM129	GB_Westray	1140	Scotland, Westray, Ness	59.2348	-2.8798	*
peripheral	KX159640	NMS.Z.2009.101.1284M	GB_Wiltshire	1140	England, Wiltshire, Corsham	51.4378	-2.1884	*
peripheral	KX159641	NMS.Z.2009.101.970M	GB_Worcester	1140	England, Worcestershire, Tardebigge	52.3218	-2.0073	*
peripheral	KX159642	NMS.Z.2009.101.244	GB_Yell_1	1140	Scotland, Yell, Rattleton	60.5994	-1.1071	*
peripheral	KX159643	NMS.Z.2009.101.951	GB_Yell_2	1140	Scotland, Yell, Cullivoe	60.7038	-1.0090	*
peripheral	KX159644	NMS.Z.2009.101.1912M	GB_York	1140	England, Yorkshire, Bishopthorpe	53.9202	-1.0955	*
peripheral	KX159644	JSH_JSY	GB_York	1140	England, Yorkshire, York	53.9460	-1.0551	*
peripheral	KX159507	U561	Britain_1_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159498	U551	Britain_2_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159499	U548	Britain_3_s	818	Britain, Kent, Canterbury	51.2800	1.0800	*
peripheral	KX159500	U559	Britain_4_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159501	U556	Britain_5_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159502	U555	Britain_6_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159503	U562	Britain_7_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159504	U553	Britain_8_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159505	U560	Britain_9_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159506	U550	Britain_10_s	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	KX159497	JSH_DK4	Britain_BI_Ireland	1140	Ireland, Louth, Knockbridge	53.9750	-6.5250	*
peripheral	KX159497	JSH_DK5	Britain_BI_Ireland	1140	Ireland, Louth, Knockbridge	53.9750	-6.5250	*

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peripheral	KX159497	JSH_WMD4	Britain_BI_Ireland	1140	Ireland, Derry, Magilligan	55.1479	-6.9346	*
peripheral	KX159497	JSH_WMD5	Britain_BI_Ireland	1140	Ireland, Derry, Magilligan	55.1479	-6.9346	*
peripheral	KX159497	JSH_WMK8	Britain_BI_Ireland	1140	Ireland, Kerry, Killarney	52.0556	-9.5333	*
peripheral	KX159497	NMS.Z.2009.101.61	Britain_BI_Ireland	1140	Scotland, North Uist, Cnoc an Torran	57.5823	-7.4735	*
peripheral	KX159497	NMS.Z.2009.101.63	Britain_BI_Ireland	1140	Scotland, North Uist, Hougharry	57.6079	-7.5059	*
peripheral	KX159497	NMS.Z.2009.101.66	Britain_BI_Ireland	1140	Scotland, South Uist, Stilligarry	57.3235	-7.3708	*
peripheral	KX159497	NMS.Z.2009.101.70	Britain_BI_Ireland	1140	Scotland, North Uist, Carinish	57.5176	-7.3233	*
peripheral	KX159497	NMS.Z.2009.101.307	Britain_BI_Ireland	1140	Scotland, South Uist, Stilligarry	57.3235	-7.3708	*
peripheral	KX159497	NMS.Z.2009.101.444	Britain_BI_Ireland	1140	Scotland, Fair Isle	59.5334	-1.6305	*
peripheral	KX159497	NMS.Z.2009.101.447	Britain_BI_Ireland	1140	Scotland, Fair Isle	59.5334	-1.6305	*
peripheral	KX159497	NMS.Z.2009.101.561	Britain_BI_Ireland	1140	Scotland, Gigha	55.6618	-5.7490	*
peripheral	KX159497	NMS.Z.2009.101.563	Britain_BI_Ireland	1140	Scotland, Gigha	55.6755	-5.7423	*
peripheral	KX159497	NMS.Z.2009.101.564	Britain_BI_Ireland	1140	Scotland, Gigha, Drumyeon More	55.6928	-5.7360	*
peripheral	KX159497	NMS.Z.2009.101.569	Britain_BI_Ireland	1140	Scotland, Shetland Mainland, Sumburgh	59.8534	-1.2753	*
peripheral	KX159497	NMS.Z.2009.101.744	Britain_BI_Ireland	1140	Scotland, Benbecula, Aird	57.4272	-7.3335	*
peripheral	KX159497	NMS.Z.2009.101.764	Britain_BI_Ireland	1140	Scotland, S. Uist, Stilligarry	57.3235	-7.3708	*
peripheral	KX159497	NMS.Z.2009.101.950	Britain_BI_Ireland	1140	Scotland, Bressay	60.1459	-1.0924	*
peripheral	KX159497	NMS.Z.2009.101.508M	Britain_BI_Ireland	1140	England, Cornwall, Bodmin	50.4617	-4.7347	*
peripheral	KX159497	NMS.Z.2009.101.1301M	Britain_BI_Ireland	1140	England, Worcestershire, Hopwood	52.3748	-1.9588	*
peripheral	KX159508	U549	Britain_Ireland	818	Britain, Oxfordshire	51.8000	-1.3000	*
peripheral	FJ389642	JM-1187	Britain_Ireland	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389643	JM-1199	Britain_Ireland	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389644	JM-1233	Britain_Ireland	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	KX159508	Ir1241	Britain_Ireland	818	Ireland, Belfast area	54.6000	-5.9000	*
peripheral	KX159509	NMS.Z.2009.101.73M	Britain_Norway	1140	Scotland, East Lothian, Kirklandhill	55.9899	-2.6075	*
peripheral	KX159509	NMS.Z.2009.101.74M	Britain_Norway	1140	Scotland, Berwickshire, Ayton	55.8484	-2.1437	*
peripheral	KX159509	NMS.Z.2009.101.76M	Britain_Norway	1140	Scotland, Berwickshire, Penmanshiel	55.9047	-2.3295	*
peripheral	KX159509	NMS.Z.2009.101.134M	Britain_Norway	1140	Scotland, Edinburgh, Grange	55.9309	-3.1812	*
peripheral	KX159509	NMS.Z.2009.101.482M	Britain_Norway	1140	England, Northumberland, Newcastle	55.0061	-1.6576	*
peripheral	KX159509	NMS.Z.2009.101.1933M	Britain_Norway	1140	Scotland, E. Lothian, Phantassie	55.9870	-2.6475	*
peripheral	KX159509	NMS.Z.2009.101.2006M	Britain_Norway	1140	Scotland, Ayrshire, Beith	55.7512	-4.6306	*
peripheral	KX159509	NMS.Z.2009.101.N12	Britain_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
peripheral	KX159509	NMS.Z.2009.101.N16	Britain_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
peripheral	KX159509	NMS.Z.2009.101.N20	Britain_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159645	JSH_A2	Germany_1	1140	Germany, Hamburg	53.5539	9.9917	*

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central	KX159645	JSH_A3	Germany_1	1140	Germany, Hamburg	53.5539	9.9917	*
central	KX159645	JSH_A14	Germany_1	1140	Germany, Hamburg	53.5539	9.9917	*
central	KX159645	JSH_A18	Germany_1	1140	Germany, Hamburg	53.5539	9.9917	*
central	KX159646	JSH_D35	Germany_2	1140	Germany, Nordfriesland, Kattinger Watt	54.2831	8.8403	*
central	KX159646	JSH_D37	Germany_2	1140	Germany, Nordfriesland, Kattinger Watt	54.2831	8.8403	*
central	AJ511893	JRM-514	Germany_3_s	948	Germany, Saxony, Leipzig	51.3398	12.3714	*
central	AJ511902	JRM-157	Germany_4_s	919	Germany, North Rhine-Westphalia, Bielefeld	52.0230	8.5331	*
central	AY180337	HB135.1.5	Germany_5_s	732	Germany, Baden-Württemberg, Rosenberg	49.4576	9.4735	Reutter <i>et al.</i> 2003
central	AY180338	HB132.4	Germany_6_s	732	Germany, Baden-Württemberg, Feldsee	47.8688	8.0329	Reutter <i>et al.</i> 2003
central	AY180339	HB136.1	Germany_7_s	732	Germany, Baden-Württemberg, Karlsruhe	49.0000	8.4833	Reutter <i>et al.</i> 2003
central	FJ389656	HB706	Germany_8_s	732	Germany, Baden-Württemberg, Karlsruhe	49.0000	8.4833	Dubey <i>et al.</i> 2009
central	JF318999		Germany_9_s	627	Germany	NA	NA	Schlegel <i>et al.</i> 2012
central	GU060537	Mu/07/817	Germany_10_s	676	Germany	NA	NA	*
central	GU060536	Mu/07/814	Germany_11_s	600	Germany	NA	NA	*
central	GU060533	Mu/07/194	Germany_12_s	654	Germany	NA	NA	*
central	KX159647	JSH_D36	Germany_Norway	1140	Germany, Nordfriesland, Kattinger Watt	54.2831	8.8403	*
central	KX159647	JSH_D38	Germany_Norway	1140	Germany, Nordfriesland, Kattinger Watt	54.2831	8.8403	*
central	KX159647	NMS.Z.2009.101.N2	Germany_Norway	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
central	KX159647	NMS.Z.2009.101.N6	Germany_Norway	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
central	KX159647	NMS.Z.2009.101.N7	Germany_Norway	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
central	KX159647	NMS.Z.2009.101.N10	Germany_Norway	1140	Norway, Rogaland, Kvernevik	58.9643	5.6020	*
central	KX159647	NMS.Z.2009.101.N11	Germany_Norway	1140	Norway, Rogaland, Kvernevik	58.9643	5.6020	*
central	KX159647	NMS.Z.2009.101.N13	Germany_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159647	NMS.Z.2009.101.N14	Germany_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159647	NMS.Z.2009.101.N17	Germany_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159647	NMS.Z.2009.101.N18	Germany_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159647	NMS.Z.2009.101.N19	Germany_Norway	1140	Norway, Rogaland, Vistnes	58.9833	5.5667	*
central	KX159647	NMS.Z.2009.101.N21	Germany_Norway	1140	Norway, Vestfold, Gran	59.4798	10.0950	*
central	KX159647	NMS.Z.2009.101.N22	Germany_Norway	1140	Norway, Vestfold, Haugestadt	59.5331	10.0983	*
central	KX159647	NMS.Z.2009.101.N23	Germany_Norway	1140	Norway, Vestfold, Haugestadt	59.5331	10.0983	*
central	KX159647	NMS.Z.2009.101.N24	Germany_Norway	1140	Norway, Vestfold, Lillehof	59.5408	10.0803	*
central	KX159647	NMS.Z.2009.101.N25	Germany_Norway	1140	Norway, Vestfold, Lillehof	59.5408	10.0803	*
central	KX159647	NMS.Z.2009.101.N26	Germany_Norway	1140	Norway, Vestfold, Lillehof	59.5408	10.0803	*
central	KX159647	NMS.Z.2009.101.N27	Germany_Norway	1140	Norway, Vestfold, Åkerholt	59.4656	10.0877	*
central	KX159647	NMS.Z.2009.101.N28	Germany_Norway	1140	Norway, Vestfold, Åkerholt	59.4656	10.0877	*

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central	KX159647	NMS.Z.2009.101.N29	Germany_Norway	1140	Norway, Vestfold, Åkerholt	59.4656	10.0877	*
central	KX159647	NMS.Z.2009.101.N30	Germany_Norway	1140	Norway, Vestfold, Åkerholt	59.4656	10.0877	*
central	KX159647	NMS.Z.2009.101.N31	Germany_Norway	1140	Norway, Vestfold, Moa	59.3640	10.1210	*
central	KX159647	NMS.Z.2009.101.N32	Germany_Norway	1140	Norway, Telemark, Øverbø	59.2822	9.7355	*
central	KX159647	NMS.Z.2009.101.N33	Germany_Norway	1140	Norway, Telemark, Gonsholt	59.2500	9.7667	*
central	KX159647	NMS.Z.2009.101.N34	Germany_Norway	1140	Norway, Vestfold, Svarstad	59.3990	9.9698	*
central	KX159647	NMS.Z.2009.101.N35	Germany_Norway	1140	Norway, Vestfold, Svarstad	59.3990	9.9698	*
central	KX159647	NMS.Z.2009.101.N36	Germany_Norway	1140	Norway, Vestfold, Svarstad	59.3990	9.9698	*
central	KX159647	NMS.Z.2009.101.N37	Germany_Norway	1140	Norway, Vestfold, Svarstad	59.3990	9.9698	*
central	KX159647	NMS.Z.2009.101.N39	Germany_Norway	1140	Norway, Vestfold, Berg	59.5944	10.0772	*
central	KX159647	NMS.Z.2009.101.N40	Germany_Norway	1140	Norway, Vestfold, Berg	59.5944	10.0772	*
central	KX159647	NMS.Z.2009.101.N41	Germany_Norway	1140	Norway, Vestfold, Berg	59.5944	10.0772	*
south-eastern	AJ511938	JRM-183	Greece_1_s	965	Greece, Peloponnese, Monemvasia	36.6877	23.0558	Michaux et al. 2003
south-eastern	AJ511940	JRM-181	Greece_2_s	965	Greece, Macedonia	41.0000	23.0000	Michaux et al. 2003
south-eastern	AJ511947	JRM-705	Greece_3_s	962	Greece, Central Greece, Mt Olympus	40.0700	22.4100	Michaux et al. 2003
peripheral	KX159648	NMS.Z.2009.101.1016	Iceland_1	1140	Iceland, Reykjavík	64.1000	-21.8000	*
peripheral	KX159649	NMS.Z.2009.101.1018	Iceland_2	1140	Iceland, Árnæssýsla, Árbær	64.1898	-20.7411	*
peripheral	KX159650	JSH_IS18	Iceland_3	1140	Iceland, Bárðardalur/Aðaldalur, Rauðá	65.6814	-17.5122	*
peripheral	KX159651	JSH_IS108	Iceland_4	1140	Iceland, Síða, Mörtunga I	63.8390	-18.0552	*
peripheral	KX159652	JSH_IS112	Iceland_5	1140	Iceland, Mýrar, Brúarhraun	64.7434	-22.2082	*
peripheral	KX159652	JSH_IS118	Iceland_5	1140	Iceland, Fitjárdalur, Efri Fitjar	65.2817	-20.6881	*
peripheral	KX159652	JSH_IS121	Iceland_5	1140	Iceland, Fitjárdalur, Efri Fitjar	65.2817	-20.6881	*
peripheral	KX159653	NMS.Z.2009.101.433	Iceland_Shetland_Norway	1140	Scotland, Shetland Mainland, Dunrossness	59.9316	-1.3005	*
peripheral	KX159653	NMS.Z.2009.101.1012	Iceland_Shetland_Norway	1140	Iceland, Rangárvallasýsla, Keldur	63.8188	-20.0607	*
peripheral	KX159653	NMS.Z.2009.101.1013	Iceland_Shetland_Norway	1140	Iceland, Kjósarsýsla, Úlfarsfell	64.1500	-21.7167	*
peripheral	KX159653	NMS.Z.2009.101.1014	Iceland_Shetland_Norway	1140	Iceland, Kjósarsýsla, Úlfarsfell	64.1500	-21.7167	*
peripheral	KX159653	NMS.Z.2009.101.1017	Iceland_Shetland_Norway	1140	Iceland, Reykjavík	64.1300	-21.9400	*
peripheral	KX159653	NMS.Z.2009.101.1021	Iceland_Shetland_Norway	1140	Iceland, Vestur-Barðastrandarsýsla, Hvallátur	65.5188	-24.4571	*
peripheral	KX159653	NMS.Z.2009.101.1022	Iceland_Shetland_Norway	1140	Iceland, Vestur-Barðastrandarsýsla, Hvallátur	65.5188	-24.4571	*
peripheral	KX159653	NMS.Z.2009.101.1023	Iceland_Shetland_Norway	1140	Iceland, Austur-Skaftafelssýsla, Smyrlabjörg	64.2167	-15.7167	*
peripheral	KX159653	NMS.Z.2009.101.1024	Iceland_Shetland_Norway	1140	Iceland, Austur-Skaftafelssýsla, Smyrlabjörg	64.2167	-15.7167	*
peripheral	KX159653	NMS.Z.2009.101.1025	Iceland_Shetland_Norway	1140	Iceland, Austur-Skaftafelssýsla, Smyrlabjörg	64.2167	-15.7167	*
peripheral	KX159653	JSH_ILN57	Iceland_Shetland_Norway	1140	Norway, Hordaland, Bergen	60.3606	5.3200	*
peripheral	KX159653	JSH_IS4	Iceland_Shetland_Norway	1140	Iceland, Skagafjörður, Efri Ás	65.7615	-19.2222	*
peripheral	KX159653	JSH_IS5	Iceland_Shetland_Norway	1140	Iceland, Skagafjörður, Efri Ás	65.7615	-19.2222	*

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159653	JSH_IS11	Iceland_Shetland_Norway	1140	Iceland, Skagafjörður, Laufskálar	65.7511	-19.1731	*
peripheral	KX159653	JSH_IS24	Iceland_Shetland_Norway	1140	Iceland, Bárðardalur/Aðaldalur, Rauðá	65.6814	-17.5122	*
peripheral	KX159653	JSH_IS73	Iceland_Shetland_Norway	1140	Iceland, Laugafell	65.0163	-18.1995	*
peripheral	KX159653	JSH_IS74	Iceland_Shetland_Norway	1140	Iceland, Laugafell	65.0163	-18.1995	*
peripheral	KX159653	JSH_IS75	Iceland_Shetland_Norway	1140	Iceland, Laugafell	65.0163	-18.1995	*
peripheral	KX159653	JSH_IS79	Iceland_Shetland_Norway	1140	Iceland, Hornafjörður, Setberg	64.3858	-15.2892	*
peripheral	KX159653	JSH_IS80	Iceland_Shetland_Norway	1140	Iceland, Hornafjörður, Setberg	64.3858	-15.2892	*
peripheral	KX159653	JSH_IS81	Iceland_Shetland_Norway	1140	Iceland, Hornafjörður, Setberg	64.3858	-15.2892	*
peripheral	KX159653	JSH_IS82	Iceland_Shetland_Norway	1140	Iceland, Hornafjörður, Setberg	64.3858	-15.2892	*
peripheral	KX159653	JSH_IS83	Iceland_Shetland_Norway	1140	Iceland, Landbrot, Eystra-Hraun	63.7186	-17.9892	*
peripheral	KX159653	JSH_IS84	Iceland_Shetland_Norway	1140	Iceland, Landbrot, Eystra-Hraun	63.7186	-17.9892	*
peripheral	KX159653	JSH_IS87	Iceland_Shetland_Norway	1140	Iceland, Landbrot, Hátún	63.7750	-17.9642	*
peripheral	KX159653	JSH_IS89	Iceland_Shetland_Norway	1140	Iceland, Síða, Mörtunga I	63.8390	-18.0552	*
peripheral	KX159653	JSH_IS92	Iceland_Shetland_Norway	1140	Iceland, Síða, Mörtunga II	63.5028	-18.0359	*
peripheral	KX159653	JSH_IS93	Iceland_Shetland_Norway	1140	Iceland, Síða, Mörtunga II	63.5028	-18.0359	*
peripheral	KX159653	JSH_IS111	Iceland_Shetland_Norway	1140	Iceland, Mýrar, Brúarhraun	64.7434	-22.2082	*
peripheral	KX159653	JSH_IS113	Iceland_Shetland_Norway	1140	Iceland, Mýrar, Brúarhraun	64.7434	-22.2082	*
peripheral	KX159653	JSH_IS117	Iceland_Shetland_Norway	1140	Iceland, Fitjárdalur, Efri Fitjar	65.2817	-20.6881	*
peripheral	KX159653	JSH_IS179	Iceland_Shetland_Norway	1140	Iceland, Hrunamannahreppur, Flúðir	64.2167	-20.5500	*
peripheral	KX159653	JSH_IS180	Iceland_Shetland_Norway	1140	Iceland, Bláskógbabyggð, Þingvellir	64.2666	-21.0892	*
peripheral	KX159653	JSH_IS181	Iceland_Shetland_Norway	1140	Iceland, Bláskógbabyggð, Þingvellir	64.2666	-21.0892	*
peripheral	KX159653	JSH_IS182	Iceland_Shetland_Norway	1140	Iceland, Bláskógbabyggð, Þingvellir	64.2666	-21.0892	*
peripheral	KX159653	NMS.Z.2009.101.N4	Iceland_Shetland_Norway	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
peripheral	KX159654	JSH_CK13	IRE_Cork	1140	Ireland, Cork, Dunderrow	51.7282	-8.5820	*
peripheral	KX159655	JSH_WMD3	IRE_Derry	1140	Ireland, Derry, Magilligan	55.1479	-6.9346	*
peripheral	KX159656	JSH_GW24	IRE_Donegal_1	1140	Ireland, Donegal, Gweedore	55.0500	-8.3917	*
peripheral	KX159656	JSH_GW32	IRE_Donegal_1	1140	Ireland, Donegal, Gweedore	55.0500	-8.3917	*
peripheral	KX159657	JSH_P1	IRE_Donegal_2	1140	Ireland, Donegal, Letterkenny	54.9483	-7.7305	*
peripheral	KX159657	JSH_P2	IRE_Donegal_2	1140	Ireland, Donegal, Letterkenny	54.9483	-7.7305	*
peripheral	KX159658	NMS.Z.2009.101.E91	IRE_Galway	1140	Ireland, Galway, Kinvarra	53.1384	-8.9342	*
peripheral	KX159659	JSH_WMK6	IRE_Kerry	1140	Ireland, Kerry, Killarney	52.0556	-9.5333	*
peripheral	KX159660	NMS.Z.2009.101.E92	IRE_Kildare	1140	Ireland, Kildare, Rathangan	53.2206	-6.9969	*
peripheral	KX159661	NMS.Z.2009.101.E90	IRE_Leitrim	1140	Ireland, Leitrim, Ballinamore	54.0515	-7.7979	*
peripheral	KX159662	JSH_DK1	IRE_Louth_1	1140	Ireland, Louth, Knockbridge	53.9750	-6.5250	*
peripheral	KX159663	JSH_DK6	IRE_Louth_2	1140	Ireland, Louth, Knockbridge	53.9750	-6.5250	*

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Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	KX159664	JSH_JS9	IRE_Meath_1	1140	Ireland, Meath, Dowth Hall	53.7067	-6.4397	*
peripheral	KX159665	JSH_JS10	IRE_Meath_2	1140	Ireland, Meath, Dowth Hall	53.7067	-6.4397	*
peripheral	KX159665	JSH_JS11	IRE_Meath_2	1140	Ireland, Meath, Dowth Hall	53.7067	-6.4397	*
peripheral	KX159666	JSH_JS12	IRE_Meath_3	1140	Ireland, Meath, Dowth Hall	53.7067	-6.4397	*
peripheral	KX159667	JSH_I1	IRE_Tipperary	1140	Ireland, Tipperary, Clonmel	52.3556	-7.6984	*
peripheral	KX159668	JSH_JS32	IRE_Wexford_1	1140	Ireland, Wexford, Begerin	52.3897	-6.8603	*
peripheral	KX159669	JSH_JS37	IRE_Wexford_2	1140	Ireland, Wexford, Camolin	52.6161	-6.4293	*
peripheral	FJ389645	JM-1188	Ireland_1_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389646	JM-1190	Ireland_2_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389647	JM-1197	Ireland_3_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389650	JM-1235	Ireland_4_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389651	JM-1239	Ireland_5_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389665	JM-1234	Ireland_6_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	FJ389666	JM-1198	Ireland_7_s	818	Ireland, Belfast area	54.6000	-5.9000	Dubey <i>et al.</i> 2009
peripheral	KX159670	Ir1191	Ireland_7_s	818	Ireland, Belfast area	54.6000	-5.9000	*
peripheral	KX159670	Ir1240	Ireland_7_s	818	Ireland, Belfast area	54.6000	-5.9000	*
peripheral	KX159671	Ir1189	Ireland_8_s	818	Ireland, Belfast area	54.6000	-5.9000	*
south-eastern	AJ511958	JRM-888	Italy_1_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
south-eastern	AJ511923	JRM-160	Italy_2_s	965	Italy, Calabria, Aspromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511924	JRM-162	Italy_3_s	964	Italy, Calabria, Aspromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511925	JRM-164	Italy_4_s	929	Italy, Abruzzo, Penne	42.4576	13.9275	Michaux <i>et al.</i> 2003
south-eastern	AJ511926	JRM-165	Italy_5_s	941	Italy, Abruzzo, Penne	42.4576	13.9275	Michaux <i>et al.</i> 2003
south-eastern	AJ511928	JRM-171	Italy_6_s	965	Italy, Latiun, San Polo	42.0156	12.8369	Michaux <i>et al.</i> 2003
south-eastern	AJ511929	JRM-172	Italy_7_s	965	Italy, Latiun, Tarquinia	42.2547	11.7585	Michaux <i>et al.</i> 2003
south-eastern	AJ511930	JRM-174	Italy_8_s	965	Italy, Latiun, Tarquinia	42.2547	11.7585	Michaux <i>et al.</i> 2003
south-eastern	AJ511936	JRM-168	Italy_9_s	965	Italy, Latiun, Rome	41.9000	12.5000	Michaux <i>et al.</i> 2003
south-eastern	AJ511937	JRM-159	Italy_10_s	965	Italy, Calabria, Aspromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511942	JRM-161	Italy_11_s	952	Italy, Calabria, Aspromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511943	JRM-163	Italy_12_s	965	Italy, Abruzzo, Penne	42.4576	13.9275	Michaux <i>et al.</i> 2003
south-eastern	AJ511944	JRM-176	Italy_13_s	962	Italy, Toscana, Grosseto	42.7629	11.1128	Michaux <i>et al.</i> 2003
south-eastern	AJ511948	JRM-822	Italy_14_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
south-eastern	AJ511949	JRM-823	Italy_15_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
south-eastern	AJ511950	JRM-824	Italy_16_s	961	Italy, Calabria, Asromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
south-eastern	AJ511951	JRM-851	Italy_17_s	961	Italy, Calabria, Asromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511952	JRM-852	Italy_18_s	961	Italy, Calabria, Asromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
south-eastern	AJ511953	JRM-853	Italy_19_s	961	Italy, Calabria, Aspromonte	42.2547	11.7585	Lalis <i>et al.</i> 2016
south-eastern	AJ511954	JRM-860	Italy_20_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Michaux <i>et al.</i> 2003
south-eastern	AJ511955	JRM-863	Italy_21_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
south-eastern	AJ511957	JRM-864	Italy_22_s	961	Italy, Calabria, Aspromonte	38.1667	16.0000	Lalis <i>et al.</i> 2016
Sicilian	AJ511959	JRM-305	IT_Sicily_1_s	964	Italy, Sicily, Alia	37.7811	13.7149	Michaux <i>et al.</i> 2003
Sicilian	AJ511960	JRM-304	IT_Sicily_2_s	964	Italy, Sicily, Alia	37.7811	13.7149	Michaux <i>et al.</i> 2003
Sicilian	AJ511961	JRM-306	IT_Sicily_3_s	965	Italy, Sicily, Alia	37.7811	13.7149	Michaux <i>et al.</i> 2003
Sicilian	AJ511962	JRM-842	IT_Sicily_4_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511963	JRM-844	IT_Sicily_5_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511964	JRM-845	IT_Sicily_6_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511965	JRM-846	IT_Sicily_7_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511966	JRM-848	IT_Sicily_8_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511967	JRM-849	IT_Sicily_9_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511968	JRM-870	IT_Sicily_10_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511969	JRM-874	IT_Sicily_11_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511970	JRM-881	IT_Sicily_12_s	916	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511971	JRM-885	IT_Sicily_13_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511972	JRM-889	IT_Sicily_14_s	961	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
Sicilian	AJ511973	JRM-891	IT_Sicily_15_s	958	Italy, Sicily, Madonie	37.8600	13.9600	Michaux <i>et al.</i> 2003
central	KX159672	JSH_LX6	Luxembourg	1140	Luxembourg	49.6000	6.1000	*
south-eastern	JF819975	BK_S5	Macedonia_1	1140	Macedonia, Popova šapka	42.0000	21.0000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819971	BK_S1a	Macedonia_2	1140	Macedonia, Mt Bistra	41.8000	20.7000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819971	BK_S1b	Macedonia_2	1140	Macedonia, Mt Bistra	41.8000	20.7000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819972	BK_S2	Montenegro_1	1140	Montenegro, Mt Orjen	42.5000	18.6000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819973	BK_S3	Montenegro_2	1140	Montenegro, Mt Orjen	42.5000	18.6000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819974	BK_S4	Montenegro_3	1140	Montenegro, Mt Orjen	42.5000	18.6000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819979	BK_S9	Montenegro_4	1140	Montenegro, Mt Lovćen	42.4000	18.8000	Kryštufek <i>et al.</i> 2012
south-eastern	JF819980	BK_S10	Montenegro_5	1140	Montenegro, Mt Lovćen	42.4000	18.8000	Kryštufek <i>et al.</i> 2012
African	AJ511916	JRM-188	Morocco_1_s	965	Morocco, Taza-Al Hoceima-Taounate, Ketama	34.7800	-4.6600	Michaux <i>et al.</i> 2003
African	AJ511919	JRM-186	Morocco_2_s	965	Morocco, Taza-Al Hoceima-Taounate, Ketama	34.7800	-4.6600	Michaux <i>et al.</i> 2003
African	AJ511921	JRM-187	Morocco_3_s	965	Morocco, Taza-Al Hoceima-Taounate, Ketama	34.7800	-4.6600	Michaux <i>et al.</i> 2003
African	AJ511922	JRM-185	Morocco_4_s	964	Morocco, Taza-Al Hoceima-Taounate, Ketama	34.7800	-4.6600	Michaux <i>et al.</i> 2003
African	KM581939	MA567	Morocco_5_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581940	MA568	Morocco_6_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581900	MA509	Morocco_6_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581862	MA379	Morocco_6_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581986	MA750	Morocco_6_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM581988	MA752	Morocco_6_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM581989	MA754	Morocco_6_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM581991	MA759	Morocco_6_s	864	Morocco, Merja Zerga	34.7920	-6.2430	Lalis <i>et al.</i> 2016
African	KM581995	MA765	Morocco_6_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM581998	MA769	Morocco_6_s	864	Morocco, Merja Zerga	34.7910	-6.2410	Lalis <i>et al.</i> 2016
African	KM582000	MA773	Morocco_6_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM582002	MA776	Morocco_6_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582003	MA777	Morocco_6_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582005	MA781	Morocco_6_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582010	MA786	Morocco_6_s	864	Morocco, Merja Zerga	34.7920	-6.2430	Lalis <i>et al.</i> 2016
African	KM581791	MA250	Morocco_6_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581941	MA570	Morocco_7_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581945	MA578	Morocco_7_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581954	MA603	Morocco_7_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581957	MA611	Morocco_7_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581943	MA573	Morocco_8_s	864	Morocco, Beni Hadifa	35.0240	-4.1620	Lalis <i>et al.</i> 2016
African	KM581947	MA586	Morocco_9_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581948	MA588	Morocco_10_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581949	MA591	Morocco_10_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581951	MA596	Morocco_11_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581952	MA597	Morocco_12_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581955	MA608	Morocco_12_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581956	MA609	Morocco_12_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581907	MA519	Morocco_12_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581935	MA557	Morocco_12_s	864	Morocco, Parc Talassemtane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581953	MA599	Morocco_13_s	864	Morocco, Beni Hadifa	35.0250	-4.1620	Lalis <i>et al.</i> 2016
African	KM581776	C096	Morocco_13_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581783	MA158	Morocco_14_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581786	MA162	Morocco_14_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581788	MA182	Morocco_14_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581789	MA201	Morocco_14_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581784	MA159	Morocco_15_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581785	MA161	Morocco_16_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581787	MA178	Morocco_17_s	864	Morocco, Ben Slimane	33.6350	-7.1060	Lalis <i>et al.</i> 2016
African	KM581761	C100	Morocco_18_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581778	C098	Morocco_18_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581764	C055	Morocco_19_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581979	MA667	Morocco_19_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581765	C056	Morocco_20_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581766	C062	Morocco_21_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581769	C067	Morocco_21_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581771	C073	Morocco_21_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581777	C097	Morocco_21_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581968	MA645	Morocco_21_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581929	MA551	Morocco_21_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581767	C065	Morocco_22_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581768	C066	Morocco_23_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581903	MA513	Morocco_23_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581914	MA532	Morocco_23_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581772	C074	Morocco_24_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581773	C076	Morocco_25_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581931	MA553	Morocco_25_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581774	C079	Morocco_26_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581775	C080	Morocco_27_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581969	MA646	Morocco_27_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581972	MA649	Morocco_27_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581973	MA655	Morocco_27_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581829	MA315	Morocco_27_s	864	Morocco, Taza	34.1040	-4.0730	Lalis <i>et al.</i> 2016
African	KM581779	C099	Morocco_28_s	864	Morocco, Chrouda	35.3700	-5.1700	Lalis <i>et al.</i> 2016
African	KM581963	MA639	Morocco_28_s	864	Morocco, Chrouda	35.3650	-5.1700	Lalis <i>et al.</i> 2016
African	KM581964	MA641	Morocco_29_s	864	Morocco, Chrouda	35.3680	-5.1720	Lalis <i>et al.</i> 2016
African	KM581965	MA642	Morocco_29_s	864	Morocco, Chrouda	35.3680	-5.1710	Lalis <i>et al.</i> 2016
African	KM581816	MA291	Morocco_29_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581818	MA293	Morocco_29_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581966	MA643	Morocco_30_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581975	MA658	Morocco_30_s	864	Morocco, Chrouda	35.3660	-5.1710	Lalis <i>et al.</i> 2016
African	KM581980	MA668	Morocco_30_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581970	MA647	Morocco_31_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581876	MA420	Morocco_31_s	864	Morocco, Ifrane	33.5000	-5.1130	Lalis <i>et al.</i> 2016
African	KM581830	MA316	Morocco_31_s	864	Morocco, Taza	34.0950	-4.0770	Lalis <i>et al.</i> 2016
African	KM581971	MA648	Morocco_32_s	864	Morocco, Chrouda	35.3660	-5.1710	Lalis <i>et al.</i> 2016
African	KM581974	MA657	Morocco_33_s	864	Morocco, Chrouda	35.3680	-5.1710	Lalis <i>et al.</i> 2016
African	KM581981	MA670	Morocco_33_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581837	MA333	Morocco_33_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581976	MA663	Morocco_34_s	864	Morocco, Chrouda	35.3660	-5.1700	Lalis <i>et al.</i> 2016
African	KM581977	MA664	Morocco_35_s	864	Morocco, Chrouda	35.3680	-5.1710	Lalis <i>et al.</i> 2016
African	KM581984	MA673	Morocco_35_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581982	MA671	Morocco_36_s	864	Morocco, Chrouda	35.3670	-5.1710	Lalis <i>et al.</i> 2016
African	KM581983	MA672	Morocco_37_s	864	Morocco, Chrouda	35.3660	-5.1710	Lalis <i>et al.</i> 2016
African	KM581919	MA538	Morocco_37_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581898	MA504	Morocco_38_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581885	MA439	Morocco_38_s	864	Morocco, Ifrane	33.4230	-5.0490	Lalis <i>et al.</i> 2016
African	KM581899	MA506	Morocco_39_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581904	MA514	Morocco_39_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581902	MA511	Morocco_40_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581905	MA515	Morocco_41_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581809	MA279	Morocco_41_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581858	MA359	Morocco_41_s	864	Morocco, Taza	34.0950	-4.0770	Lalis <i>et al.</i> 2016
African	KM581906	MA518	Morocco_42_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581908	MA520	Morocco_43_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581909	MA522	Morocco_44_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581910	MA523	Morocco_45_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581930	MA552	Morocco_46_s	864	Morocco, El Khizana	35.0300	-5.2180	Lalis <i>et al.</i> 2016
African	KM581927	MA549	Morocco_46_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581932	MA554	Morocco_46_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581894	MA473	Morocco_47_s	864	Morocco, Esperada	35.5340	-5.5340	Lalis <i>et al.</i> 2016
African	KM581993	MA761	Morocco_47_s	864	Morocco, Merja Zerga	34.7890	-6.2480	Lalis <i>et al.</i> 2016
African	KM581996	MA766	Morocco_47_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM581997	MA768	Morocco_47_s	864	Morocco, Merja Zerga	34.7950	-6.2490	Lalis <i>et al.</i> 2016
African	KM581999	MA770	Morocco_47_s	864	Morocco, Merja Zerga	34.7910	-6.2410	Lalis <i>et al.</i> 2016
African	KM582001	MA774	Morocco_47_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM582004	MA780	Morocco_47_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582011	MA787	Morocco_47_s	864	Morocco, Merja Zerga	34.7920	-6.2430	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581896	MA496	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5330	Lalis <i>et al.</i> 2016
African	KM581958	MA623	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5300	Lalis <i>et al.</i> 2016
African	KM581959	MA624	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5300	Lalis <i>et al.</i> 2016
African	KM581960	MA625	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5300	Lalis <i>et al.</i> 2016
African	KM581961	MA626	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5300	Lalis <i>et al.</i> 2016
African	KM581962	MA627	Morocco_48_s	864	Morocco, Esperada	35.5350	-5.5300	Lalis <i>et al.</i> 2016
African	KM581861	MA377	Morocco_49_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581863	MA383	Morocco_50_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581868	MA395	Morocco_50_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581872	MA414	Morocco_50_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581888	MA458	Morocco_50_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581865	MA388	Morocco_51_s	864	Morocco, Ifrane	33.4940	-5.0570	Lalis <i>et al.</i> 2016
African	KM581853	MA353	Morocco_51_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581854	MA354	Morocco_51_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581867	MA391	Morocco_52_s	864	Morocco, Ifrane	33.4940	-5.0570	Lalis <i>et al.</i> 2016
African	KM581870	MA406	Morocco_53_s	864	Morocco, Ifrane	33.5140	-5.1260	Lalis <i>et al.</i> 2016
African	KM581873	MA415	Morocco_54_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581874	MA416	Morocco_55_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581887	MA447	Morocco_55_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581875	MA419	Morocco_56_s	864	Morocco, Ifrane	33.5000	-5.1130	Lalis <i>et al.</i> 2016
African	KM581878	MA422	Morocco_57_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581879	MA423	Morocco_58_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581880	MA431	Morocco_59_s	864	Morocco, Ifrane	33.5140	-5.1251	Lalis <i>et al.</i> 2016
African	KM581881	MA432	Morocco_60_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581882	MA434	Morocco_61_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM581883	MA435	Morocco_62_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM581884	MA438	Morocco_63_s	864	Morocco, Ifrane	33.4230	-5.0490	Lalis <i>et al.</i> 2016
African	KM581886	MA440	Morocco_64_s	864	Morocco, Ifrane	33.4230	-5.0500	Lalis <i>et al.</i> 2016
African	KM581889	MA459	Morocco_65_s	864	Morocco, Ifrane	33.5140	-5.1250	Lalis <i>et al.</i> 2016
African	KM581890	MA462	Morocco_66_s	864	Morocco, Ifrane	33.4250	-5.0450	Lalis <i>et al.</i> 2016
African	KM581891	MA463	Morocco_67_s	864	Morocco, Ifrane	33.4250	-5.0450	Lalis <i>et al.</i> 2016
African	KM582021	MA944	Morocco_67_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM581892	MA465	Morocco_68_s	864	Morocco, Ifrane	33.4250	-5.0450	Lalis <i>et al.</i> 2016
African	KM581893	MA466	Morocco_69_s	864	Morocco, Ifrane	33.4210	-5.0620	Lalis <i>et al.</i> 2016
African	KM582015	MA938	Morocco_70_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM582017	MA940	Morocco_71_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582023	MA948	Morocco_71_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM582018	MA941	Morocco_72_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM581845	MA343	Morocco_72_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM582019	MA942	Morocco_73_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582020	MA943	Morocco_74_s	864	Morocco, Ifrane	33.4230	-5.0480	Lalis <i>et al.</i> 2016
African	KM582022	MA947	Morocco_75_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM582025	MA952	Morocco_76_s	864	Morocco, Ifrane	33.4230	-5.0470	Lalis <i>et al.</i> 2016
African	KM582027	OI2	Morocco_76_s	864	Morocco, Ifrane	33.5610	-5.1250	Lalis <i>et al.</i> 2016
African	KM582026	OI1	Morocco_78_s	864	Morocco, Ifrane	33.5610	-5.1250	Lalis <i>et al.</i> 2016
African	KM582028	RE1	Morocco_79_s	864	Morocco, Ifrane	33.4720	-5.1390	Lalis <i>et al.</i> 2016
African	KM582029	RE2	Morocco_80_s	864	Morocco, Ifrane	33.4720	-5.1390	Lalis <i>et al.</i> 2016
African	KM582031	RE4	Morocco_81_s	864	Morocco, Ifrane	33.4720	-5.1390	Lalis <i>et al.</i> 2016
African	KM581987	MA751	Morocco_82_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM581990	MA755	Morocco_82_s	864	Morocco, Merja Zerga	34.7890	-6.2480	Lalis <i>et al.</i> 2016
African	KM581992	MA760	Morocco_82_s	864	Morocco, Merja Zerga	34.7920	-6.2430	Lalis <i>et al.</i> 2016
African	KM581994	MA764	Morocco_82_s	864	Morocco, Merja Zerga	34.7900	-6.2410	Lalis <i>et al.</i> 2016
African	KM582008	MA784	Morocco_82_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582012	MA796	Morocco_82_s	864	Morocco, Merja Zerga	34.7890	-6.2480	Lalis <i>et al.</i> 2016
African	KM582049	TE12	Morocco_82_s	864	Morocco, Tétouan	35.6820	-5.2900	Lalis <i>et al.</i> 2016
African	KM582006	NA	Morocco_83_s	864	Morocco	NA	NA	Lalis (unpublished)
African	KM582009	NA	Morocco_83_s	864	Morocco	NA	NA	Lalis (unpublished)
African	KM582007	MA783	Morocco_84_s	864	Morocco, Merja Zerga	34.7930	-6.2490	Lalis <i>et al.</i> 2016
African	KM582013	MA797	Morocco_85_s	864	Morocco, Merja Zerga	34.7890	-6.2480	Lalis <i>et al.</i> 2016
African	KM581781	JM3	Morocco_86_s	864	Morocco, Moyen-Atlas ISR	33.5000	-4.5000	Lalis <i>et al.</i> 2016
African	KM581782	JM4	Morocco_87_s	864	Morocco, Moyen-Atlas ISR	33.5000	-4.5000	Lalis <i>et al.</i> 2016
African	KM581911	MA525	Morocco_88_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581912	MA528	Morocco_89_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581817	MA292	Morocco_89_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581819	MA294	Morocco_89_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581913	MA531	Morocco_90_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581917	MA535	Morocco_90_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581933	MA555	Morocco_90_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581916	MA534	Morocco_91_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581920	MA539	Morocco_92_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581922	MA541	Morocco_93_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581923	MA544	Morocco_94_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581924	MA545	Morocco_94_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581925	MA546	Morocco_94_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1400	Lalis <i>et al.</i> 2016
African	KM581928	MA550	Morocco_95_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581936	MA558	Morocco_96_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM581937	MA559	Morocco_97_s	864	Morocco, Parc Talassemtnane	35.1060	-5.1390	Lalis <i>et al.</i> 2016
African	KM582032	SB34	Morocco_98_s	864	Morocco, Sidi Boughaba	34.2380	-6.6730	Lalis <i>et al.</i> 2016
African	KM581790	MA249	Morocco_99_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581833	MA321	Morocco_99_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581835	MA330	Morocco_99_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581792	MA252	Morocco_100_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581793	MA253	Morocco_101_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581794	MA258	Morocco_102_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581796	MA261	Morocco_102_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581821	MA297	Morocco_102_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581795	MA260	Morocco_103_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581797	MA263	Morocco_104_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581798	MA264	Morocco_105_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581799	MA265	Morocco_106_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581800	MA266	Morocco_107_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581827	MA310	Morocco_107_s	864	Morocco, Taza	34.1040	-4.0730	Lalis <i>et al.</i> 2016
African	KM581844	MA342	Morocco_107_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581801	MA268	Morocco_108_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581802	MA269	Morocco_109_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581805	MA274	Morocco_109_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581806	MA275	Morocco_110_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581807	MA276	Morocco_111_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581808	MA278	Morocco_112_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581810	MA283	Morocco_113_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581811	MA284	Morocco_114_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581812	MA286	Morocco_115_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581813	MA287	Morocco_116_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581814	MA289	Morocco_116_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016
African	KM581815	MA290	Morocco_116_s	864	Morocco, Taza	34.0620	-4.2020	Lalis <i>et al.</i> 2016

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
African	KM581822	MA302	Morocco_117_s	864	Morocco, Taza	34.0510	-4.1870	Lalis <i>et al.</i> 2016
African	KM581823	MA303	Morocco_117_s	864	Morocco, Taza	34.0510	-4.1870	Lalis <i>et al.</i> 2016
African	KM581824	MA304	Morocco_117_s	864	Morocco, Taza	34.0510	-4.1870	Lalis <i>et al.</i> 2016
African	KM581825	MA305	Morocco_117_s	864	Morocco, Taza	34.0510	-4.1870	Lalis <i>et al.</i> 2016
African	KM581826	MA307	Morocco_117_s	864	Morocco, Taza	34.0510	-4.1870	Lalis <i>et al.</i> 2016
African	KM581831	MA318	Morocco_118_s	864	Morocco, Taza	34.0950	-4.0770	Lalis <i>et al.</i> 2016
African	KM581832	MA319	Morocco_119_s	864	Morocco, Taza	34.0950	-4.0770	Lalis <i>et al.</i> 2016
African	KM581834	MA328	Morocco_120_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581836	MA331	Morocco_121_s	864	Morocco, Taza	34.0470	-4.1860	Lalis <i>et al.</i> 2016
African	KM581838	MA335	Morocco_122_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581860	MA368	Morocco_122_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581839	MA337	Morocco_123_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581840	MA338	Morocco_123_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581859	MA367	Morocco_123_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581846	MA346	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581847	MA347	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581849	MA349	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581850	MA350	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581851	MA351	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581852	MA352	Morocco_124_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581848	MA348	Morocco_125_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581855	MA355	Morocco_126_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581856	MA356	Morocco_127_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
African	KM581857	MA357	Morocco_127_s	864	Morocco, Taza	34.0700	-4.1310	Lalis <i>et al.</i> 2016
central	FJ389641	JRM-446	Netherlands_s	818	Netherlands, Limburg	51.2400	5.8600	Dubey <i>et al.</i> 2009
peripheral	KX159673	NMS.Z.2009.101.N3	Norway_1	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
peripheral	KX159674	NMS.Z.2009.101.N5	Norway_2	1140	Norway, Rogaland, Bratland	59.6833	6.7767	*
peripheral	KX159675	JSH_ILN1831A	Norway_3	1140	Norway, Hordaland, Bergen	60.3380	5.3500	*
central	KX159676	JSH_ILN1831B	Norway_4	1140	Norway, Hordaland, Bergen	60.3380	5.3500	*
peripheral	KX159677	MRI.PAS.5466	Poland_1	1140	Poland, Nowogród	53.2261	21.8787	*
peripheral	KX159678	MRI.PAS.10302	Poland_2	1140	Poland, Darżlubie	54.6996	18.3184	*
peripheral	KX159679	MRI.PAS.15615	Poland_3	1140	Poland, Międzychód	52.5967	15.9575	*
peripheral	KX159679	MRI.PAS.15711	Poland_3	1140	Poland, Międzychód	52.5967	15.9575	*
peripheral	KX159679	MRI.PAS.15821	Poland_3	1140	Poland, Międzychód	52.5967	15.9575	*
peripheral	KX159679	MRI.PAS.19952	Poland_3	1140	Poland, Wschowa	51.8056	16.3141	*

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peripheral	KX159679	MRI.PAS.21369	Poland_3	1140	Poland, Rzepin	52.3457	14.8326	*
peripheral	KX159679	MRI.PAS.21421	Poland_3	1140	Poland, Rzepin	52.3457	14.8326	*
peripheral	KX159679	MRI.PAS.21472	Poland_3	1140	Poland, Rzepin	52.3457	14.8326	*
peripheral	KX159679	MRI.PAS.22187	Poland_3	1140	Poland, Krosno Odrzańskie	52.0573	15.0963	*
peripheral	KX159679	MRI.PAS.22238	Poland_3	1140	Poland, Krosno Odrzańskie	52.0573	15.0963	*
peripheral	KX159679	MRI.PAS.29619	Poland_3	1140	Poland, Dębno	52.7333	14.7000	*
peripheral	KX159680	MRI.PAS.15820	Poland_4	1140	Poland, Międzychód	52.5967	15.9575	*
peripheral	KX159681	MRI.PAS.15896	Poland_5	1140	Poland, Międzychód	52.5967	15.9575	*
peripheral	KX159682	MRI.PAS.19841	Poland_6	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159682	MRI.PAS.19956	Poland_6	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159682	MRI.PAS.20013	Poland_6	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159682	MRI.PAS.20029	Poland_6	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159682	MRI.PAS.20043	Poland_6	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159682	MRI.PAS.20249	Poland_6	1140	Poland, Wojsław	50.3833	21.5167	*
peripheral	KX159683	MRI.PAS.19962	Poland_7	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159684	MRI.PAS.19993	Poland_8	1140	Poland, Wschowa	51.8056	16.3141	*
peripheral	KX159685	MRI.PAS.22136	Poland_9	1140	Poland, Krosno Odrzańskie	52.0573	15.0963	*
peripheral	KX159686	MRI.PAS.22137	Poland_10	1140	Poland, Krosno Odrzańskie	52.0573	15.0963	*
peripheral	KX159687	MRI.PAS.22309	Poland_11	1140	Poland, Krosno Odrzańskie	52.0573	15.0963	*
peripheral	KX159688	MRI.PAS.23761	Poland_12	1140	Poland, Szprotawa	51.5592	15.5362	*
peripheral	KX159689	MRI.PAS.27054	Poland_13	1140	Poland, Pomorze	54.0461	23.3626	*
peripheral	KX159689	MRI.PAS.27391	Poland_13	1140	Poland, Pomorze	54.0461	23.3626	*
peripheral	KX159690	MRI.PAS.27392	Poland_14	1140	Poland, Pomorze	54.0461	23.3626	*
peripheral	KX159690	MRI.PAS.27559	Poland_14	1140	Poland, Pomorze	54.0461	23.3626	*
peripheral	KX159690	MRI.PAS.27560	Poland_14	1140	Poland, Pomorze	54.0461	23.3626	*
central	KX159691	JSH_JP1	Portugal_1	1140	Portugal, Serra da Estrela, Gouveia	40.5020	-7.5754	*
central	KX159692	JSH_JP2	Portugal_2	1140	Portugal, Serra da Estrela, Gouveia	40.5020	-7.5754	*
central	KX159693	JSH_LA2	Portugal_3	1140	Portugal, Vila Real (Vila Poca Aguiar), Lagoa	41.5493	-7.5315	*
central	KX159694	JSH_LA3	Portugal_4	1140	Portugal, Vila Real (Vila Poca Aguiar), Lagoa	41.5007	-7.6485	*
central	KX159695	JSH_LA7	Portugal_5	1140	Portugal, Vila Real (Vila Poca Aguiar), Lagoa	41.5007	-7.6485	*
central	KX159696	JSH_LA8	Portugal_6	1140	Portugal, Vila Real (Vila Poca Aguiar), Lagoa	41.5007	-7.6485	*
central	KX159697	JSH_QT7	Portugal_7	1140	Portugal, Serra da Estrela, Quinta da Taberna	40.4864	-7.4152	*
central	KX159698	JSH_QT8	Portugal_8	1140	Portugal, Serra da Estrela, Quinta da Taberna	40.4864	-7.4152	*
central	KX159699	JSH_QT9	Portugal_9	1140	Portugal, Serra da Estrela, Quinta da Taberna	40.4864	-7.4152	*
central	JX457738	ASY7_SM1153	Portugal_10	1128	Portugal, Viana do Castelo, Gerês	41.7905	-8.1546	Barbosa et al. 2012

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central	JX457737	ASY6_SM1150	Portugal_11	1128	Portugal, Viana do Castelo, Gerês	41.7905	-8.1546	Barbosa <i>et al.</i> 2012
central	JX457736	ASY5_SM1140	Portugal_12	1128	Portugal, Viana do Castelo, Gerês	41.7838	-8.1664	Barbosa <i>et al.</i> 2012
central	JX457735	ASY4_SM1104	Portugal_13	1128	Portugal, Viana do Castelo, Gerês	41.7688	-8.1469	Barbosa <i>et al.</i> 2012
central	KM581716	Murta3	Portugal_14_s	701	Portugal, Oliveira do Bairro, Murta	40.5160	-8.4680	Lalis <i>et al.</i> 2016
central	KM581715	Murta2	Portugal_15_s	701	Portugal, Oliveira do Bairro, Murta	40.5160	-8.4680	Lalis <i>et al.</i> 2016
south-eastern	AJ511941	JRM-212	Serbia_1_s	962	Serbia, Vojvodina, Šušara	45.1167	21.3036	Michaux <i>et al.</i> 2003
south-eastern	AJ511945	JRM-211	Serbia_2_s	945	Serbia, Vojvodina, Šušara	45.1167	21.3036	Michaux <i>et al.</i> 2003
south-eastern	AJ511946	JRM-210	Serbia_3_s	963	Serbia, Vojvodina, Šušara	45.1167	21.3036	Michaux <i>et al.</i> 2003
south-eastern	AJ511931	JRM-417	Slovenia_1_s	962	Slovenia, Gorenjska, Škofja	46.1672	14.3089	Michaux <i>et al.</i> 2003
south-eastern	AJ511932	JRM-434	Slovenia_2_s	965	Slovenia, Ljubljana	46.0536	14.4704	Michaux <i>et al.</i> 2003
central	KX159700	JSH_AST1	Spain_1	1140	Spain, Asturias, Illano	43.3447	-6.9047	*
central	KX159700	JSH_AST2	Spain_1	1140	Spain, Asturias, Illano	43.3447	-6.9047	*
central	KX159701	JSH_ES12	Spain_2	1140	Spain, Castilla y León, Vega de Infanzones	42.4737	-5.5308	*
central	KX159702	JSH_ES13	Spain_3	1140	Spain, Castilla y León, Vega de Infanzones	42.4737	-5.5308	*
central	KX159703	JSH_ES29	Spain_4	1140	Spain, Castilla y León, Castrojeriz	42.2699	-4.1127	*
central	KM581676	592bis	Spain_4_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581686	794	Spain_4_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KX159704	JSH_ES32	Spain_5	1140	Spain, Asturias, Picos da Europa	43.1049	-4.9997	*
central	KX159705	JSH_ES34	Spain_6	1140	Spain, Asturias, Picos da Europa	43.1059	-4.9986	*
central	KX159706	JSH_ES65	Spain_7	1140	Spain, Basque Country, El Prado	43.1423	-3.4503	*
central	KX159707	JSH_ES89	Spain_8	1140	Spain, Castilla y León, Sierra de la Demanda	42.3094	-3.2651	*
peripheral	AJ511880	JRM-131	Spain_9_s	870	Spain, Navarre, Eugi	42.9786	-1.5081	Michaux <i>et al.</i> 2003
central	AJ511881	JRM-132	Spain_10_s	915	Spain, Navarre, Eugi	42.9786	-1.5081	Michaux <i>et al.</i> 2003
central	AJ511882	JRM-133	Spain_11_s	809	Spain, Navarre, Eugi	42.9786	-1.5081	Michaux <i>et al.</i> 2003
central	AJ511897	JRM-578	Spain_12_s	965	Spain, Catalonia, Figueras	42.2675	2.9608	Michaux <i>et al.</i> 2003
central	AJ511909	JRM-700	Spain_13_s	856	Spain, Aragon, Torla	42.6279	-0.1106	Michaux <i>et al.</i> 2003
central	AJ511911	JRM-592	Spain_14_s	965	Spain, Murcia	37.9834	-1.1299	Michaux <i>et al.</i> 2003
central	AJ511912	JRM-594	Spain_15_s	965	Spain, Murcia	37.9834	-1.1299	Michaux <i>et al.</i> 2003
central	AJ511913	JRM-596	Spain_16_s	918	Spain, Murcia	37.9834	-1.1299	Michaux <i>et al.</i> 2003
peripheral	AJ511914	JRM-130	Spain_17_s	965	Spain, Navarre, Eugi	42.9786	-1.5081	Michaux <i>et al.</i> 2003
central	JX457739	ASY3_SP88	Spain_18	1128	Spain, Andaluzia	37.5000	-4.7000	Barbosa <i>et al.</i> 2012
central	JX457734	ASY2_SM428	Spain_19	1128	Spain, Galiza, Lalín	42.6400	-8.1000	Barbosa <i>et al.</i> 2012
central	JX457733	ASY1_SM344	Spain_20	1128	Spain, Bizcaia	43.0454	-8.6725	Barbosa <i>et al.</i> 2012
peripheral	KM581675	130BIS	Spain_21_s	701	Spain, Navarre, Eugi	42.9786	-1.5081	Lalis <i>et al.</i> 2016
peripheral	KM581737	VE37	Spain_22_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016

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peripheral	KM581691	1922	Spain_23_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
peripheral	KM581692	1927	Spain_24_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581704	Murcia11	Spain_25_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581707	Murcia14	Spain_25_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581687	1912	Spain_26_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581703	Murcia10	Spain_27_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581708	Murcia15	Spain_27_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581709	Murcia16	Spain_27_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581677	595	Spain_27_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581679	781	Spain_27_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581694	VV198691	Spain_28_s	701	Spain, Madrid, Rascafria	40.9040	-3.8800	Lalis <i>et al.</i> 2016
central	KM581741	VE41	Spain_29_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581683	790	Spain_30_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581682	787	Spain_31_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581689	1914	Spain_31_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581681	786	Spain_32_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581705	Murcia12	Spain_33_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581714	Murcia9	Spain_34_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581739	VE39	Spain_35_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581713	Murcia8	Spain_36_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581678	780	Spain_37_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581684	791	Spain_38_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581685	793	Spain_39_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581740	VE40	Spain_40_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581743	VE43	Spain_40_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581688	1913	Spain_41_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581710	Murcia5	Spain_42_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581711	Murcia6	Spain_43_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581736	VE36	Spain_44_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581738	VE38	Spain_44_s	701	Spain, Madrid	40.4160	-3.7020	Lalis <i>et al.</i> 2016
central	KM581706	Murcia13	Spain_45_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581712	Murcia7	Spain_45_s	701	Spain, Murcia	37.9834	-1.1299	Lalis <i>et al.</i> 2016
central	KM581690	1918	Spain_46_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KM581693	1928	Spain_47_s	701	Spain, Cataluna, Montseny	41.7590	2.3960	Lalis <i>et al.</i> 2016
central	KX159708	JSH_2S	Sweden_1	1140	Sweden, Skåne Län, Malmö	55.6000	13.0000	*

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Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
central	KX159708	JSH_5S	Sweden_1	1140	Sweden, Skåne Län, SW of Kristianstad	56.0000	14.1000	*
central	KX159709	JSH_3S	Sweden_2	1140	Sweden, Skåne Län, Malmö	55.6000	13.0000	*
central	KX159709	JSH_8S	Sweden_2	1140	Sweden, Skåne Län, SW of Kristianstad	56.0000	14.1000	*
central	KX159710	JSH_7S	Sweden_3	1140	Sweden, Skåne Län, SW of Kristianstad	56.0000	14.1000	*
central	AJ511891	JRM-452	Sweden_4_s	965	Sweden, Uppsala	59.8581	17.6446	Michaux <i>et al.</i> 2003
central	AJ511892	JRM-453	Sweden_5_s	919	Sweden, Uppsala	59.8581	17.6446	Michaux <i>et al.</i> 2003
central	FJ389620	JM-4600	Sweden_6_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	KX159711	S4603	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4605	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4611	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4620	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4634	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4635	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	S4637	Sweden_6_s	818	Sweden, southern part	NA	NA	*
central	KX159711	C4798	Sweden_6_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	FJ389627	JM-4707	Sweden_7_s	818	Sweden, Uppsala area	59.9000	17.6000	Dubey <i>et al.</i> 2009
central	FJ389632	JM-4583	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389633	JM-4584	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389634	JM-4590	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389635	JM-4592	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389631	JM-4624	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389628	JM-4796	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389629	JM-4814	Sweden_8_s	818	Sweden, Uppsala area	59.9000	17.6000	Dubey <i>et al.</i> 2009
central	FJ389630	JM-4833	Sweden_8_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	KX159712	S4582	Sweden_8_s	818	Sweden, Göteborg	57.7000	12.0000	*
central	KX159712	S4594	Sweden_8_s	818	Sweden, Göteborg	57.7000	12.0000	*
central	KX159712	S4602	Sweden_8_s	818	Sweden, southern part	NA	NA	*
central	KX159712	S4604	Sweden_8_s	818	Sweden, southern part	NA	NA	*
central	KX159712	S4618	Sweden_8_s	818	Sweden, southern part	NA	NA	*
central	KX159712	S4619	Sweden_8_s	818	Sweden, southern part	NA	NA	*
central	KX159712	S4626	Sweden_8_s	818	Sweden, southern part	NA	NA	*
central	KX159712	C4837	Sweden_8_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	FJ389638	JM-4596	Sweden_9_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389636	JM-4598	Sweden_9_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009
central	FJ389637	JM-4625	Sweden_9_s	818	Sweden, Stockholm area	59.3000	18.0000	Dubey <i>et al.</i> 2009

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
central	KX159713	S4615	Sweden_9_s	818	Sweden, southern part	NA	NA	*
central	KX159713	S4617	Sweden_9_s	818	Sweden, southern part	NA	NA	*
central	KX159713	S4627	Sweden_9_s	818	Sweden, southern part	NA	NA	*
central	KX159713	C4739	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159713	C4799	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159713	C4812	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159713	C4821	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159713	C4830	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159713	C4843	Sweden_9_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159714	C4788	Sweden_10_s	818	Sweden, Umeå area	63.8000	20.3000	*
central	KX159715	C4836	Sweden_11_s	818	Sweden, Umeå area	63.8000	20.3000	*
peripheral	FJ389649	JM-118	Sweden_12_s	818	Sweden, Stockholm	59.3000	18.0000	Dubey <i>et al.</i> 2009
peripheral	FJ389648	JM-557	Sweden_12_s	818	Sweden	NA	NA	Dubey <i>et al.</i> 2009
central	AY179493	ST56	Switzerland_1_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180340	ST28	Switzerland_2_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180336	ST29	Switzerland_2_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180341	ST58	Switzerland_3_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180342	ST30	Switzerland_4_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180343	ST27	Switzerland_5_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
central	AY180344	ST6	Switzerland_6_s	732	Switzerland, Vaud, Morges	46.5667	6.5000	Reutter <i>et al.</i> 2003
peripheral	AY180345	IZEA4858	Switzerland_7_s	732	Switzerland, Vaud, Aclens	46.5675	6.5098	Reutter <i>et al.</i> 2003
central	AY180346	BNM2218	Switzerland_8_s	732	Switzerland, Graubünden, Malix	46.8120	9.5318	Reutter <i>et al.</i> 2003
central	AY332700	P40	Switzerland_9_s	788	Switzerland, Wallbrig	47.1700	7.9600	Reutter <i>et al.</i> 2003
central	AY332701	P46	Switzerland_10_s	799	Switzerland, Wallbrig	47.1700	7.9600	Reutter <i>et al.</i> 2003
African	AJ511915	JRM-138	Tunisia_1_s	962	Tunisia, Jendouba, Aïn Draham	36.7800	8.6872	Michaux <i>et al.</i> 2003
African	AJ511917	JRM-140	Tunisia_2_s	964	Tunisia, Jendouba, Aïn Draham	36.7800	8.6872	Michaux <i>et al.</i> 2003
African	AJ511918	JRM-139	Tunisia_3_s	965	Tunisia, Jendouba, Aïn Draham	36.7800	8.6872	Michaux <i>et al.</i> 2003
African	AJ511920	JRM-141	Tunisia_4_s	965	Tunisia, Jendouba, Aïn Draham	36.7800	8.6872	Michaux <i>et al.</i> 2003
south-eastern	AJ511939	JRM-184	Turkey_1_s	963	Turkey, Zonguldak, Çaycuma	41.4264	32.0756	Michaux <i>et al.</i> 2003
peripheral	AY158455	TK67607	Ukraine_1	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
peripheral	AY158456	TK67714	Ukraine_2	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
peripheral	AY158457	TK67735	Ukraine_3	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
peripheral	AY158458	TK67803	Ukraine_4	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
peripheral	AY158459	TK67847	Ukraine_5	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
south-eastern	KX159716	MRI.PAS.UA10518	Ukraine_6	1140	Ukraine, Kharkiv Oblast, Borovaja	49.2111	37.3327	*
south-eastern	KX159716	MRI.PAS.UA10523	Ukraine_6	1140	Ukraine, Kharkiv Oblast, Borovaja	49.2111	37.3327	*
south-eastern	AY158460	TK81561	Ukraine_6	1140	Ukraine, Chernigov, Nedanchichy	51.5500	30.8600	Dunina-Barkovskaya

Lineage	GenBank #	Voucher #	Haplotype	B-P	Locality	Latitude	Longitude	Reference
peripheral	AY158461	TK96046	Ukraine_7	1140	Ukraine, Chernigov, Nedanchichy	51.5500	30.8600	Dunina-Barkovskaya
peripheral	AY158462	TK96132	Ukraine_8	1140	Ukraine, Kiev Oblast, Chornobyl	51.2900	30.0900	Dunina-Barkovskaya
south-eastern	KX159717	MRI.PAS.UA10522	Ukraine_9	1140	Ukraine, Kharkiv Oblast, Borovaja	49.2111	37.3327	*

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3 **Table S.3** Prior parameter distributions from coalescent genealogy sampling with *Beast 2.3.1*.  
4 Linked substitution and clock model parameters, unlinked tree parameters.  
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6 Parameter	7 Prior distribution	8 Range	9 Initial value
10 kappa1	11 Lognormal (1.0/1.25)	12 0 – inf	13 1.0
14 kappa2	15 Lognormal (1.0/1.25)	16 0 – inf	17 1.0
18 gamma shape	19 Lognormal (1.0/1.25)	20 0 – inf	21 1.0
22 frequencies	23 Uniform	24 1.0e-9 - 1.0	25 0.25
26 Clock rate	27 ---	28 ---	29 3.27e-4
30 Population size	31 Lognormal (1.0/1.25)	32 1.0e-9 - 1.0e9	33 10,000
34 Pop. groups ( <i>African</i> )	35 ---	36 ---	37 10
38 Pop. groups ( <i>central</i> )	39 ---	40 ---	41 10
42 Pop. groups ( <i>Channel Is</i> )	43 ---	44 ---	45 3
47 Pop. groups ( <i>peripheral</i> )	48 ---	49 ---	50 10
52 Pop. groups ( <i>south-eastern</i> )	53 ---	54 ---	55 5
57 Pop. groups ( <i>Sicilian</i> )	58 ---	59 ---	60 5
62 Tree	63 Coalescent BSP	64 ---	65 Random tree

**Table S.4** Locations with the same haplotype. Geographical coordinates for locations and pairwise geodesic distances between them, where movements between such locations would involve a sea crossing, given the present location of coastlines. Locations collapsed to mean or centroid coordinates within each land mass or archipelago.

Lineage	Haplotype name	Location land mass	Latitude	Longitude	Pairwise geodesic (km)
central	Belgium_France_Sweden_Switz	Europe mainland (centroid)	47.9529	3.3188	1611
central	Belgium_France_Sweden_Switz	Fennoscandia (centroid)	59.8557	17.4667	
central	Denmark_Sweden_s	Europe mainland (centroid)	56.2000	10.2000	579
central	Denmark_Sweden_s	Fennoscandia (centroid)	59.9099	17.0799	
central	Germany_Norway	Europe mainland (centroid)	54.2831	8.8403	571
central	Germany_Norway	Fennoscandia (centroid)	59.3795	7.8439	
peripheral	GB_Arran_Scarba	Arran, Hebrides	55.5924	-5.1501	74
peripheral	GB_Arran_Scarba	Scarba, Hebrides	56.1873	-5.6792	
peripheral	GB_Jura_N_Scotland	Jura, Hebrides (mean)	55.8959	-5.8987	271
peripheral	GB_Jura_N_Scotland	Britain mainland (mean)	58.1917	-4.4022	
peripheral	GB_Orkney_mainland_Rousay	Orkney mainland (centroid)	59.0103	-3.1172	19
peripheral	GB_Orkney_mainland_Rousay	Rousay, Orkney	59.1758	-3.0584	
peripheral	GB_Perth_Colonsay	Colonsay, Hebrides	56.0663	-6.2270	172
peripheral	GB_Perth_Colonsay	Britain mainland	56.5623	-3.6011	
peripheral	GB_Sutherland_Hoy	Britain mainland	58.1299	-5.2607	141
peripheral	GB_Sutherland_Hoy	Hoy, Orkney (centroid)	58.8730	-3.3064	
peripheral	GB_Walney_Sheep_Piel	Sheep Island, England	54.0641	-3.2024	1
peripheral	GB_Walney_Sheep_Piel	Walney, England	54.0657	-3.2239	2
peripheral	GB_Walney_Sheep_Piel	Piel Island, England	54.0626	-3.1733	3
peripheral	Britain_BL_Ireland	Britain mainland (mean)	51.4183	-3.3468	391
peripheral	Britain_BL_Ireland	Ireland mainland (centroid)	53.7454	-7.6643	416
peripheral	Britain_BL_Ireland	Uists, Hebrides (centroid)	57.4759	-7.3884	223
peripheral	Britain_BL_Ireland	Gigha, Hebrides	55.6928	-5.7360	439
peripheral	Britain_BL_Ireland	Shetland Islands (centroid)	59.8452	-1.3327	531
peripheral	Britain_Ireland_1	Britain mainland	51.8000	-1.3000	438
peripheral	Britain_Ireland_1	Ireland mainland	54.6000	-5.9000	
peripheral	Britain_Ireland_2	Britain mainland	51.8000	-1.3000	438
peripheral	Britain_Ireland_2	Ireland mainland	54.6000	-5.9000	
peripheral	Britain_Norway	Britain mainland (centroid)	55.5773	-2.9756	639
peripheral	Britain_Norway	Fennoscandia	58.9833	5.5667	
peripheral	Iceland_Shetland_Norway	Iceland (centroid)	64.5712	-20.1409	1101
peripheral	Iceland_Shetland_Norway	Shetland mainland	59.9316	-1.3005	410
peripheral	Iceland_Shetland_Norway	Fennoscandia (mean)	60.0220	6.0484	