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# Molecular studies on the colonization of the Madeiran archipelago by house mice

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**Abstract**

**To study the colonization history of the house mouse (*Mus musculus domesticus*) on the Madeiran archipelago, complete mitochondrial D-loop sequences were obtained for 44 individuals from Madeira, Porto Santo and Ilhas Desertas. Altogether, 19 D-loop haplotypes were identified which formed part of a single clade in a phylogeny incorporating haplotypes from elsewhere in the range of *M. m. domesticus*, indicating that the Madeiras were colonized from a single source. Similarities between the sequences found in the Madeiras and those in Scandinavia and northern Germany suggest that northern Europe was the source area, and there is the intriguing possibility that the Vikings may have accidentally brought house mice to the archipelago. However, there is no record of Vikings visiting the Madeiras; on historical grounds, Portugal is the most likely source area for Madeiran mice and further molecular data from Portugal are needed to rule out that possibility.**

*Keywords*: control region, D-loop, house mouse, island colonization, mitochondrial DNA, *Mus musculus domesticus*

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## Introduction

The Madeiran archipelago is a volcanic complex formed at least 12 Ma and located 600 km off the Atlantic coast of North Africa. The archipelago consists of three island groups: Madeira itself and its associated islets, Porto Santo and islets, and Ilhas Desertas (Fig. 1). The islands have long been of interest to evolutionary biologists, particularly relating to endemic beetles and snails (Wollaston 1854, 1878; Darwin 1859) that originally colonized the archipelago some millions of years ago. Our study relates to a much more recent colonization, that of the West European house mouse, *Mus musculus domesticus*. This animal has been spread around the world by humans (Sage 1981; Auffray *et al*. 1990; Baker 1994) and, given the large distance from the nearest land mass, this is the only conceivable manner by which it colonized the Madeiras. The key date for human-mediated colonization would appear to be 1419, when the islands were officially discovered by Portuguese explorers, but the islands were almost certainly visited at least 100 years before this (Mathias & Mira 1992; Goodfriend *et al*. 1994). Records of house mice on Madeira date back to the 16th century (Mathias 1993), but again it is likely that they were present before this.

Molecular markers have been invaluable in establishing the colonization history of species on oceanic islands, including the archipelagos of the West Atlantic (Thorpe *et al*. 1994; Böhle *et al*. 1996; Khadem *et al*. 1998; Widmer *et al*. 1998; Marshall & Baker 1999; Juan *et al*. 2000). In this study we used molecular data to elucidate the colonization history of the Madeiras by house mice. We used sequences of the mitochondrial D-loop (control region), building on what is already known about the geographical variation in this sequence in *M. m. domesticus* (Prager *et al*. 1993, 1996, 1998; Nachman *et al*. 1994).

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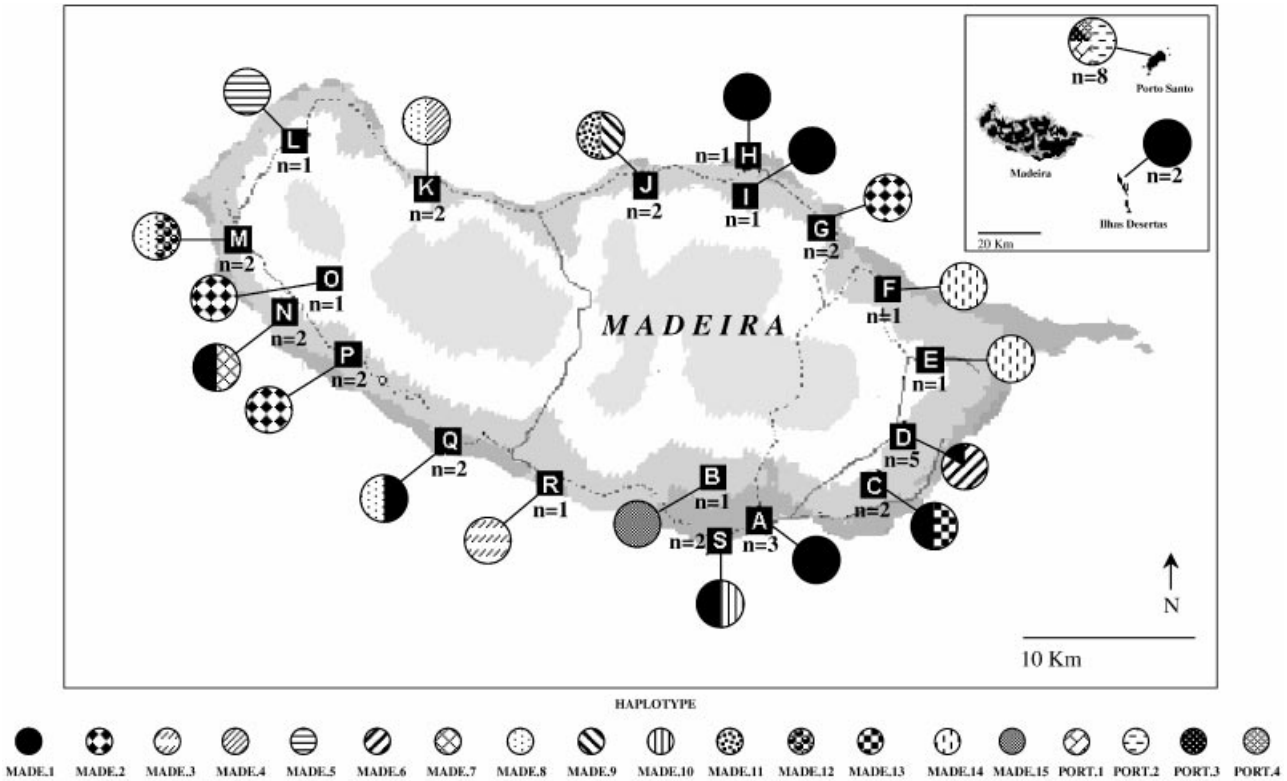



**Fig. 1** Distribution of D-loop haplotypes in house mice collected from the Madeiran archipelago.

## Materials and methods

### *Mice*

Thirty-four house mice from Madeira (collected in 1998–9), eight from Porto Santo (1999) and two from Ilhas Desertas (1994, collectors M Raymond & M Marquine) were used for molecular studies. The mice on Madeira were collected from 19 separate sites (Fig. 1), those on Ilhas Desertas from one site (on Deserta Grande) and those on Porto Santo from four well-separated sites ($n = 2$ in each case).

For phylogenetic analysis, use was made of additional specimens from another West Atlantic island (Selvagem Grande, two mice collected in 1995 by M Raymond), North Africa (one mouse from Dars Salam, Mauritania collected in 1995 by L Granjon and two from Azzemmour, Morocco collected in 1989 by F Bonhomme and K Belkhir) and Portugal (one mouse from Lisbon collected in 1999 by A Nunes).

### *DNA extraction, polymerase chain reaction (PCR) and sequencing*

In general, DNA was extracted from tail tips that were preserved in 100% ethanol and maintained at 4 °C. A standard phenol/chloroform procedure (Sambrook *et al*. 1989) was used. For all specimens, the whole D-loop (879 bp) plus the Thr-transfer (t)RNA and Pro-tRNA genes (hereafter known collectively as the 'D-loop') were amplified in two fragments: first, primers L15774 (Kocher *et al*. 1989) and H16498 (Gündüz *et al*. 2000) (numbering according to Anderson *et al*. 1981), and second, primers L15735 and H00072 of Prager *et al*. (1993) (numbering according to Bibb *et al*. 1981). In total, 1013 bp between positions 15283 and 16295 of Bibb *et al*. (1981) were sequenced in both directions on an ABI 377a automated sequencer. Further details of the methods of PCR and sequencing are described in Gündüz *et al*. (2000).

### *Data analysis*

Sequence traces were downloaded, checked with ANALYSIS software (ABI) and aligned with SEQED (ABI). For the sequences obtained from the Madeiras, nucleotide and haplotype diversities ($\pi$, $h$) were estimated according to Nei (1987) using the ARLEQUIN, version 1.1 package of Schneider *et al*. (1997).

All the D-loop haplotypes that we generated were used for phylogenetic analysis, in combination with sequences from the literature (Nachman *et al*. 1994; Prager *et al*. 1993, 1996, 1998) including representatives of all the major clades identified by Nachman *et al*. and Prager *et al*. and all haplotypes found in western North Africa and the western

and northern parts of Europe. Because of some differences between Nachman *et al*., Prager *et al*. and us in the regions sequenced, a slightly shortened segment (between positions 15363 and 16295) was used in the analysis of the combined dataset. This combined dataset was used to produce 10 000 randomly generated trees with PAUP* (Swofford 1998) and the phylogenetic signal was tested by the g1 method of Hillis & Huelsenbeck (1992). Distance, maximum likelihood and parsimony trees were generated under a range of different transition/transversion weightings; indels were zero-weighted in tree construction (see Gündüz *et al*. 2000). Pairwise distances between taxa were estimated using PHYLIP (Felsenstein 1991) either under the assumption of the Kimura 2-parameter model or a maximum likelihood model (the DNAML option within DNADIST in PHYLIP). From these estimates, PHYLIP was used to construct distance trees by the neighbour-joining method (Saitou & Nei 1987). A maximum likelihood tree was also produced with PHYLIP, applying the DNAML model and algorithm. PAUP* was used to generate maximum parsimony trees, with each analysis involving a heuristic search with stepwise addition (10 random replicates) and the tree–bisection–reconnection (TBR) setting. Given the large dataset, there were always many equally parsimonious trees generated; for each analysis a majority rule tree was produced based on the first 5000 equally parsimonious trees generated by PAUP*.

Our sequences have been deposited in the EMBL database (Accession nos AJ313361–AJ313383).

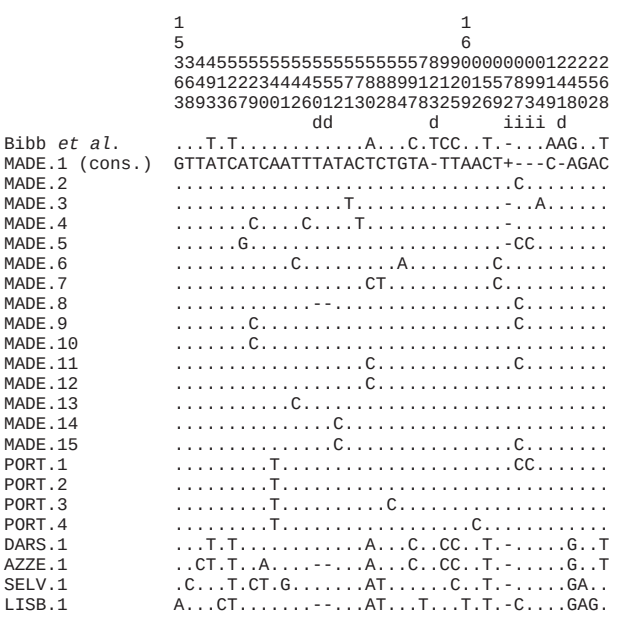



**Fig. 2** D-loop haplotypes found in mice from Madeira and Ilhas Desertas (MADE) and Porto Santo (PORT), in the Madeiran archipelago, and from western North Africa (DARS; AZZE: the two specimens had the same haplotype), Selvagem Grande (SELV: the two specimens had the same haplotype) and Portugal (LISB). Nucleotide substitutions and indels are shown with reference to the numbering system of Bibb *et al*. (1981), and a dot indicates identity to the consensus sequence (MADE.1). Each insertion or deletion relative to the sequence of Bibb *et al*. is indicated by an 'i' or a 'd', respectively. For a deletion, a dash is shown in the sequence concerned at the relevant nucleotide position. For an insertion, a dash is shown in the sequences without the insertion; the insertion occurs after the nucleotide position indicated. Note that the insertions of Cs after positions 160087 and 160093 add to a string of Cs and are positioned arbitrarily. The plus at position 16072 indicates an 11-bp insertion (TTTTAACTCTC).

## Results

### *Molecular variation in the Madeiran archipelago*

Altogether, 19 D-loop haplotypes were found in the Madeiras (Fig. 2). Of the 14 nucleotide substitutions detected, only three were transversions, consistent with the bias in favour of transitions found previously in mammalian mitochondrial DNA (mtDNA), including mouse D-loop (Prager *et al*. 1993; Nachman *et al*. 1994). One haplotype (MADE.8) showed a 2-bp deletion at positions 15550 and 15551 and there was polymorphism among the haplotypes with regards to four insertions in the region between 16072 and 16094 (Fig. 2).

The nucleotide and haplotype diversities ($\pi$, $h$) among the 44 individuals (24 localities) for the D-loop haplotypes were 0.14% and 0.90, respectively. For comparison with data collected in mainland localities of comparable geographical area (Gündüz & Searle, in preparation), the nucleotide diversity was calculated for a 305-bp stretch of sequence (between positions 15363 and 15667 of Bibb *et al*. 1981; which includes the variable left end of the D-loop). The value of 0.44% obtained compares with 1.15% for haplotypes in the vicinity of Caithness in Scotland (83 individuals, 14 localities) and 0.97% in the vicinity of Barcelona in Spain (83 individuals, 20 localities). The haplotype diversities for the 305 bp fragment were 0.82, 0.85 and 0.90 for the Madeiran archipelago, Caithness and Barcelona, respectively.

One of the sequences obtained (MADE.1) was the consensus for all the sequences from the Madeiras at all nucleotide positions (Fig. 2). MADE.1 was by far the most widespread haplotype, found at eight localities around Madeira and on Ilhas Desertas (Fig. 1). All the other D-loop sequences obtained from the Madeiran archipelago could be derived from MADE.1 by 0–3 nucleotide substitutions and 0–3 indels. The most divergent haplotypes were MADE.4 which differed by three substitutions and one indel, and MADE.5 which differed by three indels and one substitution.

All eight mice from Porto Santo differed from those on Madeira and Ilhas Desertas by a transversion at position 15540 (Fig. 2).

*Comparison with house mouse sequences from elsewhere*

The haplotypes that we found in the Madeiras differed greatly from those obtained elsewhere along the Atlantic seaboard of southern Europe and North Africa (Fig. 2). The haplotype from Lisbon was identical to one found already in the same city (Prager *et al*. 1993).

The combined dataset of our D-loop haplotypes and those from the literature showed a significant phylogenetic signal ($g1 = -0.28$; $P = 0.01$) and the distance, maximum likelihood and parsimony trees that we generated were structured (see Fig. 3). However, the major clades had little or no bootstrap support, as is normal for wide phylogenetic comparisons within *Mus musculus domesticus* (Boursot *et al*. 1996; Prager *et al*. 1993, 1996, 1998; Gündüz *et al*. 2000; Gündüz & Searle, in preparation).

In all the trees we generated, all 19 haplotypes from the Madeiran archipelago appeared in a single major 'Madeiras clade' (Fig. 3). A 'Porto Santo clade' including the Porto Santo haplotypes but none from the island of Madeira was always formed *within* the Madeiras clade. Some other haplotypes described previously in northern and western Europe also appeared in the Madeiras clade. These were very largely from northern Europe. The similarity of haplotypes from the Madeiras and northern Europe was even more striking than this; four of the Madeiran haplotypes (MADE.1, MADE.2, MADE.10 and MADE.14) were exactly the same as haplotypes described previously in northern Germany and/or Scandinavia, and another (MADE.15) has been described from central Germany (Fig. 3).

One of the north European haplotypes (haplotype 41 of Prager *et al*. 1993) was located within the Porto Santo clade in neighbour-joining trees (Fig. 3) despite the fact that the north European haplotype does not share the transversion at 15540. In the maximum parsimony and maximum likelihood trees, the Porto Santo haplotypes form an exclusive monophyletic clade, which we believe to be a more plausible result biologically.

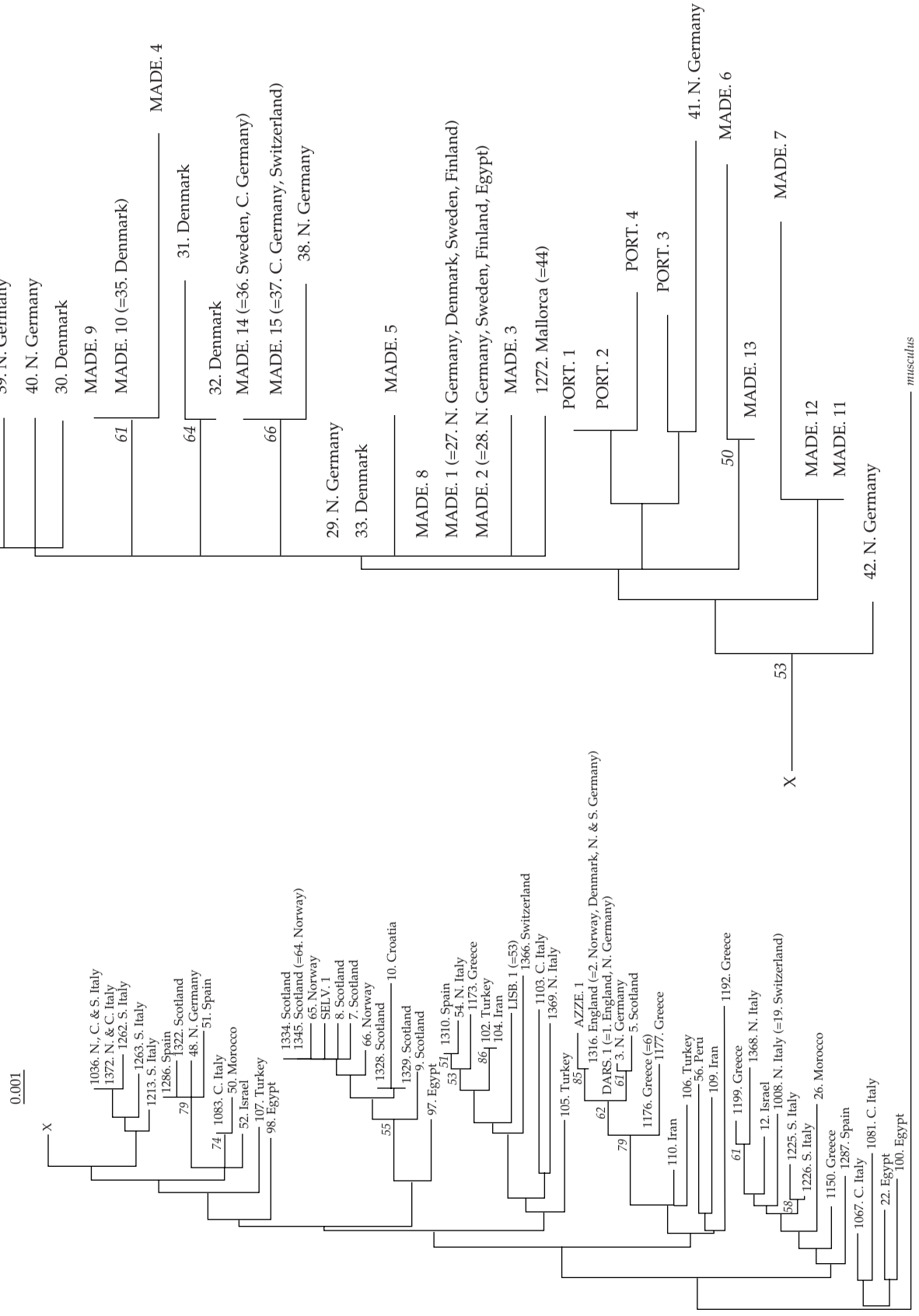
In all the trees that we generated, the single haplotype that we obtained from mice of Selvagem Grande occurs within a clade that is also predominantly north European; in this case haplotypes from Scotland and Norway.

## Discussion

In our phylogenetic analysis of D-loop sequences of *Mus musculus domesticus*, we found that all the haplotypes from the Madeiras occur in a single clade (Fig. 3), indicating either colonization of the islands by mice with a single haplotype followed by limited *in situ* diversification, or colonization by mice carrying a few closely related haplotypes. The nucleotide diversity estimates also show that mice from the Madeiras are very similar to each other in terms of mtDNA sequence. Compared with the substantial variation in D-loop sequences when *M. m. domesticus* is considered as a whole (Prager *et al*. 1993; Nachman *et al*. 1994), this occurrence of closely related D-loop haplotypes in the Madeiras suggests colonization from a single source, maybe on a single occasion. This is an extraordinarily simple pattern given that the islands have been visited innumerable times over the last 600 or more years by boats that, it may be presumed, would often have been infested with house mice. It may be, therefore, that the first mice to arrive on the archipelago and their descendants spread around the islands and were not displaced by later arrivals. Ecological studies have shown that it may be difficult for immigrant individuals to penetrate a well-established population of house mice (Lidicker 1976).

Given that the D-loop of mammals is known to be very variable (Parsons *et al*. 1997), it is not inconceivable that the variation observed among house mice on the Madeiran archipelago arose *in situ*. All the haplotypes that we found were four mutations or fewer removed from the consensus sequence for the islands that may represent the sequence of the original colonists. However, this scenario does not fit comfortably with our comparisons of complete *M. m. domesticus*-type D-loop sequences in the literature. Four of the nineteen 1013 bp haplotypes found in the Madeiras are identical to those found in northern Europe (Fig. 3). If the mtDNA variation in house mice on the archipelago is due to *in situ* diversification, there is extraordinary

**Fig. 3** (opposite) Neighbour-joining tree of all complete D-loop sequences obtained in the present study (see Fig. 2) together with selected sequences from the literature; 1–110 and 1008–1372 refer to haplotypes numbered and described by Prager *et al*. (1993, 1996, 1998) and Nachman *et al*. (1994), respectively. The known area of occurrence of each haplotype is indicated. The *Mus musculus musculus* sequence of Nachman *et al*. (1994) was used as the outgroup. This tree was constructed under the assumption of the Kimura 2-parameter model with a transition/transversion weighting of 1:4.56 (this weighting is in reverse of the relative abundance of these substitution types in the dataset used, so that the rarer substitutions were weighted more heavily in the analysis: see Nachman *et al*. 1994). All bootstrap values of 50% or more are indicated over the branches (based on a 1000 pseudoreplicates generated with PHYLIP). The 'Madeiras clade' including all haplotypes from the Madeiran archipelago is shown enlarged (it joins the main tree at position 'X'). This clade and all others with bootstrap support of 50% or more were present in all the other phylogenetic trees that we generated: Kimura 2-parameter neighbour-joining trees with alternative transition/transversion weightings (1:1, 1:2, 1:8), neighbour-joining trees with distances calculated according to a maximum likelihood model (transition/transversion weightings of 1:1, 1:2, 1:4.56 and 1:8), maximum parsimony trees (1:1, 1:2, 1:5 and 1:10) and a maximum likelihood tree (1:4.56).


0.001
X
1036. N, C. & S. Italy
1372. N. & C. Italy
1262. S. Italy
1263. S. Italy
1213. S. Italy
1286. Spain
1322. Scotland
48. N. Germany
51. Spain
79
74
1083. C. Italy
50. Morocco
52. Israel
107. Turkey
98. Egypt
1334. Scotland
1345. Scotland (=64. Norway)
65. Norway
SELV. 1
8. Scotland
7. Scotland
66. Norway
1328. Scotland
10. Croatia
55
1329. Scotland
9. Scotland
97. Egypt
51
53
1310. Spain
54. N. Italy
1173. Greece
86
102. Turkey
104. Iran
LISB. 1 (=53)
1366. Switzerland
1103. C. Italy
1369. N. Italy
105. Turkey
85
AZZE. 1
1316. England (=2. Norway, Denmark, N. & S. Germany)
62
DARS. 1 (=1. England, N. Germany)
61
3. N. Germany
5. Scotland
79
1176. Greece (=6)
1177. Greece
110. Iran
106. Turkey
56. Peru
109. Iran
1192. Greece
61
1199. Greece
1368. N. Italy
12. Israel
1008. N. Italy (=19. Switzerland)
58
1225. S. Italy
1226. S. Italy
26. Morocco
1150. Greece
1287. Spain
1067. C. Italy
1081. C. Italy
22. Egypt
100. Egypt
X
53
42. N. Germany
MADE. 12
MADE. 11
MADE. 7
MADE. 13
50
MADE. 6
41. N. Germany
PORT. 3
PORT. 4
PORT. 2
PORT. 1
1272. Mallorca (=44)
MADE. 3
MADE. 2 (=28. N. Germany, Sweden, Finland, Egypt)
MADE. 1 (=27. N. Germany, Denmark, Sweden, Finland)
MADE. 8
MADE. 5
33. Denmark
29. N. Germany
66
MADE. 15 (=37. C. Germany, Switzerland)
38. N. Germany
64
MADE. 14 (=36. Sweden, C. Germany)
32. Denmark
61
MADE. 10 (=35. Denmark)
31. Denmark
MADE. 4
MADE. 9
30. Denmark
40. N. Germany
39. N. Germany
34. Sweden
1311. Spain
0.001
musculus

convergence of mutations found in the Madeiras with those detected in mice in a single possible source area. It is more reasonable therefore, that the colonization of the Madeiras involved several closely related haplotypes from that source area, although this does not preclude at least some *in situ* evolution (see below).

The molecular similarity of mice from the Madeiras with those from northern Europe is striking. The first and second most widespread and frequent haplotypes in Scandinavia (haplotypes 27 and 28 of Prager *et al*. 1993) are exactly the same as the first and second most widespread and frequent haplotypes of the Madeiran archipelago (MADE.1 and MADE.2: Fig. 1). All the trees that we generated included a 'Madeiras clade' that contained haplotypes known only from the Madeiran archipelago, haplotypes that are known only from northern Europe and haplotypes that are found in both Madeira and northern Europe. Precisely these north European haplotypes formed a clade in the maximum parsimony tree of Prager *et al*. (1998). That 'north European clade' also included the Spanish haplotype (1311) and Mallorcan haplotype (1272) that are found in our Madeiras clade together with one extra haplotype (from central Italy) which we did not include in our analysis.

The colonization history of commensal animals is inextricably tied to the history of colonization, trading and other long-distance movement by humans. Traditionally, human history is used to infer the colonization history of the commensals. However, phylogeographic studies on the commensals can allow the reverse: molecular data may provide a rather precise scenario on source areas for the colonization of the animals which may give clues to human history. The house mice on the Madeiras may be such an example of a proxy for humans, providing new information on human movements.

The official human history of the Madeiran archipelago has been linked strongly to Portugal ever since a storm accidentally blew a Portuguese vessel to the islands in 1419, leading to subsequent settlement and Portuguese jurisdiction until the present day. So, the similarity of house mouse haplotypes in the Madeiras with those in northern Europe is unexpected and suggests that the earliest mouse colonists and, by proxy, the earliest human arrivals, may have been from northern Europe, rather than Portugal, despite the lack of historic documentation. The Vikings are obvious candidates for these earliest human arrivals. The Danish Viking kingdom in the 9th century occupied much of present-day Denmark, southern Sweden and northern Germany (Haywood 1999), where many of the haplotypes that are the same as or similar to those in the Madeiras have been found. At this time, the Danish Vikings made raiding expeditions along the coast of Iberia into the western Mediterranean (Logan 1991) and one or more boats could have been blown off course to the Madeiras, introducing northern European mice onto the islands. The occurrence of subfossil mice which appear to predate the official discovery of Madeira in 1419 (Pieper 1981; Mathias & Mira 1992) is consistent with this possible 9th century mouse colonization.

Further molecular data on house mice are needed to add weight to this hypothesis of colonization of Madeira by Vikings. In particular, more sequences are needed from Portugal to rule out more convincingly that country as a source area.

Although we suggest that several related D-loop haplotypes came in with the colonizing mice, this certainly does not preclude a degree of *in situ* evolution in the Madeiras. The nucleotide substitution (at position 15540) which differentiates Porto Santo mice from those elsewhere on the archipelago has not previously been recorded in house mice (to our knowledge), and may therefore have arisen in the islands. If so, this trait presumably became fixed or at high frequency on Porto Santo by a stochastic process (the founder effect or genetic drift). It is striking that Porto Santo should be so distinctive in terms of D-loop haplotype, given frequent human transport between Porto Santo and Madeira, which might have been expected to involve substantial inadvertent transport of mice too. Clearly, any cross-colonization between Madeira and Porto Santo has not been sufficient to homogenize mtDNA haplotypes. Once again, it suggests that mtDNA characteristics of established mouse populations in the Madeiras maybe rather resistant to change, despite frequent new arrivals of mice on the islands.

Our study not only provides information on the colonization of the Madeiras; we also analysed house mice from another Portuguese island, Selvagem Grande, which lies between the Madeiras and the Spanish-owned Canary Islands (although much closer to the latter). Clearly, on the basis of the mtDNA haplotype found there, colonization of Selvagem Grande was a separate event from the colonization of the Madeiras. Our data suggest that Scotland or Norway was a possible source of the mice on Selvagem Grande (see Fig. 3), although further studies would be worthwhile to confirm this.

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## References


Anderson S, Bankier AT, Barrell BG *et al.* (1981) Sequence and organisation of the human mitochondrial genome. *Nature, London*, **290**, 457–465.

Auffray J-C, Vanlerberghe F, Britton-Davidian J (1990) The house mouse progression in Eurasia: a palaeontological and archaeozoological approach. *Biological Journal of the Linnean Society*, **41**, 13–25.

Baker AEM (1994) Stowaway transport rates of house mice (*Mus domesticus*) and deermice (*Peromyscus maniculatus*). In: *Proceedings of the 16th Vertebrate Pest Conference* (eds Halverson WS, Crabb AC), pp. 106–112. University of California, Davis.

Bibb MJ, Van Etten RA, Wright CT, Walberg MW, Clayton DA (1981) Sequence and gene organization of mouse mitochondrial DNA. *Cell*, **26**, 167–180.

Böhle U-R, Hilger HH, Martin WF (1996) Island colonization and evolution of the insular woody habit in *Echium* L. (Boraginaceae). *Proceedings of the National Academy of Sciences of the USA*, **93**, 11740–11745.

Boursot P, Din W, Anand R *et al.* (1996) Origin and radiation of the house mouse: mitochondrial DNA phylogeny. *Journal of Evolutionary Biology*, **9**, 391–415.

Darwin C (1859) *On the Origin of Species by Means of Natural Selection*. John Murray, London.

Felsenstein J (1991) PHYLIP *(Phylogenetic Inference Package), Version 3.4*. University of Washington, Seattle.

Goodfriend GA, Cameron RAD, Cook LM (1994) Fossil evidence of recent human impact on the land snail fauna of Madeira. *Journal of Biogeography*, **21**, 309–320.

Gündüz İ, Tez C, Malikov V *et al.* (2000) Mitochondrial DNA and chromosomal studies of wild mice (*Mus*) from Turkey and Iran. *Heredity*, **84**, 458–467.

Haywood J (1999) *The Vikings*. Sutton Publishing, Stroud, UK.

Hillis DM, Huelsenbeck JP (1992) Signal, noise, and reliability in molecular phylogenetic analysis. *Journal of Heredity*, **83**, 189–195.

Juan C, Emerson BC, Oromi P, Hewitt GM (2000) Colonization and diversification: towards a phylogeographic synthesis for the Canary Islands. *Trends in Ecology and Evolution*, **15**, 104–109.

Khadem M, Rozas J, Segarra C, Brehm A, Aguadé M (1998) Tracing the colonization of Madeira and the Canary Islands by *Drosophila subobscura* through the study of the *rp49* gene region. *Journal of Evolutionary Biology*, **11**, 439–452.

Kocher TD, Thomas WK, Meyer A *et al.* (1989) Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. *Proceedings of the National Academy of Sciences of the USA*, **86**, 6196–6200.

Lidicker WZ Jr (1976) Social behaviour and density regulation in house mice living in large enclosures. *Journal of Animal Ecology*, **45**, 677–697.

Logan FD (1991) *The Vikings in History*, 2nd edn. Routledge, London.

Marshall HD, Baker AJ (1999) Colonization history of Atlantic island common chaffinches (*Fringilla coelebs*) revealed by mitochondrial DNA. *Molecular Phylogenetics and Evolution*, **11**, 201–212.

Mathias ML (1993) Historical and recent data on the mammals of the Madeira Islands. *Courier Forschsinstitut Senckenberg*, **159**, 445–450.

Mathias ML, Mira A (1992) On the origin and colonization of house mice in the Madeira islands. *Biological Journal of the Linnean Society*, **46**, 13–24.

Nachman MW, Boyer SN, Searle JB, Aquadro CF (1994) Mitochondrial DNA variation and the evolution of Robertsonian chromosomal races of house mice, *Mus domesticus*. *Genetics*, **136**, 1105–1120.

Nei M (1987) *Molecular Evolutionary Genetics*. Colombia University Press, New York.

Parsons TJ, Muniec DS, Sullivan K *et al.* (1997) A high observed substitution rate in the human mitochondrial DNA control region. *Nature Genetics*, **15**, 363–368.

Pieper H (1981) Ein subfossiles Vorkommen der Hausmaus (*Mus musculus* s.l.) auf Madeira. *Bocagiana*, **59**, 1–3.

Prager EM, Orrego C, Sage RD (1998) Genetic variation and phylogeography of central Asian and other house mice, including a major new mitochondrial lineage in Yemen. *Genetics*, **150**, 835–861.

Prager EM, Sage RD, Gyllensten U *et al.* (1993) Mitochondrial DNA sequence diversity and the colonization of Scandinavia by house mice from East Holstein. *Biological Journal of the Linnean Society*, **50**, 85–122.

Prager EM, Tichy H, Sage RD (1996) Mitochondrial DNA sequence variation in the eastern house mouse, *Mus musculus*: comparison with other house mice and report of a 75-bp repeat. *Genetics*, **143**, 427–446.

Sage RD (1981) Wild mice. In: *The Mouse in Biomedical Research* (eds Foster HL, Small JD, Fox JG), pp. 39–90. Academic Press, New York.

Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, **4**, 406–425.

Sambrook J, Fritsch EF, Maniatis T (1989) *Molecular Cloning: A Laboratory Manual*, 2nd edn. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

Schneider S, Kueffer J-M, Roessli D, Excoffier L (1997) ARLEQUIN, *Version 1.1: A Software for Population Genetic Data Analysis*. University of Geneva, Switzerland.

Swofford DL (1998) PAUP*: *Phylogenetic Analysis Using Parsimony and Other Methods*. Sinauer, Sunderland, MA.

Thorpe RS, McGregor DP, Cumming AM, Jordan WC (1994) DNA evolution and colonization sequence of island lizards in relation to geological history: mtDNA RFLP, cytochrome *b*, cytochrome oxidase, 12s rRNA sequence and nuclear RAPD analysis. *Evolution*, **48**, 230–240.

Widmer A, Schmid-Hempel P, Estoup A, Scholl A (1998) Population genetic structure and colonization history of *Bombus terrestris* s.l. (Hymenoptera: Apidae) from the Canary Islands and Madeira. *Heredity*, **81**, 563–572.

Wollaston TV (1854) *Insecta Maderensia*. van Voorst, London.

Wollaston TV (1878) *Testacea Atlantica or the Land and Freshwater Shells of the Azores, Madeira, Salvages, Canaries, Cape Verdes and Saint Helena*. Reeve, London.


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İslam Gündüz has recently completed a DPhil in Jeremy Searle's laboratory. They are continuing to collaborate in studies of colonization history and chromosomal evolution of house mice. This work was part of multidisciplinary study of the house mice in the Madeiras involving research teams in Montpellier and Lisbon.

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