

Revisiting Museum Archives to Revise Faunal Biogeography

The Paleogenomic History of Common Voles in the British Isles



Kaaviya Balakrishnan, Mateusz Baca

Laboratory of Paleogenetics and Conservation Genetics, Center for New Technologies, University of Warsaw



BACKGROUND & METHODOLOGY

The common vole (*Microtus arvalis*) is a well-studied Eurasian small mammal, yet its population history in Britain remains poorly understood. Today, the species survives only in the Orkney archipelago. The prevailing hypothesis proposes an accidental introduction by Neolithic farmers from coastal France or Belgium to Orkney, although direct archaeological evidence for this scenario is lacking. Early twentieth-century excavations recovered *Microtus* remains from several British archaeological sites (1), but ambiguous morphology and the assumption that the species was absent from mainland Britain meant these specimens received little further study. Using ancient DNA from archival material excavated between the 1910s and recent decades, we identify *M. arvalis* within faunal assemblages from mainland Britain. Material curated across eight institutions, representing nineteen archaeological sites across the British Isles and spanning the Late Pleistocene to Early Holocene, provides new data for reconstructing the species' historical distribution.

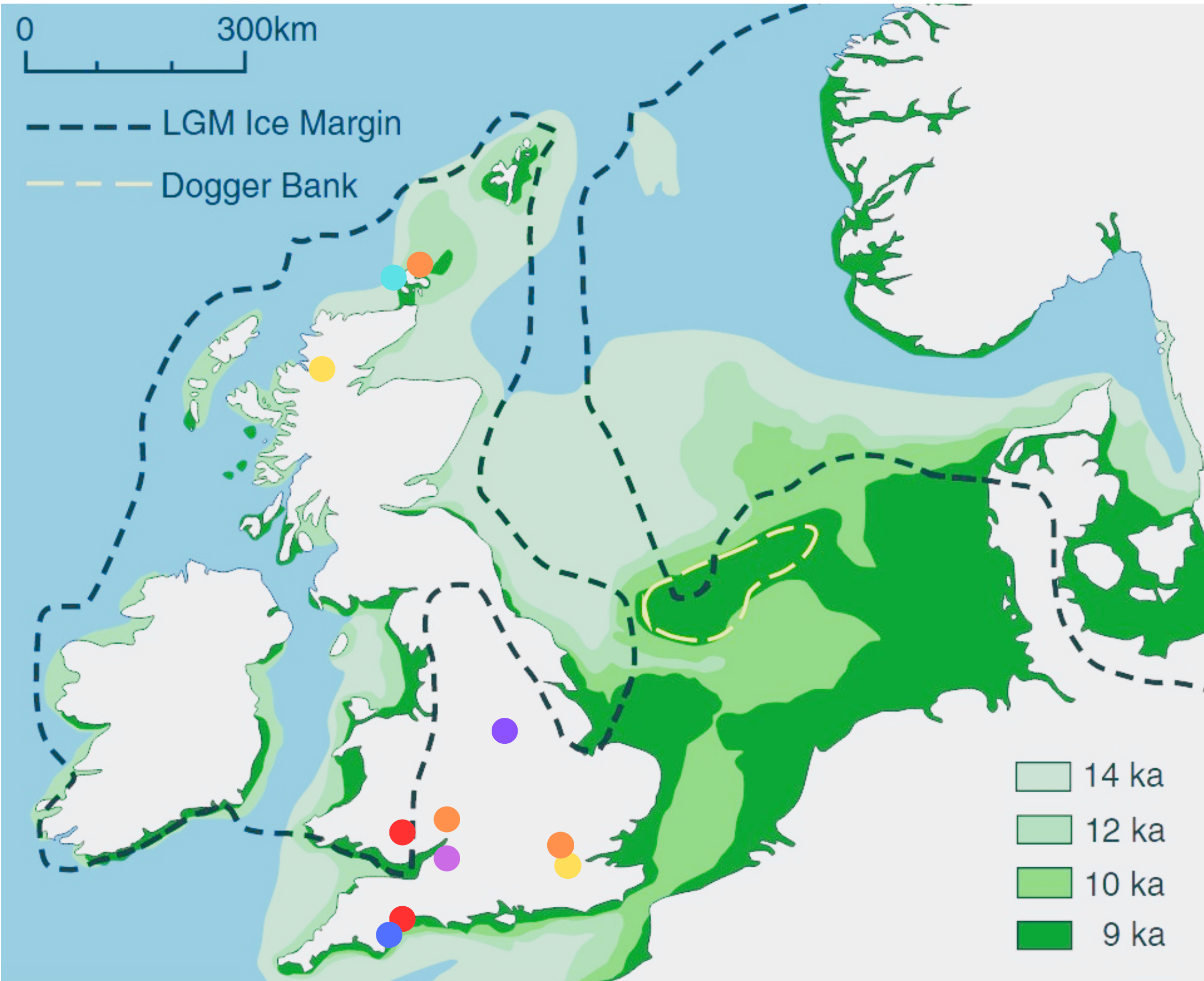


Fig 1. Archeological sites where *Microtus arvalis* specimens were identified using ancient mitochondrial DNA. Basemap demonstrating the extent of land exposed at successive stages during the progressive rise of sea level after the Last Glacial Maximum (LGM) from The Archaeology of Europe's Drowned Landscapes (Bailey et al., 2020).

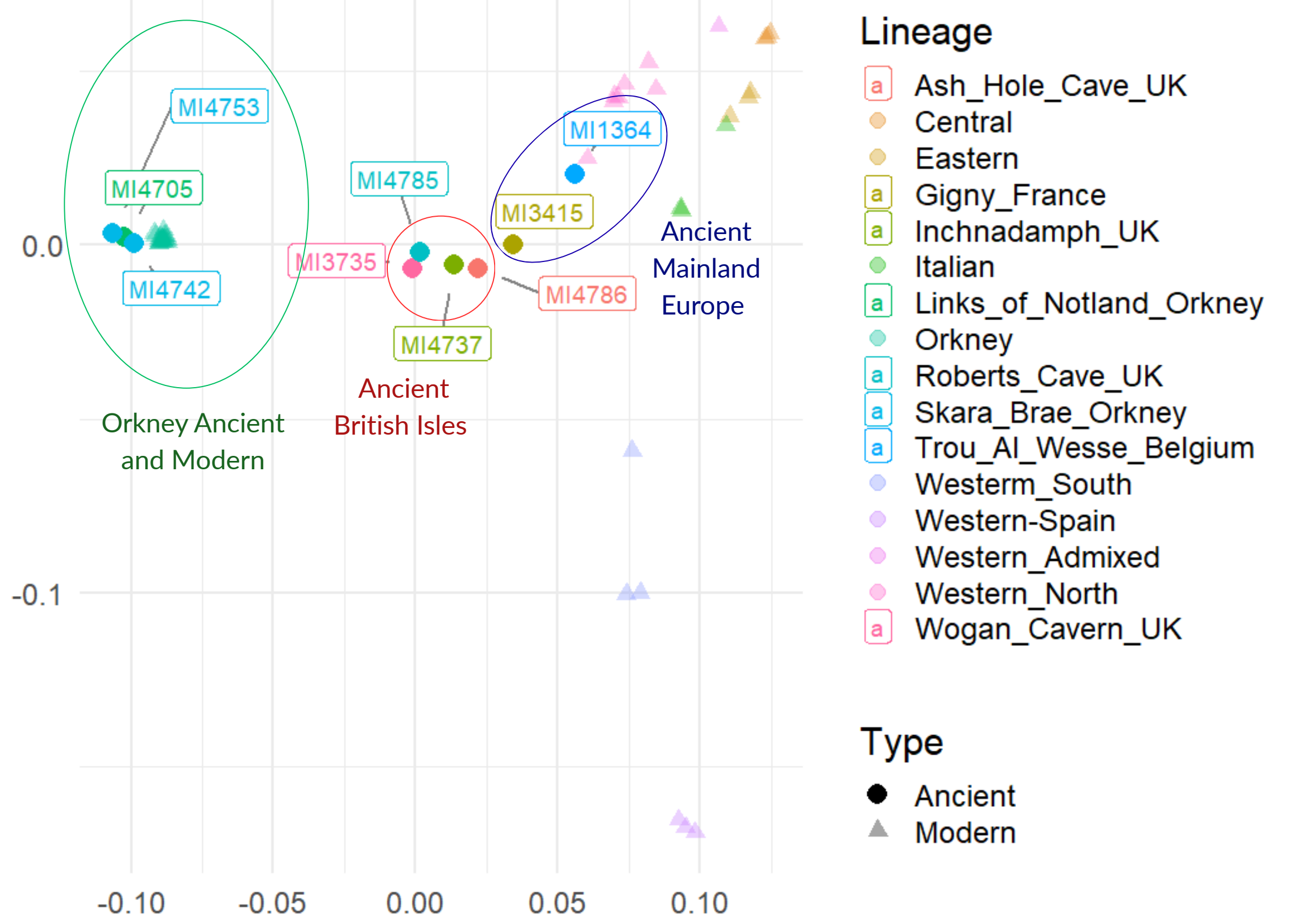


Fig 3. Multidimensional scaling (MDS) plot based on identity-by-state estimates calculated using ANGSD, including both ancient and modern samples from continental Europe and the British Isles.

ACKNOWLEDGEMENT

Samples were sourced from museum collections, archival material, and archaeological assemblages across the British Isles. We thank the archaeologists, curators, and collections staff of participating institutions for access to specimens. All laboratory work was conducted in the ancient DNA clean laboratory at the Laboratory of Paleogenetics and Conservation Genetics, University of Warsaw. This research is funded by the National Science Centre, Poland (Project Number 2020/38/E/NZ8/00431).

REFERENCES

1. Prince (2001) 2. Rohland (2018) 3. Gansauge (2020) 4. Baca (2020) 5. Wang (2023)

Ancient DNA was extracted (2) from 22 specimens, using the lower first mandible. Single-stranded libraries (3) were prepared and sequenced using shotgun sequencing on the Illumina platform. Taxonomic identification was confirmed using mitochondrial DNA, and Bayesian phylogenetic analysis was performed using BEAST2 v2.7.8 on a 4,286 bp mitochondrial dataset, combined with previously published sequences (4, 5). To explore nuclear genomic relationships, low-coverage nuclear genomes were analysed using multidimensional scaling based on identity-by-state estimates calculated with ANGSD.

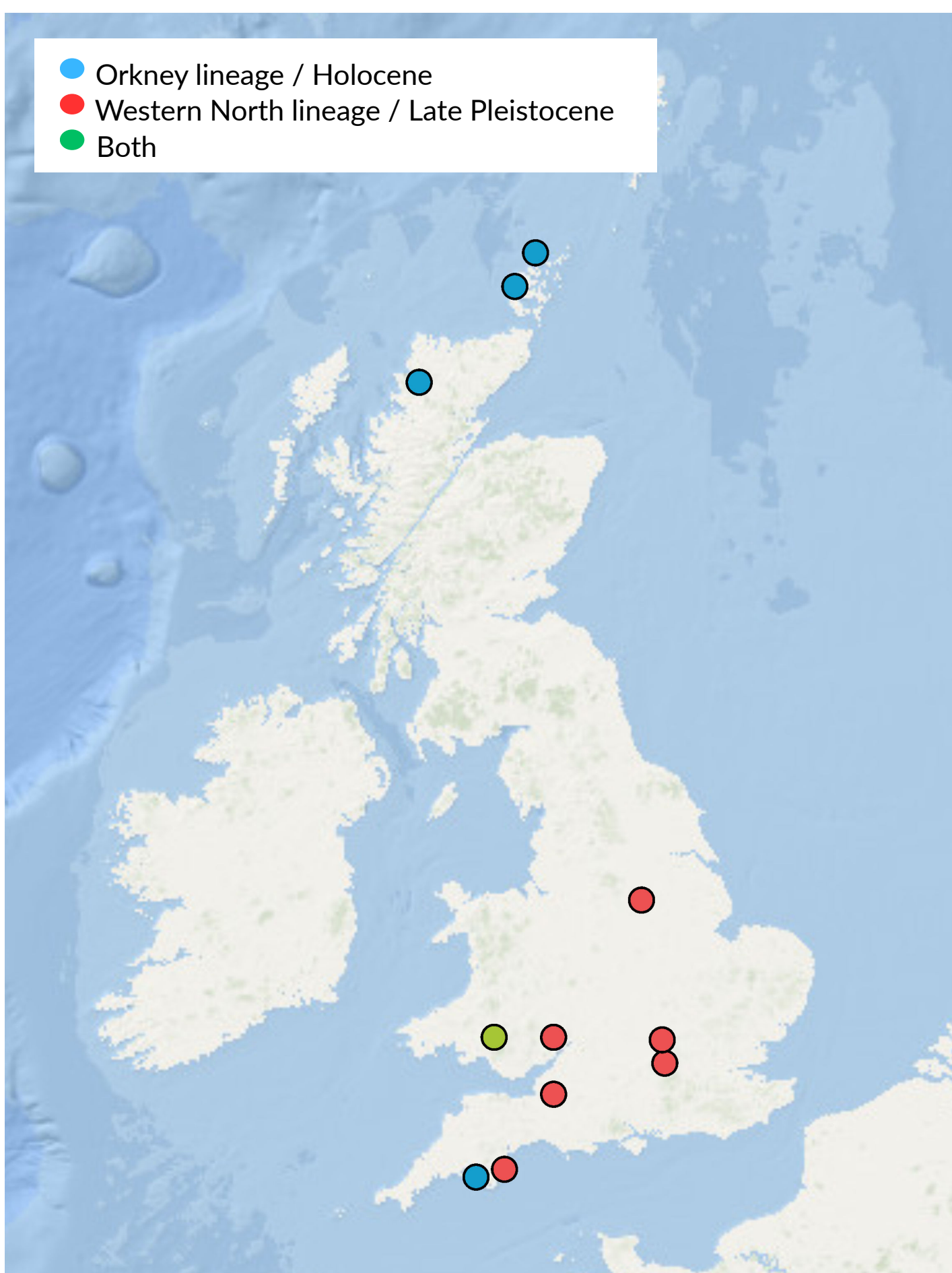
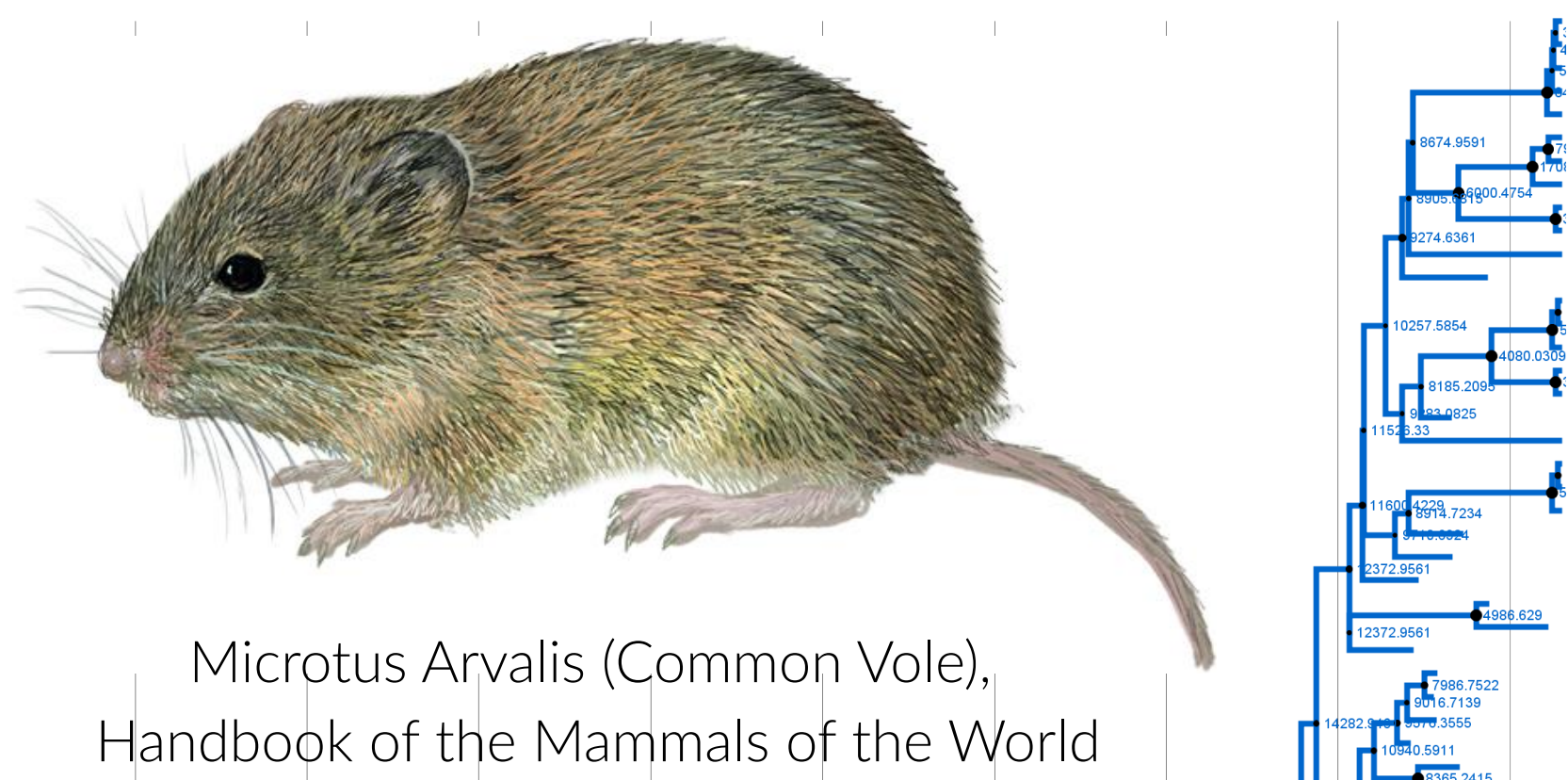


Fig 2. Site markers indicate the mitochondrial lineage detected at each locality and the estimated age of the samples.

CONCLUSION

Ancient DNA confirms the presence of *M. arvalis* in mainland Britain during the Late Pleistocene and Early Holocene, prior to Neolithic settlement. The species had a broad geographic distribution, with evidence from southern England, Wales, and northern Scotland. Divergence estimates using BEAST2 place the split between the Orkney subspecies (*M. a. orcadensis*) from the Western North lineage at ~16–17 ka BP. Phylogenetic affinities between ancient southern British specimens and modern Orkney voles suggest a natural colonisation route before the post-glacial submergence of Doggerland. These results challenge the hypothesis of a Neolithic human introduction and instead indicate that *M. arvalis* was a native species in Britain that later became locally extirpated.



Microtus Arvalis (Common Vole), Handbook of the Mammals of the World

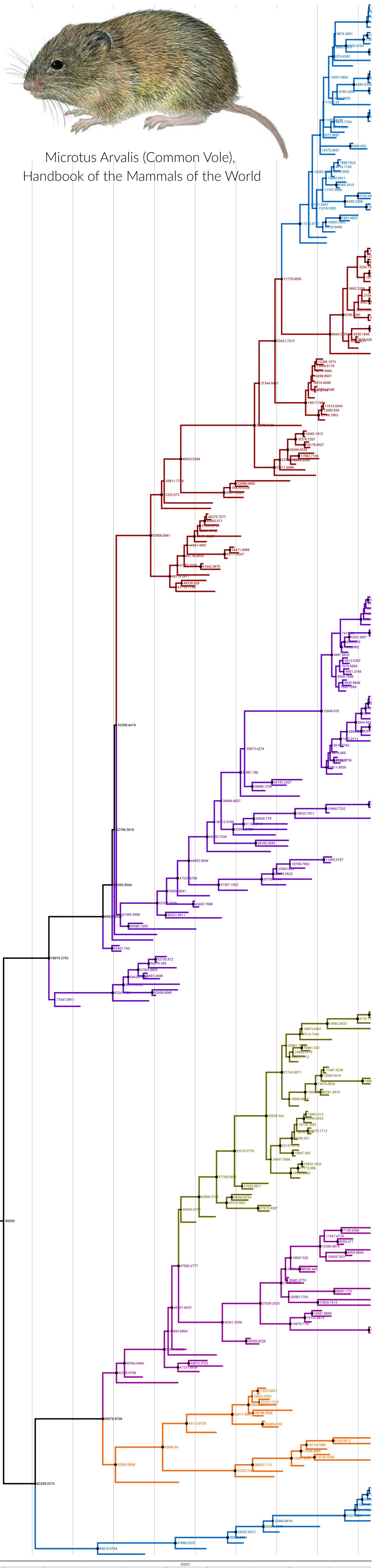


Fig 4. Bayesian phylogenetic tree of 4,286 bp mitochondrial sequences from 281 samples across mainland Europe and the British Isles (195 ancient, 86 modern). The maximum clade credibility (MCC) tree was inferred using BEAST2 v2.7.8 with tip dating (years before present), an estimated GTR+G+I substitution model, a strict molecular clock, and Coalescent Bayesian Skygrid prior.

