

CORRECTION

Correction: The Draft Genome of Extinct European Aurochs and its Implications for De-Extinction

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This article details a correction to the article: Sinding, M-H S and Gilbert, M T P 2016 The Draft Genome of Extinct European Aurochs and its Implications for De-Extinction. *Open Quaternary*, 2(7). DOI: <http://doi.org/10.5334/oq.25>

Keywords: De-extinction; back breeding; ancient genomics; aurochs-cattle hybridization

Correction

After publication of Sinding and Gilbert (2016), the publisher was made aware that **Figure 1** was incorrectly labelled. Investigation revealed that during the pre-publication proofing process the corrected figure file had not been replaced, as requested, and thus the incorrect image

was published. The corrected **Figure 1** is below, with the ‘P’ label removed from the eastern European section of the map and placed correctly. No further correction is required.

The publisher accepts that this was a production error and that the author provided the correct information prior to publication.

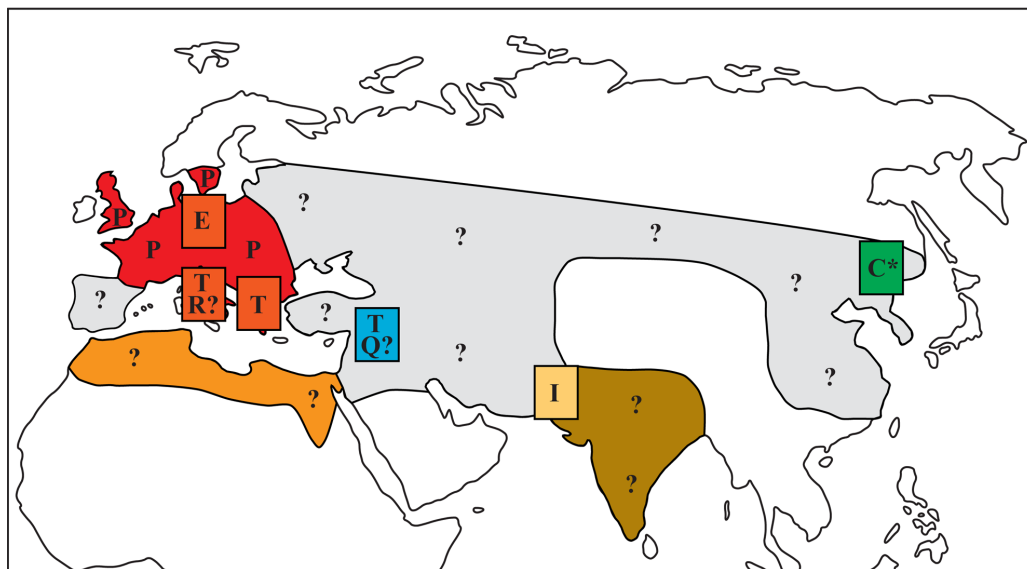


Figure 1: Map of the original wild aurochs populations. Letters refer to mitochondrial haplogroups confirmed by ancient DNA, squares refer to unique variation observed at specific location, and haplogroups followed by ‘?’ refer to haplogroups where the locality of origin is not based on sequencing of aurochs remains, but representation in either modern or ancient domestic cattle. Areas shaded in grey, labelled with ‘?’ designate unknown population affiliation and unknown original mitochondrial lineages. The “C*” implicates C is not found in any genome sequenced cattle or aurochs.

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Competing Interests

The authors have no competing interests to declare.

References

Sinding, M-H S and **Gilbert, M T P** 2016 The Draft Genome of Extinct European Aurochs and its Implications for De-Extinction. *Open Quaternary*, 2(7). DOI: <https://doi.org/10.5334/oq.25>

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