

CORRECTION

Correction: Genetic diversity, genetic structure and diet of ancient and contemporary red deer (*Cervus elaphus* L.) from north-eastern France

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Fig 2 is incorrect. Please see the corrected Fig 2 here.



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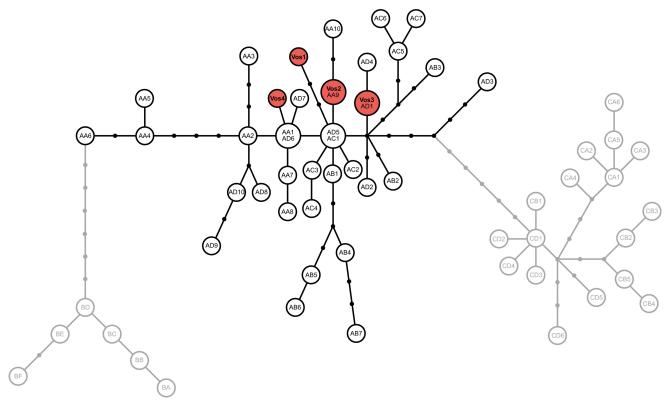


Fig 2. Haplotype genealogy based on maximum likelihood. Mitochondrial haplotype genealogy based on the mitochondrial control region and a maximum likelihood phylogenetic analysis. The haplotypes detected in red deer from the Vosges are indicated in red, all other haplotypes were taken from [3]. Haplotypes belonging to haplotype lineage A are indicated in black, those of haplotype lineages B, C are depicted in grey. Note that some of the haplotypes initially identified by Skog et al. 2009 have collapsed into a single haplotype in our analyses, which is due to the use of a shorter sequences alignment in our analysis to match the length of the newly obtained sequences.

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Reference

Schnitzler A, Granado J, Putelat O, Arbogast R-M, Drucker D, Eberhard A, et al. (2018) Genetic diversity, genetic structure and diet of ancient and contemporary red deer (*Cervus elaphus* L.) from northeastern France. PLoS ONE 13(1): e0189278. https://doi.org/10.1371/journal.pone.0189278 PMID: 29304165