

## Erratum to: Mitochondrial D-loop phylogeny signals two native Iberian red deer (*Cervus elaphus*) Lineages genetically different to Western and Eastern European red deer and infers human-mediated translocations

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**Erratum to: Biodivers Conserv**  
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This is a correction by two of the four authors of Fernández-García et al. (2014), which appears earlier in this issue. Fernández-García, the first and corresponding author, unfortunately submitted a version of the manuscript still being worked on without our knowledge and agreement. We were not informed as to the content of the manuscript submitted nor on the journal selected. The fourth author on the paper (Randi) was aware of the submission, but not that we had not had the opportunity to participate in the process. This was done despite one of us (JC) being leader of the research line and the main researcher on the projects cited in the acknowledgments section of the paper. In addition to this unacceptable behaviour, we wish to record our disagreement with some aspects of the interpretations of the results. This has practical implications for the management and conservation of red deer in the Iberian Peninsula, and need to be taken note of to avoid unfortunate decisions being made and implemented.

The main conclusion of the paper is that red deer in Iberia comprise two genetically differentiated lineages, evidenced by the two main branches for the Spanish samples in the median-joining (MJ) network (Fig. 3; all figures and tables cited refer to the original paper). We agree that there are two lineages, mostly on the basis of further research

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(Carranza et al. unpubl.). However, we do not consider that the results in the paper, or from our subsequent work, support the conclusion that the Iberian lineages are “South-Western” and “Central-Eastern”. The subdivision of haplogroups in “left and right branches” within the WERD phylogroup in Figure 3, can be attributed to the sampling locations being arbitrarily grouped into two these regions. As stated in Methods, the Spanish samples were firstly split into four geographic groups of populations, independent of genetic information: West (W), Sierra Morena (SSM), South (S) and Central-East (CE). The neighbour-joining (NJ) tree shows rather low bootstrap values, and only illustrates the structure of the three major red deer lineages already recognized in previous publications (EERD, CBRD, and WERD). The WERD node in Figure 1 is both poorly supported (bootstrap 41) and weakly structured, grouping sequences sampled in Spain and Northern Europe, with no statistical basis for the differentiation of the two cited Iberian branches. The genetic divergence of the assemblages (Tables 2 and 3) cannot support splitting Spanish sites into one group with W, SSM and S (South-West), and another one with CE (Central-East). The SSM and S sites have a higher divergence from W than the CE assemblages (see Tables 2 and 3). This suggests that the division of the WERD phylogroup in Figure 3 could have been more appropriately made at the connection between W and SSM (between WH39 and SSMH5), only differentiating the W matriline from the rest of the Spanish groups.

With respect to the final paragraph of the Discussion subsection “Two episodes of red deer mtDNA evolution in the context of WERD subspecies”, we do not consider that there is enough support from the NJ tree and the MJ network to infer the suggested evolutionary relationships among haplogroups. In particular, the interpretation of the origin of each north European subspecies from the four haplogroups found in WERD lineage requires more extensive and critical phylogenetic analyses.

There are other questionable remarks in the Discussion. Although Cabrera did describe two subspecies of red deer in Spain in 1914, the discovery of two mtDNA lineages cannot be presumed to correspond with Cabrera’s subspecies. Cabrera actually distinguished the red deer in the Doñana National Park from those in the rest of Iberian Peninsula. Similarly, the mention by Cabrera that he was informed that red deer from northern Europe might have been introduced into central Spain cannot on its own support a suggestion as to the origin of haplogroup SSMH4. The phylogenetic relationships between this haplogroup and those of other Iberian and west European red deer require new analyses.

The actual phylogenetic divergence between the two Iberian lineages, their precise composition of mitochondrial D-loop sequences and their current geographical location, merit further work based on more extensive sampling. But moreover, the phylogenetic relationships between lineages based not only on mtDNA but also on nuclear DNA are needed to inform conservation and wildlife management plans. The Iberian red deer is currently considered a separate subspecies (*Cervus elaphus hispanicus*), and therefore subject to measures aimed at preventing genetic introgression with other subspecies. For instance, the Spanish Trophy Body of the Ministry of the Environment, and the Spanish branch of the International Council for Game and Wildlife Conservation (CIC), agreed to reject as trophies deserving medals all those red deer specimens showing evidence of genetic admixture with non- Iberian genotypes. Likewise, according to Spanish legislation, regional governments include the prerequisite of genetic analyses before issuing permits for red deer introductions in hunting areas. The geographical range affected by these considerations includes Portugal, where similar genetic controls for trophies and introductions are being implemented. These conservation measures are important for the preservation of native red deer populations in Iberia, but need to be based on robust scientific knowledge. As suggested in the paper, the demonstration of the existence of two

well-differentiated lineages within Iberia would lead to recommendations aimed at preventing restocking between lineages. However, unless all restocking were stopped, even for preventive isolation between lineages, we need to rely on geographical limits. Our ongoing research is clarifying the situation, and reveals that it is only West haplogroup that strongly differs from the rest of the populations in Spain. Thus, our advice to managers and pertinent authorities, is not to use the precise geographic limits for lineages outlined in the Fernández-García et al. paper, but to implement management and conservation measures for red deer in Iberia after the additional research has come to publication.

There are also other minor modifications in the paper that should have been attended too:

(1) The current address of Carranza should have been corrected; (2) In acknowledgments add “We also thank our technician S. Martín Valle for laboratory work, and members of the Biology and Ethology Group at the University of Extremadura for their help. The Fundación Biodiversidad from the Spanish Ministry of the Environment and the Regional Government of Extremadura also contributed financial support to the early stages of the study”; and (3) We also regret some typographical errors not corrected in proof.

## Reference

Fernández-García JL, Carranza J, Martínez JG, Randi E (2014) Mitochondrial D-loop phylogeny signals two native Iberian red deer (*Cervus elaphus*) populations genetically different to western and eastern European red deer and infers human-mediated translocations. *Biodiv Conserv*. doi:[10.1007/s10531-013-0585-2](https://doi.org/10.1007/s10531-013-0585-2)