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Book of Abstracts



Mitogenomic phylogeography of the gray wolf (*Canis lupus*): ancient and contemporary data clarify the phyletic relationships across wolf populations and canine clades

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The increasing availability of genomic and paleogenomic data and tools has greatly improved our ability to reconstruct the evolutionary history of species, yet the phylogeography of the gray wolf (*Canis lupus*) and the origin of dog lineages remain only partially resolved. We assembled one of the most comprehensive mitogenomic datasets to date, comprising 950 wolf and dog mitochondrial genomes spanning the entire Holarctic region and a temporal range from ~67 kya to the present, including newly generated contemporary European and ancient Italian samples. Phylogenetic (ML and Bayesian) and tip-dated coalescent analyses were used to reconstruct evolutionary relationships, divergence times, and spatiotemporal dynamics of wolf and dog lineages. Our results confirm that most contemporary wolf mitochondrial diversity is structured into two major haplogroups (W1 and W2) and reveal a third paraphyletic assemblage (W3), composed mainly of ancient European and Beringian lineages. Temporal analyses indicate a marked turnover, with W3 dominating during

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the Pleistocene and being largely replaced by W1 and W2 around 20 kya. Contrary to previous hypotheses of a single Beringian expansion during the late Pleistocene–early Holocene, our findings support a scenario involving multiple refugia in Europe and Beringia, driving repeated dispersals and lineage replacements. Dog haplogroups show a complex origin, involving multiple maternal contributions from a structured and partially extinct wolf population. Dog haplogroup A falls outside both W1 and W2, suggesting a derivation from a more ancient wolf lineage. Overall, our results provide a refined reconstruction of the wolf matrilineal history, highlighting extensive loss of ancient diversity and supporting a complex, reticulate scenario for dog domestication involving a main ancestral source plus multiple additional matrilineal contributions.