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# Metagenomic analysis of a 35,000-year-old *Canis lupus coprolite* of the Chauvet-Pont d'Arc Palaeolithic cave

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## Résumé

To get insights into the genome and diet of ancient wolf in Europe, we performed high-throughput sequencing of DNA from coprolites collected in the Palaeolithic painted cave of Chauvet-Pont d'Arc (Ardèche, France). Shotgun sequencing of DNA from a well-preserved coprolite, radiocarbon dated to 35,600-33,600 year calBP, enabled reconstruction of the complete mitochondrial (mt) genome sequence of a Pleistocene wolf specimen. The genome sequence lies outside the diversity of the sequences that have been reported for extant dogs and Holarctic wolves. Phylogenetic analysis demonstrates that the mtDNA sequence corresponds to a hitherto unknown *Canis lupus* maternal lineage that diverged from the extant dog/Holarctic wolf lineage approximately 340,000 years ago. We found that this mitochondrial sequence is closely related to the mtDNA of other *Canis lupus* Pleistocene wolf specimens originating from Belgium that were recently described. However only the mitochondrial sequences of the Belgian wolf specimens were characterized whereas we will also discuss the conclusions that can be drawn from the study of the nuclear genomic data of the *Canis lupus* Chauvet-Pont d'Arc specimen (we obtained a 10x coverage for the nuclear genome). Analysing the coprolite for other species to indicate the diet of our specimen, we detected cave bear (*Ursus spelaeus*) DNA sequences. This finding points to the cave as a reservoir of food for carnivores when bear carcasses were abundant, some 35,000 years ago, and helps to explain wolf intrusion into the deep cave sectors. Thus, with the characterization of a vanished maternal lineage and wolf-cave bear interaction, this study provides new insights into the evolution of *Canidae* and the paleoecology of a reference archaeological site.

**Mots-Clés:** ancient DNA, *Canis lupus*, mitochondrial genome, phylogeny, Pleistocene, *Ursus spelaeus*.

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