

## HORSE MITOCHONDRIAL GENOMES: AT LEAST 17 MATRILINEAL LINEAGES UNDERWENT DOMESTICATION

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Archaeological and genetic evidences concerning the time and mode of wild horse (*Equus ferus*) domestication are still debated. High levels of genetic diversity in the horse mitochondrial DNA (mtDNA) have been detected when analyzing the control region, whose recurrent mutations, however, tend to blur the structure of the phylogenetic tree. To overcome the likely limitations of control-region data and to improve the resolution of the horse mtDNA phylogeny, we analyzed a total of 83 mitochondrial genomes (81 new and two from the literature) from modern horses (*Equus caballus*) across Asia, Europe, the Middle East and the Americas. Our data indicate a major founder event around 120,000 years ago and reveal 18 distinct haplogroups (A-R) whose radiation times are essentially confined to the Neolithic. All haplogroups were detected in Asia, but one (L) is most common and equally diverse in Europe, and another one (F) is only found in *Equus przewalskii*, the only remaining wild horse. Therefore, at least 17 matrilineal lineages from the extinct *Equus ferus* underwent domestication, probably in the Eurasian steppes but possibly even in Western Europe, and were transmitted to modern breeds. The identification of these haplogroups is a prerequisite for ancient DNA studies and for evaluating the role of mitochondrial DNA backgrounds in racecourse performance.