

## Publication

## Ancient mtDNA diversity reveals specific population development of wild horses in Switzerland after the Last Glacial Maximum

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On large geographical scales, changes in animal population distribution and abundance are driven by environmental change due to climatic and anthropogenic processes. However, so far, little is known about population dynamics on a regional scale. We have investigated 92 archaeological horse remains from nine sites mainly adjacent to the Swiss Jura Mountains dating from c. 41,000–5,000 years BP. The time frame includes major environmental turning points such as the Last Glacial Maximum (LGM), followed by steppe vegetation, afforestation and initial re-opening of the landscape by human agricultural activities. To investigate matrilinear population dynamics, we assembled 240 base pairs of the mitochondrial d-loop. FST values indicate large genetic differentiation of the horse populations that were present during and directly after the LGM. After the retreat of the ice, a highly diverse population expanded as demonstrated by significantly negative results for Tajima's D, Fu's FS and mismatch analyses. At the same time, a different development took place in Asia where populations declined after the LGM. This first comprehensive investigation of wild horse remains on a regional scale reveals a discontinuous colonisation of succeeding populations, a pattern that diverges from the larger Eurasian trend.

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