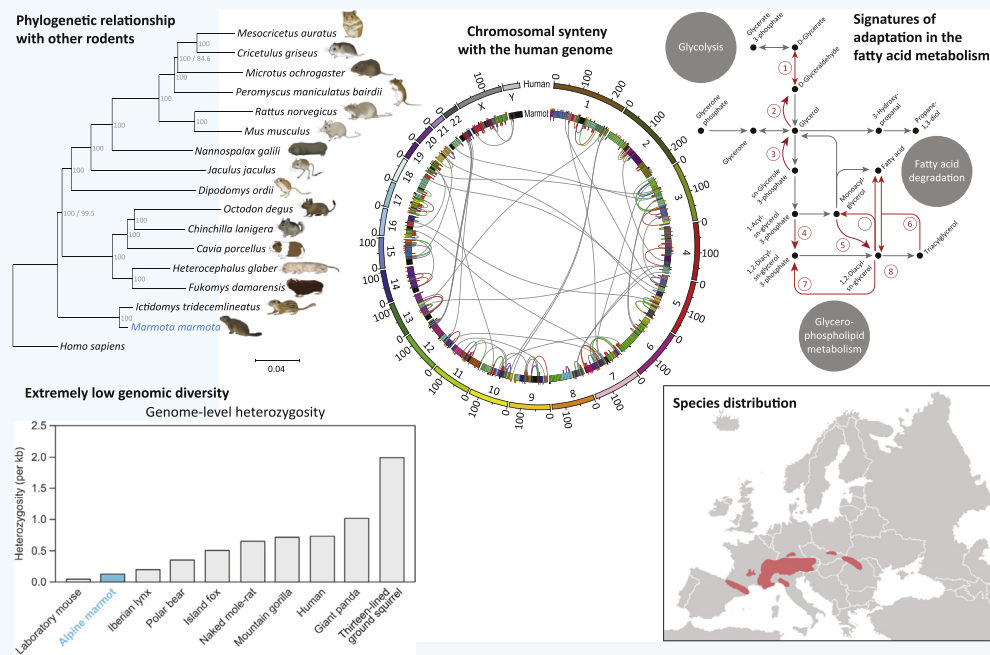


*Marmota marmota*Toni I. Gossmann¹ and Markus Ralser^{2,3,*}¹Department of Animal Behaviour, Bielefeld University, 33501 Bielefeld, Germany²Molecular Biology of Metabolism Laboratory, The Francis Crick Institute, London, NW1 1AT, UK³Department of Biochemistry, Charité, 10117, Berlin, Germany

The Alpine marmot (*Marmota marmota*) is a large squirrel that inhabits high-altitude meadows of the European Alps. The disappearance of the past ice age climate may have led them to colonize their current extreme habitat. As an ideal model to understand the impact of a changing climate and extreme lifestyle on genome evolution, it may also help us to determine whether the species is well equipped to cope with recent and ongoing human-induced climate change. Indeed, the genome of *M. marmota* reveals surprising and, in part, extreme features. As a consequence of its lifestyle, its genome shows strong signatures of slow evolution, pronounced by a high synteny with the outgroup (i.e. the human genome) and strong conservation at the molecular level. Genes involved in glycerolipid metabolism and in fat digestion and absorption show signatures of genomic adaptation. This illustrates the interplay of life history and genomic diversity, and why both factors need to be included in the determination of conservation status.

**TAXONOMY AND CLASSIFICATION:****KINGDOM:** Animalia**PHYLUM:** Chordata**CLASS:** Mammalia**ORDER:** Rodentia**FAMILY:** Sciuridae**GENUS:** *Marmota***GENOME FACTS:**

The assembly covers 2.5 Gb on 14 000 scaffolds (GenBank GCA_001458135.2) and shows higher synteny and conservation with the human genome compared to other rodents.

Features of an unusually large mitochondrial genome insertion (nuclear mitochondrial DNA segment, NUMT), which is likely to be nonfunctional, supports the notion of slow genomic evolution.

The genome comprises 21 080 inferred protein-coding genes and is predicted to contain 2384 noncoding genes (RefSeq GCF_001458135.1).

SPECIES FACTS:

The Alpine marmot (*Marmota marmota*) is a close relative of the American groundhog; during the cold period of the early Quaternary, it was widely distributed across the European Steppe.

It can persist in the harsh environment of the high altitude Alpine meadow due to its cold-adapted physiology and lifestyle, including large body size, an extensive period of winter hibernation, and a high degree of sociality, including a form of co-operative breeding, where adult subordinates warm juveniles during hibernation.

Recent surveys revealed that Alpine marmots have been affected by contemporary climate warming over the past 25 years. This direct sensitivity to the most recent changes in climate is not observed in other marmot species, consistent with the tight niche adaptation of this species.

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Fun facts about the Genome

Despite Alpine marmots having currently a very large population size, the genome is among the least genomically diverse across the animal kingdom. Its interindividual diversity is lower than that of highly endangered species, such as the Mountain gorilla (*Gorilla beringei beringei*), polar bear (*Ursus maritimus*), or Iberian lynx (*Lynx pardinus*), which suffer from declining population sizes, and count as extreme examples of low diversity. Two of the sequenced individuals from one population (Mauls, Italy) were so similar that they were not distinguishable from each other even by a single nonsynonymous (coding) SNP for most protein-coding genes. However, subsequent population genomic analyses revealed that this low genomic diversity does not necessarily mean that the Alpine marmot is at risk and, to our surprise, inbreeding could be ruled out as the main factor leading to such low diversity. Rather, it is the consequence of two consecutive climate-related events, long-term cold adaptation and a recent bottleneck, at the end of the past ice-age. These first reduced the genetic diversity while the cold-climate adapted lifestyle has prevented the marmot from recovering from it. Thus, in combination with an extreme lifestyle, changes in climate can 'trap' a highly abundant species in a state of extremely low genetic diversity.

Acknowledgements

The photograph of the Alpine marmot was kindly provided by Carole and Denis Favre-Bovin. Work in the Ralsler lab is funded by the Francis Crick Institute which receives its core funding from Cancer Research UK (FC001134), the UK Medical Research Council (FC001134), and the Wellcome Trust (FC001134).

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