

VarGoats international initiative, a 1000 goat genomes project

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Goats were domesticated ~10,000 years ago from their bezoar wild ancestor *Capra aegagrus*. These founder animals spread out from domestication centres in Europe, Asia, and Africa during the next few thousand years, which resulted in many populations becoming locally adapted to diverse environmental constraints such as heat, altitude, disease resistance, etc. After a very long period of soft selection for production traits, the situation changed dramatically with the emergence of the breed concept about 200 years ago. Selection pressure was strongly increased, and gene flow between populations (or newly formed breeds) was seriously reduced, leading to the fragmentation of the initial gene pool. Currently, there are more than 1000 goat breeds worldwide, 18% of which are either threatened or already extinct.

Through the generation of domestic breeds sequence data and their analysis together with existing data of domestic and wild animals, VarGoats collaborative project aims at becoming the first step of a 1000 goat genomes project. VarGoats Consortium is coordinated by the Institut National de la Recherche Agronomique INRA (France), and includes an international team of partners (Laboratoire d'Ecologie Alpine, France; Parco Tecnologico Padano, Italy; Agricultural Research Service, USDA, USA; International Goat Genome consortium; African Goat Improvement Network; Roslin Institute and the Centre for Tropical Livestock Genetics and Health, UK). At present, a dataset containing 829 goat genomes has been assembled, including 815 sequences from 84 local and transboundary domestic populations, and 14 genomes from 7 wild goat species. Bioinformatic infrastructures for data storage and sharing are collecting the generated sequence data and making it available to VarGoats participants. Starting from the ADAPTMAP project experience, thematic working groups are in charge of performing data analyses to (i) explore genetic diversity, (ii) study domestication, (iii) detect adaptation and selective

sweeps, and (iv) discover variants (SNPs, CNVs, structural variants, causal mutations) in various goat breeds, with the final goal to develop breeding solutions. Hybridisation between species is also under investigation, thanks to the availability of sequences from various *Capra* species. At the end of the project, data will be released in a public database.