

Conservation and sustainable utilization of camel genetic resources

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The Old-World camels consist of three species, the domesticated dromedary (*Camelus dromedarius*) and Bactrian camel (*Camelus bactrianus*), and the critically endangered wild two-humped camel (*Camelus ferus*). The domesticated species went through several demographic changes before, during and after domestication (Almathen et al. 2016, Ming et al. 2020), and although there are estimated 20 million (mio) dromedaries and 2 mio Bactrian camels their numbers are still declining (FAOstats 2020); maybe with the exception of the Australian population (Al-Jassim in this issue, Gee in this issue). The wild camels were severely reduced over the past decades and exist only in protected areas of the Mongolian Gobi and the Chinese Taklimakan and Lop Nor desert with an estimated population size of about 2000 (Yadamsuren et al. 2012, Lei et al. 2012). The current situation warrants the conservation and sustainable utilization of the existing genetic resources in camels.

Selection for specific economically important traits has led to severe inbreeding in many livestock species and to the replacement of locally adapted breeds by highly productive ones across the world. This loss of genetic diversity has been marked with increasing concern and a Global Plan of Action for Animal Genetic Resources was adopted (reviewed in Groeneveld et al. 2010). Building upon the insights gained in other livestock and on advanced genomic sequencing technologies, a sustainable development of genomic resources in camels requires comprehensive knowledge on the different camel populations, their size and structure, the production environment and genetic diversity.

The International Camel Consortium for Genomic Improvement and Conservation (ICC-GIC, www.icc-gic.weebly.com) provides a platform for collaboration, exchange of genomic and phenotypic data and the development of genomic tools with the aim of improving production traits in camels while maintaining their genetic diversity. The Greater Good Initiative of the Illumina sequencing company (<https://emea.illumina.com/company/news-center/feature-articles/greater-good-initiative-winner.html>) facilitated 400 camel genomes to be sequenced over a global distribution range to investigate genome-wide diversity in Old World camels, and to develop a camelid SNPchip including also existing genomic data (Ming et al. 2020, Fitak et al. submitted). In parallel, the development of systematic phenotype recording guidelines is in progress within the frame of the International Committee of Animal Recording (ICAR, www.icar.org). The consecutive understanding of functional important genomic regions, *i.a.*, related to (re)production traits, immune response and adaptation to different environments will lead our way to a sustainable utilization and conservation of the significant genomic resources of camels in times of global warming and increasing desertification.

References

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