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Editorial: Global green strategies and capacities to manage a sustainable animal biodiversity

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Editorial on the Research Topic
Global green strategies and capacities to manage a sustainable animal biodiversity

Livestock animals have been domesticated and raised by humans for thousands of years, providing food, fiber, and other resources (Bruford et al., 2003). Over time, farmers have selectively bred animals to improve their productive traits (Rauw et al., 1998). However, the artificial selection process has also contributed significantly to the loss of genetic diversity (Ajmone-Marsan et al., 2023). Therefore, the current Research Topic was planned and researchers around the globe were invited to explore strategies to sustainably manage animal biodiversity. This Research Topic collected a total of eight manuscripts, published by 60 authors, more than 3,331 downloads and 14 thousand views globally at the time of this editorial. Keeping in view the importance of genetic diversity for a long-term potential for survival in different livestock species, we received manuscripts regarding cattle, sheep, chickens, and camels.

Among cattle, dairy animals are particularly prone to environmental stressors because they have been exposed to intense artificial selection for milk production and composition traits, thus losing the genetic variability that could be useful for new breeding orientations in the context of climate change (Leroy, 2014; Doublet et al., 2019). Indeed, Cheruiyot et al. proposed to include in the commercial cattle SNPs chip arrays some variants associated with the nervous system and metabolic functions that are responsible for heat tolerance in dairy cattle. Dairy cattle are also the most criticized for having a rather high environmental impact associated with greenhouse gases emissions such as nitrous oxide and methane (Webster, 2021). Genetic selection is a very attractive solution to identify and breed lower-methane emitter animals, however, it requires multidisciplinary studies and a large number of methane records from individual animal. Various studies have identified genetic markers linked with methane emissions in cattle and sheep, providing opportunities for selective breeding to develop animals with reduced methane production potential (Calderón-Chagoya et al., 2019; Zhang et al., 2020; Hickey et al., 2022). On the other hand, the urinary nitrogen release leads to high levels of environmental pollution (Uwizeye et al., 2020). Accordingly, Honerlagen et al. have studied, through a GWAS approach, the genomic features behind this phenotype,

and found genomic regions and candidate genes affecting nitrogen excretion that could be included in a breeding selection scheme for animals with lower environmental impact. For a faster progress, genome editing techniques can improve livestock production efficiency and reduce environmental impacts that could have otherwise excessive cost using conventional breeding; however ethical issues regarding animal genome editing are still under debate and need to be concluded (Hallerman et al., 2022).

Specialized breeds are more likely to suffer from homozygosity, which can have a negative impact on genetic variability (Muir et al., 2008; Bosse et al., 2019). This loss of genetic diversity can lead to reduced adaptability, increased vulnerability to disease, and decreased resilience to environmental stressors (Grandin and Deesing, 2022). The conservation of genetic biodiversity in livestock animals has become a priority for a long-term sustainable agriculture (Pauls et al., 2013; DeLonge et al., 2016). Biodiversity is also crucial for ensuring adaptability to environmental stressors (Perini et al., 2020; Rovelli et al., 2020). Genomic research has provided the tools for deep characterization of genes responsible for certain phenotypes. Starting from the microsatellites, many QTLs related to interesting traits were mapped on chromosomes of livestock species (Hu et al., 2013; Badbarin et al., 2021). Moreover, the microsatellite technology, as well as the mitochondrial DNA, have been widely used to rapidly evaluate the genetic variability among and within breeds belonging to the same species (Perini et al., 2023a), and for the evaluation of their evolutionary relationships (Lasagna et al., 2020). The evolution of technology has led to the era of SNPs, a genomic tool much sharper for phenotype-genotype linkage identification. This is the case of Ben-Jemaa et al. that provides a glimpse into diverse selection signatures in semi-feral Maremmana cattle breed. The results showed a set of genes that are associated with the Maremmana breed's ability to adapt to the environment of the western-central part of Italy.

Camels are a species that used to cope with semi-arid and arid environments and their characterization regarding phenotype, microsatellites, mitochondrial DNA and SNPs have been reviewed by Yakubu et al. The authors focused on the difficulties into distinguishing sub-populations in many countries, except for the populations in Kenya. Yakubu et al. also reported that several studies have been conducted mainly to investigate the association between SNPs markers and different traits.

Since SNPs technology is used as marker of genetic variability within and between breeds (Ceccobelli et al., 2023), the study by Van Marle-Köster et al. investigated inbreeding levels and the genetic architecture of South African cattle and sheep breeds. The authors found an abundance of short ROH fragments in both species indicating ancient inbreeding. Using principal component analysis, model-based clustering, and phylogenetic analyses, the eight cattle populations studied were classified into indicine, taurine, or Sanga subspecies. Considering the sheep population, a distinct separation among dual-purpose, meat, and indigenous breeds was observed.

Since the percentage of livestock breeds at risk of extinction has increased from 15% to 17% between 2005 and 2014 (FAO, 2015), genomic characterization of indigenous breeds is an important start of point for their conservation. Soglia et al. examined the genetic diversity and the rate of extinction of 17 native Italian chicken breeds starting from microsatellite genotyping. The study revealed that 11 breeds were in endangered status. These findings highlighted the need to preserve unique genetic diversity and special attention

should be given to the introduction of different genetic lines and the use of mating schemes as a conservation strategy aimed at limiting the inbreeding increase.

RNA-sequencing is a tool which sheds light on global gene expressions of a given tissue, and it gave the possibility to discover new genomic variants with high impact on specific traits. It is also used to underline the adaptation of local livestock breeds to different environmental challenges (Perini et al., 2023b). RNA-seq has been used by Michailidou et al. for the evaluation of mammary gland transcriptional activity comparing high and low yielding ewes of two dairy sheep breeds reared intensively in Greece, the indigenous Chios, and the cosmopolitan Lacaune breed. The study demonstrated that the innate transcriptional activity of the mammary gland and the health status set the base for ewe productivity.

Finally, Peixoto et al. focused on the improvement of productive traits in Guzerá cattle. Due to its adaptation to harsh environments and low feed quality, parasite resistance, and dual-purpose characteristics, in 1994 breeding programs were implemented for the improvement of Guzerá for dairy purposes, using two joint selection strategies, the progeny test and the MOET nucleus schemes. The study provided evidence of the significant contribution of the MOET nucleus scheme to the breed's phenotypic and genetic progress for milk traits.

This Research Topic has achieved its goal of kick-starting the discussion and utilization the resources in terms of which strategies and capacities will be more efficient to solve the primary challenges that are affecting animal biodiversity around the world.

Author contributions

FP drafted the first version of the editorial manuscript. SC, RC, CT, and EL critically edited and revised the final version of manuscript. All authors contributed to the article and approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

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