Special Issue

Genomic View of Cattle Breeding and Domestication

Message from the Guest Editor

Domestication as well as artificial and natural selection have shaped the cattle genome and resulted in a large number of breeds and ecotypes. Many of these ecotypes are adapted to very different ecosystems and climates. Genome-sequencing data from cattle ecotypes and their integration with genome data from highly selected modern breeds allows us to uncover signatures of selection and likely unique and novel selection events associated with specific environments. Breeding programs should aim to incorporate newly developed indicator traits for resilience and, on the other hand, to maintain local ecotypes of cattle with lower production, but which represent an important genetic resource for production under harsh conditions.

This Special Issue of “genes” highlights recent advances in the discovery of selection signatures in cattle across a wide range of ecosystems and indicator traits for resilience in different production systems. Research articles, short communications and reviews are invited to present the latest developments and discoveries in understanding adaptation and resilience.

Guest Editor

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Deadline for manuscript submissions

closed (15 October 2022)

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Genes

an Open Access Journal by MDPI

Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/si/117010

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

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