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Genetic Diversity and Population Structure of Local Pig Breeds

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Message from the Guest Editors

Dear Colleagues,

In recent years, there has been growing awareness of the importance of local breeds in terms of adaptive traits, as a reservoir of valuable genetic variation with potential for more sustainable added-value oriented pork production.

Molecular DNA markers such as microsatellites, SNPs, CNVs, and retrotransposons are used to investigate the genetic basis of traits, supplying support to phenotypic evaluation and genealogical data analysis. The collection of phenotypic data and different genomic approaches such as high-throughput genome analysis methods and single-nucleotide polymorphism genotyping can be used to investigate the genetic basis of inheritance, QTLs, new phenotypes, genomic selection, and breeding programs.

This Special Issue will focus on recent research or reviews that investigate novel approaches and/or technologies used to identify relevant new phenotypes, as well as implement all aspects of pig genetics and genomics. Research or reviews with a focus on new phenotypes, genomic selection, breeding programs, QTLs, and breed conservation are also welcome.



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Special Issue



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Message from the Editor-in-Chief

Animals is an on-line open access journal that was first published in 2011. *Animals* adheres to rigorous peerreview and editorial processes and publishes only high quality manuscripts that address important issues in the many varied disciplines that involve animals, with a focus on animal science, animal welfare and animal ethics. *Animals* is covered in the Science Citation Index Expanded (SCIE) in Web of Science, with the latest Impact Factor: 3.0 (2022, ranks 12 /62 (Q1) in ‘Agriculture, Dairy & Animal Science’; 13/143 (Q1) in ‘Veterinary Sciences’), 5-Year Impact Factor: 3.2.

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