Special Issue

Genomic Selection for Quantitative Traits in Animals

Message from the Guest Editor

Since genomic selection started in 2009 in the US for dairy cattle, millions of animals have been genotyped. When genetic evaluation started with BLUP, genetic improvement was accelerated as accuracy in EBV increased. Now in the genomic era, because of the capacity to utilize SNP marker information as genotypes, more efficient genomic selection became possible. The genetic gain will increase significantly more, as accuracy in genomic EBV is higher using genomic relationships among animals, selection intensity is larger with more genotyped animals, and the generation interval is reduced by genotyping at younger age. In the future, genotyping embryos for many generations in a short period of time using germ cells from embryonic stem cells before having phenotypes will be possible. As a result, the genetic gain will be enormous. Genomic selection has such huge potential. Studies on genomic selection for quantitative traits will be more exciting and important than ever. Any research on genomic selection including theory, practical application, and biological aspects will be welcomed.

Guest Editor

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Deadline for manuscript submissions

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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: 2.7 (2024, ranks 15/86 (Q1) in 'Agriculture, Dairy & Animal Science'; 21/170 (Q1) in 'Veterinary Sciences'), 5-Year Impact Factor: 3.2.

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