Special Issue

Marker-Assisted Selection in the Equine

Message from the Guest Editor

Studies of equine genetics and genomics provide possibilities to track down existing diversity, risk of inbreeding, as well as discovery of mutations causing different traits and diseases. Since the release of the first equine genomic trace files in 2007, around 100 causative or possibly causative mutations of mendelian traits and disorders have been discovered in the horse. Still, there are numerous equine characteristics and disorders with an unknown genetic background. With the high-throughput genetic and genomic techniques available today, the research community has the possibility to also unravel regulatory or structural genomic variation, potentially causing complex and multivariate equine phenotypes. More knowledge about molecular genetic and/or genomic mutations and variations could assist horse breeders in how to use marker-assisted selection or genomic evaluation to produce highly-performing but still healthy and sustainable horses.

Guest Editor

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Editor-in-Chief

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