Special Issue

Genetic Disorders in Livestock

Message from the Guest Editors

Hundreds of Mendelian inherited disorders in livestock have now been published, where at least one likely causal variant has been identified. Although many of these disorders were well known long before one or more causes were identified, in more recently-discovered disorders a likely causal variant is sometimes uncovered very quickly. This is partly due to off-the-shelf availability of whole SNP panels for most livestock species. Those panels enable immediate proof of parentage to demonstrate familial inheritance, and allow GWAS to be conducted to localise the regions and therefore genes likely harbouring the causal variant. Additionally, NGS technology makes a complete screen of an individual genome both fast and relatively inexpensive. Also, population screening for SNP panel haplotypes that are never or rarely homozygous has proven to be particularly productive in uncovering deleterious mutations. We invite investigators to contribute review articles on strategies for discovery or control of likely causal variants, on their occurrence in particular species or in particular genes, as well as original research articles on topics related to genetic disorders in livestock.

Guest Editors

Prof. Dorian J. Garrick

Prof. Frank Nicholas

Dr. Keren Dittmer

Deadline for manuscript submissions

closed (31 October 2018)

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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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