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Mining the Excellent Functional Genes of Forage

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Message from the Guest Editors

Most forages, because of their perenniality and polyploidy with relatively shorter time of domestication than food crops, are more genetically diverse with versatile gene resources, showing greater tolerance to adverse environmental conditions. In the past several decades, rapid progress has been made in mining forage genes via genome sequencing, transcriptome sequencing, QTLs, GWAS, transgenic analysis, and gene editing, resulting in the identification and functional analysis of many key genes and proteins in forage.

This Special Issue aims to provide a broad and updated overview of the involvement of “Mining the Excellent Functional Genes of Forage”, with emphasis on the improvement of aboveground biomass and nutrition quality, and how forage adapts to adverse environmental conditions. Omics-related studies to elucidate omic changes in forage, gene functional analysis, and the development of genetic markers are encouraged, which might shed light on forage molecular breeding in the future. Contributions by experts in the field in the form of research papers or critical reviews are welcomed.



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Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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