

Special Issue

Genetic Mapping in Plants

Message from the Guest Editor

Genetic mapping, a research approach conceived one century ago during the juvenile period of the novel science of genetics, is still, today, one of the most powerful methods for identification of genes for which the only available information is their impact in the phenotype. It is amazing that our predecessors, based on the phenotypic analysis of progenies obtained by controlled crosses, could have identified in eukaryote genomes, the relative order, and in-between genetic distance of biological features relatively well understood today, but at that time absolute black boxes: genes. Despite the enormous amount of accumulated genomic knowledge and the most recent developments in genomic research, including the impressive improvements in genome sequencing, the establishment of an unequivocal cause–effect relationship between a phenotypic trait and a genomic feature still requires the previous genome location of that feature, either via classical mapping or by genome-wide genetic association studies. This Special Issue is dedicated to articles reporting the genome location and identification of novel genes that determine qualitative or quantitative plant traits.

Guest Editor

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closed (20 March 2024)

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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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