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Tomato Genetics

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Message from the Guest Editors

Tomato is a model species for Solanaceae. Since 2012 and following the publication of the tomato genome reference sequence by a large scientific community, genomic resources rapidly increased. Today, the genomes of more than 1000 accessions have been resequenced, and a pangenome study has allowed the discovery of new genes absent from the reference genome. The domestication of tomato has been deciphered. Many QTL have been mapped and several genes discovered, involved in fruit composition, plant architecture or disease resistances. In addition, tomato researchers have developed a plethora of tools and resources for advancing tomato genomics and gathered all this information in a few databases. In parallel, the new genome editing tools provide highly efficient ways to study and manipulate genes of interest.

For this Special Issue, we will present state-of-the-art work in tomato genetics and genomics, assembling the most recent advances in our field in one 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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