

Special Issue

Functional Genomics of Cucurbit Species

Message from the Guest Editors

The Cucurbitaceae family contains highly nutritious and morphologically diverse crops. Recent years have seen dramatic advances in the development and application of genomic tools for cucurbit species, including genome assemblies and annotations; the construction of pan-genomes; the development of high-throughput genotyping tools such as SNP, tilling and mutant platforms; the genomic analyses of germplasm collections; the identification of SNPs and structural variants; the use of bioinformatic tools such as genome-wide association studies (GWAS) and genomic prediction; fine genetic mapping and molecular marker-assisted selection (MAS); and the development of new transformation and gene editing methods. These tools provide us with the opportunity to determine the genetics behind important production, quality, and developmental traits. This Special Issue seeks to highlight the progress being made in cucurbit genomics. We invite the submission of original research and review articles dealing with any aspect of the development and/or application of functional genomic tools for cucurbit species.

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Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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