

Special Issue

Genetic Breeding and Improvement of Peanut

Message from the Guest Editor

Peanut (*Arachis hypogaea*) originated in South America through hybridization between *A. duranensis* and *A. ipaensis*, followed by chromosomal doubling, making it an allotetraploid. The genomes of the cultivated peanut and those of its progenitors have been completely sequenced, further promoting the identification of key genes associated with various phenotypes. Now, these functional genes can be used for applications in molecular breeding. Furthermore, new functional genes related to growth and development and abiotic and biotic stress can be identified using multi-omics. This Special Issue focuses on recent advances in molecular breeding and the genetic improvement of peanut.

Submitted papers can investigate the following issues:

- Identify functional genes at peanut genome level using bioinformatic approaches;
- Use molecular markers to assist in selecting breeding materials and accelerate the breeding of superior genes;
- Explore and verify genetic transformation technology in peanuts;
- Verify the gene function and molecular mechanism in the growth, development, and stress response of peanut.

Guest Editor

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Deadline for manuscript submissions

closed (25 November 2024)

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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.

Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

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