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 muti-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

Dr. Hui Song
College of Grassland Science, Qingdao Agricultural University, Qingdao 266109, China

---

Deadline for manuscript submissions

closed (25 November 2024)

Genes

an Open Access Journal by MDPI

Impact Factor 2.8
CiteScore 5.2
Indexed in PubMed

mdpi.com/si/206108

Genes
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

mdpi.com/journal/genes