

Special Issue

QTL Mapping of Seed Quality Traits in Crops, 2nd Edition

Message from the Guest Editor

This Special Issue of *Plants* aims to advance the field by focusing on the genetic and QTL mapping of seed quality traits in crops, utilizing both traditional mapping populations (such as recombinant inbred lines (RILs), F2, doubled haploid, etc.) and genome-wide association studies (GWAS). Submissions that identify candidate genes within the identified QTL regions are especially encouraged. We also welcome papers that integrate artificial intelligence (AI) and machine learning (ML) techniques in the analysis of genetic and QTL data. AI and ML offer powerful tools for uncovering hidden patterns, predicting trait outcomes, and enhancing the precision of QTL mapping and candidate gene identification. Studies leveraging these advanced computational approaches to gain new insights into seed quality traits are highly welcomed. We look forward to receiving your valuable contributions to this Special Issue.

Guest Editor

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Message from the Editor-in-Chief

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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