

Special Issue

QTL Mapping of Seed Quality Traits in Crops

Message from the Guest Editor

Seeds of major crops contain many valuable compounds for the food and feed industry. Animal feed and human nutrition and health rely largely on seed proteins, amino acids, oils, fatty acids (palmitic, stearic, oleic, linoleic, linolenic acids, etc.), sugars (glucose, galactose, sucrose, raffinose, etc.), isoflavones (daidzein, genistein, glycitein, etc.), vitamins, minerals, secondary metabolites, and other nutrients. Understanding the genetic basis of these beneficial compounds is very important, and many studies have been aimed at identifying and mapping QTL for these traits in the past 3 decades; however, most of these QTL regions are not well characterized, and candidate genes within these QTL regions are mostly unrevealed. This Special Issue of *Plants* will focus on genetic and QTL mapping of seed quality traits in crops using both traditional mapping populations (recombinant inbred lines (RILs), F2, doubled haploid, etc.) and genome-wide association studies (GWAS). Studies that also aim at identifying candidate genes within the identified QTL regions are most welcome.

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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