Special Issue

Wheat Breeding, Genomic Selection, and Phenomics

Message from the Guest Editors

Genomic selection (GS) increase the rate of genetic improvement in plant breeding programs. It allows for a comparative larger gain from selection by estimating all marker effects simultaneously, and the subsequent selection of genetically superior individuals is based on their genomic estimated breeding value (GEBV). Wheat breeding programs typically require 10–15 years to transfer novel genes into elite germplasms. Through the application of GS, it is possible to select new parents purely based on GEBV, before being entered in field trials and nurseries. We expect GS to be intensively applied in wheat breeding programs. However, there is still limited information on the implementation of GS in applied wheat breeding programmes. Therefore, this Issue is composed to address this question by focusing on empirical GS studies addressing important traits in wheat; combining GS with MAS; modelling multiple traits, epistatics, and genotypes through environmental interaction; enhancing the predictability of GS for wheat breeding through machine learning empowered high-throughput and precise phenotyping; and cost effective applications of “omics” data.

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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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