The Application of New GWAS Methods in the Genetic Dissection of Complex Traits in Plants

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Message from the Guest Editors

Genome-wide association study is widely used in the genetic dissection of complex traits. However, there is still room to improve their methodologies. In QTN, environmental interaction (QEI) and QTN-by-QTN interaction (QQI) detection, effects to be estimated are confounded, polygenic backgrounds to be controlled are imperfect, and there are limited approaches available for detecting QEIs and QQIs. Thus, single environment analyses are frequently applied in multiple environment experiments, which are inefficient and suboptimal, and very few interaction studies have been reported in plants genetics. To address these issues, we established a new framework in which all the effects to be estimated are compressed into an effect-related vector, while all the polygenic backgrounds are compressed into one polygenic background. Specifically, the compressed mixed model was integrated with mrMLM to establish the 3VmrMLM method, which is powered up to detect all types of loci and estimate their effects. This method is readily available for genetics analysis in animals, plants, forest trees, and humans. It is necessary to test this novel method with a wide range of real datasets across species.

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Special Issue

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Message from the Editor-in-Chief

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