



Plant Population Genomics

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Message from the Guest Editor

The field of plant population genomics is rapidly evolving in terms of its conceptual framework, its methodologies, and its applications, mostly due to advances in the sequencing technologies and computing capacity. For instance, the conceptual framework and practical tools have shifted from classical quantitative genetics and QTL genetic mapping to latest-generation GWAS models, genomic prediction, machine learning forecasting, and the omnigenic model. Similarly, this base knowledge has led to ecological genomic applications transcending the fields of speciation and adaptation into the frameworks of genomic islands of divergence, conservation genomics, genetic-assisted gene flow, and genomics for restoration. Plant breeding has also been boosted by developments in the population genomics field by shifting from Mendelian marker-assisted selection and marker-assisted backcrossing into genomic-enabled prediction, genomic-assisted introgression breeding, and enviromics. Therefore, this book aims to summarize, discuss, and recommend historical and modern developments that will continue enabling plant population genomics, its foundations, methodologies, and uses.





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Message from the Editor-in-Chief

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