

The Future of Rice Genomics: Sequencing the Collective Oryza Genome
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Abstract

The main objectives of the Oryza Map Alignment Project (OMAP) are to characterize the rice genome from a comparative standpoint by establishing a genus-wide and genome-scale comparative framework from representative species. Here, we report our progress in the analyses of these datasets and emerging comparative phylogenomics insights into Oryza evolution at two different resolutions chromosomal and sequence levels. We demonstrate the abundance and impact of structural variations (SV) on genome diversity using African Oryza as a model. The molecular basis of SV was inferred using three genus-wide vertical sequence datasets. Combined, these data demonstrate that a single reference genome sequence for the genus Oryza is insufficient to comprehensively capture the genomic and allelic diversity present within the genus. Towards this end, we present a strategy to generate high-quality and cost-effective de novo reference sequences of collective Oryza. The application and broader scientific impact of the OMAP resources under an international cooperative effort (I-OMAP) are discussed.