

The Future of Rice Genomics: Sequencing the Collective Oryza Genome**2010**

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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.