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**Development, Gene Discovery and Allele Mining of a Global Tropical *Japonica* Core Collection**

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Over the past 100 years, US rice variety development has focused on lines that trace back to about 40 founder parents, creating a lack of genetic diversity in modern US rice breeding programs. Most rice varieties grown in the Southern USA derive from the *tropical japonica* subpopulation, thus a tropical *japonica* Core (TRJ) panel was developed as a source of genetic diversity for improving, yield, quality, and sustainability of US rice. Accessions believed to be tropical *japonica* were selected from all available sources and subsequently genotyped with 13 molecular markers to verify subpopulation, resulting in a final panel of 529 accessions from 61 countries. From the TRJ panel, 398 accessions were sequenced with an average coverage of 3X, and single nucleotide polymorphisms (SNPs) were called using Google DeepVariant and GLnexus on the USDA-ARS SCINet HPC system. The TRJ Core was evaluated as single plots in a field experiment with two replications in 2021 and 2022. The accessions were evaluated for days to 50% heading, plant height, awns, leaf blade pubescence, lodging, growth rate, and flag leaf width and length. Additionally, yield components were measured including panicle length, seeds per panicle, seed weight per panicle, number of primary and secondary panicle branches, and grain dimensions. The panel was also scored for blast resistance under greenhouse conditions. Genome wide analyses were performed to discover associations between SNPs and the measured traits.