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Incorporation of parental phenotypic data into multi-omic models improves prediction of yield-related traits in hybrid rice

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Abstract

Hybrid breeding has been shown to effectively increase rice productivity. However, identifying desirable hybrids out of numerous potential combinations is a daunting challenge. Genomic selection holds great promise for accelerating hybrid breeding by enabling early selection before phenotypes are measured. With the recent advances in multi-omic technologies, hybrid prediction based on transcriptomic and metabolomic data has received increasing attention. However, the current omic-based hybrid prediction has ignored parental phenotypic information, which is of fundamental importance in plant breeding. In this study, we integrated parental phenotypic information into various multi-omic prediction models applied in hybrid breeding of rice and compared the predictabilities of 15 combinations from four sets of predictors from the parents, i.e., genome, transcriptome, metabolome and phenome. The predictability for each combination was evaluated using the best linear unbiased prediction and a modified fast HAT method. We found significant interactions between predictors and traits in predictability, but joint prediction with various combinations of the predictors significantly improved predictability relative to prediction of any single source omic data for each trait investigated. Incorporation of parental phenotypic data into various omic predictors increased the predictability, averagely by 13.6%, 54.5%, 19.9%, and 8.3%, for grain yield, number of tillers per plant, number of grains per panicle, and 1,000 grain weight, respectively. Among nine models of incorporating parental traits, the AD-All model was the most effective one. This novel strategy of incorporating parental phenotypic data into multi-omic prediction is expected to improve hybrid breeding progress, especially with the development of high-throughput phenotyping technologies.

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