**Quantitative genetic analysis of metabolite accumulation in rice**

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Abstract: It has been argued that metabolic content can be used as a selection marker to accelerate crop improvement because metabolic profiles in crops are often under genetic control. Evaluating the role of genetics in metabolic variation is a long-standing challenge. Rice, one of the world's most important staple crops, is known to be sensitive to recent increases in nighttime temperatures. Quantification of metabolic levels can help measure rice responses to high night temperature (HNT) stress. However, the extent of metabolic variation that can be explained by regression on whole-genome molecular markers remains to be evaluated. In the current study, we generated metabolic profiles for mature grains from a subset of rice diversity panel accessions grown under optimal and HNT conditions. Metabolite accumulation was low to moderately heritable, and genomic prediction accuracies of metabolite accumulation were within the expected upper limit set by their genomic heritability estimates. Genomic heritability estimates were slightly higher in the control group than in the HNT group. Genomic correlation estimates for the same metabolite accumulation between the control and HNT conditions indicated the presence of genotype-by-environment interactions. Reproducing kernel Hilbert spaces regression and image-based deep learning improved prediction accuracy, suggesting that some metabolite levels are under non-additive genetic control. Joint analysis of multiple metabolite accumulation simultaneously was effective in improving prediction accuracy by exploiting correlations among metabolites. The current study serves as an important first step in evaluating the cumulative effect of markers in influencing metabolic variation under control and HNT conditions.