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Causal variant effect prediction on cooked rice texture through integrative GWAS modelling

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In the study of plant breeding, genome-wide association studies (GWAS) have been employed on a widespread basis to identify relationships between genotypes and phenotypes, offering biological insights into a diverse range of species. However, it can be argued that this method has certain limitations, in that it does not directly suggest causal variants associated with phenotypes. To supplement this, variant effect prediction modelling was employed following GWAS analysis, thus facilitating the achievement of more precise results. In this study, a total of 248 accessions of the *temperate japonica* rice group were used as a GWAS panel, and texture profile analysis (TPA) was conducted to investigate cooked rice texture. GWAS was performed using high-quality single nucleotide polymorphisms (SNPs) obtained from re-sequencing and mapping against the rice reference genome (Nipponbare, IRGSP v1.0). A linkage disequilibrium (LD) analysis was also conducted to identify the LD block, which was found to be 393 kb in the GWAS panel. A model was constructed to evaluate and predict the impact of variants within the LD region, which included markers that were subjected to significant analysis in GWAS. The model was successful in identifying the variants with the strongest effect on the texture traits of cooked rice. This integrative approach should facilitate the acquisition of biological insights in future breeding programs with the goal of improving the cooked rice texture.