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RiceDBreeder: Integration and Utilization of GWAS and Korean Rice Phenotype, Pedigree, and Resequencing Data

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Modern breeding has evolved from traditional phenotype-based methods to molecular and digital breeding, which utilizes artificial intelligence and big data. Despite these advancements, Korean rice resources still face challenges due to separately managed phenotype and genomic data. Phenotypic records are individually maintained, hindering integrated analysis, while next-generation sequencing (NGS) data is fragmented, making it difficult to retrieve specific varietal information. Pedigree data is also often stored in unstructured document formats, limiting its usability in breeding strategies. To overcome these challenges, we developed RiceDBreeder, a web application that integrates phenotype data, resequencing data, and pedigree information for 8,831 Korean rice varieties. It also includes genome-wide association study (GWAS)-based marker–trait associations, enabling comprehensive and user-friendly exploration. Researchers can visually examine phenotypic data distributions, understand varietal relationships through pedigree visualization, and compare SNP markers associated with specific traits. RiceDBreeder provides tools for identifying phenotype-linked SNP alleles and exploring related varieties across the genome using pedigree analysis. By offering integrated access to diverse datasets and intuitive analysis features, RiceDBreeder supports efficient variety selection and informed breeding decisions. This platform addresses the current limitations in digital breeding for Korean rice and facilitates data-driven research and breeding innovation.