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Multi-Approach Characterization of Panicle Architecture Traits in Rice (*Oryza sativa* L.) Genotypes

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Panicle architecture is a key determinant of yield potential in rice (*Oryza sativa* L.) because it governs spikelet number per panicle and grain yield. Comprehensive characterisation integrating morphological evaluation, molecular genetic analysis and *in silico* approaches can identify trait determinants and candidate genes useful in rice breeding programs. This study evaluated diverse rice genotypes for variation in panicle architectural traits, performed molecular marker and association analyses, and used *in silico* tools to identify candidate genes and regulatory pathways associated with variation in panicle morphology.

Introduction

Rice is one of the most important staple crops worldwide. Panicle architecture—defined by panicle length, branch number, rachis structure, and spikelet distribution—is a major component of yield, and is influenced by both genetic and environmental factors. Morphological variation in panicle traits has been widely documented among rice genotypes, with correlations often found between panicle complexity and grain yield components such as spikelet number and grain weight. Genetic studies have identified numerous QTLs and genes that control panicle architecture. Notable genes include *Gn1a* (*OsCKX2*), *IPA1/OsSPL14*, *FZP/qSrn7*, *LAX1*, and *APO1*, which regulate branching and spikelet development. Genome-wide association studies (GWAS) have also revealed novel QTLs and genetic loci linked to panicle length, primary branch number, and secondary branch number. *Molecular and in silico analyses* such as sequence variation mapping, promoter haplotype analysis, protein domain prediction, and gene expression profiling provide further insight into underlying functional mechanisms. These integrative approaches allow the identification of candidate genes and marker-trait associations for use in marker-assisted selection (MAS) and genomic prediction.

Materials and Methods

Plant Materials and Morphological Evaluation:A panel of diverse rice genotypes was grown under controlled field conditions. Key panicle traits were scored, including panicle length, primary branch number (PBN), secondary branch number (SBN), spikelet number and rachis length. Correlation and principal component analyses were used to assess trait relationships.

Molecular Marker Analysis: Genomic DNA was extracted and genotyped using SSR and SNP markers linked to known panicle architecture genes and QTL regions identified in previous association studies. Marker–trait associations were tested using association mapping and linkage disequilibrium analysis.

Genome-Wide Association Study (GWAS): GWAS was conducted using high-density SNP datasets to identify genomic regions associated with panicle traits. Significant markers were cross-referenced with candidate gene databases and literature.

In Silico Characterisation: Candidate genes mapped within significant QTL regions underwent *in silico* analysis including:

- Domain prediction and functional annotation (Pfam, InterPro)
- Promoter analysis for regulatory motifs
- Expression profiling using publicly available RNA-seq data to verify tissue specificity
- Homology modelling to predict protein structure and functional impacts of allelic variation

Results

Morphological Variation: Significant variation was observed among genotypes for panicle architecture traits. Panicle length and branch number were positively correlated with grain yield and spikelet number. Phenotypic diversity indicated that architectural traits can be effective selection criteria for breeding.

Molecular Association and QTL Mapping: GWAS and marker analysis revealed several significant loci associated with PBN, SBN and panicle length. Candidate gene regions harboured known regulators such as SPL family transcription factors and hormone-responsive genes.

In Silico Functional Insights: Promoter haplotype analyses indicated regulatory variation in several gene promoters correlated with panicle trait differences. *In silico* protein models suggested functional effects of non-synonymous SNPs in key regulatory genes. Expression data supported preferential expression of candidate genes in developing panicle tissue.

Discussion

Our integrative characterisation confirms that panicle architecture is controlled by complex interactions among multiple gene networks. Genes involved in meristem identity (*IPA1/OsSPL14*), hormone biosynthesis and signalling (*Gn1a/OsCKX2*), and inflorescence meristem maintenance contribute to phenotypic variation in rice panicles.

Molecular markers linked to stable QTLs can be incorporated into MAS strategies. *In silico* characterisation adds functional context that enhances understanding of candidate genes and regulatory elements.

Conclusion

A comprehensive approach combining morphological evaluation, molecular genomics and *in silico* analysis enhances the understanding of panicle architecture variation in rice. The identified markers and candidate genes provide resources for breeding high-yield rice varieties with optimized panicle traits.

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