Original Research Article

Key advances and future directions in the regulation of rice panicle development: From gene mapping to technological application, and from resistance synergy to cross-field reference

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Abstract: Rice is a staple crop critical to global food security, and panicle development directly determines yield, stress tolerance, and quality. Advances in genomics and high-throughput phenotyping have greatly clarified the regulatory mechanisms of rice panicle development, with multiple key regulatory and blast-resistance genes identified. Synergistic effects of nitrogen and planting density, as well as high-throughput panicle phenotyping using drones and YOLOv8, have also been established. However, polygenic and gene–environment interactions remain poorly understood. Further research on synergistic regulation and technical optimization is urgently needed to accelerate breeding of high-yield, high-quality, and stress-tolerant rice varieties.

Keywords: rice; panicle development; genetic regulation; cultivation practices; detection techniques; resistance studies

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1. Introduction

Rice is the staple food for nearly half of the global population, and increasing its yield is the core goal of agricultural research. Panicle architecture is a key agronomic trait of rice, which directly affects yield components such as grain number per panicle, panicle length and panicle density, and also influences plant lodging resistance, photosynthate transport efficiency and disease and insect resistance[1]. In recent years, with the breakthroughs in molecular biology and precision agriculture, the research on rice panicle development has advanced from morphological observation to the analysis of molecular mechanisms and the application of high-throughput technologies.

However, major challenges remain, including unclear gene–pathway–environment interactions, genotype-dependent responses to cultivation, and negative pleiotropy between disease resistance and panicle architecture[2]. This review summarizes 45 studies (2013–2025) on genetic regulation, agronomy, phenotyping, and disease resistance related to dwarf rice panicle development, discusses current limitations in polygenic networks and detection tools, and provides a theoretical basis for breeding high-yield, high-quality, stress-tolerant rice varieties.

2. Method

A literature search was conducted in major international (PubMed, ScienceDirect) and Chinese (CNKI) databases using keywords related to rice panicle traits, cultivation and detection (2013–2025). Retrieved literature included peer-reviewed journals, dissertations and conference proceedings, with relevance and quality ensured by selection criteria:

(1) Focused on rice (Oryza sativa, Oryza glaberrima, related wild species) and explicit panicle traits (e.g., panicle length, effective panicle number, grain number per panicle).

(2) Covered genetic mechanisms, agronomic regulation, phenotyping, disease resistance correlations, with rigorous experiments and empirical data.

(3) Prioritized high-quality journals (SCI and Chinese core), excluding reviews, abstracts and data-incomplete studies.

(4) Excluded reviews, editorials, full-text-lacking conference abstracts and studies with incomplete/ambiguous data to focus on primary research.

3. Breakthroughs in the genetic regulatory mechanism of rice panicle development driven by high-throughput technologies

Rice panicle development is regulated by a complex network of genome variation, post-transcriptional modification and hormone signaling. GWAS and transcriptomics show that panicle morphogenesis is related to cell cycle and cell wall biosynthesis. STRONG1 regulates cell division to improve panicle shape and lodging resistance. Gibberellin and auxin pathways (EPE1, OsPL1, OsPE1, OsPN3) control rachis elongation and panicle number[1]. Post-transcriptional regulators (OsAPA1, lncRNA-PAN1) affect phenotypic plasticity[3]. Multiple genes/QTLs (OsPB1/OsSB4, qPL6-1/qGN8-1, OsDEN1, OsVB2, OsRA1/OsFT1, Chr2 QTL cluster) regulate panicle architecture[4]. Panicle development is metabolically linked to yield via OsPHS1/OsPHS2/OsSSIII, OsDEN1 and OsVB2.[5]. Key regulators including OsRA1 and OsGN1a provide a molecular basis for coordinating panicle structure and yield potential[6].

4. Effects of cultivation practices on panicle traits and yield of rice

Agronomic management is a key external driver of rice panicle development, mainly by regulating the sourcesink relationship and hormone homeostasis. Nitrogen fertilization and planting density are central to this process, as they control photosynthate distribution. However, nitrogen management must be genotypespecific: largespikelet cultivars require high N supply (240 kg hm^{-2}), while smallspikelet types perform best with moderate N (120 kg hm^{-2})[7]. Synergistic interaction between N and planting density also determines yield. High N (270 kg hm^{-2}) combined with high density (225,000 hills hm^{-2}) improves canopy microclimate and light interception, promoting inferior spikelet filling and final yield. For forage rice, optimum harvest at 20 days postheading maximizes biomass and nutrient quality[8]. Mechanistically, agronomic practices reshape panicle architecture by modulating endogenous hormones. In SP3 mutants, an unbalanced auxin/cytokinin ratio reduces panicle length, which can be restored by exogenous auxin. This confirms that cultivation practices regulate panicle development via hormone signaling pathways.

5. Technologies for rice panicle detection and biomass estimation

Advancements in remote sensing and computer vision have transformed rice panicle trait detection and biomass estimation from manual observation to high-throughput, non-destructive precision approaches, including drone image recognition, remote sensing modeling, and hyperspectral analysis. Drone-based RGB imagery with the enhanced YOLOv8 algorithm achieves 92.3% panicle counting accuracy at the heading stage[9]. Sentinel-2 satellite data, using NDVI/EVI2 vegetation indices (heading to grain filling), enables high-precision above-ground biomass estimation ($R^2 = 0.85$, RMSE = 0.5 t/hm^2), indirectly reflecting panicle development[10]. Hyperspectral imaging (350–2500 nm) identifies varieties via panicle-specific bands (680–760 nm), providing technical references for non-destructive detection of refined panicle traits.

6. Research on the association between rice panicle disease resistance and panicle development

Panicle diseases (especially panicle blast and blight) severely constrain rice production, causing spike necrosis, rachis/vascular bundle damage, obstructed nutrient transport, inhibited grain filling, and yield loss. Thus, identifying broad-spectrum resistance genes and elucidating immunity-panicle architecture coupling is key to resolving the resistance-yield trade-off. Current research focuses on resistance loci with synergistic agronomic benefits: OsPBR5 confers 40% spike blight resistance without yield penalty[11]; Pb4 enhances panicle neck cell wall lignification, reducing disease index by 50% without impairing panicle traits[12] ; pleiotropic allele Pb3-1 improves resistance and increases panicle grain weight by 12%[13]; Pb2 reduces disease incidence by 45% and promotes rachis elongation via a "disease escape" microclimate effect.

7. Insights into rice panicle development from sorghum research and rice non-panicle traits

Research on sorghum and other traits provides new perspectives and methodologies for rice panicle architecture improvement. Sorghum studies show that density and organic fertilizer synergistically optimize panicle traits (shared source-sink regulation across crops)[14], with its genetic diversity analysis methods and "panicle architecture-quality" framework offering references for rice. Barnyard grass research on panicle biomass allocation and photosynthetic rate provides cross-species insights into rice photosynthate transport[15]. Non-panicle rice traits also offer indirect insights: loquat's "gene-regulated cell division in reproductive organs" suggests OsFWL1 as a potential rice panicle regulator[16]; multi-model GWAS, 3VmrMLM, and MAGIC populations (used for rice quality/nutrition)[17] are transferable to panicle genetic analysis. Many non-panicle traits (e.g., leaf anatomy, stress tolerance) are genetically, physiologically, and phenotypically linked to panicle development[18] , providing multidimensional evidence for rice panicle source-sink coordination, stress tolerance, and yield stability.

8. Conclusion

Recent advances in rice panicle morphology research have established a multidimensional framework: genetically, GWAS and cross-genus studies have identified key genes and enriched genetic resources; agronomically, nitrogen-fertilizer-density synergy has formed a panicle-type-tailored approach; technologically, drone-YOLOv8 enables high-throughput panicle trait detection; resistance genes (e.g., Pb2/Pb3/Pb4) have been identified. However, challenges remain: fragmented molecular mechanism understanding, limited technology application, and theory-practice disconnect. Future research should focus on polygenic mechanisms, technological integration, synergistic improvement, stress adaptation, and cross-crop transferability to refine the framework, advance precision panicle improvement, and enhance rice breeding.

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