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Stage-specific drought responses in rice: shoot transcriptomes uncover tolerance genes and contrasting vulnerabilities to inform african breeding programs

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Abstract

Drought-stress critically impairs rice growth at all developmental stages, threatening global yield stability and food security. This study investigates whether genotypes previously identified as drought-tolerant during reproductive-stage field screening (Adjah et al., 2025) retain this tolerance under early-vegetative development (10–30 days) by characterising the associated differentially expressed genes (DEGs). Four genotypes previously described as drought-tolerant (APO, CRI-Enapa) or drought-sensitive (ART132–35-1–1-B-B, CRI-Amankwatia) were evaluated under controlled growth chamber conditions at early-vegetative stage. Of these, APO, CRI-Enapa, and ART132–35-1–1-B-B were also used for transcriptomic profiling after 30 days of drought exposure. Our findings show that, contrary to its field performance, APO exhibited the lowest shoot and root fresh weights under early-vegetative drought-stress, while CRI-Enapa maintained its drought resilience, outperforming ART132–35-1–1-B-B. Transcriptome profiling by RNA-Seq revealed that APO and CRI-Enapa showed 2,049 and 135 upregulated DEGs, respectively, whereas only 123 transcripts were induced in ART132–35-1–1-B-B. Analysis of shared responses revealed that APO shared 107 DEGs with CRI-Enapa and 48 with ART132–35-1–1-B-B, while only three overlapped between CRI-Enapa and ART132–35-1–1-B-B. Functional enrichment highlighted that phytohormone signalling (abscisic acid, jasmonate), transcription factors (TFs: bZIP, WRKY, ERF061), carbohydrate metabolism (SWEET transporters), and stress-response pathways (dehydrins, LEA proteins) were involved in this stress response. APO exhibited pronounced upregulation of stress-responsive genes (DREB/CBF, HVA22) and TFs linked to drought adaptation (bZIP, WRKY). Interestingly, serine/threonine protein kinases and dehydrins were uniquely upregulated in CRI-Enapa, suggesting distinct response strategies. These findings underscore genotype-specific transcriptional strategies for drought adaptation. APO's contrasting performance at earlier and later developmental stages highlights the necessity of evaluating drought tolerance at multiple growth-stages. While APO's reproductive-stage resilience correlates with robust stress-gene induction, its vegetative-stage sensitivity implies trade-offs in stage-specific regulatory pathways or resource allocation. CRI-Enapa's consistent tolerance, mediated by conserved stress-adaptive genes, positions it as a promising donor for breeding. In addition, the identified DEGs in these genotypes provide a molecular marker toolkit for enhancing drought resilience. This

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study emphasises that drought tolerance is stage-dependent, urging breeders to screen lines across different growth-stages. We recommend integrating such information into the variety passport data to enable informed and optimised cultivar selection by stakeholders under diverse drought-scenarios.

Keywords: Drought-stress, rice, RT-qPCR, transcript abundance