**Genetic mapping and transcriptome analysis of seed longevity in Taiwan weedy rice**

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Weedy red rice (Oryza sativa L.), a conspecific species of cultivated rice, substantially impacts global rice production by compromising both yield and quality. Originating from early Indica landraces, Taiwan weedy rice (TWR) has developed traits akin to modern Taiwanese rice cultivars, posing challenges in weed management through traits like crop mimicry, seed dispersal, and rapid growth. These adaptations are particularly effective in Taiwan's transplanting systems. This study explores the genetic foundations of seed longevity in TWR, a crucial trait for maintaining soil seedbank density and reproductive potential. Employing quantitative trait locus (QTL) mapping and transcriptome analysis, we identified two significant loci: qSS1 and qSS7, which are instrumental in seed longevity. The qSS1 locus includes the gene 'OsGH3-2', which modulates germination by altering hormone levels. In contrast, the contribution of the qSS7 locus remains less clear. Additionally, RNA sequencing reveals that, compared to cultivated rice, TWR seeds exhibit enhanced transcriptome stability after 12 months of room temperature storage. Genes related to chromatin remodeling, motor activity, and lateral root development are notably upregulated in these aged TWR seeds, supporting their superior longevity. This research advances our understanding of seed longevity mechanisms in weedy rice and contributes to developing effective long-term management strategies for weedy rice in both transplanting and direct seeding systems.

Keywords: Rice, Seed longevity, Weed management, Sustainability