

Three Types of Seed Dormancies and Evolutionary and Regulatory Mechanisms in Rice

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Abstract

Seed dormancy (SD) is a multigenic adaptive trait imposed by seed component tissues that vary in generation or ploidy. Several genes, or quantitative trait loci (QTL), are associated with specific types of SD in rice (*Oryza sativa*). *qSD12* is a major QTL for embryo dormancy and consists of 3 linked genes, including 2 originated from local duplications and encoding a subfamily of bHLH transcription factors (TFs). The linked genes regulate the dormancy development and were subjected to balancing selection likely before crop domestication to increase the trait diversity. *qSD1-2* controls endosperm-imposed dormancy, encodes Gibberellin20-Oxidase2, and regulates seed dehydration and physiological maturity. *qSD7-2* and *qSD4-2* control coat-imposed dormancy, both encode the other subfamily of bHLH TFs, but they vary in the size of pleiotropic effects on red/purple pericarp colors, germination velocity and soil seedbank longevity, in regulatory roles in seed flavonoid and abscisic acid biosynthesis, and in the evolutionary history. These types of SD genes are being combined into the same system to model ecological genetics of weed seedbank persistence, used as targets of genome editing or RNA interference to test a transgene-flow mitigation strategy, or introduced into cultivars to improve the resistance to pre-harvest sprouting in crop breeding.