

Learning about Rice Domestication from Domestication Genes

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The accumulation of genetic and genomic data has continued to shed light on the origin and evolution of rice cultivars. Theoretical models of rice domestication were proposed. The snowballing model considers a single origin of cultivated rice. In this model, a core of critical domestication alleles was fixed in the founding cultivar and then helped increasing the genetic diversity of cultivars through hybridization with wild populations. The combination model considers multiple origins of cultivated rice, in which initial cultivars were domesticated from divergent wild populations and fixed different sets of domestication alleles. Subsequent gene flow among these semi-domesticated cultivars resulted in the fixation of the similar set of domestication alleles in the contemporary cultivars. In both models, introgression played an important role in rice domestication. Population genetic studies of a critical domestication gene, *sh4*, suggested that artificial selection could be strong enough to have driven its fixation in cultivated rice within a period of ~100 years. The slow fixation of the non-shattering phenotype observed at the archeological sites might be a result of relatively weak selection on mutations other than *sh4* during early rice cultivation. Cloning and analyses of additional domestication genes can further test hypotheses concerning rice domestication.