

Abstract

# Diversity of Domestication Loci in Wild Rice Populations <sup>†</sup>

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**Abstract:** Domestication syndrome, i.e. seed shattering, seed dormancy and plant architecture have been selected during the domestication of wild rice around 10,000 years ago. These traits evolved through a series of genomic modifications, including selection of nucleotide polymorphisms resulting from spontaneous mutations, recombination, and fixation of alleles and were incorporated into cultivated rice by hybridization or introgression. The Australian wild rice populations are geographically and genetically distinct and free from genetic exchange with cultivated rice unlike the wild populations in Asia. Furthermore, recent studies reveal they have numerous traits of value and unique alleles. Therefore, these populations seem to be suitable to use to investigate the genetic basis of domestication traits as well as other important traits. In this study, we aim to determine the origin and role of domestication loci using two Australian wild populations: Taxa A (like *Oryza rufipogon*) and Taxa B (like *Oryza meridionalis*) endemic near Cairns, Northern Queensland. To do so, firstly, we will analyse the variation of domestication loci in these two wild populations by the comparison with cultivated rice (*Oryza sativa* spp. *japonica* cv. Nipponbare) using the whole genome sequencing. Secondly, we will look at the gene expression of the domestication loci at different seed development stages using transcriptomics. Thirdly, we will determine the variation of starch synthesis related genes using whole genome sequencing. Next generation sequencing along with a set of bioinformatics tools will be applied. This research may enlighten our understanding about the domestication process as well as provide insights into how to domesticate these species through genetic manipulation for commercial purpose.

**Keywords:** domestication traits; wild rice; diversity; next generation sequencing

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