

Category	: 8th Rice Genetics Symposium
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	: Sequencing
Genome biology Structure Function and Comparison Keyword 2	: Phylogeny
Genome biology Structure Function and Comparison Keyword 3	: Genome evolution
Title of Entry	: Contribution of wild rice introgression to the adaptation of Southeast Asian weedy rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Weedy rice is a conspecific form of cultivated rice that infests agricultural fields and causes severe production loss worldwide. Genetic and morphological assessments around the world suggest there have been multiple independent origins of weedy rice from different cultivated rice varieties. In South and Southeast Asia, weedy rice may also be influenced by local wild rice populations, which can hybridize with co-occurring cultivated and weedy rice. In this study, we examined the evolution of Southeast Asian weedy rice ecotypes by comparing high-coverage (>20X) whole genome sequences of 31 Southeast Asian accessions (13 from Malaysia and 18 from Thailand) with weedy rice genomes from the United States (38 accessions) and China (3 accessions). Phylogenetic and population structure analyses confirm multiple independent weed origins, with a major role for indica crop varieties in the origin of all Southeast Asian ecotypes. In addition, genetic contributions from wild rice have played a major role in the evolution of some Thai weedy rice accessions. These wild-like weeds are also characterized by elevated genome-wide heterozygosity, a pattern consistent with wild rice hybridization in their recent past. Genome scans for selection suggest that multiple genomic regions have been targets of selection in weedy rice evolution, and that these differ among independently-evolved weed ecotypes. These findings support growing evidence from

comparative QTL mapping and other analyses that weediness adaptations can arise through multiple genetic mechanisms, and that weedy rice evolution has not been constrained by genetic bottlenecks during rice domestication.

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