Genome evolution in rice and other grasses and possible impact of gene duplications on adaptation of rice to growth in aquatic habitats

Taikui Zhang1, Weichen Huang1,2, Lin Zhang3, Tyler Hughes1,4, Yi Hu1, Hong Ma1, \*  
1Department of Biology, the Eberly College of Science, and the Huck Institutes of the Life Sciences, the Pennsylvania State University, University Park, State College, PA 16802, USA  
2Department of Chemistry, Tufts University, 62 Talbot Ave Medford, MA 02155, USA  
3Chongqing Key Laboratory of Plant Resource Conservation and Germplasm Innovation, School of Life Sciences, Southwest University, Chongqing 400715, China  
3Plant Science and Conservation Department, Missouri Botanical Garden, 4344 Shaw Blvd, St. Louis, MO 63110, USA

\*Speaker: E-mails: H.M. (hxm16@psu.edu).

Abstract

Analyses of the rice genomes revealed that rice experienced an ancient whole-genome duplication (WGD) called rho, which has been found to be shared by other grasses (members of Poaceae) and proposed to have played crucial roles in the adaptive evolution or rice and other grasses. However, relatively little is known about the evolutionary pattern of the rho-derived duplicates in the rice genome in comparison with genomes of other grasses in different Poaceae subfamilies during the evolutionary history of the grass family, nor has there been a global evolutionary examination of possible implications of gene duplicates from rho and other events in adaptive evolution of rice and other grasses. Here we present phylogenomic/phylotranscriptomic analyses of 363 grasses covering all 12 Poaceae subfamilies, using a recently established Poaceae nuclear phylogeny as a reference. The results support nine previously unknown WGDs, including a WGD that was likely shared by woody bamboos with possible gene flow from herbaceous bamboos. Furthermore, rho duplicates showing differential retention among Poaceae subfamilies include those with functions in environmental adaptations or morphogenesis, such as *ACOT* for aquatic environments (Oryzoideae) and other genes for cold responses (Pooideae) and drought/cold responses (Panicoideae). Moreover, a separate analysis of rice and its close relatives in the same genus (*Oryza*) implicated recent paralogs of a tetraploid *Oryza* species in tolerance of seawater submergence. These results on the evolution of rice genome and other recent evolutionary genomic analyses of rice and other grasses will be present and their implications discussed.