High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences
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Chengjun Zhang1,†, Jun Wang2,†, Nicholas C. Marowsky2, Manyuan Long1, Rod A. Wing3,* and Chuanzhu Fan2,∗


1Department of Ecology and Evolution, University of Chicago, Chicago, IL 60637, USA
2Department of Biological Sciences, Wayne State University, Detroit, MI 48202, USA
3Arizona Genomics Institute, School of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA

*Author for Correspondence: Chuanzhu Fan, Department of Biological Sciences, Wayne State University, 5047 Gullen Mall, Detroit, MI 48202; Phone: 313-577-6451; Fax: 313-577-6891; email: cfan@wayne.edu.
Rod A. Wing, Arizona Genomics Institute, School of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA. Phone: 520-626-9595; Fax: 520-621-1259; email: rwing@ag.arizona.edu.

Abstract

In an effort to identify newly evolved genes in rice, we searched the genomes of Asian cultivated rice O. sativa ssp. japonica and its wild progenitors, looking for lineage specific genes. Using genome pairwise comparison of 20Mb DNA sequences from the chromosome 3 short arm (Chr3s) in six rice species, Oryza sativa, O. nivara, O. rufipogon, O. glaberrima, O. barthii, and O. punctata, combined with synonymous substitution rate tests and other evidence, we were able to identify potential recently duplicated genes which evolved within the last one million years. We identified 28 functional O. sativa genes which likely originated after O. sativa diverged from O. glaberrima. These genes account for around 1% (28/3176) of all annotated genes on O. sativa’s Chr3s. Among the 28 new genes, two recently duplicated segments contained eight genes. Fourteen of the 28 new genes consist of chimeric gene structure derived from one or multiple parental genes and flanking targeting sequences. Although the majority of these 28 new genes were formed by single or segmental DNA-based gene duplication and recombination, we found two genes which were likely originated partially through exon shuffling. Sequence divergence tests between new genes and their putative progenitors indicated that new genes were most likely evolving under natural selection. We showed all 28 new genes appeared to be functional, as suggested by Ka/Ks analysis and the presence of RNA-seq, cDNA, EST, MPSS, and/or small RNA data. The high rate of new gene origination and of chimeric gene formation in rice may demonstrate rice’s broad diversification, domestication, its
environmental adaptation, and the role of new genes in rice speciation