Global Genomic Diversity of Oryza sativa Varieties Revealed by Comparative Physical Mapping

2014

Posted by : webmaster
Posted on : 2014/1/22 21:08:47

Xiaoming Wang, David A. Kudrna, Yonglong Pan, Hao Wang, Lin Liu, Haiyan Lin, Jianwei Zhang, Xiang Song, Jose Luis Goicoechea, Rod A. Wing, Qifa Zhang and Meizhong Luo


Abstract

BAC physical maps embedding a large number of BAC end sequences (BESs) were generated for Oryza sativa ssp. indica varieties Minghui 63 (MH63) and Zhenshan 97 (ZS97), and were compared with the genome sequences of O. sativa ssp. japonica cv. Nipponbare and O. sativa ssp. indica cv. 93-11. The comparisons exhibited substantial diversities in terms of large structural variations, and small substitutions and indels. Genome-wide BAC-sized and contig-sized structural variations were detected, and the shared variations were analyzed. In the expansion regions of the Nipponbare reference sequence, in comparison to the MH63 and ZS97 physical maps, as well as to the previously constructed 93-11 physical map, the amounts and types of the repeat contents, and the outputs of gene ontology (GO) analysis, were significantly different from those of the whole genome. Using the physical maps of four wild Oryza species from OMAP (http://www.omap.org) as control, we detected many conserved and divergent regions related to the evolution process of O. sativa. Between the BESs of MH63 and ZS97 and the two reference sequences, a total of 1,532 polymorphic simple sequence repeats (SSRs), 71,383 SNPs, 1,767 MNPs, 6,340 insertions and 9,137 deletions were identified. This study provides independent whole genome resources for intra- and inter-subspecies comparisons and functional genomics studies in O. sativa. Both the comparative physical maps and the GBrowse, which integrated the QTL and molecular markers from GRAMENE (http://www.gramene.org) with our physical maps and analysis results, are open to public through our website (http://gresource.hzau.edu.cn/resource/resource.html).