Spatio-temporal patterns of genome evolution in allotetraploid species of the genus Oryza

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Abstract
Summary Despite knowledge that polyploidy is widespread and a major evolutionary force in flowering plant diversification, detailed comparative molecular studies on polyploidy have been confined to only a few species and families. The genus Oryza is composed of 23 species that are classified into ten distinct ‘genome types’ (six diploid and four polyploid), and is emerging as a powerful new model system to study polyploidy. Here we report the identification, sequence and comprehensive comparative annotation of eight homoeologous genomes from a single orthologous region (Adh1-Adh2) from four allopolyploid species representing each of the known Oryza genome types (BC, CD, HJ and KL). Detailed comparative phylogenomic analyses of these regions within and across species and ploidy levels provided several insights into the spatio-temporal dynamics of genome organization and evolution of this region in ‘natural’ polyploids of Oryza. The major findings of this study are that: (i) homoeologous genomic regions within the same nucleus experience both independent and parallel evolution, (ii) differential lineage-specific selection pressures do not occur between polyploids and their diploid progenitors, (iii) there have been no dramatic structural changes relative to the diploid ancestors, (iv) a variation in the molecular evolutionary rate exists between the two genomes in the BC complex species even though the BC and CD polyploid species appear to have arisen