Comparative Sequence Analysis of the Ghd7 Orthologous Regions Revealed Movement of Ghd7 in the Grass Genomes

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Lu Yang1, Tieyan Liu1, Bo Li1, Yi Sui1, Jinfeng Chen1, Jinfeng Shi1, Rod A. Wing2, Mingsheng Chen1*

1 State Key Laboratory of Plant Genomics, Institute of Genetics and Developmental Biology, Chinese Academy of Science, Beijing, China, 2 Arizona Genomics Institute, School of Plant Sciences, BIO5 Institute, University of Arizona, Tucson, Arizona, United States of America

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Abstract
Ghd7 is an important rice gene that has a major effect on several agronomic traits, including yield. To reveal the origin of Ghd7 and sequence evolution of this locus, we performed a comparative sequence analysis of the Ghd7 orthologous regions from ten diploid Oryza species, Brachypodium distachyon, sorghum and maize. Sequence analysis demonstrated high gene collinearity across the genus Oryza and a disruption of collinearity among non-Oryza species. In particular, Ghd7 was not present in orthologous positions except in Oryza species. The Ghd7 regions were found to have low gene densities and high contents of repetitive elements, and that the sizes of orthologous regions varied tremendously. The large transposable element contents resulted in a high frequency of pseudogenization and gene movement events surrounding the Ghd7 loci. Annotation information and cytological experiments have indicated that Ghd7 is a heterochromatic gene. Ghd7 orthologs were identified in B. distachyon, sorghum and maize by phylogenetic analysis; however, the positions of orthologous genes differed dramatically as a consequence of gene movements in grasses. Rather, we identified sequence remnants of gene movement of Ghd7 mediated by illegitimate recombination in the B. distachyon genome.