

Discussion on Relationship Between Rice and Rice Genome

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Introduction

Over the past several years, selected regions of the japonica and indica rice genomes have been sequenced. The International Rice Genome Sequencing Project was organized to achieve 99.99% accurate sequence using a mapped clone sequencing strategy. In addition, expressed gene sequencing has been actively pursued. More than 104,000 expressed sequence tags from a variety of rice tissues have been entered into the EST database. Other rice genome sequencing projects have been reported by Monsanto Co. and by the Beijing Genomics Institution [1]. The two major groups of flowering plants, monocots and dicots, diverged 200 million years before. In late 2000, the 125-Mbp genome of the dicot model plant *Arabidopsis thaliana* was reported. Similar higher accuracy sequencing projects of important cereals would be expensive and slow because their genomes are so large. Recent improvements in automated DNA sequencing have made whole-genome shotgun sequencing an attractive approach for gene discovery in both small and large genomes. Here, we describe the random-fragment shotgun sequencing of *Oryza sativa* L. ssp. japonica to discover rice genes, molecular markers for breeding, and mapped sequences for the association of candidate genes and the traits they control. Also reported are the linkages of sequence assemblies to rice bacterial artificial chromosome end sequences and fingerprints, anchoring of the physical and genetic maps, and the syntenic relationship between rice and other plants. The finding that most cereal genes have strong rice homologs suggests that the rice genome will be useful as a foundation for sequencing the genomes of related cereals. Synteny among cereals should allow placement of low-copy cereal genes on a rice genome framework. Rice and *Arabidopsis* diverged from a common ancestor about 200 million years ago [2]. Although the existence of *Arabidopsis* rice synteny has been controversial, evolutionary models based on estimated mutation rate predict some syntenic relationships between distantly related species such as *Arabidopsis* and rice. To address this issue, all annotated *Arabidopsis* proteins were compared to anchored Syd sequence contiguous. This approach links *Arabidopsis* proteins to related mapped rice sequences, forming syntenic groups. When a 99.9% significance threshold is applied, 137 *Arabidopsis*-rice syntenic groups are found at 75 rice chromosomal locations throughout the genome, with no discernible pattern [3]. This is a conservative estimate; reducing the significance threshold to 99% increases the number of syntenic groups to 508. Of the 137 high-confidence syntenic groups, the largest mapped to *Arabidopsis* chromosome 5 and rice chromosome. This syntenic block includes 119 *Arabidopsis* proteins. The predicted roles of these proteins do not suggest an obvious reason for their conservation. Within the 137 high-confidence syntenic groups, several rice blocks map to more than one site in the *Arabidopsis* genome. One such block maps to all five *Arabidopsis* chromosomes, 8 map to four *Arabidopsis* chromosomes, 10 map to three *Arabidopsis* chromosomes, 14 map to two *Arabidopsis* chromosomes, and the remaining 42 map to a single *Arabidopsis* chromosome. This observation suggests that multiple rounds of duplication occurred within the *Arabidopsis* genome, and it is consistent with the results of studies comparing distantly related dicot pairs such as tomato *Arabidopsis* and soybean-*Arabidopsis*. Syntenic protein pairs are two proteins found in close proximity in both rice

and *Arabidopsis*, excluding tandem duplications [4]. Only 2% of the syntenic protein pairs on *Arabidopsis* chromosome 5 are adjacent to one another. 52% of the syntenic protein pairs are separated by 1 to 150 intervening proteins. This distribution of related protein pairs in rice and *Arabidopsis* is not random, providing further support for a syntenic relationship between *Arabidopsis* and rice. Selective gene loss and large-scale chromosomal duplication during *Arabidopsis* genome evolution could be responsible for the distribution observed. These observations support previous hypotheses that detectable synteny exists between monocots and dicots even after 200 million years of divergence, although the conservation is less extensive than previously predicted. The rice and *Arabidopsis* genomes are rearranged to such an extent that constructing a monocot-dicot comparative framework based on these two genomes would be difficult [5]. The low but detectable synteny between rice and *Arabidopsis* may provide clues to orthologous gene identification in future functional genomics studies.

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Conflict of interest

None

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