Molecular Phylogenetics of the Genus *Oryza* L. (Poaceae): Evidence from the Sequences of the Internal Transcribed Spacer (ITS) of Nuclear Ribosomal DNA

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1 Introduction

Oryza L., a genus in the tribe Oryzeae of the family Poaceae, is composed of two cultivated rice species and 21 recognized wild species distributed across pantropical and subtripical regions of four continents. According to Vaughan's recent revision (1989, 1994), the genus *Oryza* was divided into four species complexes, Sativa complex, Officinalis complex, Meyeriana complex and Ridleyi complex, as well as two isolated species: *O. schlechteri* and *O. brachyantha*. Phylogenetic relationships among the species in the genus *Oryza* have been established on the basis of cytogenetic, biochemical and molecular data. In nuclear genome, internal transcribed spacer (ITS) has been widely used to reveal phylogenetic relationships of closely related genera and species. In present study, the ITS region of nrDNA of all known species in the genus *Oryza* was sequenced. The phylogenetic relationships among the species and genome were assessed based on nucleotide sequence of ITS region using PAUP analysis.

2 Method and Results

The sequences of the ITS region of 23 species in the genus *Oryza* together with four outgroups were sequenced, and further aligned with the CLUSTAL V multiple sequence alignment program and Multalign. The aligned sequences were analyzed employing Wagner parsimony, which assumes equal probability of character loss and character gain, with the "heruistics" option of PAUP 3.1.1 with simple sequence addition and TBR branch-swapping option in effect. As measures of the amount of homoplasy in the characters, consistency index (CI) and retention index (RI) were presented. Bootstrap values were obtained from 100 replicates parsimony analyze using "heuristics" option and "simple" addition sequence of the taxa in PAUP program.

The sequence divergence between species ranged from 0.9%-42.5%. Out of 503 aligned sequence sites from ITS1 and ITS2 regions in 29 accessions of 27 species, 151 were phylogenetically informative. Using these informative data with gaps treated as missing, PAUP found five most parsimonious trees with 1047 steps and a tree Pairwise The ITS1 in these taxa varied from 194 bp to 214 bp, and the ITS2 ranged from 228 bp to 236 bp in length. Sequence divergence ranged from 0.9% to 42.5%. The phylogenetic trees reconstructed from the ITS sequence data were in general agreement with those based on morphological, cytological, biochemical and the most of other molecular data. The Sativa group and the Officinalis group form a natural group in the genus *Oryza*. *O. ridleyi* and *O. longiglumis* show very close relationship with each other. *O. brachyantha* occupies its position between the Ridleyi group and the Meyeriana group. The ITS sequence data indicated that the genus *Porteresia* has close affinity to *O. brachyantha*, *O. granulata* and *O. meyeriana. Porteresia coarctata* may be actually a member of the genus *Oryza*.

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