

Genetic relatedness of genus *Oryza* from Eastern Himalayan region as revealed by chloroplast *matK* gene

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ABSTRACT

Phylogenetic relationship was studied in wild and cultivated rice using the chloroplast *matK* gene. The aligned sequence fragments were 826bp in length with 7.02% variable and 4.47% phylogenetically informative sites and the estimated Transition/Transversion bias (R) was 1.97. Seven hundred and two characters were constant, 74 variable characters were parsimony-uninformative and 50 were parsimony-informative. Haplotypes of Mizoram rice and wild relatives (A genome) were more similar than those of distantly related species (B, C/CD, E and G genomes). It further revealed that the EE genome species is most closely related to the CC genome and CCDD genomes. The BBCC genome species had different origins, and their maternal parents had either the BB or CC genome. An additional genome type, HHKK was recognized in *O. coarctata* and *O. schlechteri*. Within the AA genome the African, *O. glaberrima* and *O. longistaminata* and American, *O. glumipatula* and *O. barthii* were closer to the Indian *Oryza* species, *O. nivara* and *O. rufipogon*. The unknown genome *O. malampuzhaensis* from India is closer to BB and BBCC genome containing respectively *O. punctata* from Cameroon and *O. minuta* from Philippines. CpG rich *matK* sequences were rich in GG and FF genotypes, whereas CpA rich sequences belonged to BB and BBCC related genomes variety.

Key words: *Oryza* species; *matK* gene; phylogeny; genotype; divergence; eastern himalayas