

In silico Comparative Analysis of Chloroplast Genome (cpDNA) and Some Individual Genes (rbcL and trnH-psbA) in Pooideae Subfamily Members

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Abstract : An in silico analysis of *Brachypodium distachyon*, *Triticum aestivum*, *Festuca arundinacea*, *Lolium perenne*, *Hordeum vulgare* subsp. *vulgare* of the Pooideae was performed based on complete chloroplast genomes including rbcL coding and trnH-psbA intergenic spacer regions alone to compare phylogenetic resolving power. Neighbor-joining, Minimum Evolution, and Unweighted Pair Group Method with arithmetic mean methods were used to reconstruct phylogenies with the highest bootstrap supported the obtained data from whole chloroplast genome sequence. The highest and lowest values from nucleotide diversity (π) analysis were found to be 0.315813 and 0.043495 in rbcL coding region in chloroplast genome and complete chloroplast genome, respectively. The highest transition/transversion bias (R) value was recorded as 1.384 in complete chloroplast genomes. *F. arundinacea-L. perenne* clade was uncovered in all phylogenies. Sequences of rbcL and trnH-psbA regions were not able to resolve the Pooideae phylogenies due to lack of genetic variation.

Keywords : chloroplast DNA, Pooideae, phylogenetic analysis, rbcL, trnH-psbA

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