DNA BARCODES SCREENING AND PHYLETIC CLASSIFICATION OF GENUS ZEA

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Abstract

Maize and teosintes are excellent systems for study of population and ecological genomics, as well as teosintes provide excellent germplasm resources for forage maize breeding. However, genetic relationship, evolution, hybridization and introgression among the genus Zea species have not been completely resolved and effective methods for Zea species classification and identification are scarce. In current study, nuclear (ITS), mitochondrial DNA (atp6, cob and nad1) and chloroplast DNA sequences (matK, psbA-trnH and rbcL) were used to explore as a simple and efficient DNA barcode for identification and genetic study of the Zea species. Phylogenetic incongruence between nuclear and cytoplasmic sequences detected in present study. The lowest divergence value from pairwise comparisons were found between Z. mexicana and Z. parviglumis based on combined six cytoplasmic sequences and Z. mexicana and maize showed lowest divergence value based on ITS sequences. It is suggested that single-gene data sets and combined data sets of six cytoplasmic sequences failed to identify and classify every species at inter-species level, however, the combined data set containing ITS and atp6 can identify and classify Zea species perfectly. Moreover, the tetraploid Z. perennis was confirmed an autotetraploid of diploid Z. diploperennis reflecting from phylogenetic tree based on combined six cytoplasmic sequences.

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