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Assessment of candidate DNA Barcoding loci for phylogenetic relationships among *Triticum* species

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Statement of the Problem: DNA Barcoding is widely used for identification of species based on standard DNA regions. The Consortium for the Barcode of Life (CBOL) plant-working group recommended different nuclear and chloroplast loci as the standard plant barcode. Though many loci have been proposed as a DNA barcodes in plants, standardizing regions as a DNA barcode poses a challenge in many plant families. The evolutions of the chloroplast regions combine with nuclear genes are sufficiently rapid to allow discrimination between closely related species.

Material & Methods: In this study, we tested the phylogenetic utility of the DNA barcoding loci (ITS2, matK, psbA-trnH, rbcL and trnT) for efficient discrimination of *Triticum* species. For the assessment of the barcoding efficiency to resolve the species discrimination, a total of 113 accessions representing 18 species/sub-species within *Triticum* genus have been sampled. Consensus sequences of each region were manually edited with MEGA6 and the sequences were aligned and assessed for candidate DNA Barcode for phylogenetic relationships among *Triticum* species.

Findings: Topologies of the phylogenetic trees based on combination of DNA barcode analyses were similar but a few *Triticum* species were placed into distant phylogenetic groups. The 113 accessions analyzed in this study were placed into three groups supported by high bootstrap values. However, the barcoding analyses were not able to discriminate some closely related *Triticum* species.

Conclusion & Significance: We have proposed concatenated data approach to increase resolving power of candidate barcoding loci as an additional tool for phylogenetic analysis in *Triticum* species. However, molecular studies with more diverse markers and species will be required to clarify the ambiguities surrounding the phylogeny of these important genera.

Biography

Lee Gi-An has his expertise in evaluation and characterization of plant genetic resources. He has worked in National Agro-Biodiversity Center (NAC, RDA, Republic of Korea) for more 12 years as a Researcher.

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