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Genome-wide Single Nucleotide Polymorphism Marker Provide a well-resolved Phylogeny for the Genus *Triticum* (Poaceae)

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[Introduction]

Wheat (*Triticum* spp.) is one of the most widely cultivated food crop worldwide. The genus *Triticum* L. has a complex polyploidy species in which majority of the species have not yet been discriminated clearly.

[Materials and Methods]

In this study, we used Genotyping-by-sequencing (GBS) to obtain SNPs covering all seven chromosomes from 283 accessions of *Triticum* related genera.

[Results and Discussions]

After filtering low quality and redundant SNPs based on haplotype information, the GBS assay provided 14,188 high-quality SNPs that were distributed across the A (71%), B (26%), and D (2.4%) genomes. Cluster analysis and discriminant analysis of principal components (DAPC) allowed us to distinguish six distinct groups that matched well with *Triticum* species complexity. We constructed Bayesian phylogenetic tree using 14,188 SNPs, in which 17 *Triticum* species and subspecies have discriminated. The dendrogram analysis revealed that the polyploid wheat species could be divided into groups according to the presence of A, B, D and G genomes with strong nodal support and provided a new insight on the evolution of spelt wheat. This study demonstrated that GBS derived SNPs could be used efficiently in genebank management to classify *Triticum* species and subspecies that are very difficult to distinguish by their morphological characters.

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