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Phylogenetic analysis of high-throughput sequencing data for a non-transcribed spacer 5S rDNA of *Triticum aestivum* relatives

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The 5S rRNA is one of the most important structural and functional component of the large subunit of the ribosomal. 5S rDNA has long been a favored target for cytological and phylogenetic studies due to their high interspecific divergence and the tandem arrays repetitive units. The repeating unit of 5S rDNA contains a 120 bp coding region and a non-transcribed spacer sequence (NTS). The former is highly conserved in structure, whereas the NTS is polymorphic in both length and nucleotide sequence. Thus, sequencing of tandem repeats is difficult task. To multiplexing sequencing NTS of the 53 accessions of relatives of *T. aestivum* (3 acc. *T. monococcum*, 3 acc. *T. baeoticum*, 6 acc. *T. urartu*, 16 acc. *T. dicoccoides*, 6 acc. *T. araraticum*, 3 acc. *T. timopheevii*, 16 acc. *Ae. speltoides*) by high-throughput method, we have developed six pair primers to NTS for inner barcoding. Obtained results were transformed by FastX Tool Kit (www.galaxy.org). The molecular phylogenetic analysis of common sequences allowed to reveal two major evolutionary branches of NTS: Short type and Long type. Short type branch consisted of three minor types: ShortA1, ShortA2 and ShortG1 (in agreement with the classification of Baum and Bailey, 2001), and Long type branch consisted of two minor types: LongS1 (Baum and Bailey, 2001) and LongA1 (Baum and Bailey, 2004). Thus, the multiple sequence alignment problem, one of the most difficult problems in computational molecular biology, can be solve.

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