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Phylogenetic relationship of *Leymus chinensis* revealed by the ITS and chloroplast trnL-F sequences

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Key word: *Leymus chinensis*, *Psathyrostachys*, X_m genome, ITS, chloroplast trnL-F

Introduction Based on morphological observation, meiotic chromosome pairing of intergeneric hybrids, DNA hybridization patterns, and variation in repeated nucleotide sequences, previous studies have concluded that one genome in *Leymus* species originated from the genus *Psathyrostachys* (Wang *et al.*, 2006). Despite decades of intensive research, the precise phylogenetic relationship of *L. chinensis* is still unclear. The nuclear and chloroplast/mitochondrial sequences were used in many molecular phylogenetic studies for elucidating the origins and evolutionary history of polyploidy in plants, clarified their parental lineages. Particularly, internal transcribed spacers (ITS) and the intergenic spacer of trnL-trnF have been used widely in studying phylogenetic and genomic relationships of the diploid Poaceae genera. With additional abundant available sequences in public databases, ITS and trnL-trnF are the optimal choices in this study.

Materials and methods Two accessions of *L. chinensis* and *Psathyrostachys juncea* were included in this study. They were analyzed together with 18 related genera, consisting of 40 diploid species in the tribe Triticeae. *Bromus catharticus* was used as the outgroup based on previous phylogenetic studies. The aligned data set of the ITS and the trnL-F were analyzed using PAUP version 4.0. Heuristic search was implemented with 100 random additional sequence replicates, tree-bisection-reconnection (TBR) branch swapping, MULPARS option, and ACCTRAN optimization. To evaluate relative robustness of the clades found in the most parsimonious trees, bootstrap analysis was conducted using 500 replicates with a simple taxon addition.

Results It was showed that: (1) The ITS sequences revealed polyploidy *Leymus* have close phylogenetic relationships with *Psathyrostachys* and an unknown genus in Triticeae. The ITS tree suggested considerable differentiation among *Leymus* species and recurrent hybridization of *Leymus*. (2) The trnL-F tree revealed especially close relationships of partial *Leymus* species and *Psathyrostachys*, residual *Leymus* species and an unknown genus (Figure 1). The trnL-F tree showed that the mother of *Leymus chinensis* was *Psathyrostachys*, and the father was the X_m genome.

Conclusions The results indicated that it was unlikely that the unknown genome in *Leymus* species originated from a modified version of the N_s genome or any sampled diploid species in present study; The maternal of *L. chinensis* was N_s genome and the paternal genome was X_m.

Reference

Wang RRC, Zhang JY, Lee BS, Jensen KB, Kishii M, Tsujimoto H (2006). Variations in abundance of 2 repetitive sequences in *Leymus* and *Psathyrostachys* species. *Genome*, 49, 511-519.

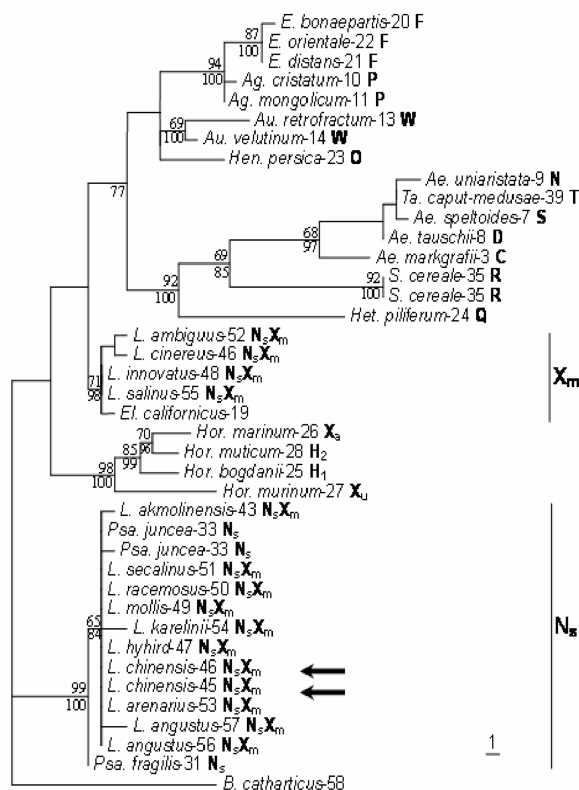


Figure 1 One of the 500 most parsimonious (MP) trees generated from the trnL-F sequences (Tree length = 147, CI = 0.7687, RI = 0.8707). The topologies obtained by Bayesian analysis are identical except for some nodes having different bootstrap values.