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## Genetic polymorphism by RAPD of *Leymus chinensis*

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**Key words :** genetic polymorphism, DNA, natural variation, RAPD, *Leymus chinensis*

**Introduction** *Leymus chinensis* (Trin.) Tzvel. is a perennial, rhizomatous species distributed widely in north China. During the long-time adaptation and evolution process, great differentiations in morphology, physiology, biochemistry and molecular biology generated. A better knowledge of genetic diversity of *L. chinensis* could be valuable in the efficient utilization, conservation and management of germplasm collections. The aims of this study were to analyze the genetic diversity of *L. chinensis* selected from cultivars of phenotypic variation.

**Materials and methods** Thirty cultivars of *L. chinensis* with different phenotype (Liang *et al.*, 2007) were cultivated in green house for 3 months and leaves were sampled for extracting the genomic DNA by the cetyltrimethylammonium bromide (CTAB) method (Puchooa, 2004), and then RNase was added. The yield of DNA was measured using UV-VIS spectrophotometer (Shimadzu). Twenty random primers were used for the amplification. Nei and Kumar's genetic diversity were calculated between accessions. Dendrogram from genetic distance was constructed by Nt-Sys software.

**Results and conclusions** The results of RAPD products electrophoresis and the dendrogram were presented in Figure 1 and Figure 2 respectively. Thirteen RAPD primers generated 98 bands, of which 88 were polymorphism, and 7 bands were generated by every primer in average. The mean genetic distance was 0.3355. Clustering analysis was performed with NTSYS and 30 clones were divided into 6 groups with threshold of 0.68. These results indicated that the genetic diversity of *L. chinensis* was very high and the cultivars with the same phenotype were not clustered into one group.

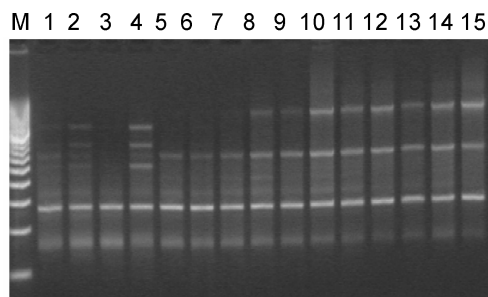


Figure 1 Electrophoresis pattern of templates L1-L15 with S8.

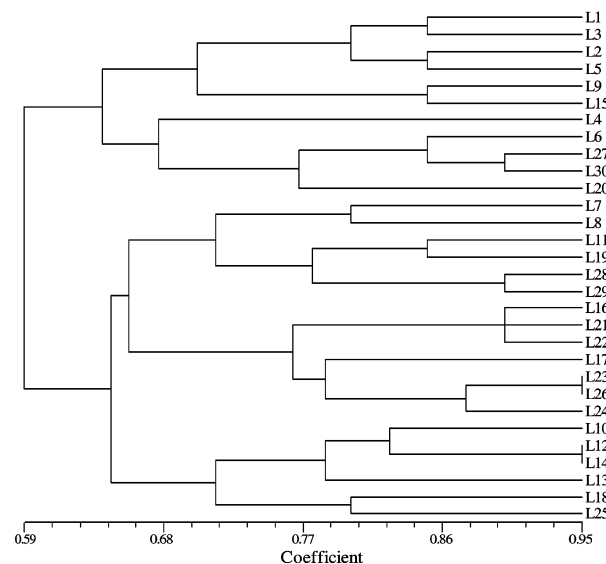


Figure 2 The dendrogram of L1~L30 constructed by UPGMA cluster analysis revealed by RAPD.

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### References

- Liang, Z. W., Ma, H. Y., Wang, Z. C., *et al.* (2007). Use of alkali tolerant plant for the improvement of high saline-alkali soil in Northeast China. Eighth Conference of the East and Southeast Asian Federation of Soil Science, pp20~25.
- Puchooa, D. (2004). A simple, rapid and efficient method for the extraction of genomic DNA from lychee (*Litchi chinensis* Sonn.) *African Journal of Biotechnology*, 3(4), 253-255.