Genetic polymorphism by RAPD of *Leymus chinensis*

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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 .

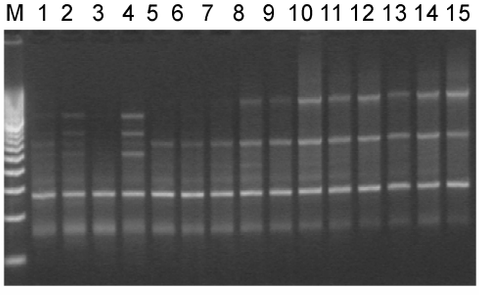

Figure 1 *Electrophoresis pattern of templates L1—L15 with S8 .*

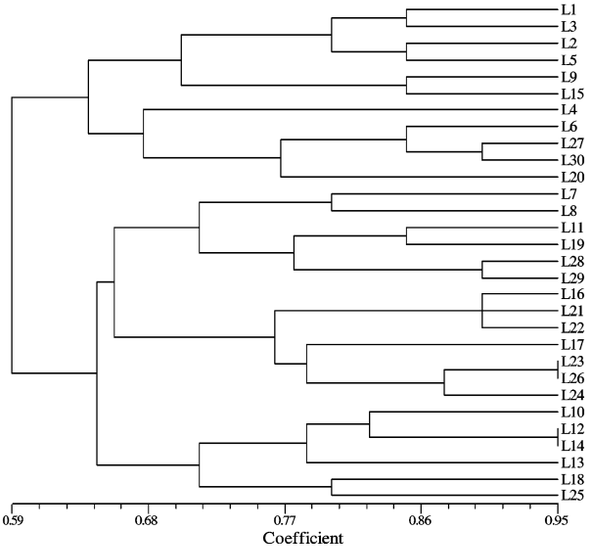

Figure 2 *The dendrogram of L1～L30 constructed by UPGMA cluster analysis revealed by RAPD .*

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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 .