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Huan Liu

Gansu Agricultural University, China

Ping Mu

Gansu Agricultural University, China

Guiqin Zhao

Gansu Agricultural University, China

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Study on AFLP based genetic diversity in oats

Liu Huan¹, Mu Ping² and Zhao Gui-qin¹

College of Grassland Science, Gansu Agricultural University, Lanzhou, 730070, E-mail: liuhuan@gsau.edu.cn

Key words: oat, genetic diversity, Amplified Fragment Length Polymorphism (AFLP), clustering analysis

Illustrations Oat (*Avena sativa* L.) is one of the major grass species used for food and forage, mostly in Europe, North America, Australia, China and other countries. China has a long history of oat cultivation, but the study focuses mainly on oat cultivation, adaptability and agronomic performance of landrace varieties, and introduction. In recent years, the research of genetic diversity on oat breeding rely on the morphological and agronomic traits, karyotype analysis, and biochemical marker, and the use of molecular markers on genetic diversity of oats is reported less.

Materials and methods AFLP analysis was conducted to assess genetic diversity of 34 covered oat varieties and 8 naked oat varieties from China, Australia, Canada Europe and other countries. Total DNA extraction with improved CTAB (Cetyl Triethyl Ammonium Bromide) methods. Extracted DNA was analyzed using the AFLP Analysis System following the protocol described by Vos et al. (1995). The factors affecting AFLP analysis in the study of genetic diversity of oats, including primer selection, digestion and ligation of DNA, amplified conditions, and detection methods were optimized. For each AFLP gel from a primer pair, the total number of AFLP bands were counted. NTSYSpc 2.1 software was used for data processing, using the Nei (1987) method to calculate genetic similarity coefficients which were used on UPGMA cluster analysis and to establish a cluster tree.

Results An optimization system of AFLP markers for oats was established. Five primer pairs with higher polymorphic and definition were selected from 30 EcoRI/MseI primer combinations, 268 informative AFLP markers were generated and 185 were polymorphic (69.0%). The highest polymorphic rate was 78.6% from primer E-AGG/M-CTA. In Nei's index calculation, average genetic diversity was 0.1664 and Shannon diversity index was 0.2206. The genetic similarity coefficient was 0.4881~0.9881, with 0.0120~0.7172 genetic distance. The fingerprinting data were further analyzed using UPGMA Cluster methods which clustered the 42 varieties into six main distinct groups at 0.748 genetic similarity coefficients.

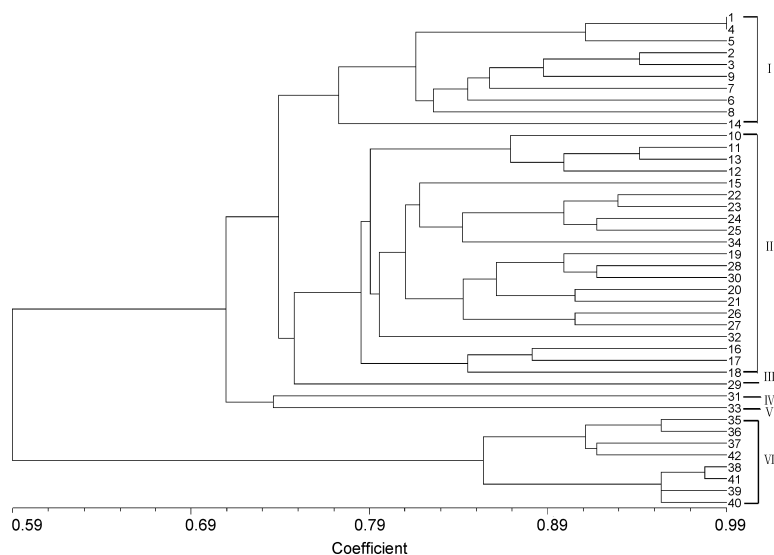


Figure 2 UPGMA cluster analysis based on Nei's genetic identities among 42 oat cultivars.

Conclusions Based on clustering results, covered oats and naked oats were divided into two groups at 0.59 genetic similarity coefficients, and genetic diversity of covered oats was higher than naked oats, which was in accordance with traditional classification. The genetic relationship revealed by AFLP was consistent with original sources; genetic distance was closely associated with geographical distributions.

Reference

Vos P, Hogers R, Bleeker M, et al, 1995. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research*. 24, 65~73.