Study on AFLP Based Genetic Diversity in Oats

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The XXI International Grassland Congress / VIII International Rangeland Congress took place in Hohhot, China from June 29 through July 5, 2008.

Proceedings edited by Organizing Committee of 2008 IGC/IRC Conference

Published by Guangdong People's Publishing House

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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 .

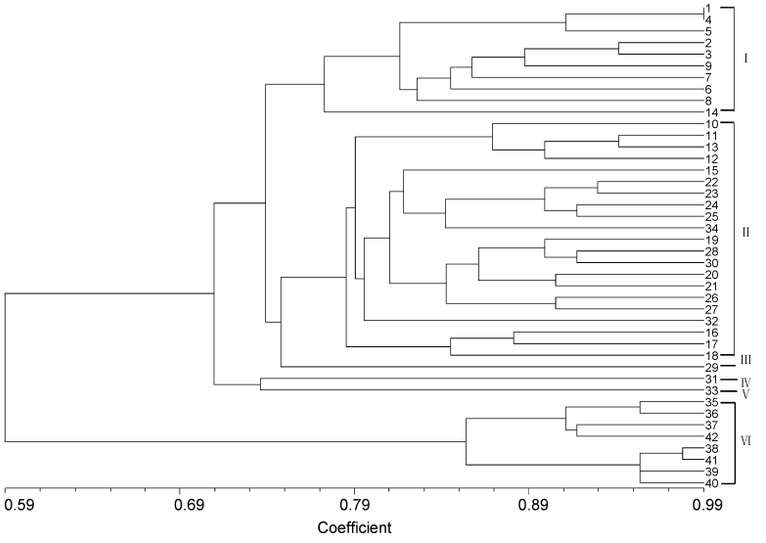

Figure 2 *UPGMA cluster analysis based on Nei's genetic identities among 42 oat cultivars .*

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 ; geneticdistance was closely associated withgeographical distributions .

Reference

Vos P , Hogers R , Bleeker M , *et* al ,1995 . AFLP : a new technique for DNA fingerprinting . *Nuclei Acids Research* . 249 , 65～73 .