

Comparisons of DNA marker-based genetic diversity with phenotypic estimates in maize grown in Pakistan

M.M. Shah¹, S.W. Hassan^{3,4}, K. Maqbool¹, I. Shahzadi¹ and A. Pervez²

¹Biotechnology Program, Department of Environmental Sciences, Commission on Science and Technology for Sustainable Development in the South, Institute of Information Technology, University Road, Abbottabad, Pakistan ²Life Sciences Community Services Center,

Commission on Science and Technology for Sustainable Development in the South, Institute of Information Technology, University Road, Abbottabad, Pakistan ³Institute of Biotechnology and Genetic Engineering,

NWFP Agricultural University, Peshawar, Pakistan

⁴Department of Applied Plant Sciences and Plant Biotechnology,

Institute of Agronomy and Plant Breeding,

University of Natural Resources and Applied Life Sciences, Vienna, Austria

Corresponding author: M.M. Shah E-mail: mmshah@ciit.net.pk

Genet. Mol. Res. 9 (3): 1936-1945 (2010) Received June 2, 2010 Accepted July 18, 2010 Published September 28, 2010 DOI 10.4238/vol9-3gmr964

ABSTRACT. We compared DNA-based genetic diversity estimates with conventional estimates by investigating agronomically important traits in maize grown in the northwestern region of Pakistan. RAPD markers were used to characterize 10 commonly cultivated maize genotypes. The same material was tested for phenotypic variation of quantitative traits using replicated field trials. The genetic distances between pairs of genotypes using RAPD data were used to generate a similarity matrix and to construct a phenogram. Statistical analyses were carried out on the data obtained from field trials of all maize genotypes for days to 50% tasseling, days to 50% silking, plant height, ear height, grain yield, grain weight per cob, and ear length. Analysis of variance and single degree of freedom contrasts were

performed on morphological data to examine the relationship between molecular-based clusters and agronomic traits. A molecular marker-based phenogram led to the grouping of all genotypes into four major clusters, some of which were distantly related. These clusters contained one to four genotypes. Analysis of variance showed significant variations among all genotypes for agronomic traits. The single degree of freedom contrasts between groups of genotypes indicated significant differences for most traits. Pair-wise comparisons between clusters were also significant. The two types of data correlated well, providing an opportunity for better choices for selection.

Key words: RAPD markers; Genetic variation; Quantitative traits; Maize; *Zea mays*