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EST-SSR-Based Phylogenetic Analysis Of USDA *Brachypodium distachyon* Collection

Yiqun Weng¹, Perumal Azhaguvel¹, Wanlong Li², Bikram S. Gill², Jackie C. Rudd¹

¹ Texas A&M University Agricultural Research & Extension Center, 6500 Amarillo Blvd. W., Amarillo, TX 79106, USA

² Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA

Brachypodium distachyon ($2n = 2x = 10$) has been proposed as a model species of the temperate grasses for genomics research. However, much basic information is lacking in this species. In this study, genetic diversity of *B. distachyon* was investigated using six accessions (Bd1-1, Bd2-3, Bd3-1, Bd18-1, Bd21 and BD29) from the USDA collection and 160 SSR (simple sequence repeats) markers developed from *B. distachyon* ESTs. The effect of inbreeding on diversity in *B. distachyon* was also evaluated by comparison of three inbred lines (Bd2-3, Bd3-1, and Bd18-1) that have undergone five or six cycles of selfing with their respective original parental line. Three grass species, rice (*Oryza sativa* cv. Nipponbare), perennial ryegrass (*Lolium perenne* cv. Palmer), and *Aegilops tauschii* (accession AL8/78) were included as outliers in phylogenetic analysis. No polymorphism was detected between each of the three inbred lines and their respective parental line. While polymorphisms among different *B. distachyon* accessions were generally low, Bd1-1 and Bd21 were more diverse than the other lines examined. The genetic divergence was correlated with geographical distances. In the phylogenetic tree, *L. perenne* was closer to *B. distachyon* than *Ae. tauschii*, and rice was the most distant. Information from this study should be useful in selecting parents for linkage mapping in *B. distachyon*.