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Population Structure and Genetic Diversity of Sudanese Pearl Millet Landraces, and Relationship Between Genetic and Agro-Morphological Diversity

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Abstract

Understanding the genetic structure and identification of distinct clusters with complementary traits is an important goal for a sustained and successful pearl millet breeding program. In this study a genotypic analysis of 214 pearl millet accessions collected from different geographical regions of Sudan, and 10 accessions from West and Central Africa, were conducted with 30 simple sequence repeat markers (SSRs) covering the pearl millet genome. A high degree of molecular diversity among the studied material was observed, with an average of 13.3 alleles per locus was detected. The average polymorphic information content (PIC), gene diversity and observed heterozygosity of the 30 SSRs were 0.77, 0.82 and 0.72 respectively. A total of seven phylogenetic groups with variable sizes were identified. Low correlation between the agro-morphological matrix and the genetic matrix was observed ($r = 0.20$). The average PIC values obtained across the seven linkage groups varied significantly. Neighbour-joining tree, principal components analyses and STRUCTURE showed that there were no clear differentiations among the geographical regions. This result indicated that there were high levels of admixture among the regions. Analysis of molecular variance (AMOVA) revealed that the variation of pearl millet accessions within the regions was much higher than among the regions. The large divergence observed among the landraces of this study would be promising for developing new varieties as well as for development of heterotic groups which can be used to develop population and hybrid varieties with higher degrees of heterozygosity and therefore hybrid vigour and stability, as well as to intensify yield production in the harsh production environments of Sudan.

Keywords: Genetic diversity, geographic regions, pearl millet, simple sequence repeats (SSRs), Sudan