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Genetic Diversity Analysis of Pearl Millet (Pennisetum glaucum [L. R. Rr.]) Accessions from Northwestern Nigeria

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Abstract: Pearl millet is the most drought tolerant of all domesticated cereals, is cultivated extensively to feed millions of people who mainly live in hash agroclimatic zones. It serves as a major source of food for more than 40 million smallholder farmers living in the marginal agricultural lands of Northern Nigeria. Pearl millet grain is more nutritious than other cereals like maize, is also a principal source of energy, protein, vitamins, and minerals for millions of poorest people in the regions where it is cultivated. Pearl millet has recorded relatively little research attention compared with other crops and no sufficient work has analyzed its genetic diversity in north-western Nigeria. Therefore, this study was undertaken with the objectives to analyze the genetic diversity of pearl millet accessions using SSR marker and to analyze the extent of evolutionary relationship among pearl millet accessions at the molecular level. The result of the present study confirmed diversity among accessions of pearl millet in the study area. Simple Sequence Repeats (SSR) markers were used for genetic analysis and evolutionary relationship of the accessions of pearl millet. To analyze the level of genetic diversity, 8 polymorphic SSR markers were used to screen 69 accessions collected based on three maturity periods. SSR markers result reveal relationships among the accessions in terms of genetic similarities, evolutionary and ancestral origin, it also reveals a total of 53 alleles recorded with 8 microsatellites and an average of 6.875 per microsatellite, the range was from 3 to 9 alleles in PSMP2248 and PSMP2080 respectively. Moreover, both the factorial analysis and the dendrogram of phylogeny tree grouping patterns and cluster analysis were almost in agreement with each other that diversity is not clustering according to geographical patterns but, according to similarity, the result showed maximum similarity among clusters with few numbers of accessions. It has been recommended that other molecular markers should be tested in the same study area.

Keywords: pearl millet, genetic diversity, simple sequence repeat (SSR)

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