Kebere Bezaweletaw Beyene 2007: Genetic Diversity Study in Finger Millet [*Eleusine coracana* (L.) Gaertn] Landraces Using Morphological Traits, Isozyme and RAPD Markers. Doctor of Philosophy (Tropical Agriculture), Major Field: Tropical Agriculture, Interdisciplinary Graduate Program. Thesis Advisor: Associate Professor Prapa Sripichitt, D.Agr. 141 pages.

Sixty-six finger millet accessions composed of 2 standard varieties and 64 landraces were evaluated using morphological traits, isozyme and RAPD markers to study the genetic diversity in finger millet landraces. In the morphological diversity study, randomized complete block design (RCBD) with three replications was employed. The estimate of diversity for six discrete morphological characters showed that accessions collected from Gojam and Welega had the highest Shannon-Weaver diversity value ($H'=0.84$), while those from Eritrea had the lowest ($H'=0.67$). The overall mean diversity was high ($H'=0.82$), revealing the existence of a vast range of diversity in the indigenous Ethiopian and Eritrean finger millet germplasm. The mean squares of genotypes were significant ($P\leq0.01$) for all the 15 morpho-agronomic characters. The phenotypic and genotypic coefficients of variations varied in the order of 8.05-31.23% and 6.52-24.21% in both cases for days to maturity and grain yield per plant, respectively. Heritability estimates ranged from 20% for grain-filling duration to 84% for days to heading. Value of expected genetic advance varied from 6.67-44.14% for grain-filling duration and finger width, respectively. Finger width and finger length exhibited high heritability coupled with high genetic advance. Grain yield per plant associated positively with productive tillers per plant, 1,000-grain weight, number of grains per spikelet and finger number per main ear and negatively with days to heading, days to maturity and leaf number per main tiller. The genotypic correlation and path-coefficient analysis showed 1,000-grain weight, finger number per main ear and productive tillers per plant as a major contributor to grain yield per plant. The cluster analysis grouped the 66 accessions into 5 major clusters. Maximum inter-cluster divergence occurred between cluster I and III ($D^2=81.47$) and the least was between cluster IV and V ($D^2=11.30$). Principal component analysis indicated that days to heading, culm thickness, leaf number per main tiller, leaf blade width and finger width contributed most towards genetic divergence. The most divergent populations and those having complementary characters could be used as parents in the improvement program of finger millet through hybridization.

Six enzyme systems were assayed for isozyme analysis but polymorphism was not found among accessions. RAPD analysis was executed using 15 primers, which were screened based on their effectiveness to discriminate among the accessions. Among the 123 RAPD fragments amplified, 89 (72.35%) were polymorphic, demonstrating the effectiveness of RAPD technique to detect intraspecific variations. The polymorphic information content (PIC) ranged from 0 to 0.50 with heterogeneous distribution and about 23% of the markers with a high discrimination power of ≥ 0.30. Genetic similarity between accessions estimated with simple matching coefficients ranged from 0.585 to 0.984. The RAPD cluster analysis successfully separated all accessions with the highest similarity value of approximately 98%. The 66 accessions were grouped into 9 clusters at similarity index of approximately 0.83, however, there was no clear-cut separation among finger millet accessions in relation to the origin of their respective region. The morphological traits and RAPD markers were better indicator of the existing diversity in finger millet landraces as opposed to the isozyme markers. The result of the present study revealed the existence of ample variability and potential in finger millet landraces from Ethiopia and Eritrea that could be employed in the genetic improvement. Moreover, the result could also help in planning future germplasm collection.

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