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Genetic variability length in maize

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Background

- The possibility of developing deep-sowing tolerant (DST) maize to absorb moisture from subsoil zones is crucial to maize adaptation to water-stress environments.
- The function of the mesocotyl in field emergence of seedlings is established in grasses. However, information is scarce on the extent of genetic variability for mesocotyl length (ML) in maize.
- Sixty-eight maize genotypes were studied using Completely Randomized Design in a laboratory experiment to investigate the extent of genetic variability for ML, and the relationship of seed biochemical components with ML. Ten seeds of each genotype were germinated for 10 days in the dark. Mesocotyl length was determined by placing cut mesocotyl against a flexible measuring tape. Biochemical contents of seeds were determined at a standard diagnostic laboratory.

- **Keywords:** adaptation; cluster; dendrogram; drought; heritability; maize; mesocotyl; variability

Results and Discussion

- Analysis of variance revealed highly-significant ($p \leq 0.01$) genotype mean square, indicating sufficient variability for genetic improvement (Table 1).
- Broad-sense heritability and genetic advance were high and implied that ML was heritable.
- Dendrogram from cluster analysis based on Ward's minimum variance cluster analysis classified 65 of the genotypes into clusters I, II, and III with ML (mean ± standard deviation) of 0.49 ± 0.18, 4.25 ± 0.96, and 9.16 ± 0.93 cm respectively (Figure 1).
- Significant ($p \leq 0.05/0.01$) associations were observed in the relationship of ML with all the measured biochemical parameters except selenium (Table 2)

Table 1. Mean squares and genetic components of maize genotypes for mesocotyl length after 10 days in the dark

Source of variation	DF	Mean square
Genotype	67	13.19**
Error	68	4.40
R^2		0.75
Genotypic variance		8.79
Environmental variance		4.40
Phenotypic variance		13.19
Broad-sense heritability		0.67
Genotypic coefficient of variation		0.57
Phenotypic coefficient of variation		0.70
Genetic Advance (% of Mean)		0.96

**, significant at 99% level of confidence; DF, degrees of freedom;
R^2, R-squared

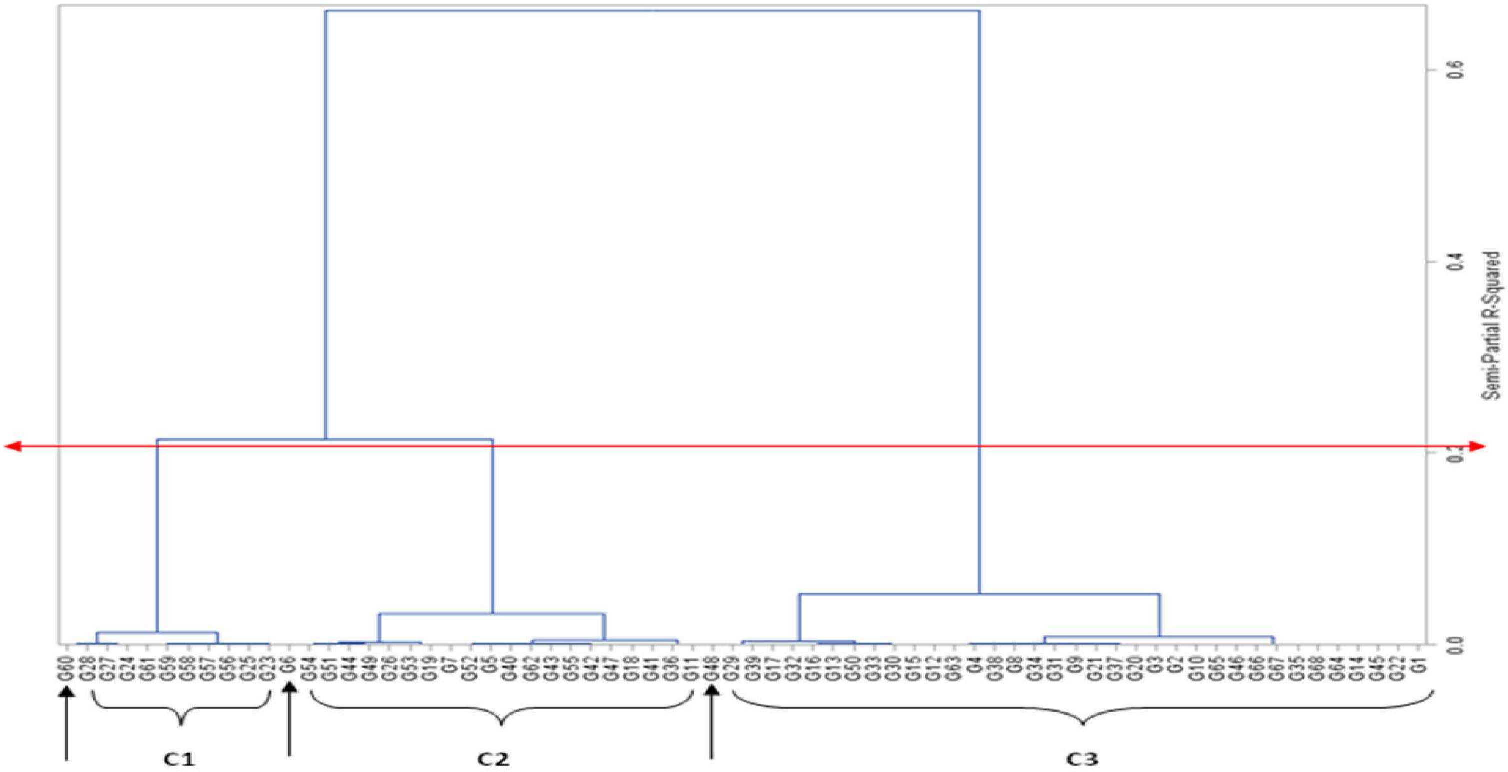

Figure 1. Dendrogram of relatedness among maize genotypes (X-axis), based on genetic similarity (Y-axis) from Ward's minimum variance cluster analysis. The red double-arrowed line delineates the genotypes into clusters at approximately 65% level of similarity; C1, C2, C3 are clusters 1, 2, and 3, respectively; single-arrowed line signifies ungrouped genotypes.

Table 2. Pearson correlation coefficients of seed biochemical parameters with mesocotyl length (ML

Biochemical content	ML
Iron	0.31*
Zinc	0.29*
Selenium	0.01ns
Crude protein	0.33**
Free fatty acid	0.26*
Oil	0.30*
Linoleic acid	0.28*
Amylase	-0.31*

* and **, significant at 5 and 1%; ns, not significant

Conclusions

- There was substantial genetic variability among the 68 maize genotypes, allowing the grouping into different clusters.
- Genotypes †PVAEH 31, †PVAEH 34, and LY1901-18 have potentials for improvement as DST maize.
- Biofortification has the potential to enhance the elongation of mesocotyl in maize during germination.
- The results obtained from this study provide basis for the development of DST maize for drought-prone environments.

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