

Genetic variability and heritability studies in F₂ and F₃ generations of QPM and NON-QPM maize crosses

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SUMMARY

The present investigation was carried out to estimate various variability parameters, *i.e.*, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad-sense heritability (h^2) and genetic advance (GA) using data derived from a number of plant characters [days to 50 per cent silking, plant height, number of leaves, cob length, cob girth, number of grain rows per cob, number of grains per row, hundred grain weight, grains per cob, grain protein, grain tryptophan, and seed yield] in F₂ and F₃ generations of four crosses involving quality protein maize (QPM) and non quality protein maize (Non-QPM) maize. The crosses exhibited moderate PCV and GCV estimates for all the traits. Genotypic coefficient of variation (GCV) was less than its corresponding estimates of phenotypic coefficient of variation (PCV) for most of the quantitative characters indicating significant role of environment in the expression of these traits. Low, medium and high estimates of broad sense heritability were found in different plant characters under study.

Key words : Heritability, Genetic advance, Crosses, Generation, PCV, GCV, Maise crosses

India is the fifth largest producer of maize in the world contributing 3% of the global production. Maize plant has a wide adaptation, and is able to grow in regions ranging from semi-arid to those where annual rainfall may exceed 400 cm. Morphologically it exhibits a greater diversity of phenotypes than perhaps any other grain crop (Kuleshov, 1933). The range of cultivation for maize crop stretches from 50° N to 40° S latitude and at altitude from sea level to 3,300 meters. Proper evaluation of genetic variability and heritability of a trait is a very important from the aspect of practical selection. Keeping this in view the study was conducted in four crosses of maize to estimate the genetic component of variance for grain yield and its related traits and to compute broad sense heritability and genetic advance for different plant traits.

MATERIALS AND METHODS

The study was conducted in the Plant Breeding Farm, Department of Agricultural Botany, Faculty of Agriculture, Annamalai University. The F₂ seeds of four crosses namely CML 176 X DMR 17 (QPM X QPM, Cross 1), UMI 124A X UMI 369 (Non-QPM X QPM, Cross 2), CML 176 X UMI 124A (QPM X Non-QPM,

Cross 3) and UMI 124 A X CML 176 (Non-QPM X Non-QPM, Cross 4) were raised in Randomized Block Design with three replications. A total of 250 plants were raised in each cross per replication and were selfed to maintain genetic purity. A total of 30 families in each of the 4 crosses were selected. The seeds of individual plants were sown as progeny rows of 4 meter length. A total of 60 seeds from each 30 families was sown at the rate of 20 seeds per replication during the month of September 2005. A population of 600 plants per replication was maintained. Observations were recorded on 90 individual earmarked plants in F₂ and F₃ of each cross @ 30 plants per replication. Genetic parameters GCV, PCV, heritability and GA were estimated by as described by Johnson *et al.* (1955).

The coefficients of variation were categorized as proposed by Sivsubramanian and Menon (1973).

Per cent of variability	Category
0-10	Low
11-20	medium
> 20	high

The heritability values were categorized as proposed by Robinson *et al.* (1949).

Per cent of heritability	Category
0-30	Low
31-60	medium
> 60	high

The genetic advance was classified as below:

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