# Heritability, genetic advance, correlation and path-coefficient estimation in high quality protein maize (*Zea mays* L.)

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**At G.B. Pant University of Agriculture and Technology, Pantnagar (Uttaranchal), 42 top crosses of 14 quality protein maize (QPM) inbred lines ($L_1$, $L_2$, ………$L_{14}$) with 3 testers ($T_1$, $T_2$, $T_3$) were evaluated using a high-lysine standard check, Shakti-1 in a randomized complete block design during kharif, 2004. Data were recorded on 50% tasselling and silking, plant height, ear height, ear length, ear diameter, kernel rows per ear, 100-kernel weight and grain yield. Significant genotypic differences and wide range of variation in mean values were observed for all the characters studied. Highest heritability in broad sense was observed for grain yield followed by ear diameter, ear length and kernel rows per ear. Maximum amount of genetic advance was found for grain yield followed by plant and ear heights. All characters except days to 50% tasselling and silking showed significant positive correlations with grain yield. Path-coefficient analysis revealed that 100-kernel weight had highest direct effect towards grain yield followed by plant and ear heights.**

**Key words:** QPM, Top crosses, Correlation, Grain yield.

## INTRODUCTION

GLOBALLY, maize (*Zea mays* L.) ranks first in production among the cereals like wheat, rice and sorghum etc. In India, it occupies an area of 7.4 m ha with the total production of 14.9 m tonnes (2004-05).

The commercially grown maize cultivars usually contain 9-12% protein which is enough to meet the physiological requirements of the human beings but the quality of the protein is nutritionally poor due to lower contents of two essential amino acids, lysine and tryptophan and high amount of leucine. Hard endosperm modified opaque-2 maize with vitreous kernels is known as quality protein maize (QPM).

The opaque-2 mutant gene which is responsible for the enhancement of lysine and tryptophan of maize protein, if incorporated into a population, inbred line or any other germplasm of maize through back cross technique, improves the nutritional status of maize.

QPM hybrids are more successful among the farmers as these are always planted by fresh $F_1$ seed every year and thus remain unaffected from contamination through normal maize cultivars. If the presently grown maize hybrids and varieties are replaced with QPM hybrids the latter will provide a definite promise in upgrading the nutritional security of maize-based population.

Yield is controlled by a number of genes i.e., polygenes and is a final product of several basic characters called yield components. All these components influence the yield directly or indirectly. A change in any of these components may bring change in other one or more characters and finally the yield. Therefore, it can be easily perceived that if these components can be improved without bringing any unfavorable associations, maximum expression of yield could be obtained.

The correlations can only reveal the direction and magnitude of association between any two characters. However, to find out the direct and indirect effects of various components on yield, the correlations are partitioned into direct and indirect effects through path-coefficient analysis which was, for the first time, given by Sewall Wright (1921). Correlation coupled with path-coefficient analysis is a powerful tool to study the character associations and their final effect on yield.

## MATERIALS AND METHODS

The experiment was conducted at the Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar (Uttaranchal), India during kharif, 2004. The experimental material comprised 42 top crosses developed by crossing 14 high QPM inbred lines of DMR series with 3 broad-based testers abbreviated as $L_1$, $L_2$, ….$L_{14}$ and $T_1$, $T_2$, $T_3$, respectively. The parental lines and top crosses were evaluated against a QPM check, Shakti-1 in a randomized complete block design with 3 replications. The net plot area was 7.5 $m^2$. Observations were recorded on whole plot basis for days to 50% tasselling and silking and fresh ear weight (later converted at 15% grain moisture for grain yield), whereas, the data on characters like plant height, ear height, ear length, ear diameter, number of kernel rows per ear, 100-kernel weight were taken on 10 randomly selected competitive plants from every plot. The average value of these plants was calculated and used for analysis of variance, heritability, genetic advance, correlation and path-coefficients using standard statistical techniques.

## RESULTS AND DISCUSSION

Heritability in broad sense and expected genetic advance were estimated for all the characters studied (Table 1). Grain yield had the highest heritability estimates (73.8%) followed by ear diameter (58.8%), kernel rows per ear (48.9%), ear length (48.2%) and 100-kernel weight (39.5%), whereas, the characters like days to 50% tasselling and silking, ear height and plant height showed moderate to low heritability. Similar observations were reported by Debnath and Sarkar (1987) and Debnath (1987). Maximum amount of genetic advance was found for the grain yield (15.69%) followed by plant height (15.15%), ear height (5.13%) and 100-kernel weight (3.90%).

Grain yield had high positive genotypic and phenotypic correlations with ear height (rg = 0.819, rp = 0.44), 100-kernel weight (rg = 0.786, rp = 0.531), plant height (rg = 0.709, rp = 0.464), ear height (rg = 0.614, rp = 0.417), kernel rows per ear (rg = 0.511, rp = 0.361) and ear diameter (rg = 0.4, rp = 0.33) as illustrated in Table 2. The environmental correlations were, however, low in magnitude. Similar results were obtained by Laptov (1980), Tyagi *et al.* (1988), Kumar and Kumar (1997), Gautam *et al.* (1999) and Umakanth and Khan (2001).

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