

Genetic Analysis of Grain Yield and its Component in Diallel Cross of Maize (*Zea Mays L.*)

Pavan. R¹, Mohan Rao. A², Gangappa.E³, Ramesh.S⁴ and Shailaja Hittalmani⁵

¹Research Associate, Department of Genetics and Plant Breeding University of Agricultural Sciences, Bangalore -65

^{2,3,4,5}Department of Genetics and Plant Breeding University of Agricultural Sciences, Bangalore -65

E-mail: ¹pavan_55agri@rediffmail.com, ²amrao8@rediffmail.com, ³egangu@gmail.com

Abstract: The present study was carried out to unravel the genetics of yield and its components by crossing 14 diverse maize inbred lines in complete diallel fashion. As there were lack of evidence for reciprocal cross differences, the trait means of straight and reciprocal crosses were pooled and the same were used for analysis using Hayman (1954) method of diallel analysis. The estimate of D, H₁ and H₂ were significant for all the traits. The ratio H₂/4H₁ suggested symmetrical distribution of increasing and decreasing genes whereas the ratio ((4DH₁)^{1/2} + F/(4DH₁)^{1/2}-F), indicated equal proportion of dominance and recessive genes controlling all the traits among the parents. The mean degree of dominance reveals that over dominance plays a major role in the expression of all the traits except for days to tasseling, days to silking and 100 grain weight.

1. INTRODUCTION

Maize (*Zea mays L.*) known as queen of cereals, ranks third after wheat and rice in the world production. Across the globe, maize is used as a staple food directly by millions. Large proportion of maize is used in the manufacture of feed for poultry and cattle. Maize is also used as a basic raw material as an ingredient to many industrial products such as starch, oil, protein, alcoholic beverages, food sweeteners, pharmaceutical, cosmetic, film, textile, gum, package and paper industries etc. In few developed countries, maize grains are used for the production of ethanol which is blended with fossil fuel for use in gasoline-powered vehicles to reduce emission. This indicates the importance of maize in India, and the role it plays in meeting the ever-increasing demand for food and also warrants the development of new, high yielding varieties and hybrids of maize. Formulation of a comprehensive breeding programme for the improvement of any crop depends on the availability of reliable information on the nature and magnitude of gene effects present for a particular trait to be improved in that population. Hayman's method of diallel analysis is one of the useful biometrical techniques for such studies. Therefore, keeping in view the crop and the utility of diallel analysis, the present investigation was undertaken to study the type of gene action involved in respect of yield and its components.

2. MATERIALS AND METHOD

The 14 parental lines were crossed by following full diallel mating design to synthesise 182 hybrids during 2012 summer and 2012 *kharif* at the experimental plots of Department of genetics and plant breeding, University of agricultural sciences, GKVK, Bangalore. The 182 hybrids along with their 14 inbred lines and four checks *viz.*, Nithyashree and Heema (public bred hybrids) and 900M and GK3018 (private bred hybrids) were evaluated in farmer's field at Sabbenahalli, Chickballapur district (Zone 5) in randomized block design with three replication during 2012 *rabi* and 2013 *kharif*. All the recommended crop production and protection practices were followed to raise a healthy crop. The mean of the traits data collected on five randomly labelled plants in each entry was used for statistical analysis. As there were lack of evidence for reciprocal cross differences, the trait means of straight and reciprocal crosses were pooled and the same were used for analysis using 'WINDOWSTAT Version 9.1 as per Hayman's analysis of diallel crosses (1954).

3. RESULTS AND DISCUSSION

In the present study, the estimate of D (additive genetic variance) and H₁(dominance genetic variance) and H₂ (proportion of dominance variance due to the positive and negative effects of genes) were significant for all the traits (Table 1). The covariance of additive and dominance gene effects (F) was significant for all the traits except for straw yield plot¹. From the ratio (H₁/D)^{1/2} it was evident that, over dominance played a major role the expression of all the traits while days to tasseling, days to silking and 100 grain weight were controlled by partial dominance. The dominance genetic variance being non-fixable, success of developing homozygous lines through selection in early segregating generations is limited. Heterosis breeding in general is likely to be most effective for the improvement of grain yield and its contributing characters. Alternatively, either biparental mating or recurrent selection in segregating material followed by conventional selection scheme is likely to lead to substantial improvement in the character. Though true overdominance at

specific loci cannot be ruled out but the observed levels of overdominance have generally been traced to mimicking effect of epistasis and linkage which do not warrant the production only of hybrids to exploit heterosis. Under such situations, chances of developing inbred lines or populations as good as or even better than hybrids that would obviate the need of costly procedure of producing hybrid seed (Chahal and Gosal, 2002).

Less than 0.25 of the ratio of $H_2/4H_1$ suggested symmetrical distribution of increasing and decreasing genes controlling all the traits among the parents. Turgut *et al.* (1995) and Perez Velasquez *et al.* (1995) also reported both symmetrical and asymmetrical distribution of genes controlling traits of economic importance. More than unity of ratio of $((4DH1)^{1/2}+F)/(4DH1)^{1/2}-F$ suggested equal proportion of dominance and recessive genes controlling all the traits in the parents. Thus, it is evident from the study that the dominance and recessive genes irrespective of whether they are increasers or decreases are symmetrically distributed among the parents. These results were in consonance with those reported by Hassaballa *et al.* (1980) and Guo *et al.* (1986).

The estimates of narrow sense heritability were relatively higher for days to tasseling (74%), days to silking (72%) and 100-grain weight (71%) compared to other traits. Hence it's proved that these traits may be largely controlled by additive genetic variance. This indicated that the individual genotype can be evaluated readily from their phenotypic expression. Simple selection or simple recurrent selection would be more effective in the sets of materials exhibiting greater additive genetic variability and desirable mean performance. Thus, breeder can go for selection in the next generation itself. As fixed effects model was used to unravel genetics of quantitative traits the inference refer to the parental lines in the study.

3.1 Figure and Table Captions

Table 1: Estimates of components of variance and genetic ratios for grain yield and its component traits in maize

Parameters	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8
X1	11.77*	6.70*	4.27*	8.07*	0.76	0.16	2.67	0.74
X2	15.45*	9.26*	5.77*	11.27*	0.77	0.16	2.78	0.72
X3	1.40*	1.86*	1.05*	1.84*	1.16	0.14	3.67	0.38
X4	440.96*	821.33*	712.94*	271.17*	1.37	0.22	1.58	0.42
X5	272.89*	386.16*	290.06*	222.27*	1.19	0.19	2.04	0.48

X6	3.55*	5.77*	3.65*	4.97*	1.28	0.16	3.42	0.24
X7	0.72*	1.89*	1.19*	0.98*	1.62	0.16	2.45	0.39
X8	24.60*	47.20*	30.69*	32.92*	1.39	0.16	2.87	0.32
X9	1.75*	2.06*	1.29*	1.47*	1.08	0.16	2.26	0.58
X10	15.03*	14.32*	7.06*	10.76*	0.98	0.12	2.16	0.71
X11	561.51*	1504.09*	968.44*	997.08*	1.64	0.16	3.37	0.15
X12	8.49*	9.63*	4.42*	11.42*	1.07	0.12	4.43	0.27
X13	0.57*	1.32*	0.87*	0.17	1.52	0.17	1.22	0.64

* Significant at $P \leq 0.05$, ** Significant at $P \leq 0.01$

X1=Days to tasseling, X2=Days to silking, X3=ASI X4=Plant height (cm), X5=Ear height (cm), X6=Ear length (cm), X7=Ear circumference (cm), X8=Kernels row-1, X9=Kernel rows ear-1, X10=100 grain weight (g), X11=Grain yield plant-1 (g), X12=Shelling (%), X13=Straw yield plot-1 (kg) Y1=D (Additive genetic variance), Y2=H1 (Dominance genetic variance), Y3=H2 (Proportion of dominance variance due to the positive and negative effects of genes), Y4=F (Covariance of additive and dominance gene effects), Y5=Degree of dominance $[(H1/D)1/2]$, Y6=Proportion of genes with positive and negative effects in parents $[H2/4H1]$, Y7=Proportion of dominant & recessive genes in parents $[(4DH1)1/2 + F/(4DH1)1/2 - F]$, Y8= h^2 (Narrow sense heritability)

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