The Bioscan 13(1): 109-112, 2018
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES
www.thebioscan.com

# GENETIC VARIABILITY AND ASSOCIATION ANALYSIS FOR YIELD AND ITS COMPONENTS IN $F_2$ AND $F_3$ SEGREGATING GENERATIONS OF THE MAIZE (*Zea mays* L.) CROSS BM125 X BM135

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**KEYWORDS**
Variability
Correlation
Path coefficients
Heritability

**Received on :**
29.05.2017

**Accepted on :**
11.02.2018

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## ABSTRACT

Crop improvement depends on, existence of genetic variability, understanding of traits inter-relations and determining the direct and indirect effects of yield determining factors. The study aimed at estimation of variability and trait associations in $F_2$ and $F_3$ generations of the cross BM-125 (high yielding) X BM-135 (low yielding) and drawn following results. PCV an indicative of environmental influence on the traits was in the range of low to medium for CLN, CGR, KRPC and KPR in both $F_2$ and $F_3$. Whereas, KPR, CWT, TW and GY exhibited high PCV in $F_2$ and $F_3$ which, means these traits are highly influenced and hence, selection based on such traits is not advisable. TW had moderate and high heritability in $F_2$ and $F_3$ respectively therefore, selection based on TW is recommended. CLN, CGR, KPR and CWT showed positive and significant association with grain yield in $F_2$ and $F_3$. The parents BM125 and BM 135 were also screened for tolerance to the disease, *Turcium* leaf blight under artificial epiphytotic conditions where, BM125 was found to be susceptible whereas, BM135 was resistant. Present study concludes superior family identification and generation advancement for high yield must be based on CLN, CGR CWT and TW.

## INTRODUCTION

The basic requirement of crop improvement is genetic variability (Allard, 1960) which is the amount of variation present among the breeding material for one or more characters. Thus, effectiveness of selection depends upon the nature, extent and magnitude of variability present among the breeding material and the extent to which it is heritable. It is measured in terms of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). To determine transmissible portion of variability, it is essential to know the heritability estimates for different characters. Genetic advance is the function of heritability of trait and is based on amount of phenotypic variation and selection differential.

Yield is a quantitatively inherited character and highly influenced by the environment hence, selection based on yield alone may limit the improvement (Grafius, 1960). Positive and significant associations between desirable traits will help improvement in a synergistic manner. Correlations cannot determine the characters which have highest direct effects on grain yield thus; path coefficient analysis permits the separation of correlation coefficient into direct and indirect effects (Garcia *et al.,* 2003).

There are number of factors which tend to reduce grain yield drastically of which, plant diseases also take up major part. The majority of maize growing areas are being affected by Turcicum leaf blight (TLB) caused by *Exorihilum turcicae* that lead to 28-98 % yield loss (Singh, 2004). TLB is common where, assured rainfall, coincidence of flowering period with cloudy weather, intermittent rains and 70-80% relative humidity prevails (Palavarsic *et al.,* 2012). These factors enhance severity of disease and it affects foliage and thus reduce grain yield drastically. Therefore, segregating populations derived using contrast parents for the above disease offer a best breeding material to select families resistant or tolerant to the disease.

In a study, $F_2$ and $F_3$ of the cross QPM X non QPM were considered to estimate the genetic variability parameters such as PCV, GCV, $h^2$ and GA and found less GCV than its corresponding estimates of PCV for most of the quantitative characters indicating significant role of environment in the expression of these traits (Murugan *et al.,* 2009). In another study, variability estimates in the $F_3$ of the cross 1491 x 1496 recoded higher genotypic variance than phenotypic variance for most of yield related traits and significantly higher values for broad sense heritability for all most all traits and they have recommended, heritability as parameter for generation advancement (Stojakovic *et al.*, 2012)

Chandrashekara *et al*. (2014) Evaluated thirty five short-duration maize inbred lines against TLB under artificial inoculation. Disease severity scoring was done according to 1-5 scale of Payak and Sharma and thus, identified twelve inbred lines as resistant against TLB and they have recommended utilization of such inbreds in disease tolerance breeding, transformation breeding and molecular breeding that is, to identify markers associated with disease resistance. Similarly, in another study (Ramdutta *et al.*, 2012) also categorized 23 inbred lines into resistant and 5 into moderately resistant based on two years evaluations.

Since, Turcicum leaf blight is a major disease of maize (Harlapur *et al.,* 2008), screening for tolerant line serve as identification of resistance resources for disease resistance breeding in maize.

With the above cited importance the paper deals with determination of various genetic parameters, estimation of inter correlations among different traits affecting grain yield, and screening of parents for resistance to Turcium leaf blight under artificial epiphytotic condition.

## MATERIALS AND METHODS

The present investigation was carried out during 2013 and 2014 using $F_2$ and $F_3$ generations of the cross BM125 and BM135. The parental line BM125 is high yielding and the other parent BM135 is low yielder. The true $F_1$ hybrids were sown and self pollinated during *kharif* 2013 to advance into $F_2$ generations. During Rabi/Summer 2014, One hundred and eighty $F_2$ plants were selfed to forward them to $F_3$ generations. The $F_2$, $F_3$ families and parents were sown by following RCBD with two replications, during *kharif*-2014 and during the same year, the parents BM125 and BM135 were also subjected to artificial inoculation conditions in separate blocks using the pathogens cultured on sorghum grains.

Data on yield and its component traits such as, cob length (CLN), Cob Girth (CGR), No of kernel rows per cob (NKRC), kernel per row (KPR), Cob weight (CWT), Test weight (TW) and grain yield per plant (GY) was recorded from one eighty plants of $F_2$ and five random plants each from one eighty $F_3$ families. GCV and PCV values were categorized (Sivasubramanian and Menon 1973) as low (10%), moderate (10.1-20%) and high (20.1% and above). Another genetic parameter, heritability was computed (Hanson *et al.,* 1956) and expressed as percentage. The heritability (Robinson *et al.,* 1949) percentage was low (0–30), moderate (30.1-60) and high (60.1 and above). Similarly, genetic advance (Johnson *et al.,* 1955) as per cent mean was categorized as low (0-10), moderate (10.1-20) and high (20.1 and above). Correlation coefficients (Weber and Morthy 1952) and path coefficients (Dewey and Lu 1959) were calculated using MRBD tool of *WINDOSTAT* v8.1 software.

*Turcium* leaf blight disease screening was done at four different intervals such as, ten day before flowering and at a regular interval of ten days after flowering till the dough stage of cobs was recorded according to the 1-5 scale (Payak and Sharma, 1983) as described in Table 5 and the score 1-2 implies resistant and scale 4-5 indicates the susceptibility.

The results and corresponding conclusion over genetic variability parameters and disease reactions of parents are described as below,

## RESULTS AND DISCUSSION

The genetic variability estimates depicted in table 1 reveals that, in both the ($F_2$ and $F_3$) populations, high phenotypic and genotypic variance was observed for the traits such as cob weight, test weight and grain yield per plant, which means these traits are controlled by non-additive genes and are influenced by the environmental factors greatly. Therefore, selection or generation advancement based on these traits is not recommendable. These results are on par with the reports of (Murugan *et al.,* 2013) where they found high GCV estimates for grain yield/plant, grains/row, plant height, ear height and 100 grain weight. Low phenotypic and genotypic variance was exhibited by cob length, cob girth and number of kernel rows per cob and these findings were similar to reports of (Hassan *et al.,* 2006). Thus, for yield improvement, traits like, cob length, cob girth and kernel rows per cob may be considered because these are least influenced by external factors and are controlled by additive genes.

In $F_2$ population, high genotypic and phenotypic coefficient of

**Table 1: Estimates of genetic parameters for yield and yield attributing characters in $F_2$ and $F_3$ of BM-125 x BM-35**

| Traits | Mean | | Range | | PCV | | GCV | | heritability | | | GAM |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $F_2$ | $F_3$ | $F_2$ | $F_3$ | $F_2$ | $F_3$ | $F_2$ | $F_3$ | $F_2$ | $F_3$ | $F_2$ | $F_3$ |
| CLN | 14.98 | 14.55 | 09.50-22.50 | 08.20-18.90 | 13.42 | 15.39 | 6.68 | 6.68 | 24.81 | 2.81 | 6.86 | 6.86 |
| CGR | 2.71 | 2.35 | 01.80-4.00 | 01.10-2.70 | 9.67 | 16.6 | 5.14 | 5.14 | 28.28 | 30 | 5.63 | 5.63 |
| KRPC | 13.79 | 13.26 | 08.00-20.00 | 08.00-18.00 | 10.97 | 56.95 | 6.17 | 6.17 | 31.63 | 2.6 | 7.13 | 7.13 |
| KPR | 31.12 | 28.97 | 14.00-60.00 | 12.00-55.20 | 15.66 | 15.56 | 4.8 | 4.8 | 9.4 | 35.3 | 3.033 | 3.033 |
| CWT | 141.19 | 108.59 | 51.00-297.00 | 22.60-259.20 | 23.76 | 26.11 | 7.43 | 7.43 | 9.79 | 14.44 | 4.79 | 4.79 |
| TW | 28.46 | 24.63 | 18.00-41.00 | 16.80-25.80 | 55.69 | 55.69 | 18.73 | 18.73 | 11.5 | 66.15 | 12.98 | 12.98 |
| GY | 112 | 87.92 | 20.00-231.00 | 12.00-210.00 | 22.28 | 22.28 | 8.48 | 8.48 | 14.5 | 14 | 6.65 | 6.65 |

**Table 2: Phenotypic correlation coefficients among the yield and yield related traits for $F_2$ (above diagonal) and $F_3$ (below diagonal) of the cross BM-125 x BM-135**

| | CLN | CGR | KRPC | KPR | CWT | TW | GY |
|---|---|---|---|---|---|---|---|
| CLN | **1** | 0.15* | -0.01 | 0.58** | 0.61** | 0.15* | 0.548** |
| CGR | 0.28* | **1** | 0.35** | 0.07 | 0.55** | 0.01 | 0.57** |
| KRPC | -0.03 | 0.03 | **1** | 0.02 | 0.19** | 0.19** | 0.130* |
| KPR | 0.38** | 0.25** | -0.02 | **1** | 0.51** | 0.024 | 0.529** |
| CWT | 0.61** | 0.41** | 0.01 | 0.52** | **1** | 0.12 | 0.937** |
| TW | 0.23** | 0.13* | -0.09 | 0.07 | 0.42** | **1** | 0.09 |
| GY | 0.58** | 0.34* | 0.01 | 0.47** | 0.93** | 0.47** | **1** |

**Table 3: Direct and indirect effects of independent variable on grain yield in $F_2$ of the cross BM-125 x BM-135**

| | CLN | CGR | KRPC | KPR | CWT | TW | GY |
|---|---|---|---|---|---|---|---|
| CLN | -0.08 | -0.01 | 0.00 | -0.05 | -0.05 | -0.01 | 0.55 |
| CGR | 0.02 | 0.12 | 0.04 | 0.01 | 0.07 | -0.01 | 0.57 |
| KRPC | 0.00 | -0.03 | -0.09 | 0.00 | -0.02 | -0.02 | 0.13 |
| KPR | 0.07 | 0.01 | 0.00 | 0.11 | 0.06 | 0.00 | 0.53 |
| CWT | 0.54 | 0.49 | 0.17 | 0.46 | 0.88 | 0.11 | 0.94 |
| TW | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.09 |

Residual effect 0.32

**Table 4: Direct and indirect effects of independent variable on grain yield in $F_3$ of the cross BM-125 x BM-135**

| | CLN | CGR | KRPC | KPR | CWT | TW | GY |
|---|---|---|---|---|---|---|---|
| CLN | 0.04 | 0.01 | 0.00 | 0.01 | 0.02 | 0.01 | 0.59 |
| CGR | -0.01 | -0.05 | 0.00 | -0.01 | -0.02 | -0.01 | 0.34 |
| KRPC | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.01 |
| KPR | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.47 |
| CWT | 0.54 | 0.36 | 0.00 | 0.46 | 0.88 | 0.38 | 0.93 |
| TW | 0.02 | 0.01 | -0.01 | 0.01 | 0.04 | 0.09 | 0.47 |

Residual effect 0.36

**Table 5: Disease scoring scale for TLB disease as given by Payak and Sharma (1983)**

| Scale | Description |
|---|---|
| 0 | No infection |
| 1 | Very slight to slight infection, one or two to few scattered lesions on lower leaves. |
| 2 | Light infection moderate number of lesions on lower leaves only. |
| 3 | Moderate infection, abundant lesions on lower leaves, few on the middle leaves. |
| 4 | Heavy infection, lesions abundant on lower, middle and extending to upper leaves. |
| 5 | Very heavy infection, lesions, leaves abundant on almost all leaves. |

variability was observed for test weight whereas, cob weight and grain yield per plant showed high PCV but low GCV indicating the influence of other genetic characters. In $F_3$ population, cob weight and grain yield per plant showed high genotypic and phenotypic coefficient of variability. High magnitude of PCV and GCV for these characters indicates presence of high degree of variability and better scope for improvement characters like cob weight, grain yield per plant and test weight can serve as key selection traits for further yield improvement. Arati *et al.* (2015) were also observed high GCV and PCV for grain yield per plant in $F_3$ generation of wheat.

The high heritability coupled with high genetic advance over per cent mean (GAM) infers the response to selection achievable in next generation. In the present investigation we found, moderate heritability with considerable level genetic advance over per cent mean for number of kernel rows per cob in $F_{2.}$ while, test weight in $F_3$ population showed high heritability and genetic advance over per cent mean, this indicates that there is low environmental influence on the character and hence can selection may be practiced to improve the traits. Similar results were also reported by (Juliet *et al.*, 2013).

Grain yield is a quantitative trait, which is greatly influenced by the environment and hence indirect selection through component traits would be an advisable strategy to increase the efficiency of selection therefore we discuss results of correlation studies (Table 2). The component traits such as cob length, cob girth, kernels per row and cob weight, were found to have positive and significant association with grain yield in $F_2$ and $F_3$ generations and these results are similar to findings of (Pavan *et al.,* 2011). Therefore, selection based on these traits may also enhance the grain yield and if the component traits have high heritability genetic gain is also more. Negative inter correlations were also observed between cob length and kernel rows per cob in $F_2$, $F_3$ and kernel rows per cob with kernels per row and test weight in $F_3$ generation whereas, all other component characters showed positive association with each other. Reports of (Tengan *et al.,* 2012) were also similar to current findings.

The phenotypic path coefficients revealed that, highest direct effect of cob weight on seed yield followed by cob girth, number of kernels per row and hundred seed weight in $F_2$ (Table 3). While in $F_3$ (Table 4) generation also, cob weight showed highest direct effect of on grain yield and similar results also recorded by (Devi and Shaik Mohammed 2001). Therefore we recommend cob weight as a most important parameter of selection and improvement of grain yield in the two different generations considered in the study. In $F_2$ residual effect was around 0.32 indicating that nearly 68 per cent of genetic variability recorded is due the characters considered and only 32 per cent of variability is due to unknown sources. Similarly, in $F_3$ genetic source of variability (66%) is higher than unknown sources (36%). From these results, it is clear that the selection based on cob weight and hundred seed weight will improve the grain yield per plant in both $F_2$ and $F_3$.

The Turcium leaf blight a common disease of maize in assured rainfall areas of India. Diseases reaction studies on parents under artificial inoculum condition confirmed that, the high yielding parent BM125, was scored 5 whereas, low yielding parent BM135, scored 2 (Table 6). Since high yielding parent is susceptible to disease, we recommend backcross breeding to develop disease resistant version of BM125. Similar reports were also made by Ramdutta *et al.* (2012) and Chandrashekara *et al.* (2014) where they categorized twenty three and thirty five maize inbred lines into resistant and susceptible lines respectively based on Payak and Sharma 1-5 scale under artificial inoculation conditions.

**Table 6: Scoring of parents for Turcium leaf blight according to Payak and Sharma scale(1983)**

| Parent | 10 days BT | 10 days AT | 20 days AT | 30 days AT | Result |
|---|---|---|---|---|---|
| BM125 | 0 | 2 | 4 | 4 | Susceptible |
| BM135 | 0 | 1 | 1 | 2 | Resistant |

Where, BT- Before tasseling/flowering; AT-After Tasseling/Flowering

The estimates of genetic parameters, associations and path coefficient in the $F_2$ and $F_3$ segregent population has revealed the existence of wide genetic variability and the traits such as cob weight, cob girth and test weigh are the major traits selection for superior families must be made based on these traits. The parents were found to be highly contrast in terms of resistance to TLB, the $F_2$ segregating generation could used for studies related identification of molecular markers associated with the above said disease.

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