Bangladesh J. Bot. **50**(1): 195-198, 2021 (March) **- Short communication**

# ASSESSMENT OF GENETICS FOR TURCICUM LEAF BLIGHT RESISTANCE IN MAIZE (*ZEA MAYS* L.)

**DAN SINGH JAKHAR*, RAJESH SINGH AND SHRAVAN KUMAR SINGH**

*Department of Genetics and Plant Breeding, Institute of Agricultural Sciences,*
*Banaras Hindu University, Varanasi- 221005, India*

*Keywords:* Maize, Genetics, Turcicum leaf blight, Inhertance, Resistance

## Abstract

Genetics of Turcicum leaf blight (TLB) was to explore the mode of inheritance in maize caused by *Exserohilum turcicum* is a serious foliar disease. The genetics was estimated with the help of two crosses (CM 212 × V 336 and CM 212 × CM 145) from data of six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$). The scaling tests as well as joint scaling tests revealed that the inadequacy of simple additive-dominance model and justifying the use of six parameter model for the detection of gene interactions in both the crosses for resistance to Turcicum leaf blight. All the scaling tests (A, B, C and D) were significant for the cross CM 212 × CM 145 and for the cross CM 212 × V 336 only A and C tests were significant. Based on the signs of [h] and [l] gene effects, complementary gene interaction for cross CM 212 × V 336 and duplicate gene interaction for cross CM 212 × CM 145 were evident in the inheritance of Turcicum leaf blight.

Maize (*Zea mays* L.) is one of the important cereal crops and it is third major crop in India after rice and wheat (Singh *et al.* 2014, Bindhu *et al.* 2017, Jakhar *et al.* 2017). It has prominent position in the agricultural economy of the world both as food for man and feed for animals. It has yield potential far higher than any other cereal and is sometimes referred to as the miracle crop or "Queen of cereals" (Kumari *et al.* 2016). It is a store house of energy with 65% starch, 12% protein and 6% oil and the rest is accounted for husk and bran (fibre). It accounts for over 30% of global cereal output and still its demand continues to soar. Maize contributes to 15% of the world's protein and 19% of the calories derived from the food crops (Kumari *et al.* 2018).

The maize crop is affected by number of fungal diseases such as Turcicum leaf blight (TLB) or Northern corn leaf blight (NCLB), common leaf rust and Southern corn leaf blight in which TLB caused by *Exserohilum turcicum* is one of the important diseases which affect the photosynthesis with severe reduction in grain yield to an extent of 28 to 91% (Robert 1953, Bindhu *et al.* 2017). The disease is more prevalent in Andhra Pradesh, Karnataka, Bihar, Himachal Pradesh and Maharashtra (Singh *et al.* 2014, Jakhar *et al.* 2017). Several disease management options have been recommended to reduce the impact of maize foliar diseases. Among these practices, planting of resistant cultivars can effectively reduce the rate of disease development and is widely recommended. Breeding for resistance is a practical, cost-effective means available to manage the diseases (Fehr 1987). So in order to breed a genotype with high level of resistance to Turcicum leaf blight the knowledge of gene action involved in the expression of resistant reaction in the material being handled, is a very important pre-requisite. Taking all above into consideration, an attempt was made in the present investigation to identify resistant inbred lines against TLB in maize.

The seeds of six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$) from the cross of CM 212 × V 336 and CM 212 × CM 145 were obtained from DMR, New Delhi; VPKAS, Almora and Maize programme, BHU, Varanasi and subjected to TLB disease screening for resistance in maize. This

---

*Author for correspondence: <dansingh410@gmail.com>.

material was sown and evaluated in artificial epiphytotic condition during Kharif, 2015 at Agricultural Research Farm of Banaras Hindu University. In these crosses, the $P_1$, $P_2$ and $F_1$ constituted 6 rows each while $F_2$, $B_1$ and $B_2$ constituted 20 rows each with 15 plants per row. The row to row distance was 75 cm and plant to plant distance was 20 cm with two replications and in each rows 15 plants were grown.

Disease severity was scored on 40 plants from each of the parents, 60 plants from $F_1$, 100 plants from $B_1$, $B_2$ and 200 plants from $F_2$ progenies in each replication using a 1 - 5 disease rating scale. Data was recorded after inoculation at three different stages: Flowering stage at 50 DAS, dough stage at 60 DAS and husk stage at 70 DAS. Generation mean analysis was undertaken using IndoStat 8.0 Advanced Plant Breeding Package (Indostat Services, Hyderabad). The pattern of inheritance was assessed by Mather's scaling test (1949) and Hayman and Mather (1955), Cavalli's Joint scaling test (1952) and Hayman six parameter model (1958).

The genetic analysis of disease severity of the two maize crosses *viz.*, CM 212 × V 336 and CM 212 × CM 145, hereafter referred to as cross I and cross II, respectively was carried out using the means and variances of six generations. The examinations of mean values for disease resistance for TLB of six generations of two crosses are presented in Table 1. Among parents, CM 212 recorded the highest disease score of 2.452 compared to the other parents CM 145 and V 336 which recorded the lowest mean disease score of 1.219 and 1.555, respectively. The $F_1$ of all the crosses for this trait exceeded both the parents indicating presence of heterobeltiosis. The $F_2$ in all the cases exhibited reduced expression than $F_1$ indicating inbreeding depression. The mean values of the back crosses exceeded the mean values of the respective back crosses parents. It was observed that both the back crosses performed better than their respective parents for all the 2 crosses.

**Table 1. Mean performance of six generations of two crosses for disease severity of Turcicum leaf blight in maize.**

| Character | Cross | Generations | | | | | |
|---|---|---|---|---|---|---|---|
| | | $P_1$ | $P_2$ | $F_1$ | $F_2$ | $B_1$ | $B_2$ |
| Disease severity | CM 212 × V 336 | 2.452± 0.077 | 1.555± 0.059 | 1.635± 0.047 | 2.091± 0.056 | 2.457± 0.051 | 1.574± 0.050 |
| | CM 212 × CM 145 | 2.452± 0.077 | 1.219± 0.058 | 1.808± 0.051 | 2.181± 0.054 | 2.514± 0.049 | 1.380± 0.047 |

**Table 2. Showing estimates of scaling test (A, B, C and D) based on six generations of disease severity of TLB in maize.**

| Character | Cross | Scaling test | | | |
|---|---|---|---|---|---|
| | | A | B | C | D |
| Disease severity | CM 212 × V 336 | –0.828±0.097** | 0.041±0.089$^{ns}$ | –1.086±0.184** | 0.150±0.094$^{ns}$ |
| | CM 212 × CM 145 | –0.767±0.095** | 0.267±0.086** | –1.436±0.183** | 0.468±0.091** |

**Significant at 0.01 probability level, ns - non significant.

The estimates along with its standard error of four scaling tests *viz.*, A, B, C and D have been presented in Table 2. The examination of values of scaling test revealed that all values were significant in the both crosses except with cross I (CM 212 × V 336) where B and D test were not significant. In general these tests indicated to go for six parameter model as well as to test the adequacy of model follow i.e. Cavalli (1952) joint scaling test.

The failure of the simple additive-dominance model was observed with significant $\chi^2$ values for disease score of the both crosses. This indicated that variation in the present material could not be ascribed to additive and dominance effects of the genes, albeit the epistatic gene effects played a significant role in the genetic control of the characters studied. The data were subjected to six parameter model of Hayman (1958) for estimation of additive, dominance and digenic interaction effects. Based on the signs of [h] and [l] gene effects, complementary gene interaction for cross CM 212 × V 336 and duplicate gene interaction for cross CM 212 × CM 145 were evident in the inheritance of Turcicum leaf blight (Table 3). The Hayman (1958) model indicated the significance of additive as well as dominant gene effect in the both crosses. Further j type (additive × dominance) of gene effect was also observed in all crosses, while*l*type (dominance × dominance) of gene effect was non-significant in the both crosses.

**Table 3. Estimates of gene effect obtained from six parameter model of Hayman (1958) in two crosses based on disease severity for TLB in maize.**

| Character | Cross | [m] | [d] | [h] | [i] | [j] | [l] | Type of epistasis |
|---|---|---|---|---|---|---|---|---|
| Disease severity | CM 212 × V 336 | 2.091 ± 0.039** | 0.883 ± 0.051** | –0.668± 0.193** | –0.299± $0.187^{ns}$ | 0.869± 0.123** | –0.487± $0.274^{ns}$ | Complementary gene interaction |
| | CM 212 × CM 145 | 2.181 ± 0.038** | 1.134 ± 0.048** | –0.963± 0.188** | –0.935± 0.181** | 1.034± 0.117** | 0.435± $0.265^{ns}$ | Duplicate gene interaction |

**Significant at 0.01 probability level, ns - non significant

To study the genetic basis of resistance is imperative in breeding for TLB resistance. Generation mean analysis is a relatively simple and statistically reliable tool which is suitable for preliminary estimation of various genetic effects. The estimation and interpretation of non-allelic interactions are more progressive with generation mean analysis (GMA) as it utilizes the first order statistics which are less compounded with each other when compared with variance estimates. Moreover, the populations evaluated in these studies can be utilized in actual breeding programmes. In the present investigation, an experiment was carried out to study the genetics of Turcicum leaf blight.

The genetics of TLB was estimated from disease severity scoring data based on six generations *viz*., $P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$ of two crosses *viz*., CM 212 × V 336 and CM 212 × CM 145 at the Agricultural Research Farm, BHU, Varanasi. The study revealed that all scaling tests (A, B, C and D) for both crosses were significant except in cross CM 212 × V 336 where B and D test was not significant. In general, the test indicated to go for six parameter model. Further, the Cavalli test (1952) also indicated its failure as observed with significant $\chi^2$ values. The data were subjected to six parameter model of Hayman (1958) for estimation of additive, dominance and digenic interaction effects. Based on the signs of [h] and [l] gene effects, complementary gene interaction for cross CM 212 × V 336 and duplicate gene interaction for cross CM 212 × CM 145 were evident in the inheritance of Turcicum leaf blight. This also revealed the presence of *i* (additive × additive) and *l* (dominant × dominant) type of higher order of gene interaction. Such results have also been reported by several workers (Carson 1995, Takamiya and Sendo 2000, Babita and Mani 2010, Ranganatha *et al.* 2017, Hegde *et al.* 2018). Gene action was mostly partial dominant or recessive. Generation means analyses with Mo17 (Carson 1995) and other germplasm (Hughes and Hooker 1971) suggested that additive gene action prevailed and that the size of non-additive effects varied among populations and between years. In this study gene action was mostly over dominance for all crosses. This result is in accordance to Srivastava (2015) who observed over dominance gene action for NCLB disease in maize.

## Acknowledgements

Authors gratefully acknowledge the support of the Department of Genetics and Plant Breeding, BHU, Varanasi, India for providing seeds of six generations of maize utilized in the experiment and the Union Grants Commission, New Delhi, India, for providing fellowship to the first author (DSJ) during the present investigation.

## References

Babita C and Mani VP 2010. Genetic analysis of resistance to Turcicum leaf blight in semi-temperate early maturing genotypes of maize (*Zea mays* L.). Indian J. Genet. Pl. Br. **70**(1): 65-70.

Bindhu KG, Pandurangegowda KT, Lohithaswa HC, Madhuri R and Mallikarjuna N 2017. Genetics of resistance to Turcicum Leaf Blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs in maize (*Zea mays* L.). Int. J. Curr. Microbiol. App. Sci. **6**(11): 964-969.

Carson ML 1995. Inheritance of latent period length in maize infected with *Exserohilum turcicum.* Plant Dis. **79**: 581-585.

Cavalli LL 1952. An analysis of linkage in quantitative inheritance. *In:* Quantitative Inheritance (eds. Rieve, ECR and Waddington, CH), HMSO, London. 135-144.

Fehr WR 1987. Principles of Cultivar Development. PB: Macmillan, New York, USA.

Hayman BI 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity **12**: 371-390.

Hayman BI and Mather R 1955. The description of genetic interaction in continuous variation. Biometric **11**: 69-82.

Hegde S, Kumar M, Ganesan NM, Chinnusamy C, Krishnamoorthy AS and Gangashetti M 2018. Genetic analysis of resistance to northern leaf blight in maize (*Zea mays* L.) reveals its population specificity. Int. J. Curr. Microbiol. App. Sci. **7**(4): 3084-3090.

Hughes GR and Hooker AL 1971. Gene action conditioning resistance to northern leaf blight in maize. Crop Sci. **11**(2): 180-184.

Jakhar DS, Singh R, Kumar S, Singh P and Ojha V 2017. Turcicum leaf blight: A ubiquitous foliar disease of maize (*Zea mays* L.). Int. J. Curr. Microbiol. App. Sci. **6**(3): 825-831.

Kumari R, Singh AK and Sharma VK 2016. Heterosis and genetic divergence correlation studies for yield and its related traits in maize (*Zea mays* L.). The Bioscan **11**(3): 1849-1854.

Kumari R, Singh AK and Sharma VK 2018. Genetic divergence studies for morpho-agronomical traits in maize (*Zea mays* L.) inbreds. Int. J. Curr. Microbiol. App. Sci. **7**: 3589-3594.

Mather K 1949. Biometrical genetics in the study of continuous variation. Methun and Company Limited, London.

Ranganatha HM, Lohithaswa HC and Pandravada AS 2017. Understanding the genetic architecture of resistance to northern corn leaf blight and southern corn rust in maize (*Zea mays* L.). Indian J. Genet. Pl. Br. **77**(3): 357-363.

Robert AL 1953. Some of the leaf blights of corn. Year Book of Agriculture, United States Department of Agriculture, North Carolina pp 380-385.

Singh R, Srivastava RP, Mani VP, Khandelwal RS and Ram L 2014. Screening of maize genotypes against northern corn leaf blight. The Bioscan **9**(4): 1689-1693.

Srivastava RP 2015. Mapping of QTLs for northern corn leaf blight in maize (*Zea mays* L.). Doctoral dissertation, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India.

Takamiya Y and Sendo S 2000. Varietal difference and genetic analysis of field resistance to northern leaf blight in maize inbred lines. Bull. Hokkaido Nat. Agric. Exper. Station **78**: 59-67.

*(Manuscript received on 12 April, 2019; revised on 23 February, 2020)*