Original Research Article

Genetics of Resistance to Turcicum Leaf Blight caused by Exserohilum turcicum (Pass.) Leonard and Suggs in maize (Zea mays L.)

K.G. Bindhu1*, K.T. Pandurangegowda1, H.C. Lohithaswa2, R. Madhuri2 and N. Mallikarjuna1

1Department of Plant Pathology, 2Department of Genetics and Plant Breeding, College of Agriculture, V. C. Farm, Mandya, Karnataka, India
*Corresponding author

A B S T R A C T

An investigation was undertaken to detect the genetic architecture of resistance of maize Turcicum leaf blight using six generation mean analysis in the two crosses viz., B-104 × CML-124 (C-I) and CML-124 × B-104 (C-II) at College of Agriculture, V. C. Farm, Mandya during Kharif 2014-15. The estimates of scaling tests A and D were significant in B104 × CML124, C and D in CML124 × B104 which suggested the significance of both additive and dominant gene effect in the inheritance of resistance in both the crosses. The scaling tests as well as joint scaling tests reveals the inadequacy of simple additive-dominance model which justified the use of six parameter model for the detection of gene interactions. The components of means, additive and dominance were significant in cross B104 × CML124. The magnitude of dominance [h] effect was more compared to additive gene effect. Among interaction components, additive × additive [i] and additive × dominance [j] interaction effects were significant in positive direction, whereas dominance × dominance [l] interaction was significant in negative direction. In the cross CML124 × B104, the mean, additive and dominant [h] gene effects were significant but dominant genetic effect was significant in the negative direction. Among interaction components [i] was significant in negative direction, which implies that biparental mating or recurrent selection programmes can be used to bring out desirable genetic improvement.

Keywords
Additive-dominance model, Biparental mating, Recurrent selection, Six generation mean, Turcicum leaf blight.

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Introduction

Maize (Zea mays L.) is one of the important cereal crops and it is third major crop in India after rice and wheat. Maize is native of Mexico and Central America by origin, (Galaniant, 1976; Pursglove, 1972 and Dowswell et al., 1996). The crop is affected by number of fungal diseases of which Turcicum leaf blight (TLB) or Northern corn leaf blight (NCLB) is one of the important diseases which affects the photosynthesis with severe reduction in grain yield to an extent of 28 to 91% (Robert, 1953). The disease is more prevalent in Andhra Pradesh, Karnataka, Bihar, Himachal Pradesh and Maharashtra. It is considered to be one of the most devastating foliar diseases in Karnataka resulting in reduction of grain yield by 28 to 91 per cent (Pandurangegowda et al., 1991 and Harlapur et al., 2000). 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. Host plant resistance is considered as most practical, feasible and economical method of plant disease management. 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 prerequisite. In this connection, an attempt has been made detect the mode of inheritance of resistance to TLB on maize using disease response of segregating lines and using generation mean analysis.

**Materials and Methods**

The present investigation was conducted during Kharif 2013-14 at Zonal Agricultural Research Station (ZARS), V.C. Farm, Mandya, which is considered as one of the ‘hot spot’ for Turcicum Leaf Blight (TLB) of maize. The experimental material consisted of two resistant inbred lines (B-61, B-104) and one susceptible (CML-124) which were obtained from the All India Co-ordinated Maize Improvement Project, New Delhi. By crossing these three inbreds during Kharif 2013, three F1s viz., C-I (B-61 × CML-124), C-II (B-104 × CML-124), C-III (CML-124 × B-104) were developed. These F1s were grown and selfed to get F2 progenies and simultaneously backcrossed with respective parents to produce BC1 and BC2 progenies, during Rabi 2013. The six generations viz., P1, P2, F1, F2, BC1 and BC2 of each of the crosses were sown in RCBD in two replications during Kharif 2014. The parents and F1’s were planted in single row each, BC1 and BC2 an eight rows and F2’s in 13 rows of 4m length with spacing of 75 × 20 cm respectively. The artificial inoculation conditions for disease development were created as described earlier. Per cent disease severity scoring was done at 60th and 80th day by visualizing the diseased leaf area using standard scale consisting of five broad categories, designated by 0 -100 per cent scale (James, 1971). Observations were recorded on all the 20 plants of P1, P2 and F1, 250 plants in F2 and 150 plants in BC1 and BC2 of all the three crosses. The pattern of inheritance was assessed by Mather’s scaling test (1945), Cavalli’s Joint scaling test (1952) and six parameter model.

**Results and Discussion**

The mean values along with standard error and variances of six generations (P1, P2, F1, F2, BC1 and BC2) of the maize in respect of Turcicum leaf blight are tabulated in (Table 1) and briefly presented below. Wide range of disease severity score was observed among non-segregating populations and the disease severity score was maximum (25.75) in the parent CML124 compared to other parents B61 (20.12) and B104 (12.13), while the F1s recorded intermediate Turcicum leaf blight score compared to its parents. Among segregating generations, the disease score of BC1 population of all the three crosses B104 × (B104 × CML124), B61 × (B61 × CML124), CML124 × (CML124 × B104) (24.88, 20.1, 24.13 respectively) was maximum compared to either BC2 (21.71, 19.68, 22.8 respectively) or F2 (19.97, 19.07, 28.22 respectively) populations.

To test the adequacy of additive-dominance model A, B, C and D scaling tests were applied. The mean and variance of six generations viz., P1, P2, F1, F2, BC1 and BC2 of the crosses C-I, C-II and C-III in respect of Turcicum leaf blight disease score were subjected to scaling tests as per the method of Mather (1949). The results of scaling tests A, B, C and D in respect of disease score of three
crosses are presented in (Table 2). The scaling tests ‘A’ and ‘D’ were significant in the cross B104 × CML124, whereas tests ‘C’ and ‘D’ were significant in the cross CML124 × B104, indicating the inadequacy of additive-dominance model, which was further confirmed by significance of additive and dominance components in joint scaling tests suggested the importance of both additive and dominance gene effects in the inheritance of resistance in both the crosses. This clearly indicated presence of digenic or still higher order epistasis in the inheritance of this trait. But in the cross B61 × CML124 all four scaling tests were non-significant indicating the adequacy of additive-dominance model which is sufficient to explain the inheritance of quantitative traits in the respective cross. The significance of ‘A’ and ‘B’ scales indicated the presence of all the three types of non-allelic interactions viz., additive × additive, additive × dominance and dominance × dominance significance of interaction effects in cross B104 × CML124 and dominance × dominance interaction effect in the cross CML124 × B104 was noticed in controlling the resistance to turcicum leaf blight. The significance of any one of the scaling tests indicated inadequacy of simple additive-dominance model which were further confirmed by significance of chi-square statistic indicating the role of epistasis.

Table 1 Estimates of means of generations with their standard error, variance and variance of mean for response to turcicum leaf blight

| Parents/generations | Turcicum leaf blight |
|---------------------|----------------------|
|                     | Mean + SE | Variance | Variance of mean |
| Parents (20)        |            |          |                  |
| CML24               | 25.75 ± 3.3 | 4.83    | 12.2             |
| B61                 | 20.12 ± 1.7 | 64.78   | 3.23             |
| B104                | 12.13 ± 0.48 | 23.33   | 1.16             |
| F1s (20)            |            |          |                  |
| B104 × CML124       | 19.38 ± 1.65 | 54.52   | 2.72             |
| B61 × CML124        | 19.250 ± 1.33 | 35.59   | 1.77             |
| CML124 × B104       | 23.82 ± 1.87 | 70.66   | 3.53             |
| F2s (250)           |            |          |                  |
| B104 × CML124       | 19.97 ± 0.42 | 45.5    | 0.18             |
| B61 × CML124        | 19.07 ± 0.39 | 39.52   | 0.15             |
| CML124 × B104       | 28.22 ± 0.67 | 112.4   | 0.44             |
| B1 (150)            |            |          |                  |
| B104 × (B104 × CML124) | 24.88 ± 0.78 | 93.4    | 0.78             |
| B61 × (B61 × CML124) | 20.1 ± 0.53   | 42.9    | 0.28             |
| CML124 × (CML124 × B104) | 24.13 ± 0.79 | 95.3    | 0.63             |
| B2 (150)            |            |          |                  |
| CML124 × (B104 × CML124) | 21.71 ± 0.58 | 51.29   | 0.34             |
| CML124 × (B61 × CML124) | 19.68 ± 0.7  | 74.35   | 0.49             |
| B104 × (CML124 × B104) | 22.8 ± 0.65  | 64.4    | 0.42             |
Table 2 Estimates of scaling tests for turcicum leaf blight scores of different generations

| CROSS                  | Scaling Test | Turcicum leaf blight |
|------------------------|--------------|----------------------|
| C-I (B104 × CML124)   | A            | 18.627**             |
|                        | B            | -1.71                |
|                        | C            | 3.29                 |
|                        | D            | -6.63**              |
| C-II (B61 × CML124)   | A            | 0.83                 |
|                        | B            | -5.13                |
|                        | C            | -7.56                |
|                        | D            | -1.63                |
| CIII (CML124 × B104)  | A            | -3.07                |
|                        | B            | 1.7                  |
|                        | C            | 17.621**             |
|                        | D            | 9.49**               |

Table 3 Estimates of components of generation means and test for adequacy of additive-dominance model for inheritance of Turcicum leaf blight

| Disease                  | Cross          | (m)     | (d)     | (h)     |
|--------------------------|----------------|---------|---------|---------|
| Turcicum leaf blight     | B104 × CML124 | 18.7**  | 2.74**  | 6.74**  |
|                          | CML124 × B104 | 21.10** | -3.13** | 1.13    |

Table 4 Estimates of components of generation means based on perfect fit solution (Joint Scaling Test) for Turcicum leaf blight

| Disease                  | Cross          | [\(\bar{m}\)] | [\(\bar{d}\)] | [\(\bar{h}\)] | [\(\bar{l}\)] | [\(\bar{t}\)] | Type of epistasis |
|--------------------------|----------------|---------------|---------------|---------------|---------------|---------------|-------------------|
| Turcicum leaf blight     | B104 × CML124 | 5.66          | -6.81**       | 43.548**      | 13.27**       | 9.98**        | -29.83**         | duplicate         |
|                          | CML124 × B104 | 42.80**       | 3.68*         | -39.3**       | -18.9**       | -2.38         | 20.35**          | duplicate         |
After ascertaining the failure of additive-dominance model in explaining the inheritance of various quantitative characters, the perfect fit six-parameter estimates of digenic interaction model were estimated following the methods of Jinks and Jones (1958) and Mather and Jinks (1971). The six generations of the crosses viz., B104 × CML124 and CML124 × B104 were used to estimate the gene effects viz., $h^+$, $i$, $j$, $l$, $h^-$, and $i$ for Turcicum leaf blight. The gene effects estimated by using perfect fit model in respect of disease score are tabulated in (Table 3 and 4). It is evident from six parameter model that in the cross B104 × CML124, the components mean, additive and dominance were significant. The magnitude of dominance effect was more compared to additive gene effect. Opposite signs of $h^-$ and $i$ components indicated the presence of duplicate gene interaction in the genetic control of Turcicum leaf blight in the crosses B104 × CML124, and CML124 × B104 which implied that biparental mating or recurrent selection programmes can be used to bring out desirable genetic improvement. Cognated results were obtained by Hettiarachchi et al., (2009), they reported the importance of additive, additive × additive, additive × dominance and dominance × dominance genetic effects which were well explained in the three crosses viz., CM139 × NA1147, CM139 × SKV18, CM139 × SKV21.

The scaling tests as well as joint scaling tests revealed inadequacy of simple additive-dominance model which justified the use of six parameter model for the detection of gene interactions. Duplicate epistasis indicated that population improvement programmes need to be utilized for substantial genetic improvement.

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