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CERTIFICATE

This is to certify that the thesis entitled "**Genetics of yield, yield components and resistance to banded leaf and sheath blight in maize (*Zea mays* L.)**" submitted to the Faculty of the Post-Graduate School, Indian Agricultural Research Institute, New Delhi, in partial fulfillment of the requirements for the award of the degree of **DOCTOR OF PHILOSOPHY** in **GENETICS** is a faithful record of *bona fide* research work carried out by **Mrs. Bhavana, P.** under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma.

It is further certified that any help or source of information that has been availed of in this connection has been duly acknowledged by her.

(**R.N. Gadag**)
Chairman
Advisory Committee

Place: New Delhi
Date: November, 2008

Genetics of yield, yield components and resistance to banded leaf and sheath blight in maize (*Zea mays* L.)

By

BHAVANA, P.

A thesis
Submitted to the Faculty of Post-Graduate School,
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In partial fulfillment of requirements for the award of the degree of

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मक्का (जी. मेज़एल) में पैदावार घटक की आनुवांशिकता एवं धारीदार पत्ती तथा शीथ अंगमारी प्रतिरोधिता

Genetics of yield, yield components and resistance to banded leaf and sheath blight in maize (*Zea mays* L.)

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CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

1. INTRODUCTION

Maize (*Zea mays* L., 2n = 20) is one of the most important food, feed and industrial crops of the world. It is widely cultivated throughout the world, and a greater weight of maize is produced each year than any other grain. It is the world's leading cereal in terms of production (694.58 m.tonnes) and productivity (4719 kg/ha) (FAO 2005). While the United States produces almost half of the world's harvest, other top producing countries are as widespread as China, Brazil, France, Indonesia, India and South Africa.

Maize is the staple food crop in tropical Asian and African countries. Apart from being human food, about 60 percent of maize output is used as nutritious animal and poultry feed. It also serves as industrial raw material for the production of starch, oil, protein, alcoholic beverages, food sweeteners and more recently fuel. Maize is increasingly used as a biomass fuel, such as ethanol, to reduce fuel costs, has unintentionally caused a rapid rise in food costs. This has led to the 2007 harvest being one of the most profitable corn crops in modern history for farmers.

India's maize production fluctuates between 10-14 m.tonnes, with 80-90% of the production being in the *kharif* season. Major states that contribute in the production are Karnataka, Andhra Pradesh, Bihar, Punjab, Uttar Pradesh and Madhya Pradesh. It is cultivated in an area of 7.4m.ha with a production of 14.5m.tonnes (FAO 2005). Its production has grown annually by a robust 4.5 percent in last 10 years to a record 18.5 m.tonnes in 2007-08 (Sud, 2008). The bulk of this increase is accounted for higher productivity and not by area expansion alone. Even with such magnificient improvement in yield potential, the present average production of maize in India is only 1959 kg/ha, which is quite low as compared to those in other countries of the world. It is, therefore, obvious that the high yield potential of improved types has not been realized in the farmer's field.

Many biotic and abiotic stresses limit the realization of yield potentiality and among the former; diseases are of utmost importance, especially in the tropical and subtropical regions. A total of 61 diseases are known to attack maize in the country (Payak and Sharma, 1985). The loss in terms of harvested grain per annum has been

determined to be the order of 13.2 percent, amounting to 1459.6million rupees (Payak and Sharma, 1985; Sharma *et* al., 1993). Availability of methods for creating aritificial epidemics in the field has resulted into critical screening and accurate identification of resistant sources of a number of such diseases which have been subsequently utilized in the development of resistant hybrids and composites. Though considerable literature is available on the resistance to these diseases, yet no single variety can be considered to possess resistance to most of the diseases and simultaneously possess the yield level of released HYV's.

During the past decade, the disease pattern has been changing dynamically and newer diseases which hitherto have never been found to attack maize are becoming progressively damaging in alarming proportions. Banded leaf and sheath blight which has never been an important disease of maize has become a major threat in the recent past throughout maize growing areas.

Banded leaf and sheath blight pathogen *Rhizoctonia solani* f.sp *sasakii* infects many crops like rice, peas and sugarbeets. This was first reported as a minor disease in maize (Payak & Renfro 1966). The destructive nature of this disease was realized only after an epidemic occurred in warm and humid foot hill areas of Mandi district of Himachal Pradesh in early 1970s (Thakur *et al.,* 1973). The disease causes extensive damage to the crop before and after flowering under warm humid conditions. Disease results in seed decay, damping off, stem canker, root rot, aerial blight and cob decay. Losses to the extent of 23 to 40 % were reported (Singh & Sharma 1976, Lal *et al.,* 1980).

The improved cultivars particularly hybrids combining high yield and disease resistance play a significant role in increasing yield. Breeding disease resistant high yielding varieties is the socio-economical and viable alternative to reduce the cost of cultivation. Development of resistant varieties appears to be the best alternative for controlling this disease.

Since banded leaf and sheath blight has become a disease of major concern in maize only recently, little work on genetic analysis and breeding for resistance to this disease has been undertaken. Moreover only a few resistance sources have been identified. So the emphasis is to screen additional inbred lines for identifying potential

new sources. In addition, genetic analysis of resistance needs to be undertaken to understand the mechanism as well as to devise appropriate strategy for incorporation of resistance.

Knowledge about the genetics of BLSB resistance is very less, more so its inter-alia relationship with yield & yield components. In order to achieve simultaneous improvement in resistance and grain yield, it is necessary to understand their nature of inheritance so as to choose a methodology to incorporate resistance as well as to improve yield.

Further, as BLSB is a major disease especially in the northern belt of the country, the reaction of elite experimental hybrids to BLSB needs to be taken into account. By involving diverse maize inbred lines, there is a possibility of generating experimental hybrids with higher productivity. Thus, the proposed study attempts to consider both the aspects *viz.*, resistance to BLSB and yield potentiality simultaneously. Keeping the above considerations in view, the present study entitled **"Genetics of yield, yield components & resistance to banded leaf and sheath blight in maize (Zea *mays* L.)"** was undertaken with the following objectives:

1) To screen maize inbred lines from diverse sources for their reaction to banded leaf and sheath blight.

2) To select maize lines with distinct responses to be used as parental lines.

3) To analyze genetic components for yield, yield components and resistance to BLSB.

3. MATERIALS AND METHODS

The present investigation was carried out in the Division of Genetics, Indian Agricultural Research Institute (I.A.R.I), New Delhi during the years, 2005, 2006 and 2007. Screening of the material against Banded leaf and sheath blight was done by artificial inoculation in the field at Maize Pathology Unit, Delhi. Crossing work was done at Maize Breeding Unit, Delhi and Maize Research Station, Hyderabad. Characters on yield and yield components and disease scoring were taken from parents, F_1 and F_2 at I.A.R.I, New Delhi. The geographical situation of the sites was as follows:

Centre	**Latitude**	**Longitude**	**Altitude**
Delhi	28.38^{o}N	77.12^{o}E	228.1m
Hyderabad	17.20^{o}N	78.30^{o}E	530.0m

3.1 MATERIALS

The material selected for the study included elite inbreds and interspecific derivatives developed at Maize Breeding Unit, I.A.R.I, New Delhi.

Screening for Banded leaf and sheath blight (BLSB) was carried on 40 lines (Table-3) during *Kharif* 2005 at Maize Pathology Unit, Delhi and 30 lines (Table-4) during *Kharif* 2006 at Maize Pathology Unit, Delhi, Pantnagar and Udaipur. Suwan-1, Pop-145 with moderate resistance on the basis of earlier reports (Sharma *et al*., 2002) served as resistant reference lines. As most of the genotypes are susceptible to BLSB, higher score of 4.0 and above would indicate sufficient build up of inoculum during screening. Thus, the requirement of reference genotypes representing the two extremes (resistant and susceptible) would be fulfilled, giving credence to the screening procedure. Screening was also carried out on 45 lines (Table-5) at Maize Pathology Unit, Delhi during *Kharif* 2006. A total of 19 lines were selected from this group and used as parents in the crossing programme. In addition CM-150 and CM-151 (the parental lines of newly released maize hybrid PEEHM-5) were also used in crossing (Table-6).

Thirty one crosses were developed during *Kharif* 2006 at Maize Breeding Unit, Delhi and these F_1s were selfed to generate F_2 generation seed at Maize Research

Station, Hyderabad during *Rabi* 2006 (Table-7). Further 86 crosses were generated at Maize Research Station, Hyderabad during *Rabi* 2006 (Table -8).

All the 19 parents, 86 F_1s and 31 F_2 s were evaluated for yield, yield components and resistance to Banded leaf and sheath blight at Maize Breeding Unit, Delhi during *Kharif* 2007.

Based on the information available, combinations were generated in Line X Tester design using nine inbreds as lines (females) and five inbreds as testers (males). Testers were selected based on diverse sources of origin and variability to yield and yield components. The particulars of parents used in L X T are provided in Table-9. The 45 F_1s along with their parents were evaluated to carry out combining ability analysis.

3.2 EXPERIMENTAL DESIGN AND LAYOUT

The entries used for screening against Banded leaf and sheath blight were sown in two rows each of 4m long at 50cm X 20cm inter and intra row spacing with non experimental rows at borders. Entries screened at three locations *viz.,* Delhi, Pantnagar and Udaipur were sown in single row of 4m long. Blsb scores were recorded from five competitive plants selected randomly from each row.

A total of 105 entries comprising 19 parents and 86 F_1s and 31 entries comprising 31 F_2 s were grown in a randomized block design with three replications at Maize Breeding Unit, Delhi. Each experimental plot had a single 4m long row with 50cm X 20cm spacing with non experimental rows at borders. Artificial inoculation for BLSB was carried out in one replication. Data on yield and yield components was recorded from three replications.

3.3 SCREENING AGAINST BANDED LEAF AND SHEATH BLIGHT

3.3.1. Artificial inoculation of Maize lines

Field inoculations were carried out as per Ahuja & Payak (1978). Inoculation was made on 35-40 day old plants with barley grain culture (using four grains) (inoculum supplied by Maize Pathology Unit, Delhi) inserted between stalk and sheath at second or third basal internode (Plate 2).

3.3.2. Rating of BLSB on maize lines

Observations on intensity of disease were recorded 45 days after inoculations following 1-5 rating scale devised by Ahuja and Payak (1983) (Plate 3).

1.0 : Disease on one leaf sheath only; few small, non-coalescent lesions present.

1.5 : Disease on two sheaths; lesions large and coalescent.

2.0 : Disease upto four sheaths, lesions many and always coalescent.

2.5 : As in 2.0 + rind discoloured with small lesions.

3.0 : Disease on all sheaths except two internodes below the ear.

3.5 : Disease upto one internode below the ear shoot; rind discolouration on many internodes with large depressed lesions.

4.0 : Disease upto the internode bearing the ear shoot but shank not affected.

4.5 : Disease on the ear; husk leaves show bleaching, bands and caking among themselves as also of silk fibres; abundant fungal growth between and on kernel rows; kernel formation normal except their being lusterless; ear size less than normal; some plants prematurely dead.

5.0 : In addition to 4.5, shrinkage of stalk, reduced ear dimensions; wet rot and disorganization of ear; kernel formation absent or rudimentary; premature dead plants common; abundant sclerotial production on husk, leaves, kernels, ear tips and silk.

The entries were evaluated against this disease using the above 1-5 rating scale. Entries with disease rating 1-2 were classified as resistant, 2.1 to 4.0 as intermediate and 4.1 to 5.0 as susceptible.

3.4 CHARACTERS STUDIED:

The following characters for yield and yield components were recorded on five randomly selected plants for each genotype under each replication:

1) **Days to 50 percent pollenshed:** It was recorded as number of days from the date of sowing till 50 percent of the plants in a plot showed pollenshed.

2) **Days to 50 percent silking:** It was recorded as number of days from the date of sowing till 50 percent of the plants in a plot showed silk emergence.

3) **Plant height:** The height from the base of the plant to the tip of the tassel**,** measured in centimeters (cm) at the time of harvest.

4) **Number of cobs per plot:** Number of cobs were counted individually before harvesting.

5) **Cob placement (cm):** The height from the base of the plant to the node bearing uppermost cob.

6) **Yield per plot (kg):** All the plants in a plot were harvested and fresh dehusked cobs were weighted in kilograms.

7) **Single cob weight (kg):** it is weight in kilograms recorded by taking the average of five cobs in each genotype.

8) **Cob length (cm):** It was measured in centimeters from the butt end to the top of the cob, by taking the average of five cobs.

9) **Cob girth (cm):** It is the cob girth recorded in centimeters on the basis of average of five cobs.

10) **Number of rows per cob:** It was recorded by counting the number of rows of kernels in the middle of the cob based on average of five cobs.

11) **Number of kernels per row:** It was recorded by counting number of kernels, in full row of the cob, taken based on the average of five cobs.

12) **100 seed weight (gm):** It was recorded in grams by weighing samples of 100 sun dried kernels from the bulk produce of plants.

13) **No. of seeds per cob:** Mean was calculated by multiplying no. of rows per cob and no. of kernels per row.

3.5. STATISTICAL ANALYSIS

Means over replications for each genotype and character were calculated and used for statistical analysis. The statistical procedures are described experiment wise.

3.5.1. Analysis of variance

The data for different characters were statistically analysed on the basis of the model by Cochran and Cox (1950) for randomised block design.

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of the j^{th} genotype in the i^{th} block
μ = general mean
b_i = true effect of i^{th} block
t_j = true effect of j^{th} genotype
e_{ij} = random error associated with i^{th} block and j^{th} genotype.

The analysis of variance for each character was carried out as indicated below :

Source of variation	**d.f.**	**MSS**	**F. ratio**
Replications	r-1	M_r	M_r/M_e
Treatments	t-1	M_t	M_t/M_e
Error	(r-1) (t-1)	M_e	
Total	(rt-1)		

Where,

r = Number of replications
t = Number of genotypes or treatments
df = degrees of freedom
MSS = Mean sum of squares

M_r, M_t and M_e = mean sum of squares due to replication, treatment and error respectively.

The test of significance was carried out by 'F' table values given by Fisher and Yates (1963) at 5% and 1% level with t-1 and (r-1)(t-1) degrees of freedom..

3.5.2. Estimation of Genetic Parameters

3.5.2.1. Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952).

$$PCV = \frac{\sqrt{\sigma^2_p}}{X} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2_g}}{X} \times 100$$

Where,

σ^2_g = Genotypic Variance = $\frac{M_t - M_e}{r}$

σ^2_e = Environment Variance = $\frac{M_e}{r}$

σ^2_p = Phenotypic Variance = $\sigma^2_g + \sigma^2_e$

X = General mean

Categorisation of the range of variation was followed as proposed by Sivasubrahmanian and Menon (1973).

Less than 10% = Low

10-20% = Moderate

More than 20% = High

3.5.2.2. Heritability in Broad sense [h^2 (b)]

Heritability in broad sense was estimated as per Allard (1960).

$$h^2(b) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

As suggested by Johnson *et al.* (1955), $h^2(b)$ estimates were categorized as

Low = 0-30%
Medium = 31-60%
High = 61% and above

3.5.2.3. Genetic advance (GA)

This was estimated as per the formula proposed by Allard (1960)

$$GA = K \times \sigma p \times h^2(b)$$

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06.
h^2 (b) = Heritability in broad sense
σ_p = Phenotypic standard deviation

3.5.2.4. Genetic advance as percent of mean (GAM)

$$GAM = \frac{GA}{X} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et. al.* (1955).

Low = Less than 10%
Moderate = 10-20%
High = More than 20%

3.5.3. Line X Tester Analysis

3.5.3.1. Analysis of variance

Analysis of variance for randomized block design including parents and F_1s was carried out as per the formulae given by Singh and Chaudhary (1977).

ANOVA for Line X Tester analysis

Source of variation	d.f.	MSS	F. ratio
Replications	r-1	M_r	M_r/M_e
Treatments (Parents & F_1s)	t-1	M_t	M_t/M_e
Parents	p-1	M_p	Mp/M_e
Crosses	c-1	M_c	M_c/M_e
Parents *vs* Crosses	1	M_{pc}	M_{pc}/M_e
Error	(r-1) (t-1)	M_e	

Where,

r = number of replications

t = number of treatments

p = number of parents

c = number of crosses

M_r, M_t, M_p, M_c, M_{pc} and $M_{e\,=}$ mean sum of squares of replications, treatments, parents, croses, parents *vs* crosses and error respectively.

3.5.3.2. Estimation of combining ability

For estimation of combining ability of various characters, the Line X Tester model suggested by Kempthorne (1957) and emphasized by Arunachalam (1974) was used. The linear mathematical model for combining ability analysis is as follows:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

Y_{ijk} = any measurable character of the cross (i X j) in the k^{th} block

μ = population mean effect

g_i = gca effect of i^{th} male parent

g_j = gca effect of j^{th} female parent

s_{ij} = sca effect of the combination $(ij)^{th}$

e_{ijk} = error associated with the observation Y_{ijk} th individual

i = number of male parents 1, 2,…….m

j = number of female parents 1, 2,……..f

k = number of replications 1, 2,……r

ANOVA for combining ability (Line X Tester mating design)

Source of variation	d.f.	SS	Expectation
Replications	r-1	-	-
Crosses	lt-1		
Lines	l-1	M_1	$\sigma^2_e + r\sigma^2_{lt} + rt\sigma^2_l$
Testers	t-1	M_2	$\sigma^2_e + r\sigma^2_{lt} + rl\sigma^2_t$
Lines X Testers	(l-1) (t-1)	M_3	$\sigma^2_e + r\sigma^2_{lt}$
Error	(r-1) (lt-1)	M_4	σ^2_e

Where,

r = number of replications

l = number of lines

t = number of testers

Cov (half sibs) and cov (full sibs) were estimated by equating the observed means squares to their expectations. Since the number of lines and testers used were different, weighted average of cov (half sibs) was computed by deriving least square estimates as proposed by Arunachalam (1974). Least squares estimates were derived as follows:

$$y = \text{cov (half sibs)} = \frac{½\,[t\,(a+c-2b) + l\,(b+c-2a)]}{lt - t^2 - l^2}$$

$$x = \text{cov (full sibs)} = \frac{[(a+c-2b) + l\,(b+c-2a)] - ½\,[t^2\,(a+c) + l^2\,(b+c) - lt\,(a+b)]}{lt - t^2 - l^2}$$

Where,

$a = (M_2-M_4)/r$

$b = (M_1-M_4)/r$

$c = (M_3-M_4)/r$

The least square estimates of x and y were used to compute components of combining ability variance as follows:

$\sigma^2_{gca} = y$ and $\sigma^2_{sca} = x-2y$

3.5.3.3. Estimation of combining ability effects

Combining ability effects were estimated as follows:

General combining ability effects (gca effects) of i th line:

$$g_i = \frac{X_{i..}}{tr} - \frac{X...}{ltr}$$

General combining ability effects (gca effects) of j th tester:

$$g_j = \frac{X_{.j..}}{lr} - \frac{X_{...}}{ltr}$$

Specific combining ability effects (sca effects) due to ij th cross:

$$s_{ij} = \frac{X_{ij}}{r} - \frac{X_{i..}}{tr} - \frac{X_{.j.}}{lr} - \frac{X_{...}}{ltr}$$

Where,

$\frac{X_{...}}{ltr}$ = overall mean

$X_{i..}$ = total of i^{th} line over all the testers and replications

$X_{.j.}$ = total of j^{th} tester over all the lines and replications

X_{ij} = total of ij^{th} cross over all the replications

3.5.3.4. Testing significance of combining ability effects:

a) SE for gca effects of lines

SE $g_i = [M_4/ rt]^{1/2}$

b) SE for gca effects of testers

SE $g_j = [M_4/ rl]^{1/2}$

c) SE for sca effects of line X tester

SE $s_{ij} = [M_4/ r]^{1/2}$

d) SE for difference between two sca effects of testers

SE $(s_{ij}-s_{kl}) = [2M_4/ r]^{1/2}$

The critical difference (CD) values in each case were computed by multiplying SE value with table't' values at error degrees of freedom at 5 % and 1% level.

The general predictability ratio *i.e.,* $(2\sigma^2_{gca}/ 2\sigma^2_{gca} + \sigma^2_{sca})$ or the relative importance of GCA and SCA variance was estimated. Utility and relevance of this ratio in determining the progeny performance was emphasised and advocated by Baker (1978).

3.5.3.5. Estimation of proportional contribution of lines, testers and their interactions to total variance:

Contribution of lines = [SS(l)/SS(c)]/100

Where SS (l) and SS (c) = sum of squares due to lines and crosses respectively

Contribution of testers = [SS(t)/SS(c)]/100

Where SS(t) = sum of squares due to testers

Contribution of line X tester = [SS(lxt)/SS(c)]/100

Where SS (lxt) = sum of squares due to interaction between lines and testers

3.5.4. Estimation of Heterosis

Heterosis (percent) of F_1 over midparent value (MP) and better parent (BP) were computed following Turner (1953) and Hayes *et al.,* (1955).

$$\text{Mid parent value} = MP = \frac{P_1 + P_2}{2}$$

Percent heterosis over MP = $[(F_1 - MP)/MP] \times 100$

Percent F_1 heterosis over BP = $[(F_1 - BP)/BP] \times 100$

3.5.4.1. Standard error of estimates

The standard error for testing significance of heterosis over midparent and better parent was worked out as follows:

SE = $[(3xM_e)/2r]^{1/2}$ for mid parent

SE = $[(2xM_e)/r]^{1/2}$ for better parent

Significance of heterosis was tested by't' test.

3.5.5. Association Analysis

3.5.5.1. Correlation Studies

Phenotypic and genotypic correlations were worked out by using formula suggested by Falconer (1964).

Phenotypic coefficients of correlation (r_p)

$$r(x_i x_j)_p = \frac{Cov(x_i . x_j)_p}{\sqrt{V(x_i)_p . V(x_j)_p}}$$

Where,

$r\ (x_i.x_j)_p$	=	Phenotypic correlation between i^{th} and j^{th} character.
$COV\ (x_i.x_j)_p$	=	Phenotypic covariance between i^{th} and j^{th} character
$V\ (x_i)_p$	=	Phenotypic variance of i^{th} character
$V(x_j)_p$	=	Phenotypic variance of j^{th} character

Genotypic coefficient of correlation (r_g)

$$r(x_i x_j)_g = \frac{Cov(x_i . x_j)_g}{\sqrt{V(x_i)_g . V(x_j)_g}}$$

Where,

$r(x_i.x_j)_g$ = genotypic correlation between i^{th} and j^{th} character.
$COV(x_i.x_j)_g$ = genotypic covariance between i^{th} and j^{th} character
$V(x_i)_g$ = genotypic variance of i^{th} character
$V(x_j)_g$ = genotypic variance of j^{th} character

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of paired observations used in the calculation.

3.5.5.2. Path Coefficient Analysis

Path coefficient analysis, suggested by Wright (1921) and elaborated by Dewey & Lu (1959) was used to calculate the direct and indirect contribution of various traits to yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots + r_{1k}P_{ky}$$
$$r_{2y} = r_{21}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots + r_{2k}P_{ky}$$
$$r_{iy} = r_{i1}P_{1y} + r_{i2}P_{2y} + r_{i3}P_{3y} + \ldots\ldots + r_{ik}P_{ky}$$
$$r_{ky} = r_{k1}P_{1y} + r_{k2}P_{2y} + r_{k3}P_{3y} + \ldots\ldots + r_{kk}P_{ky}$$

Where r_{1y} to r_{ky} = Coefficient of correlation between causal factors 1 to K and dependant character Y.

r_{12} to $r_{k-1,\,k}$ = Coefficient of correlation among causal factors
P_{1y} to P_{ky} = direct effects of characters 1 to k on character y.
The above equations were written in a matrix form as under:

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ r_{ky} \end{bmatrix} \quad \begin{bmatrix} 1 & r_{12} & r_{13} & . & . & . & r_1 \\ r_{21} & 1 & r_{23} & . & . & . & r_2 \\ . & . & . & . & . & . & . \\ . & . & . & . & . & . & . \\ . & . & . & . & . & . & . \\ r_{k1} & r_{k2} & r_{k3} & . & . & . & 1 \end{bmatrix} \quad \begin{bmatrix} p_{1y} \\ p_{2y} \\ . \\ . \\ . \\ P_{ky} \end{bmatrix}$$

Then $(C)^{-1}$ =

$$\begin{bmatrix} C_{11} & C_{12} & . & . & . & C_{1k} \\ C_{21} & C_{22} & . & . & . & C_{2k} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ C_{k1} & C_{k2} & . & . & . & C_{kk} \end{bmatrix}$$

Then direct effects were calculated as follows,

$$P_{1y} = \sum_{i=1}^{k} C_{1i} \cdot r_{iy}$$

$$P_{2y} = \sum_{i=1}^{k} C_{2i} \cdot r_{iy}$$

$$P_{ky} = \sum_{i=1}^{k} C_{ki} \cdot r_{iy}$$

The indirect effect of i^{th} variable *via* j^{th} variable was worked out as $r_{ij} \times p_{jy}$

Residual effect was calculated as under:

$$1 = P^2 R_y + P_{iy} r_{1y} + P_{2y} r_{2y} + \ldots\ldots\ldots\ldots P_{ky} r_{ky}$$

Where, P^2R_y is the square of residual effect.

REFERENCES

Ahuja, S.C. and Payak, M.M. (1978). A field inoculation technique for evaluating maize germplasm to banded leaf and sheath blight. *Indian Phytopath.* **31**: 517-520.

Ahuja, S.C. and Payak, M.M. (1981a). A laboratory method for evaluating maize germplasm to banded leaf and sheath blight. *Indian Phytopath*. **34**: 34-37.

Ahuja, S.C. and Payak, M.M. (1981b). Relationship of relative humidity and temperature levels with the development of leaf and sheath blight of maize. *Z. Pflkrankh. Schutz.*. **88**: 265-268.

Ahuja, S.C. and Payak, M.M. (1982). Symptoms and signs of banded leaf and sheath blight of maize. *Phytoparasitica.* **10**: 41-49.

Ahuja, S.C. and Payak, M.M. (1983). A rating scale for banded leaf and sheath blight. *Indian Phytopath.* **36**: 338-340.

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons Inc., London, pp. 75-98.

Altinbas, M. (1995). Heterosis and combining ability in maize for grain yield and some plant characters. *Anadolu*. **5**: 35-51.

Amin, K.S. (1975). An improved method of evaluating rice sheath blight. *Phytopathology*. **65**: 214-215.

Anderson, N.A. (1982). The Genetics and Pathology of *Rhizoctonia solani. Annu. Rev. Phytopathol.* **20**: 329-347.

Anderson, N.A., Davis, D.W. and Shehata, M.A. (1982). Screening carrots for resistance to cavity spot caused by *Rhizoctonia solani. Hort. Science.* **17**: 254-256.

Anonymous (1995). Maize at Pantnagar. Annual Report: Maize Pathology, All India Coordinated Maize Improvement Project, pp. 1-21.

Anshu, G., Prasanna, B. M., Sharma, R. C., Rathore, R. S. and Saxena, S. C. (2007). Identification of resistance sources to banded leaf and sheath blight (*Rhizoctonia solani* f.sp. *sasakii*) in maize. *Indian Phytopath.* **60**(2):162-166.

Anuradha, K. (1988). Studies on line x tester analysis for yield, its components and resistance to charcoal rot (*Macrophomina phaseolina*) in maize (*Zea mays* L.). M.Sc (Ag) Thesis submitted to Andhra Pradesh Agri. Univ., Hyderabad.

Appunu, C. Satyanarayana, E. and Rao T.N. (2007). Heterosis for grain yield and its components in maize (*Zea mays* L.). *J. Res. Angrau.* **35**(1): 124-126

Arunachalam, V.C. (1974). The fallacy behind the use of modified line x tester design. *Indian J. Genet.* **34**(2): 280-287.

Atkins, J.G. Jr. and Lewis, W.D. (1952). *Rhizoctonia* aerial blight of soybeans in Louisiana (Abstr.). *Phytopathology.* **42**: 1.

Atkins, J.G. Jr. and Lewise, W.D. (1954). *Rhizocionia* aerial blight of soybeans in Louisiana. *Phytopathology.* **44**: 215-218.

Baker, R.J. (1978). Issues in diallel analysis. *Crop Sci.* **18** : 533-536.

Balla, O., Vasal, S.K., Ceniceros, F.G., Sharma, R.C. and Shukuan, Z. (2000). Identifying resistance to some maize diseases in Asia. International Crop Science Congress, 17-21 August 2000, Hamburg, Germany.

Barham, R.W., Pfleger, P.F., Rowe, R.C. and Morrison, R.H. (1983). Studies on breeding commercially acceptable disease resistant open pollinated radish varieties (Abst.). *Hort. Science.* **18**: 48.

Barksdale, T.H. (1974). Evaluation of tomato fruit for resistance to *Rhizoctonia* soil rot. *Plant Dis. Reptr.* **58**: 406-408.

Batsa, B.K. (2003).Integrated management of banded leaf and sheath blight of maize caused by *Rhizoctonia solani* f.sp. *sasakii*. Ph.D. Thesis. I.A.R.I., New Delhi.

Bell, D.K., Harris, H. and Wells, D.H. (1973). *Rhizoctonia* blight of grain sorghum foliage. *Plant Dis. Rep.* **57**: 549-550.

Bertus, L. (1927). A sclerotial disease of maize (*Zea mays* L.) due to *Rhizoctonia solani* Kuhn. Year Book, Dept. Agric., Ceylon, pp. 46-48.

Bhatnagar, S.K., Ranwah, B.R. and Sundersan, R. (1993). Heterosis in early exotic maize. *Indian J. Genet.* **53**: 94-96.

Biswas, S., Chattopadhyay, K. and Singh, N. P. (2007). Evaluation against sheath blight disease of maize under natural conditions. *Indian Phytopath.* **60**(3) :302-305.

Boosalis, M.G. (1950). Studies on the parasitism of *Rhizoctonia solani* Kuhn on soybeans. *Phytopathology.* **50**: 820-831.

Boyette, C.D. and Lee, F.N. (1979). Reduction in rice yield caused by sheath blight. *Arkansans Farm Research.* **28**: 5.

Burr, T.J., Hunter, J.E., Ogawa, J.M. and Abawi, G.S. (1978). A root rot of apple caused by *Rhizoctonia solani. Plant Dis. Rep.* **62**: 476-479.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proceedings of the sixth International Grassland Congress, 1, Pa. State college, Aug. 17-23, National Publishing Company Washington D.C. pp. 277-283.

Campbell, C.L. and Altman, J. (1976). Rapid laboratory screening of sugarbeet cultivars for resistance to *Rhizoctonia solani. Phytopathology.* **66**: 1373-1374.

Castellanos, J.J., Hallauer, A.R. and Cordova, H.S. (1998). Relative performance of testers to identify elite lines of corn. *Maydica.* **43**: 217-226.

Cgoshi, A. (1972). Some characters of hyphal anastamosis groups in *Rhizoctonia solani* Kühn. *Ann. Phytopath. Soc. Jpn.* **38**: 123-129.

Chand, T. and Logan, O. (1984). Post harvest development of *Rhizoctonia solani* and its penetration in potatotubers in Northern Ireland. *Trans. Br. Mycol. Soc.* **82:** 615-619.

Chang, T.T. (1962). The present status of breeding for resistance to rice blast and sheath blight. IRC Newslett. **11:** 1-7.

Chattopadhyay, K. and Dhiman, K.R. (2006). Heterosis for ear parameters, crop duration and prolificacy in varietal crosses of maize (*Zea mays* L.). *Indian J. Genet.* **66**(1): 45-46.

Chauhan, L.S. and Narain, U. (1980). *Rhizoctonia* blight of sunflower. *Indian Phytopath.* **33**: 607.

Chauhan, L.S. and Singh, J. (1982). *Rhizoctonia* leaf blight of lemon grass (*cymbopogan flexuoxis*). *Indian J. Myc. Pl. Path.* **11**: 245.

Choudhary, A.K. and Choudhari, L.B. (2002). Heterotic pattern of some early generation inbreds derived from two maize (*Zea mays* L.) population. *Indian J. Genet.* **62(**2): 159-160.

Choudhary, A.K., Chaudhary L.B. and Sharma, K.C. (2000). Combining ability estimates of early generation inbred lines derived from two maize population. *Indian J. Genet.* **60**(1): 55-61.

Clarkson, J.D.S. and Griffin, M.J. (1977). Sclerotia of *Rhizoctonia solani* in wheat stems with sharp eye spot. *Pl. Path.* **26:** 98.

Cochran, G.W. and Cox, G.M. (1950). Experimental Designs. John Wiley and Sons, New York, pp. 45-67.

Crossa, J., Vasal, S.K. and Beck, D.L. (1990). Combining ability estimates of CIMMYT's tropical late yellow maize germplasm. *Maydica*. **35**: 273-278.

Dabholkar, A.R. (1999). Elements of Biometrical Genetics. Concept Publishing company, New Delhi, pp. 210-230.

Datar, V.V. and Chaure, P.S. (2007). Investigations on Leaf blight of cotton caused by *Rhizoctonia solani. J. Mycol. Pl. Pathol.* **37**(2): 292-294.

Dath, P.A., Devadath, J., Rao, S.C., Naidu, D.C. and Swain, A.V. (1976). Screening of iron against sheath blight of CRRI. *International Rice Research Newsletter.* No. 2, 7.

Datta, D., Mukherjee, B.K., Das, S.P. and Barua, N.S. (2004). Studies on heterosis and its relation to genetic divergence in maize (*Zea mays* L.) inbred lines. *Cereal Research Communications.* **32**(4): 443-450.

Davis, R.L. (1927). Report of the plant breeders – Rep. Puerto Rico Agric. Exp. Stn. Puerto Rico, pp. 14-15.

De Candolle, A.P. (1815). Memoire Sur les rhizoctones, nouveau genre de Champignons qui attaque les recines, des planteset en particular celle de la luzerne cultivee. *Mem. Mus. D'Hist. Nat.* **2**: 209-216.

Deakin, J.R. and Dukes, P.D. (1975). Breeding snap beans for resistance to diseases caused by *Rhizoctonia solani* Kühn. *Hort. Science.* **10**: 269-271.

Debnath, S.C. (1984). Heterosis in maize. I. Grain yield and some of its attributes. *Bangladesh J. Agric. Res.*. **9**: 78-83.

Debnath, S.C. and Sarkar, K.R. (1987). Genetic analysis of grain yield and some of its attributes in maize (*Zea mays* L.). *Thai. J. Agric. Sci.* **20**: 263-276.

Debnath, S.C., Sarkar, K.R. and Singh, D. (1988). Combining ability estimates in maize (*Zea mays* L.). *Ann. Agric. Res.* **9**: 37-42.

Debnath, S.C., Sarakar, K.R. and Singh D. (1987). Combining ability estimates in maize (*Zea mays* L.). *Ann. Agric. Res.* **9**(1): 37-42.

Deghanpour, Z., Ehdaie, B. and Moghaddam, M. (1996). Diallel analysis of agronomic characters in white endosperm maize. *J. Genet. And Pl. Breeding.* **50**(4): 357-365.

Devi R. Th. And Prodhan, H.S. (2004). Combining ability and heterosis studies in high oil maize (*Zea mays* L.) genotypes. *Indian J. Genet.* **64**(4): 323-324.

Dewey, D.R. and Lu, K.H. (1959). Correlation and path coefficient analysis in components of crested Wheat grass seed production. *Agronomy Journal*. **51**: 515-518.

Dhillon, B.S. and Singh, J. (1976). Combining ability and heterosis in diallel crosses of maize. *Theor. Appl. Genet.* **49**: 117-122.

Dickson, M.H. and Boettger, M.A. (1977). Breeding for multiple root rot resistance in snap beans. *J. Amer. Soc. Hort. Sci.* **182:** 373-377.

Dodiya, N.S. and Joshi, V.N. (2002). Gene action for grain yield and its attributes in maize (*Zea mays* L.). *Indian J. Genet.* **62**(3): 253-254.

Dubey, R.B., Joshi, V.N. and Pandiya, N.K.(2001). Heterosis and combining ability for quality yield and maturity traits in conventional and non conventional hybrids of maize (*Zea mays* L.). *Indian J. Genet.* **61**(4): 353-353.

Eizenga, G. C. (2002). Screening *Oryza* species plants for rice sheath blight resistance. *Plant Pathology.* **86**(7) : 808-812.

Erwin, D.C. (1954). Relation of *Stagnospora, Rhizoctonia* and associated fungi to crown rot of alfalfa. *Phytopathology*. **44:** 137-144.

Falconer, D.S. (1964). An Iintroduction to Quantitative Genetics. Second edition Oliver and Boyd Ltd, Edinburgh, pp. 312-324.

FAO (2005). FAOSTAT. Food and Agriculture Organization, Rome, Italy.

Fisher, R.A. and Yates, F. (1963). Statistical Tables for Biological, Agricultural and Medical Research. Oliver and Boyd, London, pp. 46-63.

Flentje, N.T. and Hagedorn, D.J. (1964). *Rhizoctonia* tip blight and stem rot of pea. *Phytopathology*. **54**: 788-791.

Freeman, T.E. and Zetler, F.W. (1971). *Rhizoctonia* blight of water hyaninth. *Phytopathology*. **61**: 892.

Freeman, T.E., Charudattan, R., Gullen, R.E. and Addor, E. (1982). *Rhizoctonia* blight on water hyacinth in the United States. *Plant Dis.* **66**: 861-862.

Galindo, J.J., Abawi, G.B. and Thurston, H.D. (1982). Variability among isolates of *Rhizoctonia solani* associated with snap bean hypocotyls and soils in New York. *Plant Dis.* **66**: 390-394.

Gangopadhyay, S. and Sharma, A.K. (1976). Spongy rot of pumpkin caused by *Rhizoctonia solani* and *Fusarium oxysporum. Indian Phytopath.* **29**: 423-424.

Gaskill, J.O. (1968). Breeding for *Rhizoctonia* resistance in sugar beet. *J. Am. Soc. Sugar beet Technol.* **15**: 107-119.

Gautam, A.S. (2003). Combining ability studies for grain yield and other agronomic characters in inbred lines of maize (*Zea mays* L.). *Crop. Res.* **26**(3): 482-485.

Giridharan, S., Prasad, M.N. and Rangaswamy, S.R. (1996). Diallel, triallel and quadriallel analysis for yield in maize. *Madras Agric. J.* **83**: 230-236.

Gonzalez, L.C. and Owen, J.H. (1963). Soil rot of tomato caused by *Rhizoctonia solani*. *Phytopathology*. **53**: 82-85.

Gupta, S.C., Kulmi, G.K., Nagda, A.K. and Trivedi, H.K. (1994). Heterosis and combining ability in inter-varietal crosses in some local and exotic and populations of maize (*Zea mays* L.). *Crop Res*. **8**(2): 315-319.

Hallauer, A.R. (1975). Relation of gene action and type of tester in maize breeding procedure. *Proc. Annu. Corn. And Sorghum Res. Conf.* **30** : 150-165.

Hallauer, A.R. and Miranda, J.B. (1988). Quantitative Genetics in Maize Breeding. Iowa State Univ. Press, Ames, pp. 267-294.

Hallauer, A.R. and Miranda, J.B.Fo. (1981). Quantitative Genetics In Maize Breeding. Iowa State University Press, Iowa, pp.52.

Hashiba, T. (1984). Estimating method of severity and yield loss by rice sheath blight disease. *Bull. Hokuriku Nat. Agric. Exp. Sta.* **26**: 115-164.

Hayes, H. K., Immer, F.R. and Smith, D.C. (1955). Methods in Plant Breeding. McGraw Hill Co. Inc., NewYork, pp. 551.

Heath, R.G. (1956). Annual Rept. Dept. Agric., Malaya, pp. 114.

Hecker, R.J. and Ruppel, E.G. (1973). Inheritance of resistance to *Rhizoctonia solani* root rot in sugar beet. *In Agronomy Abstract, Madison, USA. Amer. Soc. Agron.* **6**.

Hecker, R.J. and Ruppel, E.G. (1975). Inheritance of *Rhizoctonia* root rot in sugar beet. *Crop Sci.* **15**: 487-490.

Hecker, R.J. and Ruppel, E.G. (1977). *Rhizoctonia* root rot resistance in sugar beet breeding and related research. *J. Am. Soc. Sugar beet. Technol.* **19**: 246-256.

Hecker, R.J., Ruppel, E.G. and Gaskill, J.O. (1972). Development of sugarbeet with resistance to *Rhizoctonia* root and crown rot. *In Agronomy Abstracts. Amer. Soc. Agron.* **10**.

Hesegawa, T., Sugimoto, T. and Inoque, H. (1968). The process of breeding sugarbeet lines resistant to *Corticum solani. Dull. Sugarbeet Res. Tokyo.* **10**: 6-13.

Horner, E. S., Chapman, W. H., Lundy, H. W. and Lutrick, M. C. (1973). Comparison of three methods of recurrent selection in maize. *Crop Sci.* **13** : 485-489.

Hossain, M.M. and Ahmed, A.U. (1998). Rhizoctonia leaf spot of cotton, a new recode in Bangladesh. *Bangladesh J. Agric.* **13**(4): 275-276.

Howard, R.J. and Williams, P.H.. (1976). Methods for detecting resistance to *Pythium and Rhizoctonia* root diseases in seedling carrot. *Plant Dis. Rep.* **60**: 151-156.

Hull, F.H. (1945). Recurrent selection for specific combining ability in Corn. *J. Am.Soc. Agron.* **37** : 134-145.

Humaydan, H.S., Williams, P.H., Jacobsen, B.J. and Bissonnette, H.L. (1976). Resistance in radish to *Aphanomyces raphani and Rhizoctonia solani. Plant Dis. Rep.* **60**: 156-160.

Hyakumachi, M. and Ui, T. (1982a). Decline of damping off of sugarbeet seedling caused by *Rhizoctonia solani* AG-2-2. *Ann. Phytopathol. Soc. Jpn.* **48**: 600-606.

Hyakumachi, M. and Ui, T. (1982b). The role of over-wintered plant debris and sclerotia as inoculum in the field occurred with sugarbeet root rot. *Ann. Phytopathol. Soc. Jpn.* **48**: 628-633.

Iqbal, A.M., Nehvi, F.A., Wani, S.A., Qadir, R. and Dar, Z.A. (2007). Combining ability analysis for yield and yield related traits in maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics.* **1**(2): 101-105.

Jabeen F. K. Sahib Hussain and Satyanarayana, E. (2007). Combining ability analysis in quality protein maize (*Zea mays* L.). *Crop Res.* **34**(1, 2 &3): 171-175.

Jenkins, M.T. and Brunson, A.M. (1932). Methods of testing inbred lines of maize in crossbred combinations. *J. Am. Soc. Agron.* **24**: 523-530.

Jha, P.B. and Khera, A.S. (1992). Evaluation of maize inbred lines derived from two heterotic populations. *Indian J. Genet.* **52**(2):126-131.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy J.* **47**: 314-318.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and Phenotypic correlation in Soybeans and their implications in selections. *Agronomy J.* **47**: 477-483.

Joshi, V.N., Pandiya, N.K. and Dubey, R.B. (1998). Heterosis and combining ability for quality and yield in early maturing single cross hybrids on maize. *Indian J. Genet.* **58**(4): 519-524.

Joyner, B.G., Partyka, R.E and Larson, P.O. (1977). *Rhizoctonia* brown patch of Kentucky blue grass. *Plant Dis. Rep.* **61**: 749-752.

Kaiser, S.A.K.M. and Chowdhuri, B.K. (1986). Reaction of multiple disease resistant I and II Fule sib families to three disease at Kalimpong, West Bengal. *Indian J. Mycol. Res.* **24**(1): 147-150.

Kaiser, W.J. (1968). *Rhizoctonia* stem canker disease of mung bean (*Phaseolus aurens*) in Iran. *Plant Dis. Rep.* **54**: 246-250.

Kajiwara, T. (1968). Important diseases of maize in Japan. Pp. 165-172. In Proceedings of symposium on maize production in South-east Asia-Present situation and fiture problems. 187 pp. Tropical Agric. Res. Series 2, Agric. For. Fish. Res. Counc. Minist. Agric. For. Japan.

Kalia, V., Sirohi, A., Bhalla, S.K. and Rathee, V.K. (1994). Combining ability in maize composites for grain yield and other quantitative characters. *Crop Res.* **7**(1): 162-165.

Kalla, V., Kumar, R. and Basandrai, A.K. (2001). Combining ability analysis and geen action estimates of yield and yield contributing characters in maize (*Zea mays* L.). *Crop Res. Hisar*. **22**: 102-106.

Kar, A.K. (1998). Screening of maize inbred lines against maydis leaf blight and sheath blight diseases. *Plant Dis. Res.* **13**(1): 56-57.

Kataria, H.R. and Dodan, D.S. (1983). Impact of soil applied on damping off of cowpea caused by *Rhizoctonia solani. Plant and Soil.* **73:** 275-283.

Katna, G., Singh, H.B., Sharma, J.K. and Guleria, S.K. (2005). Heterosis and combining ability studies for yield and its related traits in maize (*Zea mays* L.). *Crop Res.* **30**(2): 221-226.

Kempthorne, O. (1957). An Introduction to Genetic Statistics. John Wiley and Sons Inc., New York.

Khatua, D.C. and Maiti, S. (1982). Two new leaf blight caused by *Rhizoctonia solani. Indian Phytopath.* **35**: 124-125.

Kim, W. and Kim, Wg. (1996). Pathogenicity of anastomosis groups and cultural types of *Rhizoctonia solani* on crops. *Korean J. Plant Pathol.* **12**(1): 22-32.

Knight, B.C. and Burrell, W.D. (1964). Sharp eye spot of maize. *Pl. Path.* **13**: 138.

Koinuma, K. and Mochizuke, N. (1989). Field inoculation methods for evaluating the resistance to banded leaf and sheath blight (*Rhizoctonia solani* Kuhn.) in maize. *Bulletin National Grassland and Research Institute* (Japan), **40**: 13-18.

Konak, C., Unay, A., Serter, E. and Basal, H. (1999). Estimation of combining ability effects, heterosis and heterobeltosis by line x tester method in maize. *Turkish J. Field Crops.* **4**(1): 1-9.

Krishna, M.S.R., Malhi, N.S., Singh, H. and Pal, S.S. (2005). Assessment of genetic potential of maize inbred lines belonging to different heterotic pools in maize. *Crop Improv.* **32**(1): 49-55.

Kumar, M.V.N., Kumar, S.S. and Ganesh, M. (1999). Combining ability studies for oil improvement in maize (*Zea mays* L.). *Madras Agric. J.* **61:** 111-117.

Kumar, R. and Singh, I. S. (2002). Inheritance of resistance to banded leaf and sheath blight (*Rhizoctonia solani* f.sp. *sasakii*) of maize (*Zea mays* L.). Presented. 8th Asian regional Maize Workshop, Aug. 5-8, 2002, Bangkok, Thailand.

Kumar, R. and Singh, I. S. (2004). Genetic control of banded leaf and sheath blight (*Rhizoctonia solani* f.sp. *sasakii*) in maize (*Zea mays* L.). *Cereal Res. Communications.* **32**(3): 309-316.

Lakshmanan, P., Nair, C.M. and Menon, R.M. (1970). Collar rot and web blight of cow pea caused by *Rhizoctonia solani* in Kerala. *Plant Dis. Rep.* **63**: 410-413.

Lal, S. and Butchaiah, K. (1978). A field inoculation technique for evaluating maize germplasm to *Rhizoctonia* solani (Abst.). *Indian Phytopath.* **31**: 123.

Lal, S., Baruah, P. and Butchaiah, K. (1980). Assessment of yield losses in maize cultivars due to banded sclerotial disease. *Indian Phytopath.* **33**(3): 440-443.

Lebedeva, N.A. and Lebedev, A.A. (1972). The problem of inheritance of the character resistance to *Rhizoctonia solani* in some potato forms. *Tsitologiya i Genetika.* **6***:* 500-506.

Lee, S.B., Kim, J.G., Han, M.S. and Han, H.J.(1989). Studies on the occurrence of corn sheath blight caused by *Rhizoctonia solani* I. Influence of growth season and cultural environment on the occurrence of sheath blight disease. *J. Korean Soc. Grassland Sci.* **9**:174-178.

Lewis, J.A. and Papavizas, G.C. (1977). Factors affecting *Rhizoctonia solani* infection of soybeans in the green house. *Plant Dis. Rep.* **61**: 196-200.

Lin, J.F. and Chen, C. (1986). Studies on combining ability for major agronomic characters in maize (*Zea mays* L.). *J. Agril. Assoc. China.* **136**: 6-14.

Luttrell, E.S. (1962). *Rhizoctonia* blight of tall fescue grass. *Plant Dis. Rep.* **46**: 661-664.

Malik, H.N., Malik, S.I., Chughtai, S.R. and Javed, H.I. (2004). Estimates of Heterosis among Temperate, Subtropical and Tropical Maize Germplasm. *Asian Journal of Plant Sciences.* **3**(1): 6-10.

Masajo, T.M. (1976). Varietal resistance in rice to sheath blight caused by *Thanatephorus cocumeris* (Frank) Donk. (*Rhizoctonia solani* Kühn) *Abst. Diss. Abstr.* **37**: 2007B.

Mason, L. and Zuber Marcus S. (1976). Diallel Analysis of maize for leaf area, Yield and yield components. *Crop Sci.* vol. **16**: 693-696.

Mathur, R.K., Chunilal, Bhatnagar, S.K. and Singh, V. (1998). Combining ability for yield, phenological and ear characters in white seeded maize. *Indian J. Genet.* **58**(2): 177-182.

McCoy, R.J. and Kraft, J.M. (1984a). Comparison of techniques and inoculum sources in evaluating peas (Pisum sativum) for resistance to stem rot caused by *Rhizoctonia solani. Plant Dis.* **68**: 53-55.

McLean, D.M., Hoffman, J.C. and Brown, G.B. (1968). Greenhouse studies on resistance of snap beans to *Rhizoctonia solani. Plant Dis. Rep.* **52**: 486-488.

Meena, R.L. (2004). Evaluation of Maize Genotypes for Resistance to Bandel Leaf and Sheath Blight Induced by *Rhizoctonia solani f.* sp. Sasakii (Kuhn) Exner. *Indian Journal of Plant Protection.* **32**(2): 85-88.

Mildenhall, J.P. and Williams, P.H. (1970). *Rhizoctonia* crown rot and cavity spot of muck-grown carrots. *Phytopathology*. **60**: 887-890.

Mildenhall, J.P. and Williams, P.H. (1973). Effect of soil temperature and host maturity of carrot by *Rhizoctonia solani. Phytopathology.* **63**: 276-280.

Moody, A.R., Benepal, P.S., Buckley, B. and Koch, E.J. (1980). Resistance of *Phaseolus vulgaris* L. cultivars to hypocotyls inoculation with *Rhizoctonia solani* kuhn. *J. Am. Soc. Hort. Sci.* **105**: 836-838.

Mpofu, S.I. and Julian, A.M. (1994). Characterization of *Rhizoctonia solani* associated with soreshin and leaf spot symptoms on tobacco in Zimbabwe. *J. Phytopath.* **40**: 367-374.

Mukherjee, B.K. and Saha, B.C. (1984). An analysis of heterosis and manifest for yield characteristics in intervarietal crosses of maize (*Zea mays* L.). *Egypt J. Genet. Cytol.* **13**: 41-52.

Murray, D.I.L. and Nicholson, T.H. (1979). Barley stunt disorder in Scotland. *Plant Pathology.* **28**: 200-201.

Murthy, A.R., Palanisamy, S. and Manivasakam, P. (1981). Combining ability analysis for yield in maize (*Zea mays* L.). *Crop Res.* **9**: 309-312.

Nagada, A.K., Vyas, M.C., Dubey, R.B. and Pandiya, N.K. (1995). Studies in combining ability in rabi maize (*Zea mays* L.). *Crop Res. Hisar.* **10**: 297-301.

Netaji, S.V.S.R.K., Satyanarayana, E. and Suneetha, V. (2000). Heterosis studies for yield and component characters in maize (*Zea mays* L.). *Andhra Agri. J.* **47**(1&2): 39-42.

Niza, T.J.R., Abraham, M. and Samuel, M. (1981). A new Rhizoctonia rot of carrot in storage. *Indian Phytopath.* **34**: 392-393.

O'Neill, N.R., Rush, M.C., Horn, N.L. and Carver, R.B. (1977). Aerial blight of soybeans caused by *Rhizoctonia solani*. *Plant Dis. Rep.* **61**: 713-717.

Pajic, Z. (1985). Combinig abilty of maize (*Zea mays* L.) inbred lines in different generations in inbreeding (abstract). In: Breeding of silage maize. Proc. 13 th Cong. Maize and Sorghum Section of Eucarpia, Wageningen, Netherlands. **7**: 177.

Pal, A.K. and Pradhan, H.S. (1994). Combining ability analysis of grain yield and oil content along with some other attributes in maize (*Zea mays* L.). *Indian J. Genet.* **54**: 376-380.

Pan, X.B., Rush, M.C., Sha, X.Y. Xie, Q.J., Linscobme, S.D., Stetina, S.R. and Oard J.H. (1999). Major Gene, Nonallelic Sheath Blight Resistance from the Rice Cultivars Jasmine 85 and Tequing. *Crop Sci.* **39**: 338-346.

Pandey, S., Ceballos, H., Magnavaka, R., Bahia-Falho, A.F.C., Duque-Vergae, J. and Vinasco, L.E. (1994). Genetics of tolerance to soil acidity in tropical maize. *Crop Sci.* **34**: 1511-1514.

Pangga, T. and Natural, M. P. (1988). Evaluation of corn cultivars and assessment of yield loss due to banded leaf and sheath blight. *Philippine Phytopathology*. **24** (1-2): 68.

Parmeter, J.R. Jr., Sherwood, R.T. and Platt, W.D. (1969). Anastomosis grouping among isolates of *Thanatephorus cucumeris. Phytopathology*. **59**: 1270-1278.

Payak, M.M. and Renfro, B.L. (1966). Diseases of maize new to India. *Indian Phytopath. Soc. Bull.* **3**: 14-18.

Payak, M.M. and Sharma, R.C. (1985). Maize diseases and approaches to their management in India. *Tropical Pest Management.* **31**(4): 302-310.

Perasol, C. R. G. and Silvestre, J. C. (2003). Field inoculation methods for evaluating the severity of Corn Banded leaf and sheath blight (*Rhizoctonia solani* Kuhn.). Presented. 3rd Annual scientific convention of the Philippine Society for the study of nature, May 1-3 2003, University of the Philippine Visayas, Cebu College, Gorordo Avenue, Lahug, Cebu city.

Perraton, B. and Lucas, P. (1983). Role of *Rhizoctonia solani* Kuhn in the manifestation of certain symptoms of parasitic lodging of maize. *Agronomie.* **8**: 791-796.

Pierson, V.G. and Gaskill, J.O. (1961). Artificial exposure of sugar beets to *Rhizoctonia solani*. *J. Am. Soc. Sugar Beet Technol.* **11**: 574-590.

Prasad, K. and Weigle, J.L. (1969). Resistance to *Rhizoctonia solani* in *Phaseolus vulgaris. Plant Dis. Rep.* **53**: 350-352.

Prasad, K. and Weigle, J.L. (1970). Screening for resistance to *Rhizoctonia solani* in *Phaseolus vulgaris*. *Plant Dis. Rep.* **54**: 40-44.

Prasad, R., Singh, S. and Paroda, R.S. (1988). Combinig ability analysis in a maize diallel. *Indian J. Genet.* **48**: 19-23.

Rajasab, A.H., Ahmed, A. and Rajendran, C. (1982). Leaf rot of coffee seedlings caused by *Rhizoctonia solani*. *J. Coffee Res.* **12**: 77-78.

Rameeh, V., Rezai, A. and Arzani, A. (2000). Estimates of genetic parameters of yield and yield components in corn inbred lines using diallel crosses. *J. Sci. Tech. Agric. Nat. Resources.* **4**: 95-104.

Reddy, M.V. (1983). Rhizoctonia damping off of chickpea in Syria. International Chickpea Newslett.. No. **8**. 21-22.

Rhizoctonia solani on maize. *Report of Guangxi Maize Res. Inst.* (unpublished).

Ribaut, J.M., Hoisington, D.A., Deutsch, J.A., Jiang, G. and Gonzalez-de-leon, D. (1996). Identification of quantitative trait loci under drought conditions in tropical maize. Flowering parameters and the anthesis silking interval. *Theor. Appl. Genet.* **92**: 905-914.

Rush, M.C., Hoff, B.J. and Mcllrath, W.O. (1976). A uniform disease rating system for rice diseases in the United States. In Proc. 16th Rice Tech. Working Group, Lake Charles, LA, 2-4 March, 1976, Texas Agric. Exp. Stn., College Station, TX, pp 64.

Russel, W.K. and Stuber, C.W. (1985). Genotype x photoperiod and genotype x temperature interactions for maturity in maize. *Crop Sci.* **25**: 152-158.

Saidaiah, P. Satyanarayana, E. and Ansari, N.A. (2006). Studies on combining ability for some yield and morpho-physiological characters related to drought tolerance in maize (*Zea mays* L.). *Crop Res.* **32**(1): 72-76.

Sakuri, E.A.Y. and Okamoto, H. (1971). Varietal resistance to sheath blight of rice plant caused by *Pellicularia sasakii* (*Shirai*). *S. Ito. Proc. Kansai Plant Prot. Soc.* **13**: 1-6.

Satyanarayana, E., Kumar, R.S. and Sharma, M.Y. (1994). Inheritance studies of maturity components and yield in selected hybrids of maize (*Zea mays* L.). *Mysore J. agric. Sci.* **28**(1): 25-30.

Schneider, C.L., Ruppel, E.G., Hecker, R.J. and Hogaboam, G.J. (1982). Effect of soil deposition in crown on development of *Rhizoctonia* root rot in sugar beet. *Plant Dis.* **66**: 408-410.

Seifel, H.I.N. and Leath, K.T. (1983). Crown and fungal diseases of alfalfa in Egypt. *Plant Dis*. **67**: 509-511.

Selvaraj I. C., Nagarajan, P. and Das Vijendra, L.D. (2006). Heterotic expression and combining ability analysis for qualitative and quantitative traits in inbreds of maize (*Zea mays* L.). *Crop Res.* **32**(1): 77-85.

Serry, M. and Satour, M. (1981). Major disease of sesama and source of resistance in Egypt. *FAO, Pl. Prod. And Prot. Paper.* **29**: 71-72.

Serry, M.S., Selim, A.K., Satour, M.M. and Al-Ahmar, B.A. (1976). Breeding for disease resistance in sesame (*Sesamum indicum* L.) I. Inheritance of resistance of *Rhizoctonia* root rot. *Egyptian J. Phytopath.* **8**: 9-14.

Shao, F.M.M. (1980). Investigations into a root rot complex of been *Phaseolus vulgaris* L. (Abst.). *In Dissertation Abstracts International*. **41**: 757B.

Sharma, R. C. (2005). Banded leaf and sheath blight (*Rhizoctonia solani* f.sp. *sasakii*) of maize. In: Zaidi P. H. and Singh N. N. (eds), Stresses on maize in tropics. Directorate of Maize Research, New Delhi.

Sharma, R. R., Gour, H. N. and Rathore, R. S. (2003). Identification of host resistance against Banded leaf and sheath blight of maize. *J. Mycol. Pl. Pathol.* **33**(2): 313-314.

Sharma, R. R., Gour, H. N. and Rathore, R. S. (2004). Etiology of banded leaf and sheath blight symptoms on maize. *J. Mycol. Pl. Pathol.* **34**(1) : 56-59.

Sharma, R.B., Roy, A.N. and Ahluwalia, P.S. (1981). Some new post harvest disease of *Zizhious jujuba. Ind. Jour. Myco. Pl. Path.* **11**: 116.

Sharma, R.C. Rai, S.N. and Batsa, B.K. (2005). Identifying resistance to banded leaf and sheath blight of maize. *Indian Phytopath.* **58**(1): 121-122.

Sharma, R.C., Leon, D.C. and Payak, M.M. (1993). Diseases of maize in South and South East Asia: Problems and progress. *Crop Prot*. **12**(6): 414-422.

Sharma, R.C., Srinivas, P. and Batsa, B.K. (2002). Banded leaf and sheath blight of maize its epidemiology and management. In: Rajbhadary N.P., Ransom J.K., Adhikari K. and Plamer A.F.E. (eds), Sustainable Maize Production Systems for Nepal. Proceeding of Maize Symposium, Kathmandu, Nepal, pp. 108-112.

Sharma, R.C., Vasal, S.K., Gonzalez, F., Batsa, B.K. and Singh, N.N. (2002). Redressal of banded leaf and sheath blight of maize through breeding, chemical and biocontrol agents. Presented. 8th Asian regional Maize Workshop, Aug. 5-8, 2002, Bangkok, Thailand.

Sharma, R.C., Vasal, S.K., Gonzalez, F., Batsa, B.K. and Singh, N.N. (2002). Redressal of banded leaf and sheath blight of maize through breeding, chemical and biocontrol agents. Presented. 8th Asian regional Maize Workshop, Aug. 5-8, 2002, Bangkok, Thailand.

Sharma, S.R. and Sohi, H.S. (1980). Assessment of losses n French bean due to *Rhizoctonia solani*. *Indian Phytopath.* **33**: 366-369.

Shehata, M.A. (1983). Breeding for resistance to Aphanomyces root rot, *Rhizoctonia* stem rot and interaction between stem/root rot pathogen in *Pisum sativum* (Abstr.). *In Dissertation Abstracts International.* **43**: 3442B.

Shehata, M.A., Davis, D.W. and Anderson, N.A. (1934). Resistance of *Rhizoctonia* stem rot in peas pea influenced by temperature, waterning method and period of disease development. *Plant Dis.* **68**: 22-24.

Shehata, M.A., Davis, D.W. and Pfleger, F.L. (1983). Breeding for resistance to *Aphanomyces euteiches* root rot and *Rhizoctonia solani stem rot in Peas. J. Amer. Soc. Hort. Sci.* **108**: 1080-1085.

Shehata, M.A., Devis, D.W. and Anderson, N.A. (1981). Screening peas for resistance to stem rot caused by *Rhizoctonia solani. Plant Dis.* **65**: 417-419.

Shephard, M.C. and Wood, R.K.S. (1963). The effect of environment and nutrition of pathogen and host, in the damping off of seedlings by *Rhizoctonia solani. Ann. Appl. Biol.* **51**: 389-402.

Shull, G.H. (1908). A pureline method of corn breeding. *Am. Breeders Assoc. Rep.* **5**: 51-59.

Silva, G.H. (1980). Inheritance of resistance to *Rhizoctonia solani* kuhn. In snap beans (*Phaseolus vulgaris*). In Dissertation Abstracts International. **41**: 2003B.

Silva, G.H. and Hartmann, R.W. (1982). Inheritance of resistance to *Rhizoctonia solani* Kuhn. In snap beans (*Phaseolus vulgaris* L.). *J. Amer. Hort. Sci.* **107**: 653-657.

Simmonds, N.W. (1979). Principles of crop improvement, Longman, London.

Singh, B. and Saxena, S.C. (2005). Evaluation of resistant and susceptible maize genotypes by laboratory and field method against banded leaf and sheath blight (*Rhizoctonia solani* f.sp. *sasakii*). *Advances in Plant Sciences* **18**(2): 923-926.

Singh, B.M. and Sharma, Y.R. (1976). Evaluation of maize germplasm to banded sclerotial disease and assessment of yield loss. *Indian Phytopath.* **29**: 129-132.

Singh, D.V. and Seth, M.L. (1971). White leaf blotch disease of Bermuda grass in India. *Indian Phytopath.* **24**: 207-208.

Singh, K.P., Prasad, D. and Yadav, V.K. (2007). The first report of *Rhizoctonia solani* Kuhn. on Seabuckthorn (*Hippophae salicifolia* D. Don) in Uttaranchal Himalayas. *J. Mycol. Pl. Pathol.* **37**(1) : 126.

Singh, M. (1964). Studies on four isolates of *Rhizoctonia solani* Kuhn. The causal agent of black scurf disease of potato in the Punjab. *Indian Phytopath.* **17**: 24-26.

Singh, N.N. and Gupta, N.P. and Mauria, S. (1996). Maize. In: 50 years of crop science research in India, R.S. Paroda, K.L. Chadha (eds.), ICAR, New Delhi, pp. 252-264.

Singh, P. (1978). Line x tester analysis in urd (*Phaseolus mungo)*. Ph.D. Thesis, Kanpur University, Kanpur.

Singh, P. and Narayan, S.S. (2000). Biometrical Techniques in Plant Breeding. Kalyani Publishers, New Delhi.

Singh, R.K. and Chaudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, pp 205-214.

Sivasubramanian, M.S. and Menon, M.P. (1973). Path analysis of yield components in rice. *Madras Agricultural Journal.* **60**(9/12): 1217-1221.

Sood, B.C. and Khajuria, V. (2006). Genetic and anatomical characterization of land races of maize (*Zea mays* L.) for lodging and yield related traits. *Indian J. Genet.* **66**(4): 337-338.

Sprague, G.F. and Tautum, L.A. (1942). General *vs* specific combining ability in single crosses of corn. *J. Amer. Soc. Agron.* **34**: 923-932.

Srinivas, P. (2002). Studies on genetic and pathogenic variation in *Rhizoctonia solani* f.sp. *sasakii* incident of banded leaf and sheath blight in maize. Ph.D. Thesis, IARI, New Delhi, pp.98.

Steinswat, W., Pollard, L.H. and Anderson, J.L. (1967). Inheritance of resistance to *Rhizoctonia* induced stem rot of lima beans (Abstr.). *Phytopathology*. **57**: 102.

Sterne, K.E. and Jones, J.P. (1978). Sharp eye spot of wheat in Arkansas, caused by *Rhizoctonia solani. Plant Dis. Rep.* **62**: 56-60.

Sud, S. (2008). Solving the maize puzzle. *Farm View*, New Delhi.

Sumner, D.R. and Bell, D.K. (1980). Root diseases of corm caused by Rhizoctonia solani (Abstr.) *Phytopathology*. **70**: 572.

Sumner, D.R. and Bell, D.K. (1982). Root diseases induced in corn by *Rhizoctonia solani* and *Rhizoctonia zeae. Phytopathology*. **72**: 86-92.

Sumner, D.R. and Dowler, C.C. (1983). Herbicide planting data and root disease interaction in corn. *Plant Dis.* **67**: 513-517.

Sumner, D.R. and Minton, N.A. (1989). Crop losses in corn induced by *Rhizoctonia solani* AG 2-2 and nematodes. *Phytopathology*. **79**: 934-941.

Suneetha, Y., Patel, J.R. and Srinivas, T. (2000). Studies on combining ability for forage characters in maize (Zea mays L.). *Crop Res.* **19**(2): 266-270.

Tachibana, H. (1968). *Rhizoctonia* soil root rot epidemic of soybeans in Central Iowa (1967). *Plant Dis. Rep.* **52**: 613-614.

Tachibana, H., Jowett, D. and Fehr, W.R. (1971). Determination of losses in soybean caused by *Rhizoctonia solani*. *Phytopathology*. **61**: 1444-1446.

Tang, H.T., Rong, T.Z. and Yang, J.P. (2004). Research advance on sheath blight (*Zea mays* L.) in maize. *J. Maize Sci.* **12**(1): 93-96,99.

Tangonan, N.G. and Quebral, F.C. (1992). Host index of plant diseases in the Philippines, 2nd edn, Los Banos, Philippines.

Thakur, M.S., Sharma, S.L. and Munjal, R.L. (1973). Correlation studies between incidence of banded sclerotial disease and ear yield in maize. *Indian J. Myc. Pl. Path.* **3**: 180-181.

Todkar, L.P. and Navale, P.A. (2006). Selection of Parents and Hybrids through combining ability studies in maize. *J. Maharashtra agri. Univ.* **31**(3): 264-267.

Tollenar, M. and Lee, E.A. (2002). Yield potential, yield stability and stress tolerance in maize. *Field Crops Res.* **75**: 161-169.

Tu, J.C. (1968). Physiological specialization of strains of *Pellicularia sasakii* isolated from rice plants. *Plant Dis. Rep.* **52:** 323-326.

Turner, J.H. Jr (1953). A study of heterosis in upland cotton. I. Yield of hybrids compared with varieties. *Agron. J.* **45**: 484-486.

Van Eij-Natten, C.L.M. (1961). Annual Report of the Department of Agricultural Research Federation of Nigeria for the year 1959-60, 63 pp.

Vasal, S.K., Srinivasan, G., Gonzalez, F.C., Beck, L.D. and Crossa, J. (1993). Heterosis and combining ability of CIMMYT's Quality Protein Maize. *Crop Sci.* **33**: 51-57.

Vasal, S.K., Srinivasan, G., Pandey, S., Cordora, H.C., Han, G.C. and Gonzalez, C.F. (1992). Heterotic patterns of ninety white tropical CIMMYT maize lines. *Maydica.* **37**: 259-270.

Vega, A. P. D. and Silvestre, J. C. (2003). Yield loss estimate in USM Var 9 due to banded leaf and sheath blight caused by *Rhizoctonia solani* Kuhn. Presented. 3rd Annual scientific convention of the Philippine Society for the study of nature, May 1-3 2003, University of the Philippine Visayas, Cebu College, Gorordo Avenue, Lahug, Cebu city.

Venkatesh, S., Singh, N.N. and Gupta, N.P. (2001). Use of inbred testers for evaluating combining ability in modified single cross hybrid maize. *Indian J. Genet.* **61**(4): 309-313.

Venketasubbaiah, P. and Safeeulla, K.M. (1983). Importance of inoculum density of *Rhizoctonia solani* in collar rot disease of coffee. *J. Coffee Res.* **13**: 53-55.

Venugopal, M., Ansari, N.A. and Krishnamurthy, K.G. (2002). Heterosis for yield and its component characters in maize (*Zea mays* L.). *Res. on crops* **3**(1): 72-74.

Verma, H.S. and Thapliyal, P.S. (1976). *Rhizoctonia* aerial blight of soybean *Indian Phytopath.* **29**: 389-391.

Vest, G. and Comstock, V.E. (1968). Resistance to flax seedling blight caused by *Rhizoctonia solani. Phytopathology.* **58**: 1161-1163.

Vimla, B., Mukherjee, B.K. and Ahuja, V.P. (1988). Combining ability analysis for resistance to banded leaf and sheath blight of maize. *Indian J. Genet. Plant Breed.* **48**(1): 75-79.

Walejko, R. N. and Russel, W. A. (1977). Evaluation of recurrent selection for specific combining ability in two open pollinated maize cultivars. *Crop Sci.* **17**: 647-651.

Warner, R.A., Sanders, D.C. and Handerson, R.W. (1980). Inheritance of tolerance to *Rhizoctonia* fruit rot in tomato. *J. Amer. Soc. Hort. Sci.* **105**: 819-822.

Warren, H.L. (1975). Effect of inoculum concentration on resistance of lima beans to *Rhizoctonia solani. Phytopathology.* **65**: 341-345.

Wellman, F.L. (1932). *Rhizoctonia* bottom rot and head rot of cabbage. *J. Agr. Res.* **45**: 461-469.

Werner, R.A., Sanders, D.C. and Handerson, W.L. (1978). Inheritance of *Rhizoctonia* fruit rot of tomato (Abst.). *Hort. Sci.* **13**: 355.

Widstrom, N.W., Bodari, K. and Mc Millan, W.W. (1993). Heterosis among insect resistant maize populations. *Crop Sci.* **33**: 989-994.

William, J.M. (1980). Relationship of *Rhizoctonia solani* and *Collectorichum occides* to basal stem canker to tomato. *Plant Dis.* **64**: 76-78.

Williams, P.H. and Walker, J.C. (1966). Inheritance of *Rhizoctonia* bottom rot resistance in cabbage. *Phytopathology.* **56**: 367-368.

Wiltshire, S.P. (1956). Plant Disease in British Colonial Dependencies, A half-yearly report. *FAO Plant Protection Bulletin.* **5**: 66.

Woodard, K.E. and Jones, B.I. (1980). Screening peanut plant introductions in controlled environment chambers for resistance to Rhizoctonia solani. *Plant Dis.* **64**: 949-950.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research.* **20**: 257-287.

Wu, L.C. and Lin, Y. (1967). *Rhizoctonia* aerial blight of Soybean caused by *Thanatephorus curumeris*. *Mem. Coll. Agric. Nath. Taiwan Univ.* **9**: 57-60.

Yang, A.G., Pan, G.T., Ye, H. G. and Tang, L. (2003). An evaluation of the resistance of inbred lines of maize to maize sheath blight and screening of resistant resources. *Plant Prot.* **29**(1): 25-28.

Yu, C.M. (1983). Brown sheath blight disease of rice (a new disease in Taiwan). *Plant Prot. Bull., Taiwan.* **25**: 53-56.

Yurankova, S.I., Tsitok, V.O., Rusinava, V.V. and Lamesh, V.A. (1989). Features of the expression of heterosis for yield components in first generation maize hybrids. *Verti Akad. Navuk Balaruskai SSR, Biyagi Chnykh Navuk.* **2**: 40-44.

Zambezi, B.T., Horner, E.S. and Martin, F.G. (1986). Inbred lines as testers for general combining ability in maize. *Crop Sci.* **26**: 908-910.

Zhang, P.Q., Leon, C.D. and Yang, H. (1993). Investigation on the yield loss caused by*Rhizoctonia solani* on maize. *Report of Guangxi Maize Res. Inst.* (unpublished).

Zhao, M. J., Zhang, Z. M., Li, W.C. and Pan, G. T. (2006). Advances on research of maize sheath blight and strategy for marker assisted selection. *Journal of maize sciences* **14**(1) : 161-164.

4. RESULTS

4.1. Evaluation of maize inbred lines for resistance to banded leaf and sheath blight incited by *Rhizoctonia solani*

During *kharif* 2005, a total of 40 inbred lines and interspecific derivatives from maize breeding unit, IARI, New Delhi were screened against banded leaf and sheath blight under artificial epiphytotic conditions in IARI, New Delhi. Each line was planted in two rows each of 4 metre long. Disease scoring was made at 30-40 days after inoculation. Out of the forty lines, thirty (75 percent) lines showed intermediate reaction of 2.1-4.0 score and the rest ten (25 percent) lines were rated as susceptible having disease score of 4.1-5.0 in a 1-5 scale basis (Table-10). Lines showing intermediate disease reaction of 2.5-3.0 score retained greenness till maturity.

4.2. Germplasm screening for resistance to BLSB; Field experiment-II, 2006

Studies on germplasm screening were continued in 2006. Thirty elite inbred lines were evaluated under artificial epiphytotic conditions in Delhi, Pantnagar and Udaipur taking the inoculumn of their respective centres. Each inbred line was evaluated in a single row of 4 metre long. For these lines the lowest score recorded was 2.5 at Delhi. But eight lines (27 percent) at Pantnagar and four lines (13 percent) at Udaipur showed resistant reaction (1.0-2.0) (Table-11). Line (MBL-18) with pedigree 9681-f-3-2-# showed constant score of 2.0 at Pantnagar and Udaipur centres where as it showed a disease score of 4.0 at Delhi centre. MBL-11, Pop 145 (MBL-29) and Suwan-1 (MBL-30) were resistant at Udaipur centre and moderately resistant at Pantnagar and Delhi centres (Table-12). Out of thirty lines, six lines (20 percent) and five lines (17 percent) showed susceptible reaction of 4.1-5.0 at Delhi centre and Udaipur respectively. None was susceptible at Pantnagar. Intermediate reaction of 2.1-4.0 has been recorded on 24 line (80 percent) at Delhi centre and 22 lines (73 percent) at Pantnagar and 21 lines (70 percent) at Udaipur centre.

Another set of 45 elite inbreds have also been evaluated for BLSB in *kharif* 2006 at Delhi centre. All the lines showed intermediate disease reaction of 2.1-4.0 (Table-13). Out of them 19 lines have been selected as parents to be used in crossing programme. They were evaluated in *kharif* 2007 for BLSB at Genetics field, Delhi

and Pathology field, Delhi. From year wise data DMB-3, DMB-17 and DMB-19 showed similar and consistent scores (3.5) across years (Table-14). Progeny from two cobs of the same plant has also been sown in two different rows in Pathology field to analyze the difference of disease resistance if any. While there was general conformity of magnitude of disease response in general, with very few exceptions. Five lines DMB-3, DMB-15, DMB-23, DMB-26 and DMB-27 showed consistent and same disease scores in different rows (Table-15). All F_1 s and F_2 s generated from this set of 45 lines also showed intermediate disease reaction (Table-16 and Table-17). Lines showing intermediate disease reaction of 2.5-3.0 score were also found green till maturity (Plate-4).

4.3. Line X Tester analysis among the selected inbred lines

This experiment was conducted to select superior parents for hybrid development with BLSB disease resistance. In this experiment, nine lines were crossed with five testers in Line x Tester fashion, generating 45 F_1 s (Plate-5). Lines, testers and F_1s were evaluated in a field trial and data were subjected to Line x Tester analysis to know the combining ability and choose promising parents, for their subsequent utilization. SPAR 1 computer package has been used.

4.3.1. Mean performance of parents and hybrids

The mean performance of parents and hybrids for yield and yield components has been presented in Table-18. The genotypes revealed much variation for the13 quantitative traits. The mean values for different traits have been described in the following paragraphs trait wise.

1) Days to 50 percent pollenshed

Among the parents, L_1 was the earliest to pollenshed (53.67days) and T_4 tasseled last (61.00 days). Out of the 45 hybrids, L_8 x T_3 completed 50 percent pollenshed in 52.33 days as against overall mean of 54.95.

2) Days to 50 percent silking

Among the parents, L_1 was the earliest to silking (57.00days) and the last to silk is T_4 (64.33 days). Out of the 45 hybrids, L_8 x T_3 completed 50 percent silking in 54.67 days as against overall mean of 57.94.

3) Plant height (cm)

Significant variation was observed among the genotypes for this trait. Among the parents, T_3 was shortest (128.33cm) followed by L_4 (130.00cm) and tallest was T_4 (193.33 cm). Among the hybrids, L_3 x T_1 recorded the least height (168.33cm) as compared to overall mean of 199.80cm.

4) Number of cobs per plot

L_7 recorded highest number of cobs per plot (12.33) and T_3 recorded lowest cobs per plot (3.00) among the parents. The cross L_8 x T_1 with 18.67 cobs per plot was highest among the crosses. Other promising crosses were L_1 x T_5, L_3 x T_4, L_7 x T_1, L_8 x T_3 and L_8 x T_4. The overall mean for number cobs per plot was 12.73.

5) Cob placement (cm)

Significant variation was observed among the genotypes for this trait. T_4 (91.67cm) showed higher value for cob placement. Among the parents, L_4 (46.67cm) and among the hybrids, L_1 x T_1 (81.67cm) showed the lowest cob placement as against overall mean of 100.03.

6) Yield per plot (kg)

Parents L_7 (1.367 kg) and L_5 (1.267 kg) recorded maximum yield per plot. T_3 (0.667 kg) had lowest yield per plot. The crosses L_9 x T_5 (3.000 kg), L_8 x T_5 (2.867 kg), L_7 x T_5 (2.867 kg) and L_8 x T_1 (2.800 kg) showed highest yield per plot among the crosses. Out of 45 hybrids, 37 showed higher yield per plot over the general mean of 2.00 kg.

7) Single cob weight (kg)

Among the parents, single cob weight was highest for L_2 (0.079 kg), L_6 (0.076 kg) and L_5 (0.075 kg) and lowest for L_9 (0.018 kg). L_4 x T_5, L_4 x T_3, L_6 x T_4 and L_8 x T_5 recorded highest single cob weights among the hybrids.

8) Cob length (cm)

Inbred line L_5 (14.05cm) had long cobs and T_3 (3.35 cm) had short cobs among the parents. L_4 x T_5 (19.73cm), L_4 x T_3 (19.49cm) and L_1 x T_5 (18.87cm) showed higher cob lengths as against overall mean of 15.35cm.

9) Cob girth (cm)

In case of cob girth, T_2 (3.43cm) and L_4 x T_2 (3.78cm) were highest among parents and hybrids respectively. The least was T_3 (0.66 cm) as against overall mean of 3.09 cm.

10) Number of rows per cob

For number of rows per cob, inbred T_3 (2.13) recorded lowest mean and it was highest in T_2 (15.64). L_1 x T_2, L_9 x T_2 and L_8 x T_2 had higher mean values as against overall mean of 13.18.

11) Number of kernels per row

For number of kernels per row, T_2 (28.36) and L_2 (27.16) had higher mean than other inbreds and inbred T_3 (2.07) had lowest mean. Among the hybrids, L_5 x T_3 (38.00), L_4 x T_3 (37.27) and L_3 x T_3 (37.13) had higher mean values as compared to overall mean of 29.14.

12) 100 seed weight (gm)

Among the parents, the highest 100 seed weight was recorded for L_4 (25.17 gm) and lowest for T_3 (7.67 gm). L_8 x T_4 (29.00 gm) and L_8 x T_5 (28.17 gm) recorded higher 100 seed weights. Among the 45 crosses, 34 showed higher mean values as against overall mean of 22.66 gm.

13) No. of seeds per cob

In case of number of seeds per cob, T_2 (443.55) and L_5 x T_3 (567.34) were higher among parents and hybrids, respectively. The least was T_3 (4.41) as against overall mean of 384.07.

4.3.2. Analysis of variance

Analysis of variance (ANOVA) of lines, testers and hybrids was carried out for twelve different traits and the results are presented in Table-19. ANOVA revealed significant difference among the parents, females, males and females X males for days to 50 percent pollenshed, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight. Parents showed significant variation for all characters except days to 50 percent silking and yield per plot. Variance due to females

and variance due to males showed significant difference for days to 50 percent pollenshed, plant height, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight. In addition, variance due to males was significant for single cob weight. Variance due to females X males was also significant for days to 50 percent pollenshed, number of cobs per plot, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight. Variance due to hybrids was significant for days to 50 percent silking, plant height, number of cobs per plot and yield per plot, whereas variance due to parents vs hybrids was significant for all characters except days to 50 percent silking and number of cobs per plot.

4.3.3. Combining ability analysis

General and specific combining ability analysis was carried out for the twelve characters.

4.3.3.1. Analysis of variance for combining ability

The variance due to females, males, females X males, the proportion of additive and dominance components and the contribution of lines, testers and L X T to the total sum of squares are presented in the Table-20.

Analysis of variance (ANOVA) for combining ability indicated highly significant differences among females, males and females X males for days to 50 percent silking. Variance due to females and males was significant for days to 50 percent pollenshed, days to 50 percent silking, plant height, number cobs per plot, cob placement, yield per plot and 100 seed weight. In addition variance due to females was significant for single cob weight and cob girth and variance due to males was significant for cob length and number of rows per cob. Variance due to females X males was significant for days to 50 percent silking and number of kernels per row. The contributions of lines, testers, L X T are also presented in Table-20. For yield, the L X T interaction was found to contribute more than lines and testers individually. Except for plant height, all the characters had high contribution from L X T interaction.

4.3.3.2. General predictability ratio

The general predictability ratio ($2\sigma^2g/2\sigma^2g+\sigma^2s$) or the relative importance of gca and sca variance was estimated for all the characters and presented in the

Table-20. High predictability ratio indicating high relative importance of gca over sca was observed for all characters except single cob weight, number of kernels per row and 100 seed weight. The predictability ratio for yield per plot was high indicating predominance of gca over sca.

4.3.3.3. General and specific combining ability effects of parents and hybrids

General combining ability (GCA) and specific combining ability (SCA) effects for each of the traits have been computed and the same for each has been presented in Table-21(a) and Table-21(b).

1) Days to 50 percent pollenshed

GCA effects of the lines for days to 50 percent pollenshed ranges from -0.48 (L_1) to 0.79 (L_9). Among the lines, the inbred L_5 (-0.61) recorded significant negative GCA effects while the inbred L_9 (0.79) recorded significant positive GCA effects for this trait. GCA effects among the testers ranged from -0.50 (T_3) to 0.84 (T_2). Among the testers, significant positive GCA effect was recorded for T_2 (0.84).

The SCA effects for the trait days to 50 percent pollenshed ranged from -1.57 (L_2 X T_2) to 1.18 ((L_9 X T_5). Among 45 crosses studied, three crosses recorded significant negative SCA and one cross recorded significant positive SCA. The hybrid (L_2 X T_2) recorded maximum negative and significant SCA among the hybrids.

2) Days to 50 percent silking

The significant negative and positive GCA effects, among the lines ranged from -0.93 (L_5) to 0.93 (L_2) respectively. Among the lines significant negative GCA effect was recorded for L_5 and L_9. The GCA effects for testers ranged between -0.44 (T_1) to 0.79 (T_2).

The specific combining ability effects for the trait ranged from -2.19 (L_8 X T_3) to 1.44 (L_1 X T_1). The estimate of SCA effects revealed that, out of 45 crosses, one cross (L_7 X T_1) showed significant earliness to silking.

3) Plant height (cm)

Among the lines, plant height displayed significant negative and positive GCA effects, ranging from -14.44 (L_4) to 15.56 (L_7), respectively. L_1, L_3 and L_4 showed

significant negative GCA effects and L_7 showed significant positive GCA effects. GCA effects in testers ranged from -5.93 (T_1) to 9.07 (T_5).

Plant height exhibited significant SCA effects, ranging from -22.74 (L_3 X T_1) to 18.74 (L_3 X T_2). Out of 45 crosses two crosses (L_3 X T_2) and (L_5 X T_1) recorded significant positive SCA effects and one cross (L_3 X T_1) recorded significant negative SCA effects.

4) Number of cobs per plot

Among the lines, significant GCA effects ranged from -2.47 (L_4) to 2.39 (L_8). L_7 and L_8 showed significant positive GCA effects. GCA effects in testers ranged from 0.13 (T_3) to -2.39 (T_2).

The SCA effects for number of cobs per plot ranged from -4.61 (L_5 X T_2) to 3.29 (L_4 X T_1) respectively. Out of the 45 crosses, three crosses each showed significant negative and positive SCA effects.

5) Cob placement (cm)

GCA effects among lines ranged from -9.81 (L_4) to 7.19 (L_7) respectively. L_1 and L_4 showed significant negative GCA effects and L_6 and L_7 showed positive significant GCA effects for the trait cob placement. Among testers, GCA effects ranged from -9.52 (T_1) to 6.22 (T_5) respectively. Only T_1 showed significant negative GCA effects.

Cob placement recorded significant SCA effects, ranging from -14.48 (L_3 X T_1) to 16.85 (L_4 X T_1). Among the crosses, (L_3 X T_1) and (L_6 X T_5) showed significant negative SCA effects and (L_4 X T_1) showed significant positive SCA effects.

6) Yield per plot (kg)

Among the lines, the trait yield per plot ranged from -0.35 (L_4) to 0.45 (L_8). The line L_8 showed significant positive GCA effects. GCA effects among the testers ranged from -0.31 (T_2) to 0.22 (T_5) respectively and none of them were positively significant.

The estimates of SCA effects revealed that crosses L_2 X T_2, L_5 X T_3 and L_9 X T_5 to be good specific combiners. These crosses showed significant positive SCA effects for the trait.

7) Single cob weight (kg)

GCA effects among lines and testers for the trait single cob weight, ranged between -0.02 (L_3) to 0.01 (L_4 and L_8). Among these parents only L_4 and L_8 showed significant positive GCA effects. None of the testers showed significance difference for GCA effect.

This trait displayed SCA effects from -0.03 (L_3 X T_1) to 0.02 (L_3 X T_3, L_4 X T_5, L_5 X T_3 and L_9 X T_1. Out of the 45 crosses, five crosses and four crosses recorded significant negative and positive SCA effects respectively.

8) Cob length (cm)

The estimates of GCA effects indicate line L_4 (1.15) showed significant positive GCA effect and tester T_2 (-1.32) showed significant negative GCA effect for the trait.

The SCA effects for the trait ranged from -2.77 (L_3 X T_1) to 1.58 (L_2 X T_1). Among the 45 crosses, four crosses showed significant positive SCA effects and three crosses showed significant negative SCA effects.

9) Cob girth (cm)

Among the lines, L_3 (-0.24) and L_4 (0.21) showed significant negative and positive GCA effects respectively for the trait cob girth. None of the testers showed significant difference for GCA effects.

SCA effect for this trait, ranged between -0.42 (L_5 X T_2) to 0.18 (L_4 X T_2 and L_5 X T_3). The crosses L_3 X T_1, L_5 X T_2 and L_8 X T_5 showed significant negative SCA effects.

10) Number of rows per cob

The estimates of GCA effects indicate line L_4 (0.70) showed significant positive GCA effect. Among testers, T_2 (1.10) showed significant positive GCA effect.

SCA effect estimates revealed crosses L_3 X T_1 (-1.76) and L_5 X T_2 (-2.36) were having significant negative SCA effects and the cross L_5 X T_3 (1.32) had significant positive SCA effect.

11) Number of kernels per row

There were no significant negative and positive GCA effects among the lines and testers for number of kernels per row.

The SCA effect for this trait ranged from -8.30 (L_3 X T_1) to 4.46 (L_5 X T_3). Out of the 45 crosses, three crosses each showed significant negative and positive SCA effects. L_3 X T_1, L_5 X $T_2$and L_7 X T_3 recorded significant negative SCA effects and L_5 X T_3, L_3 X T_3 and L_3 X T_2 showed significant positive SCA effects.

12) 100 seed weight (gm)

GCA effects among the lines and testers, for the trait 100 seed weight, ranged from -2.42 (L_3) to 1.58 (L_8) and -1.81 (T_2) to 1.33 (T_4 and T_5) respectively. Among the lines, L_2, L_8 and L_9 and among the testers T_4 and T_5 showed significant positive GCA effects.

Among the 45 crosses studied for 100 seed weight, two crosses each showed significant positive and negative SCA effects. The SCA effects for the trait in the crosses ranged from -2.23 (L_2 X T_5) to 2.73 (L_2 X T_1). Among the crosses L_2 X T_1 showed highest SCA effects for increased 100 seed weight. The cross L_8 X T_4 may also be considered as promising cross.

4.4. Variability, Heritability and Genetic advance

The estimates of genotypic and phenotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean were furnished in Table-22.

Heritability estimates were medium for all the traits. Genetic advance ranged from 0.05 to 35.44. Days to 50 percent pollenshed, days to 50 percent silking recorded low genetic advance as percentage of mean. Plant height, cob girth, number of rows per cob and 100 seed weight exhibited moderate genetic gain while the remaining characters recorded high genetic gain. Days to 50 percent pollenshed and days to 50 percent silking showed low genotypic and phenotypic coefficients of variation. Yield and yield components recorded medium to high genotypic and phenotypic coefficients of variation.

4.5. Heterosis

The estimates of heterosis in F_1 crosses were done in comparison with better parent and mid parent values. The parent with higher mean was considered better for all traits except plant height, days to 50 percent pollenshed and days to 50 percent silking where in parent with lower mean was considered better. Better parent and mid parent heterosis are presented in Table- 23a & Table- 23b.

1) Days to 50 percent pollenshed

When the interest of the breeder is to develop varieties with shorter duration, days to 50 percent pollenshed and silking being indicators of maturity, genotypes with minimum heterosis in positive direction and maximum in negative direction are desirable. In India, early maturing types are preferable and negative estimates indicate hybrid vigour towards early maturity.

In case of better parent heterosis all the crosses showed negative heterosis which ranged from -1.73 (L_6 X T_2) to -12.57 (L_3 X T_4). Out of 45 crosses, 43 crosses showed significant differences. In case of mid parent heterosis all crosses except L_6 X T_2 showed negative heterosis. The heterosis ranged from 0.59 (L_6 X T_2) to -11.30 (L_8 X T_3). Out of 45 crosses, 42 showed significant differences.

2) Days to 50 percent silking

All the crosses showed negative heterosis and 42 crosses had significant heterosis over better parent. The values ranged from -1.14 (L_1 X T_1 and L_3 X T_1) to -12.44 (L_5 X T_4). In case of mid parent heterosis L_1 X T_1 had positive heterosis, L_6 X T_2 had zero heterosis and all other crosses had negative heterosis. The values ranged from 0.29 (L_1 X T_1) to -11.11 (L_8 X T_3). 40 crosses showed significant differences.

3) Plant height (cm)

Shorter plant height in maize is a desirable character; therefore negative heterosis is taken as basis for the trait.

The better parent heterosis ranged from -0.98 (L_3 X T_1) to 55.13 (L_4 X T_3). Out of 45 crosses, only five crosses showed significant positive heterosis and only one cross *i.e.,* L_3 X T_1 showed negative heterosis which is not significant. In case of mid parent heterosis all crosses showed positive heterosis which ranged from 8.02 (L_3

X T_1) to 56.13 (L_4 X T_3). 23 crosses showed significant differences.

4) No. of cobs per plot

Number of cobs per plot is an important component of yield and positive heterosis is desirable which contributes to higher *per se* yield. In case of better parent heterosis all the crosses showed significant positive heterosis which ranged from 46.67 (L_4 X T_2 and L_5 X T_2) to 488.89 (L_8 X T_3). Mid parent heterosis also recorded significant heterosis for all crosses except L_5 X T_2 which showed zero heterosis.

5) Cob placement (cm)

Better parent heterosis ranged from 6.38 (L_3 XT_1) to 125 (L_4 X T_1). Out of 45 crosses, 41 crosses showed significant differences. In case of mid parent heterosis 41 crosses showed positive significant heterosis. It ranged from 5.26 (L_3 X T_1) to 68 (L_4 X T_1).

6) Yield per plot (kg)

All the 45 crosses showed highly significant heterosis in positive direction over the better parent and mid parent for the trait yield per plot. The range of better parent heterosis ranged from 25.81 (L_4 X T_2) to 328.57 (L_9 X T_5) and mid parent heterosis varied from 25.81 (L_4 X T_2) to 242.86 (L_8 X T_1).

7) Single cob weight (kg)

All the crosses exhibited highly positive significant heterosis over better parent and mid parent. The range of better parent heterosis varied from 36 (L_5 X T_2) to 2576.47 (L_4 X T_3) and mid parent heterosis varied from 13.54 (L_5 X T_2) to 378.48 (L_8 X T_3).

8) Cob length (cm)

All the crosses showed positive significant heterosis over better parent and mid parent. The better parent heterosis ranged from 8.85 (L_5 X T_2) to 481.31 (L_4 X T_3) and mid parent heterosis ranged from 5.07 (L_5 X T_2) to 219.62 (L_9 X T_3).

9) Cob girth (cm)

In case of better parent and mid parent heterosis all crosses showed significant positive heterosis but only one cross *i.e.*, L_5 X T_2 showed significant heterosis in negative direction. Better parent heterosis varied from -1.49 (L_5 X T_2) to 435.35 (L_7

X T_3) and mid parent heterosis ranged from -9.56 (L_5 X T_2) to 171.95 (L_9 X T_3).

10) No.of rows per cob

For better parent heterosis all crosses showed significant positive heterosis except the cross L_5 X T_2 which showed negative heterosis. The range of better parent heterosis varied from -3.50 (L_5 X T_2) to 600.00 (L_5 X T_3). In case of mid parent heterosis all the 45 crosses showed significant heterosis in positive direction except L_5 X T_2 which showed heterosis in negative direction. The range of mid parent heterosis varied from -13.65 (L_5 X T_2) to 222.30 (L_9 X T_3).

11) No. of kernels per row

For better parent heterosis, all the crosses showed positive heterosis which ranged from 7.38 (L_5 X T_2) to 1738.71 (L_5 X T_3). But only one cross L_5 X T_2 had non significant heterosis. In case of mid parent heterosis all crosses showed positive significant heterosis which ranged from -1.41 (L_5 X T_2) to 528.11 (L_9 X T_3) except the cross L_5 X T_2 which showed non significant negative heterosis.

12) 100 seed weight (gm)

In case of better parent heterosis, 40 crosses showed significant positive heterosis which ranged from -2.31 (L_3 X T_2) to 219.57 (L_6 X T_3 and L_9 X T_3). Only one cross L_5 X T_2 (-8.03) showed significant heterosis in negative direction. In case of mid parent heterosis 39 crosses showed significant heterosis in positive direction and one cross L_5 X T_2 showed significant heterosis in negative direction. It ranged from -10.00 (L_5 X T_2) to 127.91 (L_9 X T_3).

4.6. Correlation and Path analysis

4.6.1. Correlation

Genotypic and phenotypic correlation coefficients for 12 characters studied in the investigation are given in bold and normal respectively in Table-24.

The phenotypic correlation analysis revealed that days to 50 percent pollenshed showed high significant positive correlation with days to 50 percent silking and a negatively significant correlation with all other traits. However days to 50 percent silking had high significant negative correlation with all the traits. In case of plant

height correlation coefficient was highly significant and positive with all characters. Further number of cobs per plot, cob placement, single cob weight, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight exhibited same trend.

In respect of the phenotypic correlation for grain yield per plot with other traits, it had significant positive correlation with all other traits except days to 50 percent pollenshed and days to 50 percent silking.

The genotypic correlation analysis (figures in 'bold') indicated that all the genotypic correlation coefficients were higher in magnitude compared to phenotypic correlation coefficient. Besides all genotypic correlation coefficients for the 12 characters studied were significant and the direction of correlation was following the same trend found in phenotypic correlation.

4.6.2. Path analysis

Phenotypic and genotypic path coefficient analysis was carried out taking yield per plot as dependant variable. The results obtained in path analysis along with correlation with yield for each independent variable are given in Table-25. The analysis revealed that number of cobs per plot had highest positive direct effect on yield per plot at both phenotypic and genotypic levels.

At phenotypic level, single cob weight was ranking second with respect to direct effects on yield, where as it had second highest negative effect at genotypic level. The direct effects of all other variables were very low.

In case of indirect effects, number of cobs per plot had highest indirect effect *via* number of kernels per row at phenotypic level and *via* cob length at genotypic level. It can be observed that indirect effects of plant height, cob placement, single cob weight, cob girth, number of rows per cob and 100 seed weight were positive and higher for each *via* number of cobs per plot. The high negative indirect effects were recorded by days to 50 percent pollenshed, days to 50 percent silking. The indirect effects of other independent variables were very low.

6. SUMMARY & CONCLUSION

The present investigation was undertaken to study genetics of resistance to Banded leaf and sheath blight and yield potentiality simultaneously. Knowledge about the genetics of BLSB resistance is very scanty and only a few resistance sources have been identified so far. Hence the emphasis was to screen inbred lines to identify potential new sources. Also genetic analysis of resistance needs to be understood to devise appropriate strategy for incorporation of resistance as well as to improve yield. By involving diverse maize inbred lines with different disease reactions, experimental hybrids with higher productivity and resistance to BLSB can be generated.

Multilocation screening during *kharif* 2005 at New Delhi, Pantnagar and Udaipur centres revealed that Pop145 (MBL-29) and Suwan-1 (MBL-30) showed high degree of tolerance to BLSB.

Another set of forty five lines screened during *kharif* 2006 at Delhi center showed intermediate disease reaction to BLSB. DMB-3, DMB-15, DMB-23, DMB-26 and DMB-27 showed consistent disease scores in different rows (ear-to-row) indicating homozygous disease reaction. Dominance nature of disease reaction to BLSB was revealed by resistance reaction of F_1 s generated by crossing resistant and susceptible parents.

F_2 s of crosses DMB-9 X DMB-27 (L_2 X T_2) and CM-151 X DMB-24 exhibited lowest mean scores of 2.4 which can be used in deriving resistant lines. F_2 families of DMB-22 X DMB-27, CM-151 X DMB-27 and CM-150 X DMB-25 had more than 50% individual plants with a score of 2.0, which can be specifically targeted to yield segregants with resistance to BLSB. Those will also be relevant in the strategy of obtaining segregants with extreme reaction to banded leaf and sheath blight. Such lines after stabilization and testing for consistency in reaction could serve as potential parental lines for molecular mapping.

Nature and magnitude of gene action determines the most appropriate and efficient breeding procedure. Relative contribution of gca and sca effects are of interest to breeders as breeding methods differ appreciably based on the type of gene action.

In the present investigation, L X T analysis was done using nine lines and five testers to generate information on afforesaid parameters.

The *per se* performance of the genotypes revealed that there was substantial variability among them for all the characters. ANOVA for parents *vs* hybrids component exhibited highly significant variance for all traits indicating superior performance of hybrids over parents. The variances due to females and males (indicative of GCA variance) were significant and higher in magnitude for days to 50 percent pollenshed, days to 50 percent silking, plant height, number of cobs per plot, cob placement, yield per plot, single cob weight, cob length, cob girth, number of rows per cob and 100 seed weight. This implied that these characters are predominantly governed by additive gene action. Therefore these parents can be used for the production of synthetics and composites which can further serve as base populations for effecting selections for individual traits. Variance due to females x males, which is related to dominance variance was significant for days to 50 percent silking and number of kernels per row. Hence both additive and dominance gene action were important for days to 50 percent silking.

In LX T crosses, all the lines and testers were found to have significant gca effects for one or the other traits under study. Therefore these parents could be used for production of synthetics or composites as they possessed high additive gene effects.

The genotypes L_4 (DMB-14) and L_8 (DMB-22) were good general combiners for yield and yield associated characters. Parents with high gca effects for yield also exhibited high gca for other yield contributing characters. The best specific crosses with high sca effects in desirable direction were $L_2 \times T_1$, $L_2 \times T_2$, $L_3 \times T_3$, $L_5 \times T_3$, $L_9 \times T_1$ and $L_9 \times T_5$.

The crosses $L_4 \times T_3$, $L_5 \times T_3$, $L_7 \times T_3$, $L_8 \times T_3$, $L_9 \times T_3$ and $L_9 \times T_5$ showed high positive heterosis for yield and yield components. This indicates high heterosis for grain yield had contribution from high heterosis of yield attributes.

$L_5 \times T_3$ (DMB-16 X DMB-28) and $L_9 \times T_5$ (DMB-23 X DMB-30) with high sca effects and better parent heterosis were identified for selection on the basis of number of cobs per plot, yield per plot, single cob weight, number of rows per cob and number of kernels per row.

L_2 X T_2 (DMB-9 X DMB-27) showed high degree of tolerance to BLSB as well as high productive potentiality.

Strong positive correlation among yield and yield components was reported. This means that improvement in any yield component would result in improvement in yield. The path analysis at genotypic and phenotypic levels revealed that number of cobs per plot had higher positive direct effect on yield and correlation coefficient of number of cobs per plot was highly significant and positive.

Table 1. Review of maize genotypes screened and identified for resistance against banded leaf and sheath blight

Reference	No. of genotypes screened	Resistance source identified	Basis of classification of resistance genotype
Singh and Sharma (1976)	28 (8 inbreds, 6 single crosses, 4 double crosses & 10 composites)	CM104,CM105,CM200, CM107XCM108, RN_6Ht_1 AXGE440,JML32,JML36, JML306,JML403	Disease index of ten or less
Lal *et al.,* (1980)	10 maize composites and hybrids	Hybrid Ganga 5, VL-54, KT-41	Minimum disease severity and low percent loss in number of cobs, 1000 kernel weight and grain yield
Ahuja and Payak (1981)	31 (23 inbreds, 5 double cross hybrids, one synthetic & 2 open pollinated varieties)	CM103,CM104,CM105, CM300,CM600,PI-217407, VL43	1.0-2.0 (on 5 point scale)
Ahuja and Payak (1983)	218 (22inbreds, 23 single crosses, 42hybrids, 27synthetics & composites and 104 introductions)	51 materials proved to be resistant	1.0-2.0 (on 5 point rating scale)
Kaiser and Chowdhuri (1986)	80 full sib families of multiple disease resistance stocks I & II (MDR I& II)	64 MDR stocks	1.0-2.0 (on 5 point rating scale)
Pangga and Natural (1988)	20 corn cultivars	Pioneer hybrids	shortest lesion lengths
Vimla *et al.,* (1988)	6 inbreds and their F_1s	CM104 and 7 F_1s	1.0-2.0 (on 5 point rating scale)
Kar (1998)	33 inbreds	CM117, CM 211	1.0-1.9 (on 5 point scale)
Sharma *et al.,* (2002)	500 genotypes in inbred background received from CIMMYT	13 genotypes identified as tolerant (Pop.145co-hs-49 -1-b-b-b-b,Suwan-1(S)C#B-B)	2.5-3.0 (on 5 point rating scale)

Reference	No. of genotypes screened	Resistance source identified	Basis of classification of resistance genotype
Sharma *et al.*,(2003)	128 genotypes of different maturity groups	28 genotypes as resistant (Navjot, Ganga-11,Prabhat)	1.0-2.0 resistant (on 5 point rating scale)
Batsa 2003	1780 lines from CIMMYT	Pop.145C6-HS-16-1-B-B-B-B, Suwan-1 (S) C #-f-f	2.5-3.0 (on 5 point rating scale)
Kumar and Singh (2004)	6 inbreds and their crosses	CM104 & CML 1	1.0-4.0 (on 5 point rating scale)
Meena (2004)	127 maize genotypes of different maturity groups	HKH-1140,PRD-340,PAC-79001,NMH-9858,FH-3097, FH-3133,NECH-01,F-7001, BIO-81009	Percent disease intensity (PDI) is 20 or less
Sharma *et al.,* (2005)	44 elite inbred lines	CA14501, CA00310 (CML465), CA34507, CA14510 (CML428), CA14524 (CML474), CA003134, CA00396, CA14517, Pop.145C6 -HS-49-1-B-B-B-B, Suwan-1 (S) C #-B-B	2.5-3.0 (on 5 point rating scale)
Singh and Saxena (2005)	44maizegenotypes	CA00106, CA049Y04, CA03147, CA14509, CA141518, CA00310 (CML-465), CA 03124	1.0-2.0 resistant (on 5 point rating scale)
Sood and Khajuria (2006)	100 local cultivars/germplasm of Himachal Pradesh	PMG-47,89,90,91,94,95,96,98, 99,100,69	A score of 0 as immune (on 0-9 scale by Mayee and Datar, 1986)
Anshu *et al.,* (2007)\	29 inbreds (20 from CIMMYT & 7 CM lines)	CA 00106	Disease index of >30-60 as moderately resistant (DI by Wang and Dai, 2001)
Biswas *et al.,* (2007)	i) Six varieties and their crosses ii) 20 genotypes from NBPGR Regional station, Shillong	i) Prakash was moderately resistant ii) DRLT-180,G-RS-7,RKU-193, MZ-80	1.0-2.0 (on 5 point rating scale)

Table 2 Review on heterosis and combining ability in maize

S. no	Character	Heterosis	GCA	SCA
1.	Days to 50% pollenshed	Widstrom *et al.,* (1993) Datta *et al.,* (2004) Appunu *et al.,* (2007)	Murthy *et al.,* (1981) Russel and Stuber (1985) Choudhary *et al.,* (2000)	Widstrom *et al.,* (1993) Suneetha *et al.,* (2000) Jabeen *et al.,* (2007)
2.	Days to 50% silking	Gupta *et al.,* (1994) Altinbas (1995) Nagda *et al.,* (1995) Appunu *et al.,* (2007)	Murthy *et al.,* (1981) Vasal *et al.,* (1992) Satyanarayana *et al.,*(1994) Devi and Prodhan (2004)	Gupta *et al.,* (1994) Nagda *et al.,* (1995) Suneetha *et al.,* (2000) Jabeen *et al.,* (2007)
3.	Plant height	Bhatnagar *et al.,*(1993) Altinbas (1995) Datta *et al.,* (2004) Katna *et al.,* (2005)	Vasal *et al.,* (1992) Gautham (2003) Katna *et al.,* (2005) Krishna *et al.,* (2005)	Nagda *et al.,* (1995) Todkar and Navale (2006) Altinbas (1995) Suneetha *et al.,* (2000)
4.	No. of cobs per plot	Malik *et al.,* (2004) Chattopadhyay and Dhiman (2006)	Mason and Zuber (1976) Chattopadhyay and Dhiman (2006)	Saidaiah *et al.,* (2006)
5.	Cob placement	Pandey *et al.,*(1994) Gupta *et al.,* (1994) Katna *et al.,* (2005)	Vasal *et al.,* (1993) Altinbas (1995) Konak *et al.,* (1999) Krishna *et al.,* (2005)	Widstrom *et al.,* (1993) Nagda *et al.,* (1995) Jabeen *et al.,* (2007)
6.	Yield/ plot	Debnath and Sarkar (1987) Gupta *et al.,* (1994) Altinbas (1995) Nagda *et al.,* (1995) Katna *et al.,* (2005)	Vasal *et al.,* (1993) Pandey *et al.,* (1994) Giridharan *et al.,* (1996) Devi and Prodhan (2004) Katna *et al.,* (2005) Selvaraj *et al.,* (2006) Iqbal *et al.,* (2007)	Jha and Khera (1992) Nagda *et al.,* (1995) Altinbas (1995) Giridharan *et al.,* (1996) Joshi *et al.,* (1998) Konak *et al.,* (1999) Kalla *et al.,* (2001) Venugopal *et al.,*(2002)

cont...

S. no	Character	Heterosis	GCA	SCA
				Saidaiah *et al.,* (2006) Jabeen *et al.,* (2007)
7.	Single cob wt	Gupta *et al.,* (1994) Malik *et al.,* (2004)	Gupta *et al.,* (1994)	Kumar *et al.,* (1999)
8.	Cob length	Debnath (1984) Lin and Chen (1986) Netaji *et al.,* (2000) Katna *et al.,* (2005)	Dhillon and Singh (1976) Singh *et al.,* (1996) Gautham (2003) Katna *et al.,* (2005) Krishna *et al.,* (2005)	Pajic (1985) Pal and Prodhan (1994) Nagada *et al.,* (1995) Kalla *et al.,* (2001) Jabeen *et al.,* (2007)
9.	Cob girth	Yurankova *et al.,* (1989) Katna *et al.,* (2005) Chattopadhyay and Dhiman (2006)	Pal and Prodhan (1994) Singh *et al.,* (1996) Kalla *et al.,* (2001) Katna *et al.,* (2005)	Debnath *et al.,* (1987) Nagada *et al.,* (1995) Saidaiah *et al.,* (2006) Jabeen *et al.,* (2007)
10.	No. of rows per cob	Mukherjee and Saha (1984) Dehghanpour *et al.,* (1996) Netaji *et al.,* (2000)	Dhillon and Singh (1976) Pajic (1996) Kalla *et al.,* (2001) Devi and Prodhan (2004) Katna *et al.,* (2005)	Pal and Prodhan (1994) Nagada *et al.,* (1995) Kumar *et al.,* (1999) Todkar and Navale (2006)
11.	No. of kernels per row	Debnath *et al.,* (1988) Rameeh *et al.,* (2000) Choudhary and Chaudhari (2002) Malik *et al.,* (2004)	Prasad *et al.,* (1988) Mathur *et al.,* (1998) Katna *et al.,* (2005)	Nagada *et al.,* (1995) Kumar *et al.,* (1999) Iqbal *et al.,* (2007) Jabeen *et al.,* (2007)
12.	100-seed weight	Mukherjee and Saha (1984) Joshi *et al.,* (1998) Malik *et al.,* (2004) Katna *et al.,* (2005)	Pal and Prodhan (1994) Joshi *et al.,* (1998) Katna *et al.,* (2005) Selvaraj *et al.,* (2006)	Anuradha (1988) Nagada *et al.,* (1995) Joshi *et al.,* (1998) Konak *et al.,* (1999) Kalla *et al.,* (2001) Devi and Prodhan (2004) Jabeen *et al.,* (2007)

Table 18. Mean performance of parents and hybrids of L x T analysis

Geno-types	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)	No. of seeds per cob
L_1	53.67	57.00	165.00	9.67	68.33	1.100	0.058	13.47	2.91	13.43	24.77	17.33	332.66
L_2	58.00	60.67	161.67	7.00	85.00	1.133	0.079	12.12	3.12	12.40	27.16	20.33	336.78
L_3	55.33	58.33	141.67	6.00	80.00	0.867	0.049	13.10	2.51	10.53	18.54	21.67	195.23
L_4	55.00	57.33	130.00	7.67	46.67	1.033	0.067	12.43	3.13	12.27	19.47	25.17	238.90
L_5	54.67	57.33	188.33	9.67	80.00	1.267	0.075	14.05	2.91	12.67	24.07	23.83	304.97
L_6	55.00	57.67	163.33	7.67	75.00	1.167	0.076	13.09	3.06	12.67	24.09	23.83	305.22
L_7	55.00	57.33	158.33	12.33	83.33	1.367	0.073	12.65	3.05	12.80	23.80	22.00	304.64
L_8	58.33	60.67	175.00	5.67	85.00	0.767	0.047	8.23	2.08	9.07	14.33	15.00	129.97
L_9	58.67	62.00	170.00	3.67	68.33	0.700	0.018	6.60	1.61	6.22	7.44	13.83	46.28
T_1	56.00	58.67	170.00	5.00	78.33	0.867	0.037	9.09	1.75	8.80	15.40	12.00	135.52
T_2	57.67	60.33	175.00	5.00	81.67	1.033	0.105	13.11	3.43	15.64	28.36	22.83	443.55
T_3	59.67	62.33	128.33	3.00	55.00	0.667	0.006	3.35	0.66	2.13	2.07	7.67	4.41
T_4	61.00	64.33	193.33	3.67	91.67	0.767	0.047	8.60	1.87	7.67	15.33	15.33	117.58
T_5	58.67	61.33	168.33	8.00	86.67	1.167	0.066	11.34	2.13	9.07	19.47	15.33	176.59
$L_1 \times T_1$	54.33	58.00	185.00	12.67	81.67	2.000	0.118	16.99	3.29	13.87	34.33	21.50	476.16
$L_1 \times T_2$	54.00	57.33	210.00	12.67	101.67	2.100	0.119	14.65	3.39	16.53	29.93	20.83	494.74
$L_1 \times T_3$	53.33	56.00	190.00	14.33	91.67	2.267	0.127	17.09	3.33	14.27	33.47	22.17	477.62
$L_1 \times T_4$	54.00	57.33	200.00	17.33	106.67	2.433	0.119	16.83	3.15	13.73	34.53	22.00	474.10
$L_1 \times T_5$	53.67	56.33	215.00	18.33	113.33	2.467	0.126	18.87	3.13	13.87	34.07	24.67	472.55
$L_2 \times T_1$	54.67	57.67	218.33	12.67	88.33	2.133	0.130	18.33	3.37	13.07	33.13	27.83	433.01
$L_2 \times T_2$	54.00	58.33	225.00	15.67	110.00	2.433	0.127	16.13	3.43	15.20	31.67	24.33	481.38
$L_2 \times T_3$	55.00	59.00	201.67	14.33	110.00	2.200	0.118	15.58	3.31	14.53	32.40	23.00	470.77

cont...

Geno-types	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)	No. of seeds per cob
L_2 x T_4	55.33	59.00	210.00	16.00	110.00	2.400	0.129	17.47	3.36	13.33	32.73	26.67	436.29
L_2 x T_5	54.67	57.67	233.33	15.33	111.67	2.433	0.136	16.34	3.44	14.40	33.47	24.33	481.97
L_3 x T_1	54.33	58.00	168.33	10.00	83.33	1.433	0.072	13.18	2.64	11.70	22.87	19.50	267.58
L_3 x T_2	55.33	58.00	215.00	14.00	111.67	2.067	0.114	16.01	3.24	14.53	33.73	21.17	490.10
L_3 x T_3	53.67	56.67	195.00	13.67	108.33	2.333	0.126	17.54	3.19	14.27	37.13	21.17	529.85
L_3 x T_4	53.33	56.67	201.67	18.00	111.67	2.433	0.111	17.12	3.07	14.27	32.07	22.67	457.64
L_3 x T_5	53.33	56.67	205.00	15.00	121.67	2.333	0.112	15.95	3.11	13.87	31.53	23.50	437.32
L_4 x T_1	53.33	56.00	198.33	15.67	105.00	2.200	0.117	17.41	3.24	14.00	32.40	23.83	453.60
L_4 x T_2	55.33	57.33	181.67	7.33	98.33	1.300	0.128	16.14	3.78	15.51	30.07	22.67	466.39
L_4 x T_3	54.33	57.33	201.67	13.00	91.67	1.967	0.152	19.49	3.46	14.73	37.27	24.17	548.99
L_4 x T_4	55.00	58.00	200.00	13.00	98.33	2.200	0.135	16.83	3.53	14.40	30.20	25.17	434.88
L_4 x T_5	54.00	56.33	201.67	11.67	95.00	2.133	0.155	19.73	3.49	15.07	31.33	26.17	472.14
L_5 x T_1	53.00	55.33	226.67	15.33	105.00	2.433	0.132	16.61	3.21	14.27	33.53	24.67	478.47
L_5 x T_2	54.67	57.33	206.67	7.33	100.00	1.467	0.102	14.27	2.87	12.22	25.84	21.00	315.76
L_5 x T_3	53.33	56.67	205.00	17.33	98.33	2.733	0.147	17.64	3.37	14.93	38.00	22.33	567.334
L_5 x T_4	53.67	56.33	216.67	15.67	116.67	2.300	0.121	17.37	3.25	13.20	31.67	24.83	418.04
L_5 x T_5	54.00	56.67	228.33	16.00	115.00	2.533	0.111	16.43	3.19	12.80	31.80	23.83	407.04
L_6 x T_1	55.00	57.33	208.33	15.67	110.00	2.400	0.131	16.11	3.39	14.27	32.80	24.00	468.06
L_6 x T_2	56.67	59.00	208.33	12.67	111.67	1.933	0.125	15.13	3.46	14.93	30.13	23.00	449.84
L_6 x T_3	53.67	58.00	216.67	15.33	120.00	2.500	0.133	16.65	3.36	14.13	32.73	24.50	462.47
L_6 x T_4	55.00	58.33	210.00	14.33	123.33	2.600	0.138	17.71	3.50	14.00	34.87	24.83	488.18
L_6 x T_5	54.00	56.67	216.67	14.67	106.67	2.167	0.114	16.05	3.17	12.53	32.40	24.83	405.97
L_7 x L_1	53.67	56.00	221.67	17.67	103.33	2.767	0.124	16.35	3.37	14.13	33.60	23.33	474.77

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Geno-types	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)	No. of seeds per cob
$L_7 \times T_2$	55.00	58.33	223.33	14.00	115.00	2.033	0.120	15.81	3.41	14.93	32.07	21.00	478.81
$L_7 \times T_3$	54.00	58.33	223.33	16.67	111.67	2.233	0.115	14.73	3.53	13.87	27.07	24.33	375.46
$L_7 \times T_4$	55.00	57.67	235.00	17.00	125.00	2.600	0.128	16.50	3.39	13.07	32.53	25.33	425.17
$L_7 \times T_5$	54.33	57.00	230.00	16.00	118.33	2.867	0.141	17.72	3.42	12.80	34.67	27.33	443.78
$L_8 \times T_1$	53.67	57.00	206.67	18.67	103.33	2.800	0.128	17.43	3.28	14.13	32.73	25.33	462.47
$L_8 \times T_2$	55.33	59.00	206.67	15.33	113.33	2.700	0.133	16.05	3.46	16.13	32.60	22.00	525.84
$L_8 \times T_3$	52.33	54.67	221.67	17.67	106.67	2.533	0.126	17.77	3.09	13.33	35.40	23.50	470.88
$L_8 \times T_4$	53.67	57.33	225.00	17.67	108.33	2.900	0.141	18.30	3.40	12.80	33.00	29.00	422.40
$L_8 \times T_5$	55.00	57.33	226.67	15.67	125.00	2.867	0.138	18.07	2.71	13.73	31.47	28.17	432.08
$L_9 \times T_1$	53.67	57.33	213.33	15.33	101.67	2.333	0.137	18.35	3.37	14.53	32.87	25.00	477.60
$L_9 \times T_2$	56.33	59.00	216.67	11.00	113.33	1.933	0.135	14.81	3.56	16.27	31.80	23.83	517.37
$L_9 \times T_3$	55.00	58.00	195.00	10.33	101.67	1.733	0.116	15.91	3.09	13.47	29.87	24.50	402.35
$L_9 \times T_4$	54.33	58.00	230.00	13.33	116.67	2.333	0.136	18.37	3.33	13.20	33.40	27.67	440.88
$L_9 \times T_5$	56.33	58.67	225.00	16.00	116.67	3.000	0.106	16.71	3.08	13.20	29.80	25.33	393.34
Mean	**54.95**	**57.94**	**199.80**	**12.73**	**100.03**	**2.00**	**0.11**	**15.35**	**3.09**	**13.18**	**29.14**	**22.66**	**384.07**
SEm±	1.16	1.11	16.38	2.59	12.95	0.40	0.02	2.39	0.47	2.07	4.88	3.75	
CD at 5%	2.32	2.22	32.76	5.18	25.90	0.80	0.04	4.78	0.94	4.14	9.76	7.50	
Range	52.33-61.00	54.67-64.33	128.33-235.00	3.00-18.67	46.67-125.00	0.67-3.00	0.01-0.15	3.35-19.73	0.66-3.78	2.13-16.53	2.07-38.00	7.67-29.00	4.41-567.34

Table 19. ANOVA for yield and yield components in 9 X 5 (Line X Tester) crosses of maize

Source of variation	d.f.	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
Replication	2	5.58	25.08	573.65	13.50	361.92	0.39	0.00076	18.61	0.60	13.82	102.88	48.31
Parents (P)	13	14.79**	16.10	1095.46**	21.33*	476.42*	0.15	0.00200**	29.80**	1.85**	36.83**	168.66**	83.13**
Females (F)\	8	10.20**	10.62	894.68*	19.87	453.70	0.15	0.00110	19.58*	0.86**	16.50*	117.13**	49.54*
Male (M)	4	10.90**	13.57	1697.50**	11.06	601.67	0.12	0.00400**	40.78**	2.96**	69.40**	269.67**	92.77**
F vs. M	1	67.06**	70.09	293.63	74.00**	157.15	0.20	0.00064	67.65**	5.31**	69.14**	176.83*	313.29**
Hybrids (H)	44	2.48	30.85*	622.71**	20.56**	317.28	0.43**	0.00059	5.44	0.13	3.11	21.80	13.38
P vs. H	1	209.37**	16.46	72760.12**	19.96	31604.34**	55.60**	0.14000**	1139.88**	23.16**	429.55**	5799.49**	1048.43**
Error	116	2.01	18.32	402.33	10.07	251.66	0.24	0.00070	8.56	0.32	6.42	35.65	21.09

* significant at 5% and **significant at 1% level

Table 20. ANOVA for combining ability in 9 X 5 (Line X Tester) crosses of maize

Source of variation	d.f.	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
Replication	2	0.99	2.21	303.88	5.51	539.11	0.58	0.0011	2.36	0.063	1.47	23.15	9.54
Females (F)	8	3.54*	5.77*	1707.08**	32.12*	544.63**	0.75*	0.0010	5.92	0.30**	2.18	5.77	28.67**
Male (M)	4	7.40**	7.01*	1071.74*	53.09*	1142.86**	1.18**	0.00034	16.66**	0.18	11.75**	29.06	49.86**
F vs. M	32	1.60	1.92*	295.51	13.61	157.25	0.25	0.00050	3.914	0.089	2.26	24.90*	4.99
Error	88	1.47	1.23	328.13	9.60	176.19	0.25	0.00049	2.69	0.075	1.53	15.67	4.84
VA		0.36	0.42	104.18	2.76	65.38	0.068	0.00	0.70	0.014	0.44	-0.72	3.26
VD		0.05	0.24	-10.87	1.34	-6.31	0.0001	0.00	0.41	0.005	0.24	3.08	0.05
VD/A		0.14	0.57	-0.10	0.49	-0.10	0.0015	0.00	0.59	0.36	0.55	-4.28	0.015
Vgca		0.18	0.21	52.09	1.38	32.69	0.034	0.00	0.35	0.007	0.22	-0.36	1.63
Vsca		0.05	0.24	-10.87	1.34	-6.31	0.0001	0.00	0.41	0.005	0.24	3.08	0.05
Predictability ratio		0.88	0.64	1.12	0.67	1.11	0.99	0.00	0.63	0.74	0.65	-0.31	0.015
Contribution of													
Lines (%)		25.94	34.00	49.84	28.40	31.21	32.04	32.31	19.79	40.10	12.79	4.80	38.97
Testers (%)		27.07	20.66	15.65	23.40	32.75	25.04	5.40	27.82	11.90	34.37	12.12	33.88
L X T (%)		46.99	45.35	34.51	48.13	36.04	42.92	61.54	52.38	48.15	52.84	83.07	27.15

* significant at 5% and **significant at 1% level

Table 21 a. Estimates of GCA effects in 9 X 5 (Line X Tester) crosses of maize

S. No.	Source of variation	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
GCA effects lines													
1.	L_1	-0.48	-0.40	-11.11*	0.46	-8.48*	-0.06	0.00	0.12	-0.04	0.41	0.93	-1.79**
2.	L_2	0.39	0.93**	6.56	0.19	-1.48	0.01	0.00	0.00	0.09	0.06	0.35	1.21*
3.	L_3	-0.35	-0.20	-14.11**	-0.47	-0.15	-0.19	-0.02**	-0.81	-0.24**	-0.32	-0.87	-2.42**
4.	L_4	0.05	-0.40	-14.44**	-2.47**	-9.81*	-0.35**	0.01**	1.15*	0.21**	0.70*	-0.08	0.38
5.	L_5	-0.61*	-0.93**	5.56	-0.27	-0.48	-0.02	0.00	-0.31	-0.11	-0.56	-0.16	-0.69
6.	L_6	0.52	0.47	0.89	-0.07	6.85*	0.01	0.00	-0.44	0.08	-0.07	0.25	0.21
7.	L_7	0.05	0.07	15.56**	1.66*	7.19*	0.19	0.00	-0.55	0.13	-0.29	-0.35	0.25
5.	L_8	-0.35	-0.33	6.22	2.39**	3.85	0.45**	0.01**	0.76	-0.11	-0.02	0.71	1.58**
9.	L_9	0.79**	0.80*	4.89	-1.41	2.52	-0.04	0.00	0.06	-0.01	0.09	-0.79	1.25**
	S.E.	**0.26**	**0.24**	**3.85**	**0.66**	**2.82**	**0.11**	**0.00**	**0.35**	**0.06**	**0.26**	**0.84**	**0.47**
	Testers												
1.	T_1	-0.39	-0.44	-5.93	0.24	-9.52*	-0.03	0.00	-0.02	-0.05	-0.27	-0.30	-0.13
2.	T_2	0.84*	0.79*	-0.74	-2.39*	0.85	-0.31*	0.00	-1.32*	0.11	1.10*	-1.46	-1.81**
3.	T_3	-0.50	-0.21	-5.56	0.13	-3.04	-0.03	0.00	0.17	0.01	0.13	1.37	-0.72
4.	T_4	0.02	0.23	3.15	1.21	5.48	0.16	0.00	0.62	0.04	-0.49	0.44	1.33**
5.	T_5	0.02	-0.36	9.07*	0.80	6.22	0.22	0.00	0.55	-0.10	-0.46	-0.05	1.33**
	S.E.	**0.18**	**0.17**	**2.72**	**0.47**	**2.00**	**0.08**	**0.00**	**0.25**	**0.04**	**0.19**	**0.60**	**0.33**

* significant at 5% and **significant at 1% level

Table 21 b. Estimates of SCA effects in 9 X 5 (Line X Tester) crosses of maize

S. No.	Source of variation	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
SCA Effects of crosses													
1.	$L_1 \times T_1$	0.85	1.44**	-9.07	-2.64	-7.81	-0.22	0.00	0.12	0.08	-0.32	1.37	-0.60
2.	$L_1 \times T_2$	-0.70	-0.45	10.74	-0.01	1.81	0.16	0.00	-0.91	0.03	0.98	-1.87	0.41
3.	$L_1 \times T_3$	-0.04	-0.79	-4.44	-0.87	-4.30	0.05	0.00	0.04	0.06	-0.31	-1.17	0.66
4.	$L_1 \times T_4$	0.11	0.10	-3.15	1.06	2.19	0.02	-0.01	-0.68	-0.14	-0.23	0.82	-1.57
5.	$L_1 \times T_5$	-0.22	-0.30	5.93	2.47	8.11	-0.01	0.00	1.43*	-0.02	-0.13	0.85	1.10
6.	$L_2 \times T_1$	0.32	-0.23	6.59	-2.38	-8.15	-0.15	0.01	1.58*	0.04	-0.77	0.76	2.73**
7.	$L_2 \times T_2$	-1.57**	-0.79	8.07	3.25*	3.15	0.43*	0.00	0.68	-0.06	0.00	0.45	0.91
8.	$L_2 \times T_3$	0.76	0.88	-10.44	-0.60	7.04	-0.09	-0.01	-1.36	-0.08	0.30	-1.65	-1.51
9.	$L_2 \times T_4$	0.58	0.44	-10.81	-0.01	-1.48	-0.08	0.00	0.08	-0.06	-0.28	-0.39	0.10
10.	$L_2 \times T_5$	-0.09	-0.30	6.59	-0.27	-0.56	-0.11	0.01	-0.98	0.16	0.75	0.84	-2.23*
11.	$L_3 \times T_1$	0.72	1.24**	-22.74**	-4.38**	-14.48*	-0.65**	-0.03**	-2.77**	-0.36**	-1.76**	-8.30**	-1.97*
12.	$L_3 \times T_2$	0.50	0.01	18.74*	2.25	3.48	0.26	0.01	1.38	0.08	-0.29	3.73*	1.38
13.	$L_3 \times T_3$	0.16	-0.32	3.56	-0.60	4.04	0.25	0.02**	1.41**	0.13	0.41	4.30*	0.29
14.	$L_3 \times T_4$	-0.69	-0.76	1.52	2.66	-1.15	0.16	0.00	0.54	-0.02	1.03	0.16	-0.27
15.	$L_3 \times T_5$	-0.69	-0.17	-1.07	0.07	8.11	-0.01	0.00	-0.56	0.16	0.60	0.12	0.57
16.	$L_4 \times T_1$	-0.68	-0.56	7.59	3.29*	16.85**	0.27	-0.02**	-0.49	-0.21	-0.47	0.45	-0.44
17.	$L_4 \times T_2$	0.10	-0.45	-14.26	-2.41	-0.19	-0.35	-0.01	-0.46	0.18	-0.33	-0.73	0.08
18.	$L_4 \times T_3$	0.43	0.55	10.56	0.73	-2.96	0.04	0.01	1.40	-0.05	-0.13	3.64	0.49
19.	$L_4 \times T_4$	0.58	0.77	0.19	-0.34	-4.81	0.08	-0.01	-1.72**	-0.01	0.15	-2.50	-0.57
20.	$L_4 \times T_5$	-0.42	-0.30	-4.07	-1.27	-8.89	-0.05	0.02**	1.26	0.09	0.78	-0.87	0.43
21.	$L_5 \times T_1$	-0.35	-0.70	15.93*	0.76	7.52	0.17	0.01	0.16	0.09	1.05	1.67	1.46
22.	$L_5 \times T_2$	0.10	0.08	-9.26	-4.61**	-7.85	-0.51**	-0.02**	-0.87	-0.42**	-2.36**	-4.86**	-0.52
23.	$L_5 \times T_3$	0.10	0.41	-6.11	2.87*	-5.63	0.47*	0.02*	1.01	0.18	1.32*	4.46*	-0.28
24.	$L_5 \times T_4$	-0.09	-0.36	-3.15	0.13	4.19	-0.15	0.00	0.28	0.03	0.20	-0.95	0.17

cont...

S. No.	Source of variation	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
25.	$L_5 \times T_5$	0.24	0.56	2.59	0.87	1.78	0.02	-0.01	-0.59	0.11	-0.22	-0.32	-0.83
26.	$L_6 \times T_1$	0.52	-0.10	2.26	0.89	5.19	0.11	0.01	-0.21	0.07	0.56	0.52	-0.10
27.	$L_6 \times T_2$	0.96	0.35	-2.93	0.52	-3.52	-0.07	0.00	0.13	-0.02	-0.14	-0.99	0.58
28.	$L_6 \times T_3$	-0.70	0.35	10.22	0.67	8.70	0.21	0.00	0.16	-0.02	0.03	-1.22	0.99
29.	$L_6 \times T_4$	0.11	0.24	-5.15	-1.41	3.52	0.12	0.01	0.76	0.09	0.52	1.84	-0.73
30.	$L_6 \times T_5$	-0.89	-0.84	-4.41	-0.67	-13.89*	-0.38	-0.02*	-0.83	-0.11	-0.98	-0.14	-0.73
31.	$L_7 \times T_1$	-0.35	-1.03*	0.93	1.16	-1.81	0.30	0.00	0.14	0.00	0.64	1.92	-0.80
32.	$L_7 \times T_2$	-0.24	0.08	-2.59	0.12	-0.52	-0.15	0.00	0.91	-0.12	0.08	1.54	-1.45
33.	$L_7 \times T_3$	0.10	1.08*	2.22	0.27	0.04	-0.23	-0.01	-1.66*	0.10	-0.02	-6.29**	0.79
34.	$L_7 \times T_4$	0.58	-0.03	5.19	-0.47	4.85	-0.06	0.00	-0.34	-0.08	-0.20	0.10	-0.27
35.	$L_7 \times T_5$	-0.09	-0.10	-5.74	-1.07	-2.56	0.14	0.01	0.95	0.10	-0.50	2.73	1.73
36.	$L_8 \times T_1$	0.05	0.37	-4.74	1.42	1.52	0.07	0.00	-0.07	0.15	0.38	0.00	-0.14
37.	$L_8 \times T_2$	0.50	1.15*	-9.93	0.72	1.15	0.25	0.00	-0.16	0.16	1.01	1.02	-1.79
38.	$L_8 \times T_3$	-1.17*	-2.19**	9.89	0.53	-1.63	-0.19	-0.01	0.08	-0.11	-0.82	0.99	-1.38
39.	$L_8 \times T_4$	-0.36	0.04	4.52	-0.54	-8.48	-0.02	0.00	0.15	0.17	-0.74	-0.48	2.07*
40.	$L_8 \times T_5$	0.98	0.63	0.26	-2.13	7.44	-0.12	0.00	0.00	-0.37**	0.17	-1.52	1.23
41.	$L_9 \times T_1$	-1.08*	-0.43	3.26	1.89	1.19	0.10	0.02*	1.54*	0.14	0.67	1.62	-0.14
42.	$L_9 \times T_2$	0.36	0.01	1.41	0.19	2.48	-0.02	0.01	-0.70	0.17	1.04	1.71	0.38
43.	$L_9 \times T_3$	0.36	0.01	-15.44	-3.00*	-5.30	-0.50*	-0.01	-1.09	-0.21	-0.79	-3.05	-0.04
44.	$L_9 \times T_4$	-0.82	-0.43	10.85	-1.07	1.19	-0.09	0.01	0.92	0.01	-0.44	1.41	1.07
45.	$L_9 \times T_5$	1.18*	0.83	-0.07	2.00	0.44	0.51*	-0.02*	-0.67	-0.10	-0.47	-1.70	-1.27
	S.E.	**0.52**	**0.47**	**7.70**	**1.32**	**5.64**	**0.21**	**0.01**	**0.70**	**0.12**	**0.53**	**1.68**	**0.94**

* significant at 5% and **significant at 1% level

Table 22. Estimates of Heritability, genetic advance, genetic advance as per cent mean, GCV and PCV

S. No.	Characters	Heritability (%)	Genetic advance	Genetic advance as per cent of mean	Genotypic coefficient variation	Phenotypic coefficient variation
1.	Days to 50% pollenshed	0.529	2.26	4.11	2.74	3.76
2.	Days to 50% silking	0.559	2.34	4.04	2.63	3.52
3.	Plant height (cm)	0.565	35.44	17.74	11.45	15.23
4.	No. of cobs per plot	0.597	6.15	48.31	30.32	39.24
5.	Cob placement (cm)	0.459	20.40	20.39	14.61	21.56
6.	Yield/ plot (kg)	0.594	0.95	47.50	29.93	38.83
7.	Single cob wt. (kg)	0.569	0.05	45.45	27.82	36.88
8.	Cob length (cm)	0.460	3.78	24.63	17.60	25.94
9.	Cob girth (cm)	0.377	0.56	18.12	14.36	23.38
10.	No. of rows per cob	0.376	2.48	18.82	14.92	24.34
11.	No. of kernels per row	0.526	9.40	32.26	21.58	29.76
12.	100-seed weight (gm)	0.289	3.25	14.34	12.93	24.04

Table-23a. Estimates of better parent heterosis for 12 characters studied

Crosses	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield per plot (kg)	Single cob weight (kg)	Cob length (cm)	Cob girth (cm)	Number of rows per cob	Number of kernels per row	100-seed weight (gm)
$L_1 \times T_1$	-2.98*	-1.14	8.82	153.33**	19.51	130.77**	221.82**	86.80**	88.17**	57.58**	122.94**	79.17**
$L_1 \times T_2$	-6.36**	-4.97**	20.00	153.33**	48.78**	103.23**	104.57**	11.77**	16.74**	23.08**	20.86**	20.19**
$L_1 \times T_3$	-10.61**	-10.16**	15.15	377.78**	66.67**	240.00**	2141.18**	409.74**	404.04**	568.75**	1519.35**	189.13**
$L_1 \times T_4$	-11.48**	-10.88**	3.45	372.73**	56.10**	217.39**	155.71**	95.74**	68.93**	79.13**	125.22**	43.48**
$L_1 \times T_5$	-8.52**	-8.15**	27.72	129.17**	65.85**	124.24**	116.00**	66.43**	47.34**	52.94**	75.00**	60.87**
$L_2 \times T_1$	-5.75**	-4.95**	28.43	153.33**	12.77	146.15**	255.55**	101.54**	92.75**	48.48**	115.15**	131.94**
$L_2 \times T_2$	-6.90**	-3.85**	28.57	213.33**	34.69*	135.48**	60.48**	33.09**	9.93**	22.58**	16.61**	19.67**
$L_2 \times T_3$	-7.82**	-5.35**	24.74	377.78**	100.00**	230.00**	1982.35**	364.61**	402.02**	581.25**	1467.74**	200.00**
$L_2 \times T_4$	-9.29**	-8.29**	8.62	336.36**	29.41*	213.04**	176.43**	103.10**	80.00**	73.91**	113.48**	73.91**
$L_2 \times T_5$	-6.82**	-5.98**	38.61*	119.05**	31.37*	114.71**	105.53**	44.09**	61.69**	58.82**	71.92**	58.70**
$L_3 \times T_1$	-2.98*	-1.14	-0.98	100.00**	6.38	65.38**	97.27**	44.90**	51.15**	32.95**	48.48**	62.50**
$L_3 \times T_2$	-4.05**	-3.87**	22.86	180.00**	39.58**	138.46**	134.93**	22.27**	29.08**	37.97**	81.95**	-2.31
$L_3 \times T_3$	-10.06**	-9.09**	37.65*	355.56**	96.97**	250.00**	2123.53**	423.06**	383.84**	568.75**	1696.77**	176.09**
$L_3 \times T_4$	-12.57**	-11.92**	4.31	390.91**	39.58**	217.39**	138.57**	99.07**	64.64**	86.09**	109.13**	47.83**
$L_3 \times T_5$	-9.09**	-7.61**	21.78	150.00**	52.08**	169.23**	130.82**	40.68**	46.08**	52.94**	70.08**	53.26**
$L_4 \times T_1$	-4.76**	-4.55**	16.67	213.33**	125.00**	153.85**	218.18**	91.50**	85.50**	59.09**	110.39**	98.61**
$L_4 \times T_2$	-4.05**	-4.97**	3.81	46.67**	110.71**	25.81**	91.50**	29.84**	21.00**	26.44**	54.45**	-0.73
$L_4 \times T_3$	-8.94**	-8.02**	55.13**	333.33**	96.43**	195.00**	2576.47**	481.31**	424.24**	590.62**	1703.23**	215.22**
$L_4 \times T_4$	-9.84**	-9.84**	3.45	254.55**	110.71**	186.96**	189.29**	95.66**	89.29**	87.83**	96.96**	64.13**
$L_4 \times T_5$	-7.95**	-8.15**	19.80	52.17**	103.57**	106.45**	133.17**	74.02**	63.95**	66.18**	60.96**	70.65**
$L_5 \times T_1$	-5.36**	-5.68**	20.35	206.67**	34.04*	180.77**	260.00**	82.62**	83.97**	62.12**	117.75**	105.56**
$L_5 \times T_2$	-5.20**	-4.97**	9.73	46.67**	25.00	41.94**	36.00**	8.85**	-1.49**	-3.50	7.38	-8.03*
$L_5 \times T_3$	-10.61**	-9.09**	8.85	477.78**	78.79**	310.00**	2488.23**	426.04**	411.11**	600.00**	1738.71**	191.30**
$L_5 \times T_4$	-12.02**	-12.44**	12.07	327.27**	45.83**	200.00**	158.57**	101.94**	73.93**	72.17**	106.52**	61.96**
$L_5 \times T_5$	-7.95**	-7.61**	21.24	100.00**	43.75**	117.14**	66.83**	44.86**	50.16**	41.18**	63.36**	55.43**
$L_6 \times T_1$	-1.79	-2.27*	22.55	213.33**	46.67**	176.92**	257.27**	77.13**	93.89**	62.12**	112.99**	100.00**
$L_6 \times T_2$	-1.73	-2.21	19.05	153.33**	48.89**	87.10**	64.91**	15.58**	13.07**	17.89**	25.09**	0.73
$L_6 \times T_3$	-10.06**	-6.95**	32.65	411.11**	118.18**	275.00**	2252.94**	396.62**	409.09**	562.50**	1483.87**	219.57**
$L_6 \times T_4$	-9.84**	-9.33**	8.62	290.91**	64.44**	239.00**	195.71**	105.89**	87.50**	82.61**	127.39**	61.96**

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Crosses	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield per plot (kg)	Single cob weight (kg)	Cob length (cm)	Cob girth (cm)	Number of rows per cob	Number of kernels per row	100-seed weight (gm)
$L_6 \times T_5$	-7.95**	-7.61**	28.71	91.30**	42.22**	85.71**	71.86**	41.50**	48.90**	38.24**	66.44**	61.96**
$L_7 \times T_1$	-4.17**	-4.55**	30.39	253.33**	31.91*	219.23**	238.18**	79.77**	93.13**	60.61**	118.18**	94.44**
$L_7 \times T_2$	-4.62**	-3.31**	27.62	180.00**	40.82**	96.77**	64.84**	24.99**	12.03**	16.67**	34.73**	-4.55
$L_7 \times T_3$	-9.50**	-6.42**	41.05*	455.56**	103.03**	235.00**	1935.29**	339.36**	435.35**	550.00**	1209.68**	217.39**
$L_7 \times T_4$	-9.84**	-10.36**	21.55	363.64**	50.00**	239.13**	173.57**	91.86**	81.43**	70.43**	112.17**	65.22**
$L_7 \times T_5$	-7.39**	-7.07**	36.63*	100.00**	42.00**	145.71**	112.06**	56.26**	60.82**	41.18**	78.08**	78.26**
$L_8 \times T_1$	-8.00**	-6.04**	18.10	273.33**	31.91*	265.22**	248.18**	111.91**	87.79**	60.61**	128.37**	111.11**
$L_8 \times T_2$	-5.14**	-2.75*	18.10	206.67**	38.78**	252.17**	182.27**	95.06**	66.35**	77.94**	127.44**	46.67**
$L_8 \times T_3$	-12.29**	-12.30**	26.67	488.89**	93.94**	280.00**	2123.53**	430.02**	367.68**	525.00**	1612.90**	206.52**
$L_8 \times T_4$	-12.02**	-10.88**	16.38	381.82**	27.45*	278.26**	201.43**	122.45**	82.14**	66.96**	130.23**	93.33**
$L_8 \times T_5$	-6.25**	-6.52**	29.52	176.47**	47.06**	273.91**	194.33**	119.69**	30.45**	51.47**	119.53**	87.78**
$L_9 \times T_1$	-8.52**	-7.53**	25.49	318.18**	48.78**	233.33**	673.58**	178.08**	109.11**	133.53**	341.56**	108.33**
$L_9 \times T_2$	-3.98**	-4.84**	23.81	200.00**	65.75**	176.19**	662.26**	124.34**	121.12**	161.38**	327.23**	72.29**
$L_9 \times T_3$	-7.82**	-6.95**	14.71	244.44**	84.85**	160.00**	1947.06**	374.35**	367.68**	531.25**	1345.16**	219.57**
$L_9 \times T_4$	-10.93**	-9.84**	18.97	263.64**	70.73**	233.33**	671.70**	178.38**	107.04**	112.10**	348.72**	100.00**
$L_9 \times T_5$	-3.98**	-5.38**	32.35	336.36**	70.73**	328.57**	498.11**	153.13**	91.30**	112.10**	300.36**	83.13**
S.E.	**1.15**	**1.10**	**16.37**	**2.59**	**12.95**	**0.40**	**0.021**	**2.39**	**0.46**	**2.07**	**4.87**	**3.75**

Table 23b. Estimates of mid parent heterosis for 12 characters studied

Crosses	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield per plot (kg)	Single cob weight (kg)	Cob length (cm)	Cob girth (cm)	Number of rows per cob	Number of kernels per row	100-seed weight (gm)
$L_1 \times T_1$	-0.91	0.29	10.45	72.73**	11.36	103.39**	148.42**	50.59**	41.26**	24.74**	70.95**	46.59**
$L_1 \times T_2$	-2.99**	-2.27*	23.53	72.73**	35.56**	96.88**	46.42**	10.27**	7.05**	13.72**	12.69**	3.73
$L_1 \times T_3$	-5.88**	-6.15**	29.55**	126.32**	48.65**	156.60**	296.87**	103.25**	86.54**	83.30**	149.44**	77.33**
$L_1 \times T_4$	-5.81**	-5.49**	11.63	160.00**	33.33**	160.71**	127.30**	52.57**	32.12**	30.17**	72.24**	34.69**
$L_1 \times T_5$	-4.45**	-4.79**	29.00*	107.55**	46.24**	117.65**	102.14**	52.16**	24.50**	23.26**	54.03**	51.02**
$L_2 \times T_1$	-4.09**	-3.35**	31.66*	111.11**	8.16	113.33**	124.71**	72.81**	38.26**	23.27**	55.71**	72.16**
$L_2 \times T_2$	-6.63**	-3.58**	33.66*	161.11**	32.00**	124.62**	38.04**	27.85**	4.73**	8.40**	14.09**	12.74**
$L_2 \times T_3$	-6.52**	-4.07**	39.08**	186.67**	57.14**	144.44**	177.65**	101.42**	75.15**	100.00**	121.74**	64.29**
$L_2 \times T_4$	-7.00**	-5.60**	18.31	200.00**	24.53*	152.63**	104.76**	68.62**	34.67**	32.89**	54.08**	49.53**
$L_2 \times T_5$	-6.29**	-5.46**	41.41**	104.44**	30.10*	111.59**	87.19**	39.32**	31.00**	34.16**	43.56**	36.45**
$L_3 \times T_1$	-2.40**	-0.85	8.02	81.82**	5.26	65.38**	69.53**	18.76**	24.04**	21.03**	34.75**	15.84**
$L_3 \times T_2$	-2.06*	-2.25*	35.79*	154.55**	38.14**	117.54**	49.13**	22.21**	9.03**	11.04**	43.86**	4.87
$L_3 \times T_3$	-6.67**	-6.08**	44.44**	203.70**	60.49**	204.35**	363.80**	113.25**	101.47**	125.26**	260.40**	44.32**
$L_3 \times T_4$	-8.31**	-7.61**	20.40	272.41**	30.10*	197.96**	133.57**	57.81**	40.44**	56.78**	89.33**	22.52**
$L_3 \times T_5$	-6.43**	-5.29**	32.26*	114.29**	46.00**	129.51**	95.36**	30.57**	34.00**	41.50**	65.94**	27.03**
$L_4 \times T_1$	-3.90**	-3.45**	32.22*	147.37**	68.00**	131.58**	125.81**	61.78**	32.97**	32.91**	85.85**	28.25**
$L_4 \times T_2$	-1.78	-2.55*	19.13	15.79**	53.25**	25.81**	49.03**	26.40**	15.35**	11.14**	25.74**	5.56
$L_4 \times T_3$	-5.23**	-4.18**	56.13**	143.75**	80.33**	131.37**	319.35**	146.96**	82.75**	104.63**	246.13**	47.21**
$L_4 \times T_4$	-5.17**	-4.66**	23.71	129.41**	42.17**	144.44**	138.24**	60.00**	41.52**	44.48**	73.56**	24.28**
$L_4 \times T_5$	-4.99**	-5.06**	35.20	48.94**	42.50**	93.94**	132.58**	66.01**	32.74**	41.25**	60.96**	29.22**
$L_5 \times T_1$	-4.22**	-4.60**	26.51	109.09**	32.63**	128.13**	136.42**	43.49**	37.91**	32.92**	69.93**	37.67**
$L_5 \times T_2$	-2.67**	-2.55*	13.76	0.00	23.71*	27.54**	13.54**	5.07*	-9.56**	-13.65**	-1.41	10.00**
$L_5 \times T_3$	-6.71**	-5.29**	29.47*	173.68**	45.68**	182.76**	263.64**	102.68**	88.81**	101.80**	190.82**	41.80**
$L_5 \times T_4$	-7.20**	-7.40**	13.54	135.00**	35.92**	126.23**	98.36**	53.33**	35.84**	29.84**	60.74**	26.81**
$L_5 \times T_5$	-4.71**	-4.49**	28.04	81.13**	38.00**	108.22**	56.60**	29.38**	26.72**	17.79**	46.09**	21.70**
$L_6 \times T_1$	-0.90	-1.43	25.00	147.37**	43.48**	136.07**	132.54**	45.19**	40.92**	32.92**	66.12**	33.95**
$L_6 \times T_2$	0.59	0.00	23.15	100.00**	42.55**	75.76**	38.75**	15.51**	6.57**	5.50**	14.91**	1.43
$L_6 \times T_3$	-6.40**	-3.33**	48.57**	187.50**	84.62**	172.73**	226.53**	102.51**	80.65**	90.99**	150.29**	55.56**

cont....

Crosses	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Yield per plot (kg)	Single cob weight (kg)	Cob length (cm)	Cob girth (cm)	Number of rows per cob	Number of kernels per row	100-seed weight (gm)
$L_6 \times T_4$	-5.17**	-4.37**	17.76	152.94**	48.00**	168.97**	125.00**	63.25**	42.08**	37.70**	76.88**	26.81**
$L_6 \times T_5$	-4.99**	-4.76**	30.65*	87.23**	31.96**	85.71**	60.19**	31.35**	22.11**	15.34**	48.77**	26.81**
$L_7 \times T_1$	-3.30**	-3.45**	35.03*	103.85**	27.84*	147.76**	126.14**	50.38**	40.75**	30.86**	71.43**	37.25**
$L_7 \times T_2$	-2.37**	-0.85	34.00*	61.54**	39.39**	69.44**	35.46**	22.74**	5.35**	5.00**	22.96**	6.32
$L_7 \times T_3$	-5.81**	-2.51**	55.81**	117.39**	61.45**	119.67**	193.22**	84.17**	90.65**	85.71**	109.28**	64.04**
$L_7 \times T_4$	-5.17**	-5.21**	33.65*	112.50**	42.86**	143.75**	113.37**	55.32**	37.86**	27.69**	66.27**	35.71**
$L_7 \times T_5$	-4.40**	-3.93**	40.82**	57.38**	39.22**	126.32**	101.91**	47.75**	32.22**	17.07**	60.25**	46.43**
$L_8 \times T_1$	-6.12**	-4.47**	19.81	250.00**	26.53*	242.86**	205.18**	101.31**	71.43**	58.21**	120.18**	87.65**
$L_8 \times T_2$	-4.60**	-2.48*	18.10	187.50**	36.00**	200.00**	74.95**	50.41**	25.51**	30.58**	52.73**	16.30**
$L_8 \times T_3$	-11.30**	-11.11**	46.15**	307.69**	52.38**	253.49**	378.48**	206.97**	125.30**	138.10**	331.71**	107.35**
$L_8 \times T_4$	-10.06**	-8.27**	22.17	278.57**	22.64	278.26**	200.36**	117.51**	72.30**	52.99**	122.47**	91.21**
$L_8 \times T_5$	-5.98**	-6.01**	32.04*	129.27**	45.63**	196.55**	144.12**	84.74**	29.00**	51.47**	86.19**	85.71**
$L_9 \times T_1$	-6.40**	-4.97**	25.49	253.85**	38.64**	197.87**	403.07**	133.90**	100.60**	93.48**	187.76**	93.55**
$L_9 \times T_2$	-3.15**	-3.54**	25.60	153.85**	51.11**	123.08**	120.16**	50.25**	41.18**	48.78**	77.65**	30.00**
$L_9 \times T_3$	-7.04**	-6.70**	30.73*	210.00**	64.86**	153.66**	894.29**	219.62**	171.95**	222.30**	528.11**	127.91**
$L_9 \times T_4$	-9.19**	-8.18**	26.61	263.64**	45.83**	218.18**	323.83**	141.75**	91.75**	90.06**	193.28**	89.71**
$L_9 \times T_5$	-3.98**	-4.86**	33.00*	174.29**	50.54**	221.43**	151.59**	86.25**	64.85**	72.66**	121.48**	73.71**
S.E.	**1.00**	**0.96**	**14.18**	**2.24**	**11.22**	**0.35**	**0.018**	**2.07**	**0.40**	**1.79**	**4.22**	**3.25**

Table 24. Phenotypic & Genotypic correlations

Genotypes	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No.of cobs per plot	Cob placement (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)
Days to 50% pollenshed		0.909	-0.336	-0.572	-0.309	-0.519	-0.518	-0.586	-0.454	-0.464	-0.581	-0.414
	1.000	**0.979**	**-0.582**	**-0.899**	**-0.502**	**-0.785**	**-0.755**	**-0.970**	**-0.860**	**-0.858**	**-0.861**	**-0.923**
Days to 50% silking			-0.296	-0.539	-0.256	-0.482	-0.501	-0.573	-0.438	-0.456	-0.568	-0.408
		1.000	**-0.502**	**-0.788**	**-0.434**	**-0.692**	**-0.690**	**-0.907**	**-0.792**	**-0.787**	**-0.790**	**-0.880**
Plant height (cm)				0.629	0.823	0.694	0.642	0.556	0.446	0.406	0.592	0.474
			1.000	**0.877**	**0.937**	**0.952**	**0.897**	**0.843**	**0.727**	**0.703**	**0.850**	**0.832**
No. of cobs per plot					0.567	0.884	0.649	0.642	0.503	0.451	0.655	0.510
				1.000	**0.922**	**0.998**	**0.891**	**0.975**	**0.808**	**0.806**	**0.964**	**0.908**
Ear placement (cm)						0.642	0.588	0.497	0.413	0.399	0.554	0.421
					1.000	**0.977**	**0.889**	**0.852**	**0.728**	**0.739**	**0.875**	**0.788**
Yield/ plot (kg)							0.754	0.699	0.527	0.461	0.701	0.574
						1.000	**0.926**	**0.954**	**0.779**	**0.788**	**0.948**	**0.907**
Single cob wt. (kg)								0.889	0.797	0.768	0.901	0.744
							1.000	**0.986**	**0.946**	**0.910**	**0.974**	**0.918**
Cob length (cm)									0.837	0.805	0.922	0.843
								1.000	**0.848**	**0.807**	**0.967**	**0.898**
Cob girth (cm)										0.911	0.823	0.840
									1.000	**0.978**	**0.947**	**0.806**
No. of rows per cob											0.834	0.718
										1.000	**0.905**	**0.719**
No. of kernels per row												0.716
											1.000	**0.873**
100-seed weight (gm)												
												1.000

All the values are significant at 5% and 1% level

Figures in ‘bold’ indicate genotypic correlation coefficients

Table 25. Direct and indirect effects of yield components on grain yield per plot

Characters	Days to 50% pollenshed	Days to 50% silking	Plant height (cm)	No. of cobs per plot	Cob placement (cm)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)	'r' values Yield/ plot (kg)
Days to 50% pollenshed	**-0.019 (0.004)**	0.039 (-0.068)	-0.010 (-0.134)	-0.356 (-0.514)	-0.026 (-0.299)	-0.195 (0.141)	-0.026 (-0.259)	0.039 (-0.263)	0.086 (0.059)	-0.015 (0.466)	-0.035 (0.013)	-0.519**
Days to 50% silking	-0.017 (-0.002)	**0.043 (-0.070)**	-0.009 (-0.115)	-0.335 (-0.450)	-0.022 (-0.199)	-0.189 (0.129)	-0.025 (-0.242)	0.037 (-0.242)	0.085 (0.054)	-0.014 (0.427)	-0.035 (0.013)	-0.482**
Plant height (cm)	0.006 (-0.003)	-0.013 (0.035)	**0.031 (0.230)**	0.391 (0.501)	0.069 (0.428)	0.242 (-0.167)	0.024 (0.225)	-0.038 (0.222)	-0.075 (-0.048)	0.015 (-0.460)	0.041 (-0.012)	0.694**
No. of cobs per plot	0.011 (-0.002)	-0.023 (0.055)	0.020 (0.202)	**0.622 (0.571)**	0.048 (0.421)	0.245 (-0.166)	0.028 (0.260)	-0.043 (0.247)	-0.084 (-0.055)	0.017 (-0.521)	0.044 (-0.013)	0.884**
Cob placement (cm)	0.006 (-0.003)	-0.011 (0.030)	0.026 (0.216)	0.353 (0.527)	**0.084 (0.457)**	0.222 (-0.166)	0.022 (0.228)	-0.035 (0.223)	-0.074 (-0.051)	0.014 (-0.473)	0.036 (-0.011)	0.642**
Single cob wt. (kg)	0.010 (-0.003)	-0.021 (0.048)	0.020 (0.206)	0.404 (0.509)	0.049 (0.406)	**0.377 (-0.187)**	0.039 (0.259)	-0.068 (0.289)	-0.143 (-0.062)	0.023 (-0.527)	0.064 (-0.013)	0.754**
Cob length (cm)	0.011 (-0.003)	-0.025 (0.063)	0.017 (0.194)	0.400 (0.557)	0.042 (0.390)	0.335 (-0.181)	**0.044 (0.267)**	-0.071 (0.259)	-0.150 (-0.055)	0.023 (-0.523)	0.072 (-0.013)	0.699**
Cob girth (cm)	0.009 (-0.003)	-0.019 (0.055)	0.014 (0.167)	0.313 (0.462)	0.035 (0.333)	0.301 (-0.177)	0.037 (0.226)	**-0.085 (0.306)**	-0.169 (-0.067)	0.021 (-0.512)	0.072 (-0.012)	0.527**
No. of rows per cob	0.009 (-0.003)	-0.020 (0.055)	0.013 (0.162)	0.281 (0.460)	0.034 (0.338)	0.290 (-0.170)	0.035 (0.216)	-0.078 (0.299)	**-0.186 (-0.069)**	0.021 (-0.490)	0.062 (-0.010)	0.461**
No. of kernels per row	0.011 (-0.003)	-0.024 (0.055)	0.018 (0.196)	0.407 (0.551)	0.047 (0.400)	0.340 (-0.182)	0.041 (0.258)	-0.070 (0.290)	-0.155 (-0.062)	**0.025 (-0.541)**	0.061 (-0.013)	0.701**
100-seed weight (gm)	0.008 (-0.003)	-0.017 (0.061)	0.015 (0.191)	0.317 (0.519)	0.035 (0.360)	0.281 (-0.171)	0.037 (0.240)	-0.072 (0.247)	-0.133 (-0.049)	0.018 (-0.472)	**0.086 (-0.014)**	0.574**

Residual effect = 0.1337

Figures in 'bold' are direct effects and all other values are indirect effects Figures in parentheses are genotypic estimates

2. REVIEW OF LITERATURE

Maize (*Zea mays* L.) is the world's leading cereal in terms of production and productivity. The total area under maize cultivation in the world is about 147.17 m.ha with a total production of 694.58 m.tonnes and an average yield of 4719 kg/ha (FAO 2005). Maize is adaptable under varied agro climatic conditions of the world. Despite its high potential, the productivity of maize is at a low level of 1959 kg/ha in India. It is, therefore, obvious that the high yield potential of improved types have not been realized in the farmer's field. Many biotic and abiotic stresses limit the realization of yield potentiality and among the former; diseases are of utmost importance, especially in the tropical and subtropical regions. Of the various pathogens affecting maize, banded leaf and sheath blight is a major threat throughout maize growing areas.

2.1. BANDED LEAF AND SHEATH BLIGHT

2.1.1. History and geographical distribution of the disease

Banded leaf and sheath blight has become increasingly severe and economically important disease of maize during the last two decades. The disease occurs in moderate to severe intensities every year in several countries resulting in significant loss in grain yield (Balla *et al.*, 2000).

The genus *Rhizoctonia* was first observed by De Candolle (1815) as the sterile mycelia attacking the roots of alfalfa. *Rhizoctonia solani* is the most widespread, destructive, versatile pathogen capable of attacking several types of host plants, causing major share of root rot and foliage diseases. It infects plants belonging to 32 families and 188 genera. The fungus is primarily known to cause diseases such as pre-and post-emergence damping-off, collar, crown and bud rots and cankers. In addition to its damaging role at soil level, it is capable of producing diseases on aerial parts. Such diseases are expressed in the form of leaf spots, leaf blights and web blights. On Graminacious hosts, it produces necrotic lesions, alternating with unaffected portions which appear in the form of characteristic bands.

Bertus (1927) first recorded the ‘sclerotial disease’ of maize from Sri Lanka. Subsequently, it was recorded in Philippines under the name banded sclerotial disease (Reyes, 1941), in Malaysia as banded sheath rot (Heath, 1956; Wiltshire, 1956) and as summer sheath blight in Japan (Kjiware, 1968). In recent years the disease outbreaks have occurred in more countries and have assumed epidemic dimensions. Besides India and Sri Lanka, it has been found to occur in Bhutan, Indonesia, Cambodia, Bangladesh, Japan, Korea, Malaysia, Myanmar, Nepal, Pakistan, Philippines, South China, Thailand, Vietnam, Sierra Leone, Ivory Coast, Nigeria, England, USA (Arkansas) and Venezuela (Sharma *et al.,* 2002; Sharma *et al.,* 1993). In most of these countries, the disease has been a priority item in maize research programmes due to its increasing incidence and economic damage (Fig.1).

In India, it was first recorded in UP (Tarai area) in 1960 by Ullstrup (Payak and Renfro, 1966). In early sixties the disease was considered only as a disease of minor importance till it appeared in an epidemic form in the warm foothill regions of Himachal Pradesh in the Mandi district (Thakur *et al.,* 1973). Now it is considered as one of the major diseases of maize and is present in the states of Himachal Pradesh, Madhya Pradesh, West Bengal, Orissa, Bihar, Haryana, Punjab, Rajasthan, Meghalaya, Uttaranchal, Uttar Pradesh, Assam, Nagaland and Andhra Pradesh (Fig. 2).

2.1.2. Anastomosis and interspecific groups in Rhizoctonia

The anastomosis group (AG) concept in *Rhizoctonia solani* can make the difference between the progress and failure in a breeding programme for disease resistance (Anderson, 1982). Fusions occur only between isolates of the same AG. *R. solani* is not a single species but a collection of non inter-breeding populations (Anderson, 1982). Parmeter *et al.* (1969) proposed four AGs and Ogoshi (1972) identified two subgroups within AG1 and AG2.

Atleast 14 AGs (AG-1 through AG-13 plus AG-BI) have been reported till recently in *Rhizoctonia* sp., five of the twelve AGs have been further divided into subgroups according to culture appearance, pathogenicity and thiamin requirement. In the past, many workers have tried to group isolates of *R. solani* on the basis of their anastomosis behaviour. However, on the basis of available information it appears

that *R. solani* anastomosis group AG-1-1A (*sasakii* type) is the main isolate for leaf and sheath blight disease, distributed in areas where maize and rice are the main crops.

The pathogenicity of different AGs of *Rhizoctonia solani* causing leaf blight or leaf rot and sheath blight on different crops was proved by Kim and Kim (1996).

2.1.3. Economic Importance and Losses

The disease causes direct losses, resulting in premature death, stalk breakage and ear rot, indirect losses by reducing grain yield and also grain quality in terms of human consumption. In India, loss in grain yield has been estimated in the range of 23.9 to 31.9 per cent in ten cultivars (Lal *et al.*, 1980). An yield reduction of 5-6 per cent was observed in disease score 3, 19.2 per cent in Hybrid Ganga Safed-2 and 15.1 per cent in composite D-745 for a disease score of 4 and 97.7 and 97.3 per cent at a score of 5 for Ganga-2 and D-745 respectively. 40.50 per cent reduction in grain yield for a disease index of 71 per cent has been recorded by Singh and Sharma (1976).

Thakur *et al.* (1973) found that there was negative correlation between the disease incidence and yield in corn. Vega and Silvestre (2003) observed that as the level of disease intensity increased from 25-100 per cent, the measured yield and yield components decreased proportionally in the cultivar USM Var 9. Percent loss in grain yield based on 20 infected plants/plot ranged from 4.9-18.2% (Pangga and Natural 1988).

In Guangxi province in South China, yield losses of 87.5 and 57.8 per cent have been determined under natural conditions in the hybrids Luyu 13 and Guiding planted at Bao Qiao and Chen Xiang counties (Zhang *et al.*, unpublished). In Georgia, USA, Sumner and Minton (1989) reported yield reduction of 47, 42 and 8 per cent in soils infested with the high inoculum level and 15, 19 and 1 per cent in the low inoculum levels for a three year period. When the ear rot phase of the disease predominates, yield losses approached 100 percent in South China (Tang *et al.*, 2004). Further it was estimated that in India 1 per cent of total grain yield is lost by this disease (Payak and Sharma, 1985).

2.1.4. Disease and Symptoms

The disease appears at pre-flowering stage in 40-50 day old plants. Symptoms and signs of disease have been described in detail and illustrated (Ahuja and Payak,

1982, Knight and Burrill, 1964). Bertus (1927) recorded disease on the lower sheaths and ears of maize. He found spots below the stalk of the affected sheath and outright death of the plant. Reyes (1941) and Ullstrup (Payak and Renfro, 1966) found the disease only on drooping leaves and some leaves get fully blotched and their leaf sheath became diseased (Reyes, 1941). Van Eij-natten (1961) recorded it on leaves, sheaths, ear husks and ears. Wiltshire (1956) and Heath (1956) observed it on the lower sheaths only. Knight and Burrell (1964) reported that disease appeared as 'sharp eye spots' both on lodged and standing plants.

The disease manifests on leaves, sheaths, stalks and ears as leaf and sheath blight, stalk lesion or rind spotting and stalk breakage, clumping and caking of style (silk fibre), horse-shoe shaped lesions with banding on caryopsis, ear rots etc (Plate 1). As the disease is soil borne, initial infection appears on the lowest leaf sheath or on the leaves that are in contact with soil and progresses up to the ear. Symptoms are more common on the leaf sheath than on the leaf lamina. The disease lesions show alternate bleached areas or zones that are initially water soaked and narrow purple brown bands oriented perpendicular to long axis of leaves or leaf sheaths resulting in the characteristic symptom of banded blight. Severely affected leaves and sheaths become thin and papery and resemble, from a distance, a cast off snake skin which ultimately results in torn and tattered foliage. If infection occurs prior to ear emergence, the development of ear is completely suppressed or at best it remains rudimentary with bleaching of entire husk leaves. If the pathogen reaches the ear shoot after ear emergence, the stalk fibres at the tip become darkened caked up and turn into a hard lump leading to poor filling. But infection after grain formation stage results in light weight, chaffy and lusterless kernels.

This pathogen produces similar types of aerial symptom on crops like rice, wheat, soybean, sorghum, sugarbeet, cowpea, radish, etc.

In Philippines, this fungus causes banded leaf and sheath blight in maize, rice and sorghum, damping-off in cotton, aerial blight and stem rot in mungbean and soybean, sheath rot in sugarcane, heart rot in cabbage, black scurf and sprout canker in potato and foliar blights of fruits and plantation crops (Tangonan and Quebral, 1992).

In rice, the disease appears as gray oblong lesions with definite reddish brown borders and these lesions coalesce, overlap and form typical cobra skin pattern on the

inoculated sheath (Amin, 1975). Yu *et al.* (1980) found faster disease development at heading stage than at booting and tillering stage. At booting stage, the development was more rapid on the lower leaf sheath than on the upper leaves but the reverse occurred at the heading stage. According to Boyette and Lee (1979), maximum sheath blight in rice occurs at half internode elongation growth stage and yield was reduced by 22 per cent.

Atkins and Lewis (1952, 1954) found that in soybean, disease manifests as definite spots on leaves, pods and young stems. These spots of various sizes and shape cover the entire leaflet as necrotic areas with distinct reddish brown margin. O'Niell *et al.* (1977) found the symptoms as water soaked areas on the leaves, stem, petioles and immature pods of soybean and they become reddish brown or necrotic lesions. The infection starts at the base of the blade and spreads in a 'fan-shaped' manner to the rest of the blade. Verma and Thapliyal (1976) reported that during *kharif* season all aerial parts of soybean plants show light to dark brown spots, vein reddening, superficial cob web like mycelium and development of sclerotia after six weeks of planting.

The leaf and leaf sheath of sorghum shows large purple bordered irregular shaped lesions which often cover the entire leaves (Bell *et al.*, 1973). Khatua and Maiti (1982) observed that leaf blight in radish appears as water-soaked faded green patches on any part of the leaf lamina and following rain, these lesions increase leading to the complete brightening and damage of the foliage within seven days. Ahuja and Payak (1982) noticed that in maize, disease appears at the pre-flowering stage; but infection can occur on young plants by artificial inoculation and in the latter case severe blight occurs accompanied by death of the apical growing point.

The infected seedling showed stunted growth in rice (Amin, 1975) and yellowing of older leaves of tomato (William, 1980). This pathogen causes 'barley stunt Disorder' (Murray and Nicholson, 1979) in Scotland. The barley plants, grown on the sandy soil of Scotland, show severe stunting of root and shoot.

Wu and Lin (1967) stated that *Rhizoctonia* aerial blight of soybean is the most destructive disease in Taiwan in the vicinity of rice fields affected by sheath blight. Lakshmanan *et al.*, (1979) also reported that collar rot and web blight of cow pea is a serious disease near the rice growing areas in Kerala. *Rhizoctonia* causes leaf rot disease

of coffee seedlings (Rajasab *et al.,* 1982) which appears as necrotic spots spread over the leaves causing defoliation.

Rhizoctonia 'brown patch' of Kentucky blue grass was observed by Joyner *et al.* (1977). Regular or irregular patches of healthy green in the centre got encircled by light green grass giving 'frog eyed' appearance. The circular patches were noticed from several centimeters to several meters giving blighted turf grass appearance.

This pathogen also caused aerial blight in lemon grass (Chauhan and Singh, 1982), sunflower (Chauhan and Narain, 1980), water hyacinth (Freeman and Zetler, 1971, Freeman *et al.,* 1982), seedling and tip blight in peas (Flentje and Hagedorn, 1964, Shehata *et al.,* 1981), white leaf blotch disease of Bermuda grass (Singh and Seth, 1971), and brown sheath blight disease of rice (Yu, 1983). In Zimbabwe, Mpofu and Julian (1994) recorded leaf spot symptoms on tobacco due to *Rhizoctonia solani.*

Brown lesions on the leaves and stem were observed on cotton by Hossain and Ahmed (1988), Datar and Chaure (2007). In cabbage, about 22 per cent of damage occurs as a result of head rot or bottom rot (Williams and Walker, 1966). The symptom starts as drooping of leaves, decay of the lower leaves, petioles and head leaves and finally produced head rot or bottom rot.

The tomato fruits touching the soil showed extensive rot called fruit rot or soil rot (Gonzalez and Owen, 1963; Barksdale, 1974). The fungus causes 'spongy rot' in pumpkin (Gangopadhyaya and Sharma, 1976) and post-harvest disease of *Ziziphus jujuba* (Sharma *et al.,* 1981).

This pathogen causes pre-and post-emergence damping-off of seedlings. Damping-off refers to the decay of the stem at about soil level causing it to fall over because it has, as yet, no thickened supporting tissue, ultimately leads to the death of the plants. This results into poor stand of the crop in the field. Damping-off of seedlings has been reported in number of crop plants like sugarbeet (Pierson and Gaskill, 1961), snap beans (Prasad and Weigle, 1970), cowpea (Kataria and Dodan, 1983) and conifers (Wall, 1984). This fungus is also responsible for post-emergence mortality and collar rot in French bean (Sharma and Sohi, 1980) and hypocotyls rot in peas (Moody *et al.,* 1980). In beans, cotyledons are the primary site of infection (McLean *et al.,* 1968).

Some crop plants are attacked by *Rhizoctonia solani* even after the seedling stage. In cabbage, the cortex of the stem decays but the stele provides the support. The stem is wiry and slender at the point of lesion called 'wire stem' (Wellman, 1932). McLean *et al.,* (1968) noticed brown cankers on infected seedlings and sunken lesions on the stem of peas. In wheat, the symptoms appear as "sharp eye spot" on the stem (Clarkson and Griffin, 1977; Sterne and Jones, 1978).

Cankers appear on mung bean as reddish lesions in the cortex of hypocotyl and these lesions enlarge, coalesce and girdle the stem (Kaiser, 1970). William (1980) found that the stem cankers in tomato begin as decay of the cortex which changes into brown gray, sunken and often zonate cankers. This fungus is also responsible for collar rot in french bean (Sharma and Sohi, 1980), coffee (Venketasubbaih and Safeeulla, 1983) and crown rot in carrot (Mildenhall and Williams 1973; Howard and Williams, 1976). Anderson *et al.* (1982) reported that the crown cankers in carrot developed at the base of the leaf and shoulder of the tap root. The crown phase of the disease often kills the plant causing gap in the stand. The cavity spots of carrot show wilting, chlorosis and death of the plant (Mildenhall and Williams 1973; Howard and Williams, 1976). In alfalfa, cankers were formed by this fungus (Erwin, 1954).

This pathogen is responsible for the major share of root diseases on various crop plants. In 1967, an outbreak of root rot disease of soybean occurred in USA (Tachibana, 1968). It appears as brown sunken lesions on the hypocotyls (Boosalis, 1950; Tachibana, 1968). Tachibana *et al*. (1971) stated that an yield loss of 42-44 per cent occur if the root rot appears after flowering period. In snap beans, Galindo *et al.* (1982) reported that the brown lesions encircling the hypocotyls caused the death of the plant.

About 44 per cent of young apple trees wilted, followed by necrosis of leaves and shoot which eventually resulted into the death of the trees when the infection extended from roots to woody stem (Burr *et al.,* 1978). Singh *et al.,* (2007) gave the first report of root rot caused by *Rhizoctonia solani* on seabuckthorn (medicinal plant) in Uttaranchal Himalayas.

Rhizoctonia solani induces severe root rot in corn (Sumner and Bell, 1980, Perraton and Lucas, 1983). Sumner and Bell (1982), observed that about 10-100 per

cent of lateral and crown roots of maize rotted in numerous irrigated corn fields in USA. Leaning and lodging of the plants were common after high winds or heavy rains since at least one side of the roots were completely disintegrated.

In alfalfa, crown rot and root rot caused by *Rhizoctonia solani* and *Fusarium* spp show cortical necrosis, vascular browning and stellar necrosis (Seifel and Leath, 1983). Root rot caused by *Rhizoctonia* is a destructive disease in sugarbeet (Campbell and Altman, 1976; Hecker and Ruppel, 1977; Hyakumachi and Ui, 1982a).

This pathogen also causes considerable damage to the stored tubers. In potato, it causes black scurf disease. Singh (1964) noticed the black sclerotial encrustations adhered closely to the skin of potato tubers which when sown, might give rise to infected seedlings. Niza *et al.* (1981) observed *Rhizoctonia* rot in stored carrot. The infected tissue softened causing depression on the surface, enlarged into a sunken crator and was covered with a mycelial mat. The decayed tissue beneath the lesion became watery and emitted foul small.

2.1.5. Screening techniques

A large number of varieties belonging to different crop species have been screened for resistance to *Rhizoctonia solani* by different methods. Some of the methods normally used are as follows:

2.1.5.1. Soil inoculation

Hesegawa *et al.* (1968) reported that selection in sugarbeet for resistance to root rot was effective only when the population was grown in heavily infested land. Infected hypocotyls and root sections were added to the bench soil in the glasshouse to build a high inoculum potential to screen peas against root rot. Seeds were planted in this soil and disease rating was done after twenty-one days (Prasad and Weigle, 1969, 1970).

Mildenhall and Williams (1973) inoculated carrot seedlings with infected corn meal in the pots. Severe crown rot and cavity spot developed 12-15 weeks after seeding at 20-28^{o}C. Barksdale (1974) tested tomato fruit against soil rot by keeping the matured green fruits on the infested soil bed. After ten days, each fruit was turned over and the side touching the soil examined for number of fruits and percentage of surface area affected.

Deakin and Dukes (1975) opened 5 cm deep furrow in the soil benches in glasshouse. Seeds of snap bean breeding lines were sown along with checks. Inoculum was placed in contact with the soil and covered with well mixed pulverised soil. The disease reaction was scored by 1-5 scale for seed rot and hypocotyle lesion (5-healthy resistant no lesion and 1-susceptible with deep lesion and girdling stem).

Two methods were used to screen carrot seedlings by Howard and Williams (1976). One week old carrot seedlings grown in muck soil were inoculated by burying a solid line of infected corn meal 1.0 cm apart and 1.5 cm deep on both sides of the rows. After fourteen weeks the roots were rated for normal, healthy and abnormal or rotted roots. In the other method plastic pots were filled with 500 gm of soil and infested with inoculum mixture. Seeds were planted and placed in a growth chamber at 20-28^{o}C and 12 hr photoperiod. The survival of seedlings was observed after twenty-one days of planting and compared to non-inoculated seedlings.

Lewis and Papavizas (1977) mixed 900 gm of soil with oat inoculum to plant ten soybean seeds per pot and damping-off and hypocotyls rot rated by 0-4 scale (0=healthy seedlings, 4= hypocotyl girdled with lesions or secondary roots destroyed or both). Dickson and Boettger (1977) prepared soil benches with 3:1 sand and peat and inoculated them with race-2 *Rhizoctonia solani* from beets. Seeds of susceptible snap beans were planted first to build up the inoculum uniformly throughout the bench and afterwards the cultivars were tested.

Anderson *et al.* (1982) screened carrot cultivars by placing one infected corn per root at a depth of 4-5 cm from the roots ten weeks after planting and used 1-5 Rhizoctonia disease index to evaluate the roots. Woodard and Jones (1980) screened peanut introductions on metal flats containing infected soil inoculum. The seeds were planted and kept at 28-30^{o}C for seven days. The emerged seedlings were transferred to greenhouses and seedling survival was tested after twenty-one days.

Moody *et al.* (1980) tested bean cultivars by inoculating the hypocotyls of seven day old seedlings with *Rhizoctonia solani* and the seedlings were incubated at 32^{o}C for 72 hrs. Root rating was done by measuring the length of the lesion. Schneider *et al.*, (1982) observed in greenhouses, the hilled plant (soil deposition around the crown) had root rot sooner and more severe than the unhilled sugarbeet plants.

Reddy (1983) grew the chick pea varieties in pots containing field soil and inoculated by floodings with mycelia and sclerotial suspension of *Rhizoctonia solani.* McCoy and Kraft (1984a) evaluated peas by planting the seeds in soil infested with sclerotia. Twenty sclerotia were added per one gram of soil. They also inoculated the epicotyl by using mycelial discs of *Rhizoctonia solani.*

Koinuma and Mochizuke (1989) used six maize inbred lines with different levels of resistance to *R. solani* and employed four inoculation methods. Of the four methods hill inoculation by putting whole barley grains with the mycelia in the hill with soil cover yielded maximum disease spread on the plants. They used infected sheath ratio (ISR) scale (height of the uppermost lesion on the sheath/height of the flag leaf collar of the plant) for BLSB assessment and have come up with the results that increased ISR is the indication of susceptibility of plants to disease.

2.1.5.2. Sheath inoculation

Luttrell (1962) inoculated Fescue grass by placing a single culture in the centre of ten matured leaves. Chang (1962) placed a straw culture in between the tillers of rice during the tillering stage. Tu (1968) put sclerotia culture on the innerside of the leaf sheath of rice. Sakuri and Okamoto (1971) tested the rice seedlings by inserting agar culture inside the sheath at 7-8 leaf stage and field inoculation was done by placing a straw culture around the stem. Amin (1975) developed a stem tape inoculation method. The inoculum was covered with scotch brand 202.2 masking tape or cellophane tape and inoculum placed directly on the sheath.

Paddy tillers were inoculated with colonized toothpicks placed in the leaf sheath at the collar, without wounding, in up to five leaves (Eizenga *et al.,* 2002). Disease ratings were made about 30 days after heading using a 0-9 rating scale as described by Rush *et al.* (1976), where 0 indicates no disease and 9 indicates plants dead or collapsed. Gaskill (1968) tested sugarbeet seedlings by placing the fungal culture on the leaf cluster of each plant at 3-5 weeks after thinning. Dath *et al.,* (1976) screened rice cultivars by inserting a sterile stem colonized with the fungus into the leaf sheath. After fifteen days of inoculation, varieties were grouped into four grades based on the length of stem affected.

Lal and Butchaiah (1978) used seven methods to screen maize germplasm. Of the seven methods, sorghum grain culture placed on the leaf sheath and stem followed by toothpick and syringe inoculation resulted into more disease development than other methods. They found that disease development was the highest when four or eight infected grains were placed on all leaf sheaths of 45-day old plant. Two inoculations were significantly better than one for maximum disease development.

Kumar and Singh (2002) inserted two sorghum grains between leaf sheath and stem on lower third/fourth internode above ground level just before onset of tassel emergence stage. Sorghum grains infested with the pathogen were inserted between leaf sheath and stem upto ear placement (Lal *et al.,* 1980). Two wheat seeds infected by AG1-1A were placed into third sheath at jointing stage of maize (Zhao *et al.*, 2006).

Disks of actively growing mycelium (three days old cultures) were placed between leaf sheath of lower most leaf and internode (Singh and Sharma 1976). Sclerotia collected in previous season (four sclerotia per plant) were inserted inside the lowermost leaf sheath on seven week old plants (Kar, 1998).

Perasol and Silvestre (2003) found no significant differences among several inoculation methods of corn banded leaf and sheath blight *viz.*, basal sheath inoculation, sheath inoculation, basal sheath inoculation with soil cover, basal sheath inoculation with paper cover and basal sheath inoculation with rice hull cover, in terms of per cent highest relative lesion height.

Singh and Sharma (1976) categorized maize germplasm on the basis of average discolouration of internodes and average number of internodes infected and on the extent of ear rotting when inoculation was made on ears. Disease index was calculated by multiplying average discoloration of the internodes in a plot with average number of internodes infected. Plants with disease index of ten or less were considered resistant and those with 11-20 as moderately susceptible and those with a disease index of more than 20 as susceptible.

Disease index (DI) to score genotype response suggested by Wang and Dai (2001) is as follows: DI = [$\sum$ (severity class or disease score X number of plants in this class)/ the highest possible severity class or disease score X total number of

investigated plants] x100. DI of 0-30 was classified as resistant, >30-60 as moderately resistant, >60-90 as susceptible and >90-100 as highly susceptible.

Percent disease intensity (PDI) was calculated to differentiate resistant and susceptible genotypes as follows: PDI = [sum of all individual disease ratings / (total number of plants assessed X maximum rating)] x 100. PDI of 20 or less were categorized as resistant (Meena 2004).

Ahuja and Payak (1981a) developed excised leaf inoculation technique that allows evaluating large number of germplasm in *in vitro.* Field inoculation and evaluation technique developed by Ahuja and Payak (1978) which allows satisfactory disease development is widely used today for evaluating large number of germplasms in the field. Inoculation should be carried out during wet season on 30-45 day old plants with barley/oat grain culture (using four grains) inserted between stalk and sheath at second or third internode from soil level. A grade of 1 to 5 disease scoring scale (1 indicating non coalescent lesion limited to one sheath and 5 coalescent lesions covering upto ear and above or prematured death of plants) has been universally used. This method has been used by Sharma *et al.* (2002) to screen more than 500 maize genotypes.

2.1.6. Environmental conditions

Rhizoctonia solani constitutes numerous strains with diverse characters having wider adaptability to different environmental conditions.

Warm temperature and high humid conditions are quite congenial for the development of banded leaf and sheath blight in maize (Thakur *et al.,* 1973, Ahuja and Payak, 1978, 1981b and 1982). In maize, Ahuja and Payak (1981b) observed that temperature influenced mycelial growth, infection cushion formation, length of incubation period, initiation of disease and its intensity. The disease intensity appeared to be directly related to rise in relative humidity and disease did not develop at 70 per cent but appeared at 75 per cent and above. Relative humidity of 100 per cent and temperature between 25-30^{o}C were most suitable for disease development. Optimum temperature of about 28^{o}C and a high relative humidity of 88-90% were essential for infection and disease development. Rainfall of 100 mm in the first two weeks of infection favoured early infection and disease development. (Sharma, 2005).

Sumner and Bell (1982) reported that root rot in maize could be induced at all temperatures but was most severe at 16-18^{o}C. High humidity and 25-30^{o}C temperature were most suitable for sheath blight development in rice (Amin, 1975). *Rhizoctonia* rot in stored carrot develops very rapidly at 28^{o}C (Niza *et al.*, 1981) and damping off of carrot seedling occurred at 24-28^{o}C (Mildenhall and Williams, 1970, 1973).

Campbell and Altman (1976) observed that the differences in survival of the sugarbeet cultivars were not significant at 16^{o}C and testing for resistance at 26^{o}C was more rapid and economical than field trial. *Rhizoctonia* bottom rot or head rot in cabbage occurs in warm wet season (Williams and Walker, 1966). The tip blight in pea seedlings was more severe when soil moisture was 12 per cent (Shephard and Wood, 1963).

Gonzalez and Owen (1963) stated that the highest infection of soil rot in tomato occurs when the soil had more than 60 per cent water holding capacity. High atmospheric humidity was essential for penetration of the pathogen into the tomato fruit and once infection occurs, the disease was not affected by air humidity.

Datar and Chaure (2007) found that high humidity (80-90%) and continuous rainfall (duration 19-24 days and precipitation of 1.00 mm to 42.00 mm) during august and September was conducive for development of leaf blight in cotton. Extensive soil rot in tomato occurs at 24-26^{o}C (Barksdale, 1974). For detached fruit, optimum temperature for disease development was 24^{o}C (Gonzalez and Owen, 1963).

Lewis and Papavizas (1977) found that high temperature (26-32^{o}C), high moisture holding capacity (more than 70 per cent) and soil pH (more than 6.6) were favourable for disease development in soybean plants in the greenhouse. The disease severity, as measured by lesion development was not affected by soil pH. According to Chand and Logan (1984) black scurf incidence in potato was least under low pH.

Williams and Walker (1966) found that increase in the severity of head rot or bottom rot in cabbage occurred when the disease incidence of sugarbeet seedlings was as low as 20 per cent, in comparison to the first crop which showed 60 per cent (Hyakumachiu and Ui, 1982b).

Warren’s (1975) studies showed that there was linear relationship between disease incidence and inoculum concentration in limabeans. He suggested that disease

reaction should be assessed with low level of inoculum especially the lines with intermediate resistance. Venketasubbaiah and Safeeulla (1983) also obtained linear relationship between inoculum density and disease expression in coffee. Maxium infection of 100 per cent was observed when the inoculum density was 5-25 per cent on sterilised soil and 25-50 per cent in unsterilised soil. When the inoculum exceeded the limit present in natural conditions, moderate and partial resistant varieties become susceptible (Anderson *et al*., 1982).

Sumner and Dowler (1983) stated that soil temperature and planting date affected the root disease expression in maize. Shehata *et al.*, (1984) found that in peas no differences in disease severity were observed by age of inoculum or by the age of plant at inoculation.

2.1.7. Review of maize genotypes screened and analysed against BLSB

Rapid spread of Banded leaf and sheath blight of maize is due to lack of resistant sources. Most of the inbred lines used in maize breeding and the commercial cultivars used in production are susceptible to BLSB (Yang *et al.,* 2003). Adopting good resistant material for maize BLSB breeding will be an effective method to control quick spreading of BLSB. Sources of resistance to BLSB in maize have been elusive in Asian countries (Sharma *et al.,* 1993). Identification of diverse and stable field sources of resistance to BLSB is imperative and prerequisite to a resistance breeding programme.

Screening for BLSB resistance is being practiced in national programmes in India, Guangxi province in South China, Indonesia and Philippines. A variety of maize materials including inbred lines, single crosses, double crosses, double top crosses and composites have been evaluated in Indian maize programme. Among the inbred lines CM104 and CM300 were determined to be the elite lines in terms of resistance (Sharma *et al.,* 2002). In Guangxi, China, B 44-1, SZ-1, B 84-2, MS 08, BS-1, WP-4, WP-5, H 138, H 158, KI 1414 and several other materials were rated as resistant during 1994-95 crop season. Maize varieties Jinguok, Suweon 83, Suweon 87, Suweon 89, P 3055, P 3160, DK 689 and XCG 51 showed high tolerance levels to BLSB in Korea (Lee *et al.,* 1989). Selection of disease resistance has been intensified through collaborative project initiated by CIMMYT in collaboration with national programmes in the Asian region. A number of CML lines and other materials have been evaluated in India,

China and Indonesia and many lines have been identified having reasonable levels of resistance. In the early maturing group, some genotypes have been found to be tolerant in testing at China and Indonesia. These include CA 001056, CA 03149, CA 03147, CA 14509, CA 14518, CA 030106, CA 03103, CA 03147, CA 14518, CA 03106, CA 03137 and CA 03131. Similarly in late maturing group also lines with pedigree CA 003134, CL 02846, CA 00396, CA 00310, CA 34506, CA 03806, CA 00334 and CA 34516 were selected as tolerant lines in China, India and Indonesia (Balla *et al.*, 2000). Among 45 inbred lines evaluated against BLSB, resistance of R 15 was higher than that of R 09. Out of the 45 inbred lines tested, none were immune to the disease. CML 270 was found to be highly resistant (Yang *et al.,* 2003). Out of 200 maize germplasm including inbred lines evaluated at Pantnagar only six inbred lines CM 105, CM 117, CM 600, CM 201, CM 205 and CML 265 showed moderate level of resistance to BLSB (Anonymous, 1995). Srinivas (2002) evaluated 10 inbred lines against 10 isolates of *R. solani* f.sp. *sasakii* and found a differential response of the inbreds to the tested isolates. Inbred line CM 104 was found moderately resistant (disease score of 2) to the isolates tested.

Maize genotypes screened and identified for resistance against banded leaf and sheath blight by several workers are summarized and presented in Table 1.

2.1.8. Inheritance studies on disease resistance

Even though a very large number of crop plants have been screened for resistance to *Rhizoctonia solani,* only limited information is available regarding the mode of inheritance. Hybrids developed from tolerant inbred lines have given inconsistent level of inheritance to this disease.

Williams and Walker (1966) first studied the inheritance of *Rhizoctonia* bottom rot in cabbage. Their studies indicated that resistance to bottom rot was monogenic and was inherited as a dominant character.

Steinswatt *et al.* (1967) obtained 3:1 ratio in F_2 indicating that resistance to stem rot in limabean was inherited as a single dominant factor designated as Pd. Dominant. Serry *et al.* (1976) reported that resistance to *Rhizoctonia* rot in *Sesamum indicum* was governed by two recessive genes. But in another cross, tolerance was controlled by a single dominant gene.

The resistance of soil rot in tomato appeared under polygenic control since no segregation occurred in F_2 classes, and they ranged over the entire range of disease shown by the parents (Barksdale, 1974). According to Lebedeva and Lebedev (1972), the resistance in potato to *Rhizoctonia solani* was a dominant character inherited polygenically. The studies of Hecker *et al.,* (1972) showed that two advanced selections in sugarbeet exhibited partial dominance for resistance and both had more than one gene for resistance. This type of resistance was effective against all races of *Rhizoctonia* rot and crown rot in sugarbeet.

Deakin and Dukes (1975) reported that, resistance in snap beans was heritable. They found recessive epistasis (9:3:4) between the seed colour and resistance. Resistance was associated with coloured seed. Masajo (1976) found that resistance in rice to sheath blight was partially dominant over susceptibility. The difference in susceptible parents was controlled by two genes. Heritability estimates ranged from 62.6 to 82.3 per cent for 4 crosses. To date only partial resistance to sheath blight has been identified as evidenced by a survey of 6000 rice cultivars from 40 countries from which no cultivar exhibiting a major gene for rice sheath blight resistance was identified (Hashiba 1984).

Vest and Comstock (1968) stated that resistance in flax to *Rhizoctonia solani* was multigenic. The yellow seeded variety was represented by three colour genes. There was transgressive segregation towards high resistance in crosses involving one or more resistant parent. All the crosses of relatively resistant parent were resistant than the parental lines. Heritability of resistance in broad sense was relatively high.

The partitioning method of genetic analysis in sugarbeet by Hecker and Ruppel (1973, 1975) indicated that a three locus model with partial dominance best fitted the experimental data. They also reported that modifying gene or epistatic interaction was involved in the disease resistance. Based on the study of progenies for 3 years, Hecker and Ruppel (1975) confirmed that two loci accounted for majority of the expression of resistance. Year x genotype interaction also affected the resistance but their magnitude was not important. Two resistant parents did not have exactly the same genotype for resistance. Broad sense heritability was influenced by intensity of infection and ranged from 0.07 to 0.65 in the F_2s.

According to Humaydan *et al.*, (1976), disease resistance to *Aphanomyces raphani* and *Rhizoctonia solani* and root quality improved by a single cycle of selection. He suggested that resistance to these two pathogens in radish was highly heritable.

The inheritance of resistance to *Pythium, Fusarium* and *Rhizoctonia* in snap bean was studied by Dickson and Boettger (1977).The low correlation between these pathogens indicated that the resistance to all the three pathogens was independently and quantitatively inherited. Heritability estimates of *Rhizoctonia* resistance were 0.75 and 0.65 in the broad sense and 0.32 and 0.29 in the narrow sense. In the Rhizoctonia selections, generation to generation correlation was high (r = 0.90) among those with best resistance but only moderate among those with moderate resistance. Since the narrow sense heritability was low, they suggested that resistance in later generation should be more effective than in the earlier generation.

Shao (1980) investigated the resistance to root rot complex caused by *R. solani* and *F. solani* in snap beans. The results indicated that resistance was quantitatively inherited and the resistance to the above two pathogens was independent.

According to Hecker and Ruppel (1977), back-crossing for two generations was slightly effective in incorporating the root rot resistance into susceptible varieties of sugarbeet. They found that selection solely for resistance did not drastically reduce the genetic variance for components of sugar yield.

Silva (1980) reported that broad sense heritability of resistance of *Rhizoctonia solani* in peas range between 73.4 to 91.4 per cent while narrow sense heritability was greater than 68.3 per cent. The resistance in peas appeared to be controlled by three pairs of genes and their actions were equal and additive without dominance (Silva, 1980; Silva and Hartmann, 1982).

The inheritance studies in tomato to fruit rot (Werner *et al.*, 1978) showed that resistance was determined by two major genes in one line and by a polygenic system with three contributing genes in another line. The heritability estimates for these lines were 71 per cent and 30 per cent respectively.

Werner *et al.* (1980) crossed two susceptible tomato varieties and studied the performance of parents, F_1, F_2 and back-crosses. They observed that tolerance depended upon a major gene with dominance and had 71 per cent narrow sense heritability. In

another variety, tolerance was polygenic involving four major genes and heritability was 30 per cent. In both families, correlation between fruit rot tolerance and resistant to mechanical puncturing of the epidermis was high but correlation between family having dominance for tolerance and oblong fruit shape was high and positive (Werner *et al.,* 1978, 1980).

The inheritance studies on resistant in sesame gave contradictory results (Serry and Satour, 1981). In one cross, susceptibility was dominant over tolerance to *Rhizoctonia solani* and *Macrophomina phaseoli* and was controlled by two to three pairs of alleles. In four other crosses, tolerance was dominant involving one or two pair of alleles. According to Burham *et al.* (1983) in radish, heritability for disease resistance ranged as high as 0.65 for *R. solani* and as low as 0.19 for *A. raphani*.

Shehata (1983) and Shehata *et al.* (1983) reported that in peas resistance to *Aphanomyces* root rot and *Rihizoctonia* stem rot was inherited independently. Broad sense heritability ranged between 0.45 and 0.57 in *A. euteiches* and 0.39 and 0.44 in *R. solani*. However, heritability based on selection gain in the F_3 ranged from 0.28 to 0.46 and from 0.21 to 0.44 for resistant to A. *etuteiches* and *R. Solani* respectively. Frequency distribution of resistant and susceptible plants suggested quantitative inheritance of resistance to both diseases.

Polygenic interaction to Turcicum leaf blight, common rust and banded leaf and sheath blight was observed in eighty full sib families of maize originated from multiple disease resistance stocks I & II (Kaiser & Chowdari 1986). Pan *et al.* (1999) demonstrated that significant levels of partial resistance to sheath blight of rice can be controlled by single major genes and that the effects of these genes may be additive.

Combining ability analysis for resistance to BLSB has been carried out by Vimla *et al.* (1988). On the basis of two location data they concluded that both general and specific combining ability variances significantly controlled disease resistance but general combining ability variance was predominant. In their study CM104 was found to be the most promising combiner for conferring resistance. Kumar and Singh (2002) studied inheritance using 10 crosses between resistant and susceptible lines and concluded that the resistance was governed by two genes. They also concluded that

resistance in crosses involving resistant line CM104 was controlled by duplicate dominant genes (15:1) while crosses of another resistant line CML 1 showed dominance and recessive interaction (13:3).

2.2. GENETIC ANALYSIS OF METRIC TRAITS

Quantitave characters are governed by several genes and exhibit continuous variation from one extreme to other. They assume great importance in plant breeding because many economically important characters are quantitative in nature. Their polygenic control and influence by environment necessitates use of biometrical techniques for evaluating the inbred lines in terms of combining ability variances and effects.

2.2.1. Combining ability

Combining ability is a measure of gene action which refers to the capacity or ability of a genotype to transmit superior performance to its crosses. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbreds (Sprague and Tatum, 1942). Combining ability one of the most important areas in hybrid research, has significant impact on inbred line evaluation and population improvement in maize breeding (Hallauer and Mirinda, 1988; Crossa *et al.*, 1990). It also provides information about the gene action involved in the expression of various quantitative characters and thus helps in deciding the breeding procedure for genetic improvement of such traits.

Sprague and Tatum (1942) partitioned the total combining ability of the lines into general combining ability (gca) and specific combining ability (sca). Gca was defined as the average performance of a line in a series of hybrid combinations and estimated from half-sib families. Sca refers to those instances in which certain hybrid combinations are either better or poorer than would be expected based on the average performance of the parent inbred lines included and estimated from full-sib families. They interpreted gca as an indication of genes having largely additive effects and sca as indicative of lines having dominance and epistatic effects. Among the two parameters, gca is relatively more important than sca for unselected inbred lines, whereas, sca is more important than gca for previously selected lines.

The estimates of combining ability provide information about the components of genetic variance involved in the expression of various polygenic characters and thus help in the selection of desirable parents for hybridization and also in deciding the breeding procedure for genetic improvement of such characters. Three biometrical designs, namely, diallel, partial diallel and Line X Tester analysis are commonly used for the analysis of combining ability (Singh, 2000).

Joshi *et al.* (1998) studied heterosis and combining ability for quality and yield in early maturing single cross hybrids in maize and identified good general and specific cross combinations.

A review of heterosis and combining ability for important traits in maize is presented in Table 2:

2.2.2. Line X Tester analysis

Estimation of genetic components requires use of appropriate mating designs. Line X Tester design (Kempthorne, 1957) is one of the most important mating designs permitting the estimation of combining ability effects and also partitioning of the genetic variance. It is a modified form of top cross scheme. In case of top cross only one tester is used, while in case of Line X Tester cross several testers are used as male parents and crossed with set of inbreds as females (Singh, 2000).

Line X Tester is useful in deciding the relative ability of number of female and male inbreds to produce desirable hybrid combinations. This mating design can also provide information regarding the usefulness of male and female inbreds as parents for hybridization to generate segregating population which is expected to give superior segregates.

This is a very good technique for evaluation of large number of germplasm lines in terms of combining ability variances and effects and D and H components (Singh, 1978; Dabholkar, 1999).

Vasal *et al.* (1992) characterized 92 white tropical lines of CIMMYT using four inbred testers in a Line X Tester model for estimation of combining ability and heterosis. Additive genetic variance was found to be important for days to tasseling, cob placement and plant height, non additive genetic variance for brown stripe downy

mildew and bacterial stalk rot. However grain yield per plant and days to 50% silking were observed to be governed by both additive and non additive genetic variance. For grain yield per plant, experimental variety AB(Y) EV and composite Navjot were good general combiners in a 7X2 line X tester design (Kalia *et al.*, 1994).

Using Line X Tester design, Castellanos *et al.* (1998) determined the relative performance of seven inbred testers in ranking a specific set of 21 lines from different origins and identified the most convenient tester for evaluating lines for a hybrid breeding programme. Pre ponderance of non additive gene action was observed for grain yield and yield component characters in 6 x 4 Line X Tester design (Kumar *et al.,* 1999). Venkatesh *et al.* (2001) reviewed from a Line X Tester analysis from modified single cross hybrids, derived from inbred testers and found sca effects to be significant and positive for grain yield and related traits. Line X Tester analysis was used by Dubey *et al.* (2001) to study combining ability for yield and maturity traits in conventional and non conventional hybrids of maize and reported significant positive sca effect for grain yield, 100 grain weight and negative sca for 50 percent silking respectively. Dodiya and Joshi (2002) studied gene action for grain yield and its attributes in maize by using Line X Tester analysis and reported significant positive SCA effect for grain yield, plant height, ear size and 100-grain weight.

Additive effects, dominance effects & epistatic effects were found to be significant for grain yield & yield components in various crosses under different growing conditions (Jayant 2003). Also Subba Rao (1992) & Rameeh *et al.* (2000) reported significant additive, dominance & epistatic effects for various yield & yield components. Non additive gene effects for grain yield were found to be significant in maize (kalla *et al.,* 2001).

Additive gene effects were predominant in the expression of grain yield, days to silk, ear length and kernel rows/ear and non additive gene effects were important for ear diameter, 100 grain weight, embryo weight, oil content and starch content in a line X tester design of high oil maize inbreds of ICRISAT. The cross ICRISAT-346 X FRD-73 was identified as best for both grain yield and oil content (Devi and Prodhan 2004). Additive gene effects were found important for all yield components and non additive gene effects for grain yield in assessment of genetic potential of maize inbreds belonging to different heterotic pools (Krishna *et al.,* 2005).

Saidaiah *et al.,* (2006) concluded that non additive components of genetic variance were involved in inheritance of various morpho-physiological, yield and yield components in a 10X4 line X tester design and suggested that the inbreds DMR-156, DMR-274 and EI-34 were good general combiners for most of the characters associated with drought tolerance. A line X tester analysis with five lines and 10 testers performed by Selvaraj *et al.* (2006) indicated preponderance of non additive gene action for all 19 characters except leaf width, ear length, number of grains per row, 100 grain weight, grain yield per plant and starch content for which variance due to general combining ability was more.

Ratio of GCA: SCA indicated predominance of non-additive gene action for all the traits studied except days to 50% silking. GPM 201 and GPM 302 were identified good general combiners yield and most of the yield contributing characters in a 4X10 line X tester design (Todkar and Navale 2006). Combining ability analysis using 15 lines and three testers by Iqbal *et al.* (2007) revealed higher magnitude of dominance variance for number of kernel rows per ear, number of kernels per row and 1000 grain weight, while additive genetic variance was higher for ear length, ear diameter and grain yield per plot.

2.2.2.1. Use of inbred lines as testers

Use of common tester to evaluate lines for general combining ability was suggested by Davis (1927) and Jenkins and Brunson (1932). Earlier breeders used heterogenous open pollinated cultivar as a common tester. Top cross was employed to evaluate combining ability of inbred lines. The choice of tester that provides best discrimination among genotypes is very essential. Hull (1945) concluded that the most efficient tester would be one that is homozygous recessive at all loci. A tester should be poor in the trait for which the lines are to be evaluated. The most desirable tester is the one that provides maximum information about the performance of a line in cross combinations (Allard, 1960). The characters of an ideal tester include simplicity in use, provide information that correctly classifies merit of lines and maximize genetic gain (Hallauer, 1975).

Prior to 1970’s it was commonly accepted that use of a tester with narrow genetic base would improve combining ability with the specific tester but would have

less improvement for gca. Testers with broad genetic base were used to improve gca (Hallauer and Mirinda, 1981).

Use of inbred lines as testers resulted in significant improvement of combining ability with specific testers and also of gca as measured by crosses with unrelated broad base populations (Horner *et al.,* 1973; Wajeko and Russel, 1977). Zambezi *et al.* (1986) evaluated 20 parents for effectiveness as testers for gca and supported earlier results regarding the utility of inbred testers to improve gca and sca. The practical reasons for preferring inbreds as testers to broad based testers are 1) sampling error is less with inbred testers and 2) use of inbred as tester permits quicker utilization of new lines in commercial hybrids, especially if the tester is already in commercial use (Zambezi *et al.,* 1986).

In view of various points elaborated above, it is essential to analyze and characterize the new inbred lines that are generated in the maize improvement programmes. By using practically or potentially useful maize inbred lines as testers, in addition to testing the potentiality of lines, the promising combinations can be directly evaluated for their commercial viability. Further as BLSB is a major disease, the reaction of elite experimental hybrids to BLSB needs to be taken into account. By involving diverse maize inbred lines, there is a possibility of generating experimental hybrids with higher productivity.

Table-3 Screening of elite breeding lines at Delhi during *Kharif* 2005

Genotype Code No.	Pedigree	Source Population/ Remarks
DBL-1	CM-135-3-6-1	A-64
DBL-2	CM-135-3-6-2	A-64
DBL-3	CM-135-3-8-1	A-64
DBL-4	CM-135-3-8-2	A-64
DBL-5	CM-135-1-1-1	A-64
DBL-6	CM-135-1-1-2	A-64
DBL-7	CM-135-1-1-3	A-64
DBL-8	CM-135-1-1-4	A-64
DBL-9	CM-135-1-4	A-64
DBL-10	CM-137-3-#	MDR-1
DBL-11	CM-137-3-3	MDR-1
DBL-12	CM-137-2-1	MDR-1
DBL-13	CM-137-2-2	MDR-1
DBL-14	CM-138(-3)-3-1	AD-609
DBL-15	CM-138(-3)-3-2	AD-609
DBL-16	IPA34-62-F-#(CM213)-2-#	MDR-1
DBL-17	SC-7-2-1-2-7-F-1	MDR-1×A-64
DBL-18	CM-111-1-#	From DMR, New Delhi
DBL-19	CM-136-9-1	MDR-1
DBL-20	CM-136-9-2	MDR-1
DBL-21	9678C-1-3-#	Interspecific derivatives
DBL-22	9680F-2-3-#	Interspecific derivatives
DBL-23	9679A-1-1-#-1	Interspecific derivatives
DBL-24	9679A-1-1-#-2	Interspecific derivatives
DBL-25	9679A-1-2-#	Interspecific derivatives
DBL-26	CM-142-2	A-64
DBL-27	CM-142-3	A-64
DBL-28	IPA21-10-F-1-⊗-B-1	AD609
DBL-29	90-1(MnHYD R01)-4	Hybrid derivatives
DBL-30	90-1(MnHYD R01)-4-1	Hybrid derivatives
DBL-31	IPA-3-20-⊗-⊗-B-1-2-1	A-64
DBL-32	IPA-9-7-F-⊗- #-B(CM-137-1)	MDR-1
DBL-33	PC_2HS-34-1-3-4-1-1-1-⊗-B-2	From composite
DBL-34	IPA-34-5-F-1-1-1	MDR-1
DBL-35	Comp8527 X 85164-⊗-1-2-7-51-5-2-2	From composite crosses
DBL-36	IPA-3-28-5-⊗-#	A-64
DBL-37	IPA-22-6- #-10F-1-⊗-B-1	AD-609
DBL-38	IPA-9-7-F-1-⊗-⊗-#-1	MDR-1
DBL-39	IPA-29-3-18-#-10F-F-⊗-B-2-1	MDR-1
DBL-40	FSA-17-2-1-#-12-1-2-1-1-#	From fullsib

Table 4. Multilocation screening of elite breeding lines during *Kharif* 2006

Genotype Code No.	Pedigree	Source Population/ Remarks
MBL-1	CM-135	A-64
MBL-2	CM-136	MDR-1
MBL-3	CM-137-7	MDR-1
MBL-4	CM-138-2	AD-609
MBL-5	CM-142	From DMR New Delhi
MBL-6	CM-213	MDR-1
MBL-7	SC-7	MDR-1 × A-64
MBL-8	IPA-1-F-16-2-# -F-1-# -F	A-64
MBL-9	PC_2MHS-36-F-1-⊗-B-2-1	From Composite
MBL-10	FSA-17-2-1-# -12-1-2-1-1-#	From Fullsib
MBL-11	IPA-34-6-2-F-# -1-1-2-F-2	MDR-1
MBL-12	IPA-34-5-F_1-1-1-#	MDR-1
MBL-13	9679-1-1-#	Interspecific derivatives
MBL-14	9679-1-1-#	Interspecific derivatives
MBL-15	9679A-1-2-#	Interspecific derivatives
MBL-16	9678C-1-2-#	Interspecific derivatives
MBL-17	9680-F-2-1-#	Interspecific derivatives
MBL-18	9681-F-3-2-#	Interspecific derivatives
MBL-19	9679-A-1-1-#	Interspecific derivatives
MBL-20	9680A-1-2- #	Interspecific derivatives
MBL-21	8683C_2-110-C-2-99-⊗	Interspecific derivatives
MBL-22	NE-19008	Introduction
MBL-23	PC_2HS-36-F-1-⊗-B-2-1	From composite
MBL-24	SC-7-2-1-1-2-7-F-1	MDR-1 × A-64
MBL-25	IPA-29-3-18-# -10-F-⊗-B-1	MDR-1
MBL-26	CM-136	MDR-1
MBL-27	90-1-(MN – R01)-4	Hybrid derivatives
MBL-28	IPA-79-3-18-# -10-F-⊗-B	NA
MBL-29	Pop 145	From Pathology Division, IARI
MBL-30	Suwan-1	From Pathology Division, IARI

Table-5 Screening of 45 lines at Maize Pathology Unit, Delhi during *Kharif* 2006

Genotype Code No.	Pedigree	Source Population/ Remarks
DMB-1	IPA-1-F-16-2-# -F-1- # - F	A-64
DMB-2	IPA-1-F-16-2-# -F-1- # - F-1	A-64
DMB-3	IPA-9-7-F-1-⊗-B- # -1	MDR-1
DMB-4	SC-30-(92)-4-F-1-1	Single cross derivatives*
DMB-5	PC_2HS-36-F-1-⊗-B-2-1	From halfsib
DMB-6	PC_2HS-36-F-1-⊗-B-2-1-1	From halfsib
DMB-7	FSA-17-2-1- # -12-⊗-2-F	From fullsib
DMB-8	SC-7-2-1-2-7-F-1	MDR-1 × A-64
DMB-9	IPA-29-3-18- # -1-F-B-2-1	MDR-1
DMB-10	IPA-29-3-18- # -1-F-B-2-1-1	MDR-1
DMB-11	IPA-29-3-18- # -1-F-B-2-1-1-1	MDR-1
DMB-12	IPA-9-7-F-1-⊗-B- # -1- #	MDR-1
DMB-13	A-61-HS-91-F-1-⊗-B-1	A-61
DMB-14	A-61-HS-91-F-1-⊗-B-1-1	A-61
DMB-15	A-61-HS-91-F-1-⊗-B-1-1-1	A-61
DMB-16	SC-35-(92)-4-F-1-1-2-1	Single cross derivatives*
DMB-17	SC-35-(92)-4-F-1-1-2-1-1	Single cross derivatives*
DMB-18	IPA-34-5-F-F	MDR-1
DMB-19	IPA-34-5-F-F-1	MDR-1
DMB-20	A-61-HS-91-F-1-⊗-B-1-1-1-1	A-61
DMB-21	IPA-22-6- # -10-1-⊗-B-1	AD609
DMB-22	IPA-3-20- ⊗-⊗-B-1-2-1	A-64
DMB-23	IPA-3-20- ⊗-⊗-B-1-2-1-1	A-64
DMB-24	PC_2HS-34-1-3-4-1-1-1-⊗-B	From halfsib
DMB-25	PC_2HS-34-1-3-4-1-1-1-⊗-B-1	From halfsib
DMB-26	SC-35-(92)-4-F-1-1-2-1	Single cross derivatives*
DMB-27	Comp8527 X 85169-⊗-1-2-7-5-1-1-5-2-2	Composite cross
DMB-28	IPA-3-20-⊗-⊗-B-1-2	A-64
DMB-29	IPA-9-7-F-1-⊗-B- # -1	MDR-1
DMB-30	IPA-9-7-F-1-⊗-B- # -1-1	MDR-1
DMB-31	IPA-3-6-10-3- # -1-1-2-1-1-1-⊗-B-1	A-64
DMB-32	IPA-3-6-10-3- # -1-1-2-1-1-1-⊗-B-1-1	A-64
DMB-33	IPA-3-6-10-3- # -1-1-2-1-1-1-⊗-B-1-1-1	A-64

cont...

DMB-34	SC-35-(92)-4-F-1-1-2-1	Single cross derivatives*
DMB-35	SC-30-(92)-4-F-1-1	Single cross derivatives*
DMB-36	IPA-29-3-3-18- # -10-F-⊗-B-2-1- #	MDR-1
DMB-37	SC-7-2-1-1-2-7-F-1	MDR-1 × A-64
DMB-38	IPA-9-7-F-1-⊗-B- #	MDR-1
DMB-39	IPA-23-92-F-1- # -1-12-2- #	AD609
DMB-40	IPA-3-20-⊗-⊗-B-1-2-1	A-64
DMB-41	IPA-34-5-F-1-1-1-1	MDR-1
DMB-42	IPA-34-62-F- # -1-1	MDR-1
DMB-43	TCA-22-3-1-1-2-F- # -1-1-2-F	A-64
DMB-44	IPA-3-28-5-⊗- #	A-64
DMB-45	IPA-22- # -10-F-1-⊗-B-1	AD609

Single cross derivatives*- referes to elite single crosses evaluated in respective years.

Table 6. Parents used in crossing programme

S.no	Pedigree	Origin (DL-6K)
1	IPA-1-F-16-2-# -F-1- # - F-1	DMB-2
2	IPA-9-7-F-1-⊗-B- # -1	DMB-3
3	PC_2HS-36-F-1-⊗-B-2-1	DMB-5
4	IPA-29-3-18- # -1-F-B-2-1	DMB-9
5	IPA-9-7-F-1-⊗-B- # -1- #	DMB-12
6	A-61-HS-91-F-1-⊗-B-1-1	DMB-14
7	A-61-HS-91-F-1-⊗-B-1-1-1	DMB-15
8	SC-35-(92)-4-F-1-1-2-1	DMB-16
9	SC-35-(92)-4-F-1-1-2-1-1	DMB-17
10	IPA-34-5-F-F	DMB-18
11	IPA-34-5-F-F-1	DMB-19
12	IPA-3-20- ⊗-⊗-B-1-2-1	DMB-22
13	IPA-3-20- ⊗-⊗-B-1-2-1-1	DMB-23
14	PC_2HS-34-1-3-4-1-1-1-⊗-B	DMB-24
15	SC-35-(92)-4-F-1-1-2-1	DMB-26
16	Comp8527 X 85169-⊗-1-2-7-5-1-1-5-2-2	DMB-27
17	IPA-3-20-⊗-⊗-B-1-2	DMB-28
18	IPA-9-7-F-1-⊗-B- # -1	DMB-29
19	IPA-9-7-F-1-⊗-B- # -1-1	DMB-30
20	CM-151	978 (DK05)
21	CM-150	976 (DK05)

Table 7. Crosses developed during *Kharif* 2006

Cross No.	Crosses
1	DMB-14 X DMB-26
2	DMB-18 X DMB-26
3	DMB-19 X DMB-26
4	DMB-23 X DMB-26
5	DMB-5 X DMB-27
6	DMB-9 X DMB-27
7	DMB-12 X DMB-27
8	DMB-17 X DMB-27
9	DMB-18 X DMB-27
10	DMB-19 X DMB-27
11	DMB-22 X DMB-27
12	DMB-24 X DMB-27
13	CM-150 X DMB-27
14	CM-151 X DMB-27
15	DMB-2 X DMB-28
16	DMB-9 X DMB-28
17	DMB-12 X DMB-28
18	DMB-16 X DMB-28
19	DMB-17 X DMB-28
20	DMB-18 X DMB-28
21	DMB-24 X DMB-28
22	DMB-30 X DMB-28
23	DMB-12 X DMB-30
24	DMB-14 X DMB-30
25	DMB-23 X DMB-30
26	CM-151 X DMB-30
27	CM-150 X DMB-23
28	CM-151 X DMB-23
29	CM-150 X DMB-24
30	CM-151 X DMB-24
31	CM-150 X DMB-25

Table 8. Crosses developed during *Rabi* 2006

Cross No.	Crosses
1	DMB-2 X DMB-28
2	DMB-2 X DMB-30
3	DMB-3 X DMB-26
4	DMB-3 X DMB-28
5	DMB-3 X DMB-29
6	DMB-3 X DMB-30
7	DMB-5 X DMB-26
8	DMB-5 X DMB-27
9	DMB-5 X DMB-28
10	DMB-5 X DMB-29
11	DMB-5 X DMB-30
12	DMB-9 X DMB-26
13	DMB-9 X DMB-27
14	DMB-9 X DMB-28
15	DMB-9 X DMB-29
16	DMB-9 X DMB-30
17	DMB-12 X DMB-26
18	DMB-12 X DMB-27
19	DMB-12 X DMB-28
20	DMB-12 X DMB-29
21	DMB-12 X DMB-30
22	DMB-14 X DMB-26
23	DMB-14 X DMB-27
24	DMB-14 X DMB-28
25	DMB-14 X DMB-29
26	DMB-14 X DMB-30
27	DMB-15 X DMB-27
28	DMB-16 X DMB-26
29	DMB-16 X DMB-27
30	DMB-16 X DMB-28
31	DMB-16 X DMB-29
32	DMB-16 X DMB-30
33	DMB-17 X DMB-26
34	DMB-17 X DMB-27
35	DMB-17 X DMB-28
36	DMB-17 X DMB-29
37	DMB-17 X DMB-30
38	DMB-18 X DMB-26
39	DMB-18 X DMB-27
40	DMB-18 X DMB-28
41	DMB-18 X DMB-29

42	DMB-18 X DMB-30
43	DMB-19 X DMB-26
44	DMB-19 X DMB-27
45	DMB-19 X DMB-28
46	DMB-19 X DMB-30
47	DMB-22 X DMB-26
48	DMB-22 X DMB-27
49	DMB-22 X DMB-28
50	DMB-22 X DMB-29
51	DMB-22 X DMB-30
52	DMB-23 X DMB-26
53	DMB-23 X DMB-27
54	DMB-23 X DMB-28
55	DMB-23 X DMB-29
56	DMB-23 X DMB-30
57	DMB-24 X DMB-27
58	DMB-24 X DMB-28
59	DMB-24 X DMB-29
60	DMB-24 X DMB-30
61	DMB-26 X DMB-27
62	DMB-26 X DMB-28
63	DMB-26 X DMB-29
64	DMB-26 X DMB-30
65	DMB-27 X DMB-28
66	DMB-27 X DMB-29
67	DMB-28 X DMB-26
68	DMB-28 X DMB-27
69	DMB-28 X DMB-29
70	DMB-28 X DMB-30
71	DMB-29 X DMB-26
72	DMB-29 X DMB-27
73	DMB-29 X DMB-28
74	DMB-29 X DMB-30
75	DMB-30 X DMB-26
76	DMB-30 X DMB-28
77	DMB-30 X DMB-29
78	CM-151 X DMB-26
79	CM-151 X DMB-28
80	CM-151 X DMB-29
81	CM-151 X DMB-30
82	CM-150 X DMB-26
83	CM-150 X DMB-27
84	CM-150 X DMB-28
85	CM-150 X DMB-29
86	CM-150 X DMB-30

Table 9. Parents used in Line X Tester

Lines/ Testers (DL-6K)	Origin
L_1	DMB-5
L_2	DMB-9
L_3	DMB-12
L_4	DMB-14
L_5	DMB-16
L_6	DMB-17
L_7	DMB-18
L_8	DMB-22
L_9	DMB-23
T_1	DMB-26
T_2	DMB-27
T_3	DMB-28
T_4	DMB-29
T_5	DMB-30

Table 10. Frequency distribution of banded leaf and sheath blight score in maize inbred lines (*Kharif* 2005).

Disease score (1.0-5.0)	No. of lines	Percent	Reaction type*
1.0	0	0	Resistant
1.5	0	0	Resistant
2.0	0	0	Resistant
2.5	3	7.5	Intermediate
3.0	7	17.5	Intermediate
3.5	13	32.5	Intermediate
4.0	7	17.5	Intermediate
4.5	8	20.0	Susceptible
5.0	2	5.0	Susceptible
Total	40	100%	

*Score 1.0-2.0 = Resistant; 2.1-4.0 = Intermediate; 4.1-5.0 = Susceptible

Table 11. Frequency distribution of banded leaf and sheath blight score in maize inbred lines (*Kharif* 2006)

Disease score (1.0-5.0)	No. of lines			Percent			Reaction type*
	Delhi	Pant nagar	Udaipur	Delhi	Pant nagar	Udaipur	
1.0	0	0	0	0	0	0	Resistant
1.5	0	0	2	0	0	6.6	Resistant
2.0	0	8	2	0	27.0	6.6	Resistant
2.5	1	13	6	3.3	43.3	20.0	Intermediate
3.0	3	7	5	10.0	23.3	16.6	Intermediate
3.5	10	2	7	33.3	6.7	23.3	Intermediate
4.0	10	0	3	33.3	0	10.0	Intermediate
4.5	5	0	4	16.6	0	13.3	Susceptible
5.0	1	0	1	3.3	0	3.3	Susceptible
Total	30	30	30	100	100	100	

*Score 1.0-2.0 = Resistant; 2.1-4.0 = Intermediate; 4.1-5.0 = Susceptible

Table 12. Multilocation screening (1-5 score) of inbred lines for banded leaf and sheath blight during *Kharif* 2006.

Inbred lines Genotype (Code No.)	Locations		
	Delhi	Pant nagar	Udaipur
MBL-1	4.0	3.5	4.5
MBL-2	3.5	2.5	2.5
MBL-3	3.5	2.5	3.5
MBL-4	4.5	3.0	4.5
MBL-5	3.5	2.5	3.5
MBL-6	4.0	2.0	3.0
MBL-7	4.5	3.0	3.5
MBL-8	5.0	2.0	5.0
MBL-9	4.0	2.5	2.5
MBL-10	4.5	2.0	3.5
MBL-11	4.0	3.5	1.5
MBL-12	3.5	2.5	2.5
MBL-13	4.0	3.0	4.5
MBL-14	3.5	2.0	3.5
MBL-15	3.0	2.5	2.5
MBL-16	3.0	3.0	2.5
MBL-17	3.5	2.0	3.0
MBL-18	4.0	2.0	2.0
MBL-19	4.0	2.0	3.0
MBL-20	4.0	2.5	4.0
MBL-21	4.0	2.5	3.0
MBL-22	3.5	2.5	3.0
MBL-23	3.0	3.0	2.5
MBL-24	3.5	2.5	3.5
MBL-25	4.5	3.0	4.5
MBL-26	4.0	3.0	3.5
MBL-27	3.5	2.5	4.0
MBL-28	4.5	2.0	4.0
MBL-29	2.5	2.5	2.0
MBL-30	3.5	2.5	1.5

Table 13. Frequency distribution of banded leaf and sheath blight score in maize inbred lines (*Kharif* 2006).

Disease score (1.0-5.0)	No. of lines	Percent	Reaction type*
1.0	0	0	Resistant
1.5	0	0	Resistant
2.0	0	0	Resistant
2.5	1	2.0	Intermediate
3.0	16	35.6	Intermediate
3.5	17	38	Intermediate
4.0	11	24.4	Intermediate
4.5	0	0	Susceptible
5.0	0	0	Susceptible
Total	45	100%	

* score 1.0-2.0 = Resistant; 2.1-4.0 = Intermediate; 4.1-5.0 = Susceptible

Table 14. Disease scores for maize inbred lines during two consecutive years

Inbred lines	*Kharif* 2006	*Kharif* 2007
DMB-2	3.0	2.5
DMB-3	3.5	3.5
DMB-5	3.0	4.0
DMB-9	3.5	3.0
DMB-12	3.0	2.5
DMB-14	3.0	3.5
DMB-15	3.5	2.5
DMB-16	4.0	2.5
DMB-17	3.5	3.5
DMB-18	2.5	3.0
DMB-19	3.5	3.5
DMB-22	3.0	3.5
DMB-23	4.0	3.0
DMB-24	4.0	2.5
DMB-26	3.5	3.0
DMB-27	4.0	3.0
DMB-28	3.0	4.0
DMB-29	3.5	2.5
DMB-30	4.0	3.0

Table 15. Ear to row wise disease scores during *Kharif* 2007

Inbred lines	Ear-1	Ear-2
DMB-2	2.5	3.5
DMB-3	4.0	4.0
DMB-5	4.5	4.0
DMB-9	3.5	3.0
DMB-12	3.0	4.0
DMB-14	4.0	3.5
DMB-15	3.0	3.0
DMB-16	3.5	4.0
DMB-17	4.0	2.5
DMB-18	3.0	3.5
DMB-19	4.0	3.5
DMB-22	3.5	4.0
DMB-23	3.0	3.0
DMB-24	4.0	3.5
DMB-26	4.0	4.0
DMB-27	3.5	3.5
DMB-28	4.0	3.5
DMB-29	4.0	3.0
DMB-30	3.5	4.0

Table 16. BLSB disease reaction of F_1s

S. no.	Pedigree	BLSB scores
1	DMB-2 X DMB-28	2.5
2	DMB-2 X DMB-30	3.0
3	DMB-3 X DMB-26	3.5
4	DMB-3 X DMB-28	3.0
5	DMB-3 X DMB-29	2.5
6	DMB-3 X DMB-30	2.5
7	DMB-5 X DMB-26	3.5
8	DMB-5 X DMB-27	2.5
9	DMB-5 X DMB-28	3.0
10	DMB-5 X DMB-29	3.0
11	DMB-5 X DMB-30	3.0
12	DMB-9 X DMB-26	2.5
13	DMB-9 X DMB-27	3.0
14	DMB-9 X DMB-28	3.5
15	DMB-9 X DMB-29	3.0
16	DMB-9 X DMB-30	3.0
17	DMB-12 X DMB-26	2.5
18	DMB-12 X DMB-27	2.5
19	DMB-12 X DMB-28	3.0
20	DMB-12 X DMB-29	3.0
21	DMB-12 X DMB-30	3.0
22	DMB-14 X DMB-26	3.5
23	DMB-14 X DMB-27	2.5
24	DMB-14 X DMB-28	3.0
25	DMB-14 X DMB-29	2.5
26	DMB-14 X DMB-30	3.0
27	DMB-15 X DMB-27	3.0
28	DMB-16 X DMB-26	3.5
29	DMB-16 X DMB-27	3.0
30	DMB-16 X DMB-28	3.0
31	DMB-16 X DMB-29	3.0
32	DMB-16 X DMB-30	3.0
33	DMB-17 X DMB-26	2.5
34	DMB-17 X DMB-27	3.0
35	DMB-17 X DMB-28	3.0
36	DMB-17 X DMB-29	3.0
37	DMB-17 X DMB-30	3.0
38	DMB-18 X DMB-26	3.0
39	DMB-18 X DMB-27	2.5
40	DMB-18 X DMB-28	3.5
41	DMB-18 X DMB-29	3.0
42	DMB-18 X DMB-30	3.0

cont...

S. no.	Pedigree	BLSB scores
43	DMB-19 X DMB-26	3.0
44	DMB-19 X DMB-27	3.0
45	DMB-19 X DMB-28	3.5
46	DMB-19 X DMB-30	2.5
47	DMB-22 X DMB-26	3.0
48	DMB-22 X DMB-27	2.5
49	DMB-22 X DMB-28	3.5
50	DMB-22 X DMB-29	3.5
51	DMB-22 X DMB-30	3.0
52	DMB-23 X DMB-26	3.5
53	DMB-23 X DMB-27	2.5
54	DMB-23 X DMB-28	3.5
55	DMB-23 X DMB-29	2.5
56	DMB-23 X DMB-30	3.5
57	DMB-24 X DMB-27	2.5
58	DMB-24 X DMB-28	2.5
59	DMB-24 X DMB-29	2.5
60	DMB-24 X DMB-30	3.0
61	DMB-26 X DMB-27	3.0
62	DMB-26 X DMB-28	2.5
63	DMB-26 X DMB-29	3.0
64	DMB-26 X DMB-30	3.0
65	DMB-27 X DMB-28	2.5
66	DMB-27 X DMB-29	2.5
67	DMB-28 X DMB-26	3.0
68	DMB-28 X DMB-27	3.0
69	DMB-28 X DMB-29	3.0
70	DMB-28 X DMB-30	3.0
71	DMB-29 X DMB-26	3.0
72	DMB-29 X DMB-27	2.5
73	DMB-29 X DMB-28	2.5
74	DMB-29 X DMB-30	3.0
75	DMB-30 X DMB-26	3.0
76	DMB-30 X DMB-28	3.0
77	DMB-30 X DMB-29	3.0
78	CM-151 X DMB-26	2.5
79	CM-151 X DMB-28	2.5
80	CM-151 X DMB-29	2.5
81	CM-151 X DMB-30	3.0
82	CM-150 X DMB-26	2.5
83	CM-150 X DMB-27	3.0
84	CM-150 X DMB-28	3.0
85	CM-150 X DMB-29	3.0
86	CM-150 X DMB-30	3.0

Table 17. BLSB disease reaction of F_2s

S. no.	Pedigree	Mean BLSB scores
1	DMB-14 X DMB-26	3.5
2	DMB-18 X DMB-26	3.3
3	DMB-19 X DMB-26	3.8
4	DMB-23 X DMB-26	3.08
5	DMB-5 X DMB-27	2.9
6	DMB-9 X DMB-27	2.4
7	DMB-12 X DMB-27	2.86
8	DMB-17 X DMB-27	3.42
9	DMB-18 X DMB-27	3.0
10	DMB-19 X DMB-27	2.8
11	DMB-22 X DMB-27	2.55
12	DMB-24 X DMB-27	3.58
13	CM-150 X DMB-27	3.6
14	CM-151 X DMB-27	2.5
15	DMB-2 X DMB-28	2.9
16	DMB-9 X DMB-28	3.7
17	DMB-12 X DMB-28	3.3
18	DMB-16 X DMB-28	3.66
19	DMB-17 X DMB-28	3.2
20	DMB-18 X DMB-28	2.8
21	DMB-24 X DMB-28	2.8
22	DMB-30 X DMB-28	3.1
23	DMB-12 X DMB-30	3.6
24	DMB-14 X DMB-30	2.9
25	DMB-23 X DMB-30	2.6
26	CM-151 X DMB-30	3.6
27	CM-150 X DMB-23	2.5
28	CM-151 X DMB-23	3.75
29	CM-150 X DMB-24	4.0
30	CM-151 X DMB-24	2.4
31	CM-150 X DMB-25	2.7

ABSTRACT

Improved cultivars particularly hybrids combining high yield and disease resistance play a significant role in increasing yield. Breeding disease resistant varieties is the socio-economical and viable alternative to reduce the cost of cultivation. Since Banded leaf and sheath blight (*Rhizoctonia solani* f.sp *sasakii*) has become a disease of major concern in maize only recently, little work on genetic analysis and breeding for resistance to this disease has been undertaken. Moreover only a few resistance sources have been identified. So the emphasis was to screen additional inbred lines for identifying potential new sources. Also genetic analysis of resistance needs to be undertaken to understand the mechanism as well as to devise appropriate strategy for incorporation of resistance as well as to improve yield. By involving diverse maize inbred lines with different disease reactions, experimental hybrids with higher productivity and resistant to BLSB can be generated.

Multilocation screening during *kharif* 2005 at New Delhi, Pantnagar and Udaipur centres revealed that Pop145 (MBL-29) and Suwan-1 (MBL-30) had high degree of tolerance to BLSB. Another set of forty five lines screened during *kharif* 2006 at Delhi centre showed intermediate disease reaction to BLSB. DMB-3, DMB-15, DMB-23, DMB-26 and DMB-27 showed consistent disease scores in different rows (ear-to-row) indicating homozygous disease reaction. Dominance nature of disease reaction to BLSB was revealed by resistance reaction of F_1 s generated by crossing resistant and susceptible parents. F_2 s of crosses DMB-9 X DMB-27 (L_2 X T_2) and CM-151 X DMB-24 exhibited lowest mean scores of 2.4 which can be used in deriving resistant lines. F_2 families of DMB-22 X DMB-27, CM-151 X DMB-27 and CM-150 X DMB-25 had more than 50% individual plants with a score of 2.0, which can be specifically targeted to yield segregants with resistance to BLSB.

L X T analysis was done using nine lines and five testers to generate information on nature and magnitude of gene action for yield and yield components. Genotypes under study exhibited substantial variability for all the characters. ANOVA for parents *vs* hybrids component exhibited highly significant variance for all traits indicating superior performance of hybrids over parents. The variances due to females

and males (indicative of GCA variance) were significant and higher in magnitude for almost all the characters indicating predominance of additive gene action.

The genotypes L_4 (DMB-14) and L_8 (DMB-22) were good general combiners for yield and yield associated characters. Parents with high gca effects for yield also exhibited high gca for other yield contributing characters. The best specific crosses with high sca effects in desirable direction were L_2 x T_1, L_2 x T_2, L_3 x T_3, L_5 x T_3, L_9 x T_1 and L_9 X T_5. High sca effects involved not only high x high parents but also high x low and low x low gca effects. High heterosis for grain yield had contribution from high heterosis of yield attributes. L_5 x T_3 (DMB-16 X DMB-28) and L_9 X T_5 (DMB-23 X DMB-30) with high sca effects and better parent heterosis were identified for selection on the basis of number of cobs per plot, yield per plot, single cob weight, number of rows per cob and number of kernels per row. L_2 X T_2 (DMB-9 X DMB-27) showed high degree of tolerance to BLSB with high productive potentiality.

The path analysis at genotypic and phenotypic levels revealed that number of cobs per plot had higher positive direct effect on yield and correlation coefficient of number of cobs per plot was highly significant and positive.

5. DISCUSSION

Banded leaf and sheath blight (BLSB) caused by *Rhizoctonia solani* f.sp. *sasakii*, here after referred to as *R. solani* is one of the major diseases of maize in hot and humid regions. The disease is present in many parts of the world and has a potential to reduce the economic yield upto the extent of 100 percent (Payak and Sharma, 1985).

5.1. Evaluation of maize inbred lines for response to banded leaf and sheath blight

Host plant resistance is one of the important components of any integrated disease management system. It provides an opportunity to cut down the costs of disease control over other methods. Sources of disease resistance can be found in existing varieties, local collections, exotic materials and wild relatives. Evaluation and selection of desired materials from a large number of genetically diverse groups is one of the effective methods to identify desired resistant genotypes. In order to find out the sources of resistance to BLSB a large number of inbred lines were screened under artificial epiphytotic condition during *kharif* seasons of 2005 and 2006 at IARI. During 2005 season, out of 40 lines evaluated, 25 percent were found susceptible (4.1-5.0), 75 percent intermediate (2.1-4.0). But none were found showing resistant reaction (1.0-2.0) to BLSB indicating paucity of resistant genotypes or higher virulence of the pathogen or both.

However multilocation screening of 30 lines during *kharif* 2006 showed 27 percent and 13 percent resistant (1.0-2.0) to BLSB at Pantnagar and Udaipur respectively. None of the lines were resistant at Delhi centre. Out of 30 lines screened, 20 percent and 17 percent were rated as susceptible (4.1-5.0) at Delhi and Udaipur centres respectively. None was susceptible at Pantnagar. And 80 percent, 73 percent and 70 percent lines showed intermediate reaction (2.1-4.0) at Delhi, Pantnagar and Udaipur centres respectively. In general Delhi centre recorded high scores of disease when compared to other centres. MBL-18 with pedigree 9681-f-3-2-# showed constant score of 2.0 at Pantnagar and Udaipur centres where as it showed a disease score of 4.0 at Delhi centre. This indicates involvement of different races of BLSB and different environment conditions. Inbred lines Pop 145 (MBL-29) and Suwan-1 (MBL-30)

showed high degree of tolerance (1.5-3.0) to BLSB. Similar results were also obtained by Sharma *et al.,* (2002), Batsa (2003) and Sharma *et al.,* (2005).

Of the 45 lines screened during *kharif* 2006 at Delhi centre, all of them showed intermediate disease score (2.1-4.0) to BLSB. Year wise data indicates DMB-17 and DMB-19 showed consistent scores (3.5) across years (Table-14). Progeny from two cobs of the same plant has been sown in two different rows in Pathology field to analyze the differences, if any, in the genotypes for disease resistance. This is specifically relevant for the inbred lines used by maize breeders, which may harbour subtle differences for responses to specific pathogens and would be uncovered only after the exposure to those conditions. Five lines DMB-3, DMB-15, DMB-23, DMB-26 and DMB-27 showed consistent disease scores in different rows. This indicates homozygous disease reaction of these lines and they can be utilized in breeding programmes along with high reliability of their response to BLSB (Table-15).

All F_1 s and F_2 s generated from this set of 45 lines also showed intermediate disease reaction (Table-16 and Table-17). Out of all F_2 s the lowest mean scores of 2.4 were exhibited by two crosses DMB-9 X DMB-27 and CM-151 X DMB-24, which could be of potential utility in deriving resistant line if large number of segregants from respective families were screened under artificial conditions. By looking into individual scores of individual plants of each F_2 family, three crosses *viz.,* DMB-22 X DMB-27, CM-151 X DMB-27 and CM-150 X DMB-25 were found to be having 50 percent or more plants with a score of 2.0. Advancement of these families in large family size will also be expected to give useful segregants with resistance to banded leaf and sheath blight. Those will also be relevant due to prospects of obtaining segregants with extreme reaction to banded leaf and sheath blight. Such lines after stabilization and testing for consistency in reaction could serve as potential parental lines for molecular mapping.

During the test seasons or years (0-35 days after inoculation) weekly average maximum temperature of 31-35^0 C, minimum temperature of 23-27^{0}C, average relative humidity of 75-85 percent and rainfall >150mm were recorded. This indicated that the field environment of IARI was suitable for screening large number of germplasm against BLSB.

Germplasm evaluation was extensively carried out in the past using a large number of maize varieties, hybrids and inbred lines (Singh and Sharma, 1976; Ahuja and Payak, 1981; Balla *et al.*, 2000 and Sharma *et al.,* 2003) in order to find materials resistant to BLSB, but the success in achieving true resistance still seems to be far. As of know, the genetic variability for resistance to BLSB has been found to be limited (Sharma *et al.,* 2002) which is a bottleneck for an effective resistance breeding programme. This is convincing because maize varieties, hybrids and inbreds derived from these diverse gene pools and evaluated across the environment are not showing true or absolute resistance so far.

However, the lines which have shown constantly tolerant reaction in different countries may be utilised as such or resistance can be transferred using cyclic breeding programme into commercial varieties to meet the immediate challenge posed by BLSB.

Another useful and practically relevant approach might be to take into account disease reaction of the elite genotypes (parents and crosses) in the decision making process. Thus, suitable importance and weightage might be given to the reactions to BLSB, in addition to other parameters related to productivity and combining ability. This would ensure minimum or tolerable impact of the disease on one hand and not compromising on the productivity on the other hand. This could be a sensible step for the maize breeders specifically in the northern belt of the country, where the menace of BLSB is mainly felt.

5.1.1. Genetics of BLSB resistance

F_1 of cross between DMB-5 and DMB-27 with disease scores 4.0 and 3.0 respectively, showed disease score of 2.5 and all F_2 showed intermediate resistance reaction. Similarly F_1 between DMB-18 and DMB-27 with disease scores 3.0 and 4.0 respectively showed disease score of 3.5 and all F_2 plants were moderately resistant. This indicates dominant nature of disease resistance. Other such crosses were:

DMB-2 X DMB-28

DMB-17 X DMB-28

DMB-30 X DMB-28

DMB-9 X DMB-27

DMB-12 X DMB-27

DMB-18 X DMB-27

DMB-14 X DMB-30

DMB-23 X DMB-30

These crosses might be specifically targeted for making selections for resistant lines under artificial inoculation conditions.

5.2. Line x Tester analysis

Line x tester design is basically an extension of top cross analysis in the sense that, instead of one tester, used in top crossing, more testers are employed under L x T mating designs (Kempthorne, 1957). Top cross and poly cross designs provide only halfsibs where as L x T mating design provides both halfsib (HS) and fullsib (FS) relatives simultaneously. Hence L x T analysis also referred as FS/HS analysis. Here specific combining ability of each cross can be determined (Sharma, 1998). When compared to diallel analysis, L x T analysis can include more parents for a given level of resources and two independent estimates of σ^2 A are available and greater number of parents can be included by subdividing parent into sets (Hallauer and Miranda, 1988).

Nature and magnitude of gene action determines the most appropriate and efficient breeding procedure. Relative contribution of GCA and SCA effects are of interest to breeders as breeding methods differ appreciably based on the type of gene action. In the present investigation, L x T analysis was done using nine lines and five testers to generate information on afforesaid parameters.

Further, as BLSB is a major disease, the reaction of elite experimental hybrids to BLSB needs to be taken into account. By involving diverse maize inbred lines with different disease reactions, there is a possibility of generating experimental hybrids with higher productivity along with reasonable disease resistance which would meet the practical and field requirements.

5.2.1. *Per se* performance of parents and hybrids

The mean performance of parents and hybrids concerning to L x T (9 x 5) analysis is presented in Table-18. The data on mean performance is the basis on which all other analysis is done. The *per se* performance of the genotypes revealed that there

was substantial variability among them for all the characters. Based on the mean performance L_7 among the lines and T_5 among the testers were the best for grain yield per plot. Also L_7 recorded highest *per se* performance for number of cobs per plot (12.33). For single cob weight L_2 and T_2 among lines and testers respectively were the best. Some other inbreds worth mentioning with respect to yield per plot and single cob weight where L_5 (1.267kg, 0.075kg) and L_6 (1.167kg, 0.076kg) and T_5 (1.167kg, 0.066kg).

The inbred L_2 had also the highest per se performance for number kernels per row (27.16). The inbred L_4 recorded highest mean for 100 seed weight (25.17gm). L_5 also recorded highest mean for cob length (14.05cm) with good performance for yield and yield parameters. T_2 showed highest *per se* performance for cob girth (3.43cm), number of rows per cob (15.64), number of kernels per row (28.36) and number of seeds per cob (443.55). L_1 among lines and T_1 among testers were the earliest to 50 percent pollenshed and 50 percent silking. Since inbred with highest desirable mean value for all the characters was not observed, best performer across the characters could not be identified. However, there were inbreds that performed better for one or more characters. Hence, while selecting for Line x Tester analysis yield per plot and single cob weight were taken as primary characters. While selecting for testers, three testers with higher yield per plot and two with low yield per plot, and while selecting lines, seven lines with higher yield and two with low yield were selected. The selection for high and low performers based on the fact that high heterosis results not only due to high x high process but also high x low or low x high process. Among such combinations high x low and low x high combinations frequently show high heterosis (Hallauer and Miranda, 1988).

BLSB disease reaction of 2.5 to 3.5 was exhibited by seven lines and two lines had a score of 4.0. Among the testers three testers recorded a disease score of 3 to 3.5 and two a disease score of 4.0. Thus testers as a group comprised of genotypes with relatively higher scores than the lines.

Days to 50 percent pollenshed and days to 50 percent silking are very important physiological traits that give a clue to duration of maturity and expected date of harvesting. Silking is greatly influenced by environment. In hybrid seed production, better synchrony of male and female lines improves the seed quality and reduces the

cost of seed production. Early maturing hybrids are important under Indian conditions to avoid ill effects of late season drought, as most of maize in India is grown under rainfed conditions (Chapmon and Edmedes, 1999). The hybrid L_8 x T_3 was earliest (52.33 and 54.67 days) followed by L_5 x T_1 (53.00 and 55.33 days) both of which were significantly earlier than the earliest inbred L_1 (53.67 and 57.00 days). These hybrids can further be utilized for the extraction of early inbred lines.

Short and robust plant stature is preferred for most of the cereals. The mean performance with respect to plant height had a range of 128.33cm to 235.00cm indicating most significant variability for the trait among highest yields. However in the present investigation the highest yielding hybrid (L_9 x T_5) had a height of 225cm.

The character cob placement is positively correlated with plant height and negatively correlated with silking. The range of cob placement was broad (81.67cm to 125.00cm).

Improvement of grain yield is the prime objective in all the breeding programmes and also in resistance breeding. Plant productivity in broad sense includes not only yield but also number of direct and indirect components (Arunachalam, 1988). Among hybrids L_9 x T_5 had highest grain yield per plot, (3.00Kg), L_8 x T_1 had highest number of cobs per plot (18.67), L_4 x T_5 had highest single cob weight (0.155kg) and cob length (19.73cm), L_4 x T_2 for cob girth (3.78cm), L_1 x T_2 for number of rows per cob (16.53), L_5 x T_3 for number of kernels per row (38.00), L_5 x T_3 (567.34) for number of seeds per cob and L_8 x T_4 for hundred seed weight (29.00gm). The above said high yielding crosses justified selection of parents indicating high x low or low x high combinations resulting in high heterosis. There were some notable crosses for one or more individual traits and none of the crosses had highest performance for all the traits. The crosses L_1 x T_5 for number of cobs per plot (18.33) and cob length (18.87cm), L_4 x T_3 for single cob weight (0.152 kg) and cob length (19.49cm) and number of kernels per row (37.27), L_8 x T_1 for number of cobs per plot (18.67) and yield per plot (2.800 kg), L_8 x T_5 for yield per plot (2.867 kg) and single cob weight (0.138 kg). This means that even in hybrids simultaneous improvement of all traits is difficult. Therefore it is advisable to improve individual traits and the above hybrids can be utilized to derive better inbred lines through the process of recycling of inbreds. The strength and sustainable gain in a continuous hybrid breeding programme lies in the inbred based

germplasm. It is important that enough inbreds should form the base and preferably should be diverse.

5.2.2. ANOVA for parents and hybrids

In L x T analysis total variance is partitioned into variances due to replication, parents, females, males, females x males, hybrids, parents *vs* hybrids and error. Significant variation was detected for parents to days to 50 percent pollenshed, plant height, number of cobs per plot, cob placement, single cob weight, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight. It was observed that there were significant differences for plant height with respect to variance due to all source components of ANOVA except due to females x males. Significant differences for days to 50 percent pollenshed, cob length, cob girth, number of cobs per row, number of kernels per row and 100 seed weight was observed for all sources of variation except due to hybrids. Variance due to hybrids was significant for days to 50 percent silking, plant height, number of cobs per plot and yield per plot. The parents *vs* hybrids component exhibited highly significant variance for all traits except days to 50 percent silking and number of cobs per plot. This implies that the performance of hybrids was significantly different from one another and performance of parents as a group was significantly different from hybrids as a group. This can also be seen from the data (Table-19) that the performance of hybrids was superior compared to parents.

5.2.3. Combining ability of inbred lines

Combining ability of inbred lines is the ultimate factor determining the usefulness of the lines for hybrid breeding. Combining ability is useful in classifying an inbred line in relation to its cross performance. Sprague and Tatum in 1942 refined the concept of combining ability and for the first time suggested partition of total combining ability of lines into GCA and SCA. They defined general combining ability as the average performance of line in hybrid combination and specific combining ability as those instances in which certain cross combinations are either better or poorer than would be expected on the average performance of the parent inbred lines included. They also emphasized that the estimates of GCA and SCA are relative and dependent on the particular set of inbred lines included in the hybrids under test, an important

principle that is often forgotten (Hallauer and Miranda, 1988). They interpreted GCA as indication of genes having largely additive effect and SCA as indicative of genes having dominance and epistasis effect. The conclusion of Sprague and Tatum (1942) are equally valid in the present breeding programme because of interest of production and growing of single cross hybrids.

Kempthorne (1957) gave the method of analysis of combining ability using Line x Tester mating designs. This mating design yields information on GCA and SCA variances, GCA and SCA effects and an extent of heterosis in cross combinations. Thus combining ability analysis is one of the important tools for identifying prospective parents and shifting productive hybrids from set crosses in F_1 hybrids. In the present study also an attempt has been made to obtain information on combining ability employing L x T analysis.

The variances due to females and males (indicative of GCA variance) were significant and higher in magnitude for days to 50 percent pollenshed, days to 50 percent silking, plant height, number of cobs per plot, cob placement, yield per plot, single cob weight, cob length, cob girth, number of rows per cob and 100 seed weight (Table -11). This implied that these characters are predominantly governed by additive gene action. This result was in agreement with the reports of Murthy *et al.*, 1981, Vasal *et al.*,1993, Satyanarayana *et al.*, 1994, Gupta *et al.*,1994, Choudhary *et al.*, 2000, Devi and Prodhan 2004, Katna *et al.*, 2005, Kishan *et al.*, 2005, Chattopadhyay and Dhiman 2006, Selvaraj *et al.*, 2006 and Iqbal *et al.*, 2007.

Variance due to females x males, which is related to dominance variance was significant for days to 50 percent silking and number of kernels per row. Hence both additive and dominance gene action were important for days to 50 percent silking. Similar results were obtained by Widstrom *et al.*, 1993, Kumar *et al.*, 1999 and Jabeen *et al.*, 2007.

The GCA effects of L_1 and T_3 for days to 50 percent pollenshed and L_5 for days to 50 percent pollenshed and days to 50 percent silking were significant in desirable direction. Therefore these inbreds can be used to produce early maturing hybrids. L_1 was good general combiner for plant height, cob placement and 100 seed weight.

Significant negative SCA effect was detected in L_8 x T_3 for days to 50 percent silking. It was observed that this hybrid did not show any desirable SCA effect for yield and yield components, emphasizing the difficulty in combining earliness and yield. L_3 and L_4 can be used to produce short stature hybrids which may be useful where lodging is a problem. This was evident with significant negative SCA effect for plant height in the cross combination L_3 x T_1. For cob placement, L_4 and T_1 were significant in desirable direction. Significant negative SCA effect was detected in L_3 x T_1.

The estimates of GCA effects indicated that L_4 was best general combiner for single cob weight, cob length, cob girth and number of rows per cob, L_8 for number of cobs per plot, yield per plot, single cob weight and 100 seed weight, L_7 for cob placement and L_9 for 100 seed weight. Among the testers, T_1 for cob placement, T_2 for number of rows per cob and T_4 and T_5 for 100 seed weight recorded significant positive GCA effects. To sum up L_4 and L_8 were good general combiners for yield and yield components. None of the parents displayed desirable GCA effects for all the traits. This means that there is scope for improving GCA of parents.

A highly significant SCA effect for number of cobs per plot was observed in the cross L_4 x T_1, L_4 x T_5 for single cob weight and L8 x T_4 for 100 seed weight. Other notable crosses with desirable effect include L_1 xT_5 for cob length, L_2 x T_1 for cob length and 100 seed weight, L_2 x T_2 for days to 50 percent pollenshed, number of cobs per plot and yield per plot, L_3 x T_2 for number of kernels per row, L_3 x T_3 for single cob weight, cob length and number of kernels per row, L_4 x T_1 for number of cobs per plot, L_5 x T_3 for number of cobs per plot, yield per plot, single cob weight, cob girth, number of rows per cob and number of kernels per row, L_9 x T_1 for single cob weight and cob length and L_9 x T_5 for yield per plot. These hybrids with higher effects are useful for deriving high performing inbreds.

5.3. Variability, Heritability and Genetic advance

Success of any plant breeding programme largely depends upon the knowledge of genetic variability present in a given crop species for the character under improvement. The genotypic coefficient of variation measures the range of variability available in a crop and also enables to compare the amount of variability available in

a crop and also enables to compare the amount of variability present in different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence the total variance needs to be partitioned into heritable and non-heritable components to assess the inheritance pattern of the particular character under study.

Heritability indicates the relative degree at which a character is transmitted from parent to offspring. High heritability values indicate that the character under study is less influenced by environment in their expression and such characters could be improved by adopting simple selection methods. Further, the information on genetic variation, heritability and genetic advance helps predict the genetic gain that could be obtained in later generations, if selection is exercised for improving the particular trait under study. A relative comparison of heritability values and expected genetic advance expressed as percent of means gives an idea about the nature of gene action governing a particular character.

Yield per plot recorded high genotypic and phenotypic coefficients of variation with moderate heritability and genetic advance as percent of mean indicating presence of additive gene action in controlling the expression of this trait. Hence response to selection would be expected in improvement of this character.

Low genotypic and phenotypic coefficients of variation, moderate heritability with low genetic advance as percent of mean for days to 50 percent pollenshed and days to 50 percent silking indicates the preponderance of non additive gene action in controlling these traits. Selection and intermating the selected plants will improve these traits. Other characters recorded moderate to high genotypic and phenotypic coefficients of variation, moderate to high genetic advance as percent of mean indicating presence of additive gene action and simple selection is effective in improving them.

5.4. Heterosis

The subject of heterosis has continued to be of prime importance to the plant breeder in general and the maize breeder in particular, even after nine decades of its reveal by Shull (1908). Heterosis exploitation has become an accepted component of hybrid maize breeding, as seen by the role of hybrid cultivars in revolutionizing maize productivity over the past five decades. By the cobly 80’s, majority of maize growing

area in USA was under single cross hybrid cultivation (Hallauer and Miranda, 1988). The magnitude and extent of heterosis in desired direction is of paramount importance in deciding as to whether or not heterosis is practically and economically feasible.

In the present investigation, heterosis over mid parent and better parents were worked out for all the characters. The results obtained have been discussed below:

The results obtained in present investigation were very encouraging and tremendous increase in yield has been recorded in all the crosses. The results obtained with regard to grain yield have proved the validity of the fact that inbreds derived from the geographically and genetically diverse maize populations but improved through half sib and full sib method of selection for few cycles, when crossed, would provide substantial heterosis to surpass the yield level of the best heterotic released hybrids under cultivation.

Majority of the hybrids expressed more than 100 percent better parent heterosis with one hybrid L_9 X T_5 expressing more than 300 percent better parent heterosis for grain yield. The crosses L_4 X T_3, L_5 X T_3, L_7 X T_3, L_8 X T_3 and L_9 X T_3 showed high positive heterosis for yield and yield components. This indicates high heterosis for grain yield had contribution from high heterosis of yield attributes. High and significant heterosis for grain yield accompanied by significant heterosis for one or more yield components was earlier reported by several workers (Rameeh *et al.* 2000; Kalla *et al.* 2001; Tollenar & Lee 2002).

All crosses recorded negative heterosis for days to 50 percent pollenshed and days to 50 percent silking indicating early maturity of crosses. The highest negative better parent heterosis for days to 50 percent silking was observed in L_5 X T_4 (-12.44) followed by L_8 X T_3 (-12.30). Similar results were obtained by Dubey *et al.* (2001). L_8 X T_3 (-11.11) followed by L_8 X T_4 (-8.27) exhibited highest negative mid parent heterosis. The hybrids L_3 X T_4 followed by L_8 X T_3 exhibited high better parent heterosis indicating operation of negative over dominance for days to 50 percent flowering. Under Indian conditions early maturing hybrids are of prime importance and hence negative heterosis for this trait is desirable. Existence of negative heterosis for days to 50 percent pollenshed and silking, resulting in the reduction in days to 50 percent silking for few days has been reported by Crossa *et al.* (1990) and Choudhary & Choudhary (2002).

The mid parent heterosis was positive and significant in 23 crosses for plant height and 41 crosses for cob placement. This indicated the superiority of hybrids over its mid parent value.

5.5. Correlation and Path analysis

Knowledge of character association provides better understanding of the contribution of yield components and other characters towards yield and a positive correlation between desirable characters is favourable to plant breeder because it helps in simultaneous improvement of both the characters. A highly correlated character with high heritability is chosen to make selection more effective through indirect selection (Simmonds, 1979). However, simple correlation does not give the direct and indirect effects of characters on yield. The path coefficient analysis is a useful method of estimating direct and indirect contribution of an attribute towards yield (Dewey & Lu, 1959).

Correlation coefficients among the 12 characters are presented and described in the preceding chapter (Table-24). Yield per plot was positively correlated with plant height, number of cobs per plot, cob placement, single cob weight, cob length, cob girth, number of rows per cob, number of kernels per row and 100 seed weight and negatively correlated with days to 50 percent pollenshed and days to 50 percent silking. Strong positive correlation among yield and yield components was earlier reported by Kalla *et al.*(2001).

According to Tollenar and Lee (2002) most of the yield components had positive correlation among themselves, this means that improvement in any yield component would result in improvement in yield. The correlation coefficients of days to 50 percent pollenshed and silking were negative with yield and yield components implying selection for earliness leads to selection for lower yield.

In general the genotypic correlations were higher in magnitude than phenotypic correlations. This indicates that there is strong inherent association between the most of the characters studied, but its expression, was lessened due to influence of environment, for which reason phenotypic correlations were lower in magnitude.

The path analysis at genotypic and phenotypic levels (Table-25) revealed that number of cobs per plot had highest positive direct effect on yield and correlation

coefficient of number of cobs per plot was highly significant and positive. It can be noted that indirect effects of other yield components *via* number of cobs per plot were high on yield per plot, meaning number of cobs per plot is the most important trait among yield components. The direct effects of days to 50 percent silking was positive but low and days to 50 percent pollenshed was negative and low, the correlation of these with yield was negative because of the fact that indirect effect of these traits *via* number of cobs per plot was high. Therefore they are *per se* not responsible for negative correlation with yield. If negative correlation between flowering traits and grain yield are broken it is possible to have genotype with early maturity and high yield (Ribaut *et al.* 1996). The recent success in Basmati indicates that unholy linkage between yield and maturity can be broken. Also the success story of green revolution was based on breaking linkage between tall stature and small panicle.

5.6. Prominent and potential genotypes identified on the basis of present study:

5.6.1. Resistance to banded leaf and sheath blight:

- Multilocation screening revealed that Pop145 (MBL-29) and Suwan-1 (MBL-30) showed high degree of tolerance to BLSB.
- Segregants from F_2 s of crosses DMB-9 X DMB-27 (L_2 X T_2) and CM-151 X DMB-24 exhibited lowest mean scores of 2.4 which can be used in deriving resistant lines.
- Similarly F_2 families of DMB-22 X DMB-27, CM-151 X DMB-27 and CM-150 X DMB-25 had more than 50% individual plants with a score of 2.0, which can be specifically targeted to obtain segregants with resistance to BLSB

5.6.2. L X T analysis

- All the lines and testers were found to have significant GCA effects for one or the other traits under study.
- Therefore these parents could be used for production of synthetics or composites as they possess high additive gene effects.
- L_2XT_1, L_2XT_2, L_3XT_3, L_5XT_3, L_9XT_1 and L_9XT_5 were found to have very high SCA status for yield and yield components.

Cross	No. of cobs per plot	Cob place-ment (cm)	Yield/ plot (kg)	Single cob wt. (kg)	Cob length (cm)	Cob girth (cm)	No. of rows per cob	No. of kernels per row	100-seed weight (gm)	No. of seeds per cob	Hetero-sis for Yield /plot	BLSB score
L_2XT_2	15.67	110.00	2.433	0.127	16.13	3.43	15.20	31.67	24.33	481.38	135.48**	3.0
L_5XT_3	17.33	98.33	2.733	0.147	17.64	3.37	14.93	38.00	22.33	567.34	310.00**	3.0
L_9XT_5	16.00	116.67	3.000	0.106	16.71	3.08	13.20	29.80	25.33	393.36	328.57**	3.5

- The crosses L_4XT_3, L_5XT_3, L_7XT_3, L_8XT_3, L_9XT_3 and L_9XT_5 were found to heterotic for yield and yield components and these may be evaluated under multilocations to identify potential single cross hybrids.

5.6.3. Comparison among the superior crosses

- The above three crosses can be specifically forwarded to multilocation trails for identifying high yielding and BLSB resistant hybrids in the northern belt of the country, where the disease is endemic.

5.7. Future line of work

The following suggestions are made to efficiently exploit the material developed in this programme:

- Utilization of resistant genotypes in molecular breeding programme
- Advancement of the identified crosses under multilocation trails
- Phytotron studies to verify and replicate the artificial screening technique.
- Refinement in techniques of isolation of pathogen to facilitate race specific inheritance studies.