SYNOPSIS OF POST GRADUATE RESEARCH PROBLEM
ON
“LINE x TESTER ANALYSIS IN RIDGE GOURD
(Luffa acutangula (Roxb.) L.)”

UNDER THE GUIDANCE OF
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SYNOPSIS OF P.G. RESEARCH PROBLEM

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7. Title of research problem : “Line x Tester Analysis in Ridge gourd
   (Luffa acutangula (Roxb.) L.).”

8. Introduction:

   Ridge gourd (Luffa acutangula (Roxb.) L.) belongs to the family Cucurbitaceae which includes about 118 genera and 825 species. Ridge gourd or angled gourd is cultivated in all tropical regions of the world. In India, it is grown as summer and kharif season crop in well drained sandy loam soil with a pH range of 6.5-7.5. The somatic chromosome number of ridge gourd is 2n=2x=26. It is a monoecious and cross pollinated annual crop characterized by long vines having branched tendrils. The leaves are glabrous, five to seven lobed while the flowers are yellow coloured, having corolla of five petals. The staminate flowers grow in raceme while pistillate flowers are solitary. The anthers are free and five in number, pistil has three bilobate stigma and ovary with three placentae and many ovules. The fruit is large oblong pepo and ribbed. The dry fruit consists of a hard shell surrounding a stiff, dense network of cellulose fibers. The seeds are generally black and may have either smooth or pitted surface. The immature tender fruits are used as a cooked vegetable. These soft fruits are easily digestible and appetizing and therefore prescribed for malaria and other seasonal fevers.
Nutritively, ridge gourd contains 95.4% water, 3.7% carbohydrates, 0.5% protein, 0.1% minerals, 0.4% calcium, traces of iron, vitamin B and vitamin C. It also contains a gelatinous compound called luffein. The genus derives its name from loofah, fibre of mature dry fruit which is used as bathing sponge, scrubber pad, doormat, in mattresses and also as an insulator.

In India, vegetables occupy an important place in diversification of agriculture and play a vital role in food and nutritional security of ever growing population of our country. India is the second largest producer of vegetables in the world. In Ridge gourd covers a total area of 1737.16 hectare with an annual production of 21310.46 million tonnes and productivity of 1226 kg/ha. In Gujarat, the crop covers a total area of 181.57 hectare with an annual production of 2899.67 million tonnes and productivity is 1596 kg/ha. (Anon., 2014).

9. Practical utility of research problem :-

Ridge gourd is grown extensively and exhibits a wide range of variability in fruit and vegetable characters. It is a cross pollinated crop and thus exhibits considerable heterozygosity in population and does not suffer from inbreeding depression. The natural variability in ridge gourd provides ample scope for exploitation of hybrid vigour. However, the same has not been assessed and utilized. The hybrid vigour remains unexploited and nationwide released hybrids from public sector or institutions are not available. Even now, local strains of ridge gourd are commercially grown by farmers which result into very low yield. Poor performance of local varieties is due to genetic impurities.

Exploitation of hybrid vigour has been recognized as an important tool for making genetic improvement of yield and its attributing characters in ridge gourd by earlier workers. Therefore, preliminary evaluation of the genetic stock available for use in hybridization programme is important to identify heterotic hybrids and to select elite parents. These may then be utilized to build up population with favourable fixable genes for effective crop yield and quality improvement.

For successful breeding programme genetic information on variability, combining ability, gene action and extent of heterosis is of paramount importance. Line x Tester analysis is one of the appropriate methods in preliminary screening of breeding material and to obtain the above data. It helps the breeder in critical choice of parents to be incorporated in breeding programme. Therefore, the present investigation was under taken with seven genotypes used as lines and crossed with three common testers as per the Line x
Tester method of Kempthorne (1957). This would allow the comparison of the performance of the crosses, evaluate heterosis as well as select best combiner parental lines for future breeding programmes to help bridge the gap between production and productivity in this crop.

10. Objectives:

Keeping in view all the above aspects, the present study on ridge gourd will be undertaken with the following objectives.
1. To estimate the general and specific combining ability effects for yield and its related characters.
2. To study the nature and magnitude of heterosis for fruit yield and its component traits.
3. To estimate the nature and magnitude of gene action involved in the inheritance of fruit yield and its component traits.
4. To identify superior cross combinations and parents for future use.

11. Review of literature:

A brief review related to the following sub-heads is presented here.

(1) Heterosis in ridge gourd
(2) Combining ability and gene action

11.1. Heterosis:

Prabhakar (2008) studied heterosis in 18 ridge gourd hybrids derived by crossing six lines and three testers. The crosses Pusa Nasdar x LA-12, Pusa Nasdar x LA-17 recorded the maximum standard heterosis of more than 23% over the high fruit yielding commercial hybrid Surekha.

Karmakar et al. (2014) studied heterosis in ridge gourd (Luffa acutangula (Roxb.) L.) using seven parental lines including two hermaphrodite lines and 21 F1 hybrids of ridge gourd obtained from half diallel mating design to investigate the extent of heterosis for yield and its contributing characters during spring, summer and rainy season for two years. The top three performing parents, viz. P1 (DRG-2), P2 (Pusa Nasdar) and P7 (Satputia Small) were observed for total yield per plant. Appreciable heterosis was observed over better parent and top parent for all the characters studied. In order of merit, P1 x P7, P1 x P6 and P2 x P7 were found to be best heterotic combinations as they exhibited significant heterosis percentage for yield per plant over the top parent. The high yielding F1 hybrids
P1 x P7 (DRG-2 x Satputia Small), P1 x P6 (DRG-2 x Satputia Long) and P2 x P7 (Pusa Nasdar x Satputia Small) were found early in maturity, had high number of fruits per plant and showed 91.36 %, 84.84 % and 73.11% heterosis for yield over top parent and may be recommended for commercial exploitation.

Naransannavar et al. (2014 a) carried out an experiment on heterosis in ridge gourd with 51 crosses and 20 parents from L x T design. They evaluated heterosis for growth, earliness, yield and quality parameters. Maximum standard heterosis for vine length (9.20%) was observed in KRG-7 x ASM, for number of leaves in KRG-11 x PN (172.12%), for number of branches in KRG-11 x PN (141.38%), for days to first male flower appearance in KRG-3 x PN (-19.48%), for node to first female flower appearance in KRG-9 x ASJ (-56.92%), for node to first female flower appearance in KRG-2 x ASM (-19.35%), for sex ratio in KRG-17 x PN (-40.34%), for per cent fruit set in KRG-16 x PN (36.45%), for number of fruits per vine in KRG-10 x PN (13.95%), for average fruit weight in KRG-6 x ASJ (36.34%), for fruit length in KRG-1 x ASJ (36.91%), for fruit diameter in KRG-12 x PN (55.09%), for fruit yield per plot in KRG-3 x ASM (26.53%), for fruit yield per hectare in KRG-3 x AS (26.46%), for rind thickness in KRG-12 x PN (8.07%), for flesh thickness in KRG-12 x PN (70.27%), for number of seeds per fruit in KRG-16 x ASM (238.80%) and for seed yield per fruit in KRG-4xASM (201.11%). The four best performing F1 hybrids viz., the cross KRG-3 x ASJ (23.61%) followed by KRG-3 x PN (13.80%), KRG-10 x PN (12.45%) and KRG-11 x PN (6.00%) exhibited the highest standard heterosis for total yield per vine in order of merit. The higher yield recorded by these hybrids could be due to increased per cent fruit set and number of fruits per plant.

Poshiya et al. (2015) studied heterosis in ridge gourd for fruit yield and its attributes through 8 x 8 diallel mating design. The magnitude of heterotic effects was high for fruit yield per vine (kg) and number of fruits per vine. No heterosis was observed for fruit yield per vine and some of its component traits were recorded in the crosses Pusa Nasdar x JRG-05-6, Pusa Nasdar x JRG-05-4, JRG-05-4 x ARGS-05-31, Pusa Nasdar x Jaipur Long and JRG-05-4 x ARGS-07-41. Such crosses could be exploited for practical plant breeding programme in ridge gourd.

11.2. Combining ability and Gene action:

Mehta et al. (2005) carried out a study with 8 parents of ridge gourd in a diallel mating design in ridge gourd. The study revealed over dominance effects for most of the characters viz., number of primary branches per vine, length of vine, internodal length, fruit
length, fruit diameter, number of fruits per vine, average fruit weight, fruit yield per vine, partial dominance for days to first picking and complete dominance for days to last picking. The dominance component of genetic variance was higher than that of additive for all the traits except days to first picking. The presence of over dominance for all the traits (except days to first and last picking) suggested that heterosis breeding is worthwhile to get higher gain in ridge gourd.

Prabhakar (2008) estimated nature of gene action in 18 ridge gourd hybrids derived by crossing six lines and three testers during summer 2000 and 2001. The genotypic differences were significant for all the characters. The L x T sum of squares were significant for fruit yield per plant indicating predominant role of non-additive gene action for fruit yield and most of its components. The parental lines Pusa Nasdar, Jaipur long and LA-17 were good general combiners for fruit yield and contributed maximum favorable genes. The cross combinations Jaipur long x LA-97, Pusa Nasdar x LA-12 were best specific crosses for both the seasons. In Jaipur long x LA-97, both the parents were poor combiners therefore, this cross can be used for heterosis breeding. In the cross Pusa Nasdar x LA-12 both the parents were good combiners and governed by additive gene action which is fixable in nature.

Lodam et al. (2009) studied combining ability in ridge gourd using eight parental lines crossed in diallel fashion excluding reciprocals during summer, 2008. The mean sum of squares due to gca and sca were highly significant for all the characters, indicating the importance of both additive and non-additive genetic components for traits under study. None of these parents showed good gca effect for all the characters. Parent ARG5-98-06 and ARG5 03 – 18 showed high gca effect for important characters, high per se performance for fruit yield and yield component characters. The crosses viz., ARG5 98 – 06 x ARG5 00 – 03, ARG5 04 – 23 x ARG5 00 -03 and ARG5 02 – 14 x ARG5 03 – 18 which recorded significant sca effects for fruit yield, resulted from good x average, average x average and average x good combiners, respectively. This indicated the inconsistent expression of sca effects in specific crosses irrespective of gca effects of the parents.

Deshpande (2010) carried out genetic studies in ridge gourd using line x tester analysis and observed that contribution of lines towards gca variance were higher than testers for all characters except days to appearance of first female flower, fruit girth and acidity. She found existence of both additive and non-additive gene action with prominent role of non- additive gene action. Parents ARG5-00-03, JRG-05-4, ARS-05-31 and ARS-06-33 were found to be good general combiners for fruit yield per plant. Hybrid
ARGS-00-03 x RGM-6 was the best specific combiner for fruit yield per plant. This cross also exhibited significant sca effects in desirable direction for first male flowering node, number of primary branches per plant, fruits per plant, fruit length, fruit girth, fruit weight and acidity.

Tyagi et al. (2010) studied combining ability in 45 ridge gourd hybrids derived from a 10 x 10 diallel mating design. Additive and non-additive genes were found to be important for all the traits. Additive gene effects were more important for vine length, days to opening of the first male flower, number of male and female flowers/plant, number of nodes, number of fruits/plant, fruit length, fruit diameter, and number of seeds/fruit. Slumber Long was the best general combiner, among ten parental lines, for fruit yield/plant and fruit size.

Poshiya (2011) performed combining ability analysis in a set of 8 x 8 diallel fashion in ridge gourd. The study revealed that the general and specific combining ability variances were highly significant for all the characters. This indicated that both additive and non-additive type of gene effects played a vital role in the inheritance of all these traits. The estimates of gca effects indicated that parents Pusa Nasdar, Jaipur Long, JRG-05-4, JRG-05-6 and ARGS-05-31 were found to be the good general combiners for fruit yield per vine and some of its component traits. The parents ARGS-05-31 and ARGS-07-41 were found to be good specific combiner for earliness and fruit fly infestation. The cross HARG-109 x HARG-110 had high sca effects for fruit yield per vine due to poor x poor general combiner parents. The crosses displaying high sca effects did not always involve parents with high gca effects.

Dodiya et. al (2013) studied heterosis and combining ability for fruit yield and yield components in ridge gourd (Luffa acutangula (Roxb.) L.) through Line x Tester (ten x five) mating design (excluding reciprocal). The highest, positive and significant standard heterosis for fruit yield per vine and some of its traits were recorded in the crosses viz., ARGS-07-45 x Jaipur Long, ARGS-07-45 x Swarna Manjari, ARGS-07-45 x Pusa Nasdar and ARGS-09-59 x GARG-1. Such crosses could be exploited for practical heterosis plant breeding programme in ridge gourd. Parents Swarna Manjari, Jaipur Long, ARGS-07-45 and ARGS-09-59 were found to be the good general combiners for fruit yield and some of the yield contributing characters. The four cross combinations viz., JRG-05-6 x GARG-1, ARGS-09-59 x GARG-1, ARGS-07-46 x Swarna Uphar and ARGS-07-46 x Pusa Nasdar were found to be good specific cross combinations for fruit yield per vine and would be exploited for heterosis breeding in ridge gourd.
Karmakar et al. (2013) conducted an experiment with the objective to evaluate the breeding potential of hermaphrodite lines and to suggest suitable breeding approaches following half-diallel mating design for genetic improvement of antioxidant content and activity in ridge gourd (*Luffa acutangula* (Roxb) L.) fruits. Twenty-eight genotypes, including seven parental lines and 21 crosses, were grown in randomized block design with three replications for fruit sample collection. The highly significant mean squares due to parents, hybrids and parents versus hybrids; and gca and sca for yield and antioxidants (ascorbic acid, total carotenoids, total phenolics, DPPH-RSA, ABTS-RSA and CUPRAC assay) indicate the existence of abundant genetic variation. The *per se* performance and combining ability of hermaphrodite parents (Satputia Long and Satputia Small) and hybrids of monoecious x hermaphrodite cross were found to be superior for antioxidants along with yield potential. The cross combinations with superior *per se* performance coupled with high SCA estimates and having at least one hermaphrodite parent would be useful for concentrating desirable alleles to improve the antioxidants and yield simultaneously. Thus, hermaphrodite lines in combination with monoecious counterpart have enormous potential to breed genotypes for higher antioxidants without compromising yield in ridge gourd.

Narasannavar et al. (2014 b) studied gene action and combining ability for yield and yield related traits in ridge gourd. Fifty-one cross combinations obtained from L x T mating design were evaluated for 15 traits. The variance due to SCA was higher than the GCA for all the characters, indicating the importance of non-additive gene action. Comprehensive assessment of parents considering the gca effects of 15 characters studied identified lines KRG-2, KRG-3, KRG-4, KRG-11, KRG-16 and tester ASM as good combiners while PN as average combiners for all characters. Maximum and positively significant sca effects was observed in the cross KRG-9 x ASJ (0.24) followed by KRG-10 x PN (0.22), KRG-6 x ASM (0.16), KRG-5 x ASM (0.15) and KRG-3 x ASJ (0.14) for fruit yield per vine as well as fruit yield per plot and fruit yield per hectare. KRG-9 x ASJ showed significant sca effects for earliness characters like days to first female flower appearance (-6.19), node to first female flower appearance (-5.31) and days to first harvest (-8.61).
12. Material and Methods:

12.1 Experimental details:

<table>
<thead>
<tr>
<th>Location</th>
<th>a. Crossing Programme</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Vegetable Research Station</td>
</tr>
<tr>
<td></td>
<td>Junagadh Agricultural University,</td>
</tr>
<tr>
<td></td>
<td>Junagadh.</td>
</tr>
<tr>
<td>b. Evaluation</td>
<td>Instructional Farm,</td>
</tr>
<tr>
<td></td>
<td>Junagadh Agricultural University,</td>
</tr>
<tr>
<td></td>
<td>Junagadh.</td>
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</table>

<table>
<thead>
<tr>
<th>Year and season of experiment</th>
<th>a. For development of crosses <em>kharif</em>, 2015</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>b. For evaluation of experimental material summer, 2016</td>
</tr>
</tbody>
</table>

| Experimenal design          | Randomized Block Design (RBD)                                 |

<table>
<thead>
<tr>
<th>Number of Genotypes</th>
<th>32 (Thirty two) = (21 Hybrids + 10 Parents+ 1 Check variety- GJRGH-1)</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Number of Replications</th>
<th>3 (Three)</th>
</tr>
</thead>
</table>

| Spacing                      | 200 x 100 cm                                                    |

12.2 Name of Genotypes:-

**Testers:-**

- P1 = Arka Sujat (T1)
- P2 = Pusa Nasdar (T2)
- P3 = Jaipur Long (T3)

**Lines :-**

- P4 = JRG – 13-01 (L1)
- P5 = JRG - 13-02 (L2)
- P6 = JRG - 13- 03 (L3)
- P7 = JRG - 13- 04 (L4)
P8 = JRG - 13-05 (L5)
P9 = JRG - 13-06 (L6)
P10 = JRG - 13-07 (L7)

Check variety :-
GJRGH-1

12.3 Observations to be recorded:-

Five single plants will be randomly tagged for recording the observations on various morphological and yield traits before initiation of flowering. Observations will be recorded for parents and hybrids in each replication from the randomly selected plants in each plot for all the characters except for days to 50% flowering which will be recorded on the whole plot basis. Average value of the observations will be used for the statistical analysis.

The details of the procedure to be followed for recording data for various characters are described below:

i. Days to 50 % flowering:-
The number of days taken from the date of sowing to the date of anthesis of main umbel in 50 % plants in a plot will be recorded.

ii. Days to opening of first female flower:
The days required for opening of first female flower from the date of sowing will be counted.

iii. Days to opening of first male flower:
The days required for opening of first male flower will be counted from the date of sowing.

iv. Node number of first female flower:
The node number on which first female flower appears on the main shoot will be counted from the base of stem.

v. Node number of first male flower:
The node number on which first male flower appears on the main shoot will be counted from the base of stem.

vi. Days to first picking:
The number of days required for first picking of green tender, marketable fruits will be counted from the date of sowing.
vii. **Length of main vine (m):**
The length of main vine will be measured in meter with the help of measuring tape from the base of the vine to the growing tip of main stem at the final harvest.

viii. **Number of primary branches per vine:**
The number of primary branches on main stem will be counted at final harvest.

ix. **Number of fruits per vine:**
The number of fruits from all pickings, harvested from the five randomly selected plants, will be counted and averaged.

x. **Fruit weight (g):**
Ten fruits from five randomly tagged plants will be selected during peak period of harvesting for recording fruit weight in grams.

xi. **Length of fruit (cm):**
The length of the ten selected tender edible fruits will be recorded in centimeter from peduncle end to the blossom end of the fruit.

xii. **Girth of fruit (cm):**
The girth of the ten selected tender edible fruits will be recorded in centimeter by measuring at the mid-portion of the fruit with the help of the measuring tape.

xiii. **Rind thickness: (mm)**
The rind thickness of the ten selected tender edible fruits will be recorded in millimeter.

xiv. **Flesh thickness: (mm)**
The flesh thickness of the ten selected tender edible fruits will be recorded in millimeter.

xv. **Fruit yield per vine (kg):**
The weight of harvested fruits of all pickings from each randomly selected plant will be summed up after the last picking and the average fruit yield per vine will be calculated in kilogram.

xvi. **No. of seeds per fruit:**
In each plot, five randomly selected fruits will be allowed to mature on the untagged plants. The ripened fruits will be harvested and seeds will be collected individually from the five fruits.

xvii. **100-seed weight (g):**
Hundred seeds will be collected and weighed on an electrical balance to obtain the test weight in grams.

13. **Statistical Analysis:**

The mean values of parents and hybrids for all the characters will be subjected to statistical analysis on following aspects.

15.1 Analysis of Variance for experimental design

15.2 Heterosis

15.3 Combining ability

13.1 **Analysis of variance for experimental design:**

ANOVA will be performed to test the significance of difference among genotypes for all the characters following fixed effect model as suggested by Panse and Sukhatme (1985).

\[ Y_{ij} = \mu + g_i + r_j + e_{ij} \]

\[ i = 1,2,\ldots, g \]

\[ j = 1,2,\ldots, r \]

Where,

- \( Y_{ij} \) = Value of \( i^{th} \) genotype in \( j^{th} \) replication
- \( \mu \) = Population mean
- \( g_i \) = An effect of \( i^{th} \) genotype
- \( r_j \) = An effect of \( j^{th} \) replication
- \( e_{ij} \) = Uncontrolled variation associated with \( i^{th} \) genotype and \( j^{th} \) replication

**Analysis of variance : breakup of variance components**

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>d.f.</th>
<th>M.S.</th>
<th>E.M.S.</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>(r-1)</td>
<td>( M_1 )</td>
<td>( \sigma_e^2 + g\sigma_r^2 )</td>
<td>( M_1/M_6 )</td>
</tr>
<tr>
<td>Genotypes</td>
<td>(g-1)</td>
<td>( M_2 )</td>
<td>( \sigma_e^2 + r\sigma_g^2 )</td>
<td>( M_2/M_6 )</td>
</tr>
<tr>
<td>Parents</td>
<td>(p-1)</td>
<td>( M_3 )</td>
<td>( \sigma_e^2 + p\sigma_p^2 )</td>
<td>( M_3/M_6 )</td>
</tr>
<tr>
<td>Hybrids</td>
<td>(h-1)</td>
<td>( M_4 )</td>
<td>( \sigma_e^2 + h\sigma_h^2 )</td>
<td>( M_4/M_6 )</td>
</tr>
<tr>
<td>Parents Vs. hybrids</td>
<td>1</td>
<td>( M_5 )</td>
<td>( \sigma_e^2 + ph\sigma_{ph} )</td>
<td>( M_5/M_6 )</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1)(g-1)</td>
<td>( M_6 )</td>
<td>( \sigma_e^2 )</td>
<td></td>
</tr>
</tbody>
</table>
13.2. Heterosis:

a. Heterobeltiosis

It will be calculated as the deviation of $F_1$ from the better parent (Fonseca and Patterson, 1968) and expressed on per cent basis by the following formula:

\[
\text{Heterosis over better parent (Heterobeltiosis)} = \frac{F_1 - BP}{BP} \times 100
\]

b. Standard Heterosis

It will be calculated as the deviation of $F_1$ from the standard check variety (GJRGH-1) and expressed on percent basis by the following formula:

\[
\text{Heterosis over standard check (Standard Heterosis)} = \frac{F_1 - SC}{SC} \times 100
\]

c. Relative Heterosis

Heterosis over mid-parent (Relative heterosis) = \[
\frac{F_1 - MP}{MP} \times 100
\]

Where,

$\overline{F_1} = \text{Mean of the hybrid}$

$\overline{MP} = \text{Mean of the parents involved in the crosses or mid-parent value.}$

$\overline{BP} = \text{Mean of the better parent in the particular cross value.}$

$\overline{SC} = \text{Mean of the standard check in the particular cross value.}$

13.3. Combining ability analysis:-

Analysis of variance for combining ability was computed according to the model given by Kempthorne (1957) which is related to design-II of Comstock and Robinson (1952) in terms of covariance of half-sibs (H.S.) and full-sibs (F.S.).

\[
Y_{ijk} = \mu + G_i + G_j + S_{ij} + r_k + \epsilon_{ijk}
\]

Where,

$Y_{ijk} = \text{Phenotypic expression of } ij^{th} \text{ genotypes in } k^{th} \text{ replication}$

$\mu = \text{General mean}$

$G_i = \text{General combining ability of } i^{th} \text{ female parent (line)}$

$G_j = \text{General combining ability of } j^{th} \text{ male parent (tester)}$

$S_{ij} = \text{Specific combining ability of cross between } i^{th} \text{ line and } j^{th} \text{ tester}$
\[ r_k = \text{The } k^{\text{th}} \text{ replication effect} \]
\[ \epsilon_{ijk} = \text{Random error associated with } ij^{\text{th}} \text{ genotype and } k^{\text{th}} \text{ replication} \]

13.3.1 General combining ability effects of lines
\[ \hat{g}_i = (Y_{i...}/ltr) \]

13.3.2 General combining ability effects of testers
\[ \hat{g}_j = (Y_{.j.}/lr) - (Y_{...}/ltr) \]

13.3.3 Specific combining ability effects of crosses
\[ S_{ij} = (Y_{ij.}/r) - (Y_{i.}/tr) - (Y_{.j.}/lr) + (Y_{...}/ltr) \]
14. REFERENCES:


