

**M.S. Swaminathan School of Agriculture
Centurion University of Technology and Management,
Paralakhemundi, Odisha
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**Assignment of M.Sc. Agriculture Department of
Genetics & Plant breeding and Seed Science &
Technology**

Student Name:-----*S. Teja Dugga*-----

Registration Number:-----*20805210002*-----

Course Title:-----*Principles of Quantitative Genetics*-----

Course Code:-----*MACP 1204*-----

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**Practical Record of M.Sc. Agriculture
Department of Genetics & Plant breeding and Seed
Science & Technology**

Student Name:-----S. Teja Durga
Registration Number:-----21080511002
Course Title:-----Principles of Quantitative Genetics
Course Code:-----MAGP1204 (2+1)

**Department of Genetics & Plant breeding
and Seed Science & Technology
M.S. Swaminathan School of Agriculture
Centurion University of Technology and Management,
Paralakhemundi, Odisha**

Certificate

Certified that this is a bonafide record of practical work done by Mr./
Ms. S. Teja Durga Regd.
No. 210805210002 M.Sc. Ag. (Genetics & Plant breeding)
Degree programme, Course No. MAGP 1204
entitled Principle of Quantitative of 2nd semester of the academic
year 2020-21. Genetics

Date:

14/7/22
Faculty In-charge

Internal Evaluation

Course Title: Principle of Quantitative Genetics
Course No.: MAGP 1204

| Sl. No. | Marks distribution | Total marks | Marks obtained |
|---------|--|-------------|----------------|
| 1 | Record | 5.0 | 5.0 |
| 2 | Attendance | 5.0 | 4.0 |
| 3 | Field Crop / Assignment, Continuous evaluation | 10.0 | 10.0 |
| 4 | Viva voce | 5.0 | 5.0 |
| Total | | 25.0 | 24.0 |

14/7/22
Signature of Faculty In-charge

List of Experiments

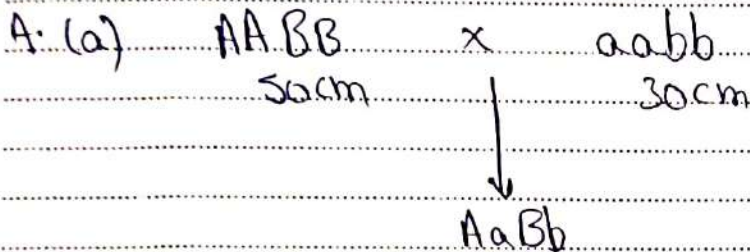
| Exp. No. | Date of Exp. | Date of Submission | Title | Page No. | Signature | Remarks |
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| 1. | 2-4-22 | 21-4-22 | problems on multiple factor inheritance | 1-4 | Atul 21/4/22 | 8/5 |
| 2. | 21-4-22 | 28-4-22 | partitioning of variance - Estimation of heritability & genetic advance analysis | 5-9 | Atul 28/4/22 | 8/5 |
| 3. | 28-4-22 | 5-5-22 | Multigraph analysis, D analysis - grouping of clusters & interpretation cluster analysis - construction of cluster diagrams & dendrogram - interpretation | 10-16 | Atul 6/5/22 | 8/5 |
| 4. | 5-5-22 | 12-5-22 | Correlation analysis & path analysis - parent progeny regression analysis | 17-31 | Atul 14/5/22 | 8/5 |
| 5. | 19-5-22 | 19-5-22 | Diallel analysis - Griffings method I & interpretation of results | 32-37 | Atul 21/5/22 | 8/5 |
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| 9. | 26-5-22 | 2-6-22 | Line tester analysis & interpretation of results | 55-61 | Atul 4/6/22 | 8/5 |
| 10 | 2-6-22 | 9-6-22 | Estimation of heterosis & inbreeding depression | 62-68 | Atul 11/6/22 | 8/5 |
| 11 | 16-6-22 | 23-6-22 | G x E interaction & stability analysis using Eberhart & Russell Model | 69-79 | Atul 21/6/22 | 8/5 |
| 12 | 23-6-22 | 30-6-22 | Biparental mating, RCI & their interpretations | 80-82 | Atul 3/7/22 | 8/5 |

List of Experiments

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| 1 ³ | 23-6-22 | 30-6-22 | Biparental mating, NCD-II & their interpretations | 83-85 | Aradhya 11/7/22 | 5/5 |
| 1 ² | 23-6-22 | 30-6-22 | Biparental mating NCD-III & their interpretations | 86-88 | Aradhya 11/7/22 | 5/5 |
| 1 ³ | 7-7-22 | 8-7-22 | QTL mapping - strategies for QTL mapping, methods, marker linkage studies & software | 89-92 | Aradhya 14/7/22 | 5/5 |
| 4. | | | | | | |
| 5. | | | | | | |
| 6. | | | | | | |
| 7. | | | | | | |
| 8. | | | | | | |
| 9. | | | | | | |
| 10 | | | | | | |
| 11 | | | | | | |
| 12 | | | | | | |

Assume that two pairs of genes of 2 allele which determine plant height additively in a population. The homozygotes $AABB$ and $aabb$ have 50cm and 30cm height respectively.

- What is the height of F_1 ?
- After one generation of selfing which genotypes of F_2 plant height 40cm?
- What will the F_2 frequency of these 40cm plants?

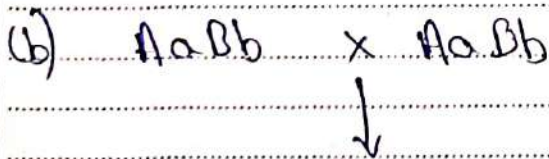


No. of dominant alleles = 2

$50 - 30 = 20$ cm height controlled by 4 alleles

Contribution of each contributing allele = $20 / 4 = 5$ cm

\therefore The ~~pl~~ height of F_1 plant will be = $30 + (2 \times 5) = 40$ cm



| $ \sigma $ | $ \text{AB} $ | $ \text{aB} $ | $ \text{Ab} $ | $ \text{ab} $ |
|---------------|---------------|---------------|---------------|---------------|
| $ \text{AB} $ | $ AABB $ | $ AaBB $ | $ AABb $ | $ AaBb $ |
| $ \text{aB} $ | $ AaBB $ | $ aaBB $ | $ AaBb $ | $ aaBb $ |
| $ \text{Ab} $ | $ AABb $ | $ AaBb $ | $ AAbb $ | $ Aabb $ |
| $ \text{ab} $ | $ AaBb $ | $ aaBb $ | $ Aabb $ | $ aabb $ |

To get 40cm height in F_2 generation, there must be contributing 2 alleles. So the genotypes having 2 contributing alleles are $AaBb$, $AABb$, and $aaBb$. These 3 genotypes show 40cm ht in F_2 generation.

(c) The F_2 frequency

- i) 4 dominant allele = 50cm
- ii) 3 dominant allele = 45cm
- iii) 2 dominant allele = 40cm
- iv) 1 dominant allele = 35cm
- v) 4 recessive allele = 30cm

| | | | | | | | | |
|------|---|------|---|------|---|------|---|------|
| 1 | : | 4 | : | 6 | : | 4 | : | 1 |
| 30cm | | 45cm | | 40cm | | 35cm | | 30cm |

Total no. of population is

$$1/16 \times 100 = 0.0625 \times 100 = 6.25$$

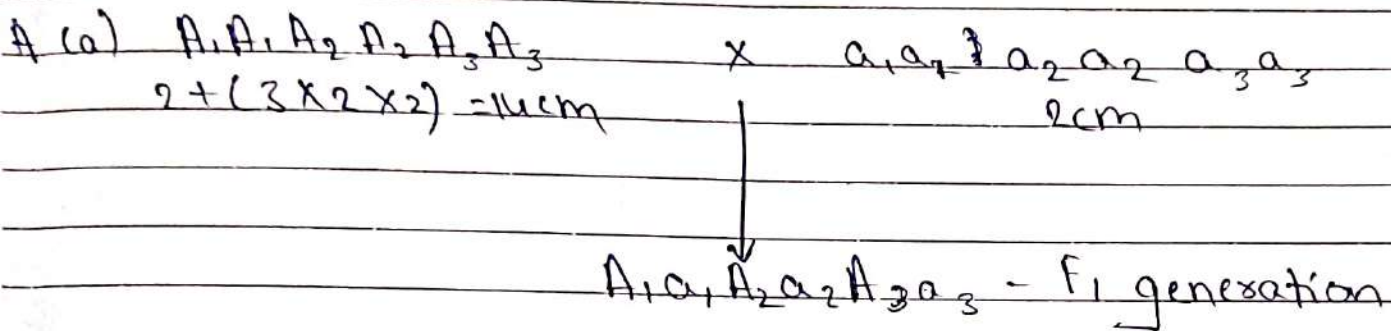
$$4/16 \times 100 = 0.25 \times 100 = 25$$

$$6/16 \times 100 = 0.375 \times 100 = 37.5$$

The frequency of plants having 40cm height = 37.5%.

4) Three independently segregating genes each with 2 alleles determine height in a particular plants. The presence of each contributing allele adds 2cm to the base height of 2cm.

- a) calculate the expected height of F_1 .
- b) Give the distribution of heights expected in $F_1 \times F_1$ cross.
- c) What proportion of F_2 progeny had a exactly height of parental population.



\therefore Expected height in F_1 generation is $2 + (3 \times 2) = 8 \text{ cm}$

- b) Since 3 genes are controlling the characters F_2 ratio

$$\begin{array}{l}
 1 : 6 : 15 : 20 : 15 : 6 : 1 \rightarrow F_2 \text{ ratio} \\
 6 : 5 : 4 : 3 : 2 : 1 : 0 \rightarrow \text{no. of contributing alleles}
 \end{array}$$

Height of each class is:

$$1 = (2 \times 6) + 2 = 14 \text{ cm}$$

$$6 = 2 + (5 \times 2) = 12 \text{ cm}$$

$$15 = 2 + (4 \times 2) = 10 \text{ cm}$$

$$20 = 2 + (3 \times 2) = 8 \text{ cm}$$

$$15 = 2 + (2 \times 2) = 6 \text{ cm}$$

$$6 = 2 + (2 \times 1) = 4 \text{ cm}$$

$$1 = 2 + (2 \times 0) = 2 \text{ cm}$$

Title:

Experiment No.:

Date:

c) proportion of plants in F_2 with parental heights is

$$= \frac{1+1}{64} \times 100$$

$$= \frac{2}{64} \times 100$$

$$= 3.125\%$$

Conclⁿ?

An experiment with seven varieties of line seed was conducted in RBD with 3 replications. The following are the data recorded for seed yield (x) & no. of capsules/plant (y). Estimate the components of co-variance.

| Genotypes | Seed yield (g) | | | | No. of capsules | | | |
|-----------|----------------|----------------|----------------|-------|-----------------|----------------|----------------|-------|
| | R ₁ | R ₂ | R ₃ | Total | R ₁ | R ₂ | R ₃ | Total |
| 1 | 40 | 35 | 40 | 115 | 95 | 100 | 100 | 295 |
| 2 | 50 | 50 | 50 | 150 | 120 | 125 | 120 | 365 |
| 3 | 55 | 59 | 50 | 164 | 120 | 130 | 130 | 380 |
| 4 | 60 | 65 | 65 | 190 | 140 | 150 | 145 | 435 |
| 5 | 40 | 40 | 40 | 120 | 110 | 110 | 115 | 335 |
| 6 | 50 | 55 | 55 | 160 | 125 | 130 | 130 | 385 |
| 7 | 65 | 60 | 70 | 195 | 145 | 145 | 135 | 445 |
| Total | 360 | 364 | 370 | 1094 | 855 | 890 | 895 | 2640 |

$$A. \text{ Correlation factor} = \frac{\sum Tx - \sum Ty}{\sqrt{\sum x^2 \sum y^2}} = \frac{1094 \times 2640}{21}$$

$$= 137531.43$$

~~$$\text{Total sum of products} = \sum (xy) - CF$$~~

~~$$= (40 \times 95) + (50 \times 120) + \dots + (70 \times 152) - CF$$~~

~~$$= 140820.00 - 137531.43 =$$~~

~~$$= 3289.57$$~~

$$\text{Treatment sum of products} = \frac{\sum (Tx - Ty)^2}{r} - CF$$

$$= \frac{(115 \times 295) + \dots + (195 \times 445)}{3} - CF$$

$$= \frac{422220}{3} - 137531.43$$

$$= 3208.57$$

$$\text{Replication sum of products} = \frac{\sum (P_x - P_y)}{t} - CF$$

$$= \frac{(360 \times 855) + (364 \times 890) + (370 \times 895)}{7} - CF$$

$$= 137558.57 - 137531.43$$

$$= 27.14$$

$$\text{Error sum of products} = \text{Total sum of products} - \text{Treatment SP} - \text{Replication SP}$$

$$= 3288.57 - 3208.57 - 27.14$$

$$= 52.86$$

ANACOVA Table

| SOV | df | SP | MP | F |
|-------------|-------------------|---------|--------|--------|
| Replication | $(x-1) = 2$ | 27.14 | 13.57 | |
| Treatment | $(t-1) = 6$ | 3208.57 | 534.76 | 121.26 |
| Error | $(x-t)(t-1) = 12$ | 52.86 | 4.41 | |
| Total | $(xt-1) = 20$ | 3288.57 | - | |

$$\text{Environmental covariance} = \sigma_{b_{xy}} = 4.41$$

$$\text{Genotypic co-variance} = \sigma_{gxy} = \frac{\text{HP due to genotype} - \text{HP due to error}}{2}$$

$$= \frac{534.76 - 4.41}{3}$$

$$= 176.78$$

$$\text{phenotypic co-variance } \sigma_{pxy} = \sigma_{gxy} + \sigma_{exy}$$

$$= 176.78 + 4.41$$

$$= 181.19$$

Title: Estimation of Heritability
& Genetic Advance

Experiment No: ?

Date: ?

using the different variance components, estimate heritability and genetic advance expected for lint index from problem. Also workout co-heritability for seed yield & no. of capsules per plant.

A. phenotypic variance = 38.91

Genotypic variance = 36.97

Environmental variance = 1.94

Heritability in broad sense = $\frac{\sigma_g^2}{\sigma_p^2} \times 100$

= $\frac{36.97}{38.91} \times 100$

= 95.01%

Genetic advance = $kh^2\sigma_p$

where,

k = Selection differential at 5% selection intensity = 2.06

h^2 = heritability coefficient = 0.95

σ_p = phenotypic standard deviation = $\sqrt{38.91}$
= 6.24

\therefore Genetic advance = $2.06 \times 0.95 \times 6.24 = 12.21$

% Genetic advance as percent of mean =

$\frac{GA}{\text{Grand mean}} \times 100$

= $\frac{12.21}{50.76} \times 100 = 24.05\%$

The heritability of (95.01%) for lint index is very high indicating the low influence of environment on lint index. The genetic advance expected (24.05%) is also high.

Co-heritability b/w seed yield and no. of capsules per plant.

$$\text{Co-heritability} = \frac{\sigma_{gxy}}{\sigma_{pxy}} \times 100$$

σ_{gxy} = genotypic covariance b/w x and y = 176.78

σ_{pxy} = phenotypic covariance b/w x and y = 181.19

$$\text{Co-heritability} = \frac{176.78}{181.19} \times 100 = 97.57\%$$

Conclusion:

The co-heritability no. of capsules / plant and seed yield is high. Therefore, selection on no. of capsules / plant will result in increased grain yield in in seed.

Title: Diversity Analysis by using
Molecular Markers

Experiment No: 3

Date: 28-4-22

Q) 24^{ncc} genotypes evaluated using 6 molecular markers & scored in presence (0) absence of the band in gel pictures. Scoreings of the markers given below. calculate the A.F & P.I.c value & construct dendrogram using unweighted neighbour hood joining methods [DAR win-5]

| | M ₁ | M ₁ | M ₂ | M ₂ | M ₂ | M ₃ | M ₄ | M ₄ | M ₅ | M ₅ | M ₆ | M ₆ |
|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| G ₁ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂ | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 0 |
| G ₃ | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₄ | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₅ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₆ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₇ | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| G ₈ | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| G ₉ | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| G ₁₀ | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 |
| G ₁₁ | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₁₂ | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₁₃ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₁₄ | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 1 |
| G ₁₅ | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 0 |
| G ₁₆ | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 |
| G ₁₇ | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 0 |
| G ₁₈ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₁₉ | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂₀ | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂₁ | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂₂ | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂₃ | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |
| G ₂₄ | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 |

$$\text{Total} = 1 - \sum_{i=1}^k p_i^2$$

$$\text{Avg} = \frac{\text{Sum of observation}}{\text{Total observation}}$$

Marker -1 (a)

$$\text{Allelic frequency} = \frac{4}{24}$$

$$= 0.166667$$

$$= (0.166667)^2$$

$$= 0.027778$$

$$(b) \text{ Allelic frequency} = \frac{20}{24}$$

$$= 0.833333$$

$$= (0.833333)^2$$

$$= 0.694444$$

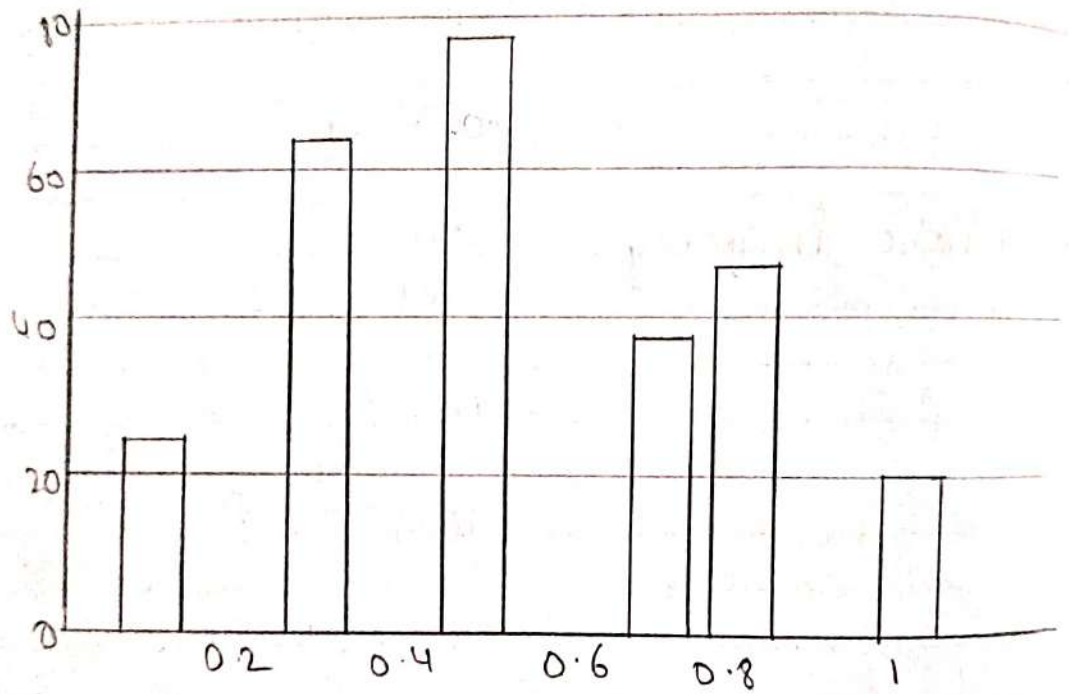
$$\text{Sum of values (a+b)} = 0.027778 + 0.694444$$

$$= 0.72222$$

$$P_{Tc} = 1 - 0.72222$$

$$= 0.27778$$

As the marker value is 0.27778, these are not useful.



Bar graph

Marker-2 (a)

$$A.F = \frac{6}{24}$$

$$= 0.25$$

$$= (0.25)^2$$

$$= 0.0625$$

(b)

$$A.F = \frac{18}{24}$$

$$= 0.75$$

$$= (0.75)^2$$

$$= 0.5625$$

$$\text{Sum of values (a+b)} = 0.0625 + 0.5625$$

$$= 0.625$$

$$P.I.C = 0.375$$

These markers are used for analysis but of its value is 0.375.

Marker-3 (a)

$$A.F = \frac{10}{24}$$

$$= 0.416667$$

$$= (0.416667)^2$$

$$= 0.173611$$

(b)

$$AF = \frac{14}{24}$$

$$= 0.58333$$

$$= (0.58333)^2$$

$$= 0.3402778$$

$$\text{Sum of values (a+b)} = 0.173611 + 0.3402778$$

$$= 0.513888$$

$$PTC = 1 - 0.513888$$

$$= 0.486112$$

These markers are useful for analysis based on their value 0.486112.

Marker-4 (a)

$$AF = \frac{4}{24}$$

$$= 0.166667$$

$$= (0.166667)^2$$

$$= 0.0277778$$

(b)

$$AF = \frac{20}{24}$$

$$= 0.83333$$

$$= (0.83333)^2$$

$$= 0.694444$$

$$\text{Sum of values (a+b)} = 0.0277778 + 0.694444$$

$$= 0.7222218$$

$$PIc = 1 - 0.7222218$$

$$= 0.2777782$$

These markers are not useful for its low value.

Marker \rightarrow (a)

$$AF = \frac{5}{24}$$

$$= 0.208333$$

$$= (0.208333)^2$$

$$= 0.0434027$$

Title:

Experiment No:

Date:

(b)

$$A.F = \frac{19}{24}$$

$$= 0.7916667$$

$$= (0.7916667)^2$$

$$= 0.626736$$

$$\text{Sum of values (a+b)} = 0.0434027 + 0.626726$$

$$= 0.6701387$$

$$P.T.c = 1 - 0.6701387$$

$$= 0.3298613$$

These max.ces are useful for analysis for it value 0.3298613.

Max.ces - 6 (a)

$$A.F = \frac{8}{24}$$

$$= 0.33333$$

$$= (0.3333)^2$$

$$= 0.1111$$

(b)

$$A.F = \frac{16}{24}$$

$$\begin{aligned}
 &= 0.6667 \\
 &= (0.6667)^2 = 0.44489 \\
 \text{sum of values} &= 0.1111 + 0.44489 \\
 &= 0.55599
 \end{aligned}$$

$$\begin{aligned}
 \text{PIC} &= 1 - 0.55599 \\
 &= 0.44401
 \end{aligned}$$

These markers are useful for its high value i.e., 0.44401.

Conclusion

According to the dendrogram, clusters are categorized to 3. Among those clusters 1A and 1B has the maximum no. of genotypes i.e., 12 and 2A, 2B & 3A, 3B are having less genotypes, each 6 and the Markers 2, 3, 5, 6 are useful for analysis:

clusters - 1A - G7, G8, G9, G10, G16, G15, G20, G19, G21, G11

1B - G17, G2

2A - G18, G13, G5, G6, G22

2B - G1

3A - G4, G3, G12, G14

3B - G24, G23

Markers \rightarrow (2) - 0.375, (3) 0.486112, (5) 0.3298613, (6) 0.44401

List index of an experiment with 25 cotton genotypes is given below. These genotypes have been evaluated in RBD with 3 replications. Workout components of variance of lint index.

Lint Index (g)

| Genotypes | Replication I | Replication II | Replication III | Total |
|-----------|---------------|----------------|-----------------|-------|
| 1 | 36.5 | 36.0 | 36.4 | 108.9 |
| 2 | 51.0 | 54.0 | 53.5 | 160.5 |
| 3 | 42.1 | 44.8 | 42.9 | 129.8 |
| 4 | 46.5 | 51.0 | 49.5 | 147.0 |
| 5 | 49.5 | 48.0 | 47.3 | 144.8 |
| 6 | 51.0 | 49.5 | 51.5 | 152.0 |
| 7 | 50.0 | 49.0 | 49.8 | 148.8 |
| 8 | 54.5 | 52.0 | 53.5 | 162.0 |
| 9 | 50.5 | 48.5 | 52.0 | 151.0 |
| 10 | 53.8 | 54.0 | 53.5 | 161.3 |
| 11 | 57.0 | 56.0 | 53.0 | 168.0 |
| 12 | 52.5 | 51.0 | 50.0 | 153.5 |
| 13 | 47.5 | 48.0 | 48.5 | 144.0 |
| 14 | 57.0 | 56.0 | 57.5 | 170.5 |
| 15 | 39.0 | 37.0 | 40.0 | 116.0 |
| 16 | 47.5 | 49.0 | 48.0 | 144.5 |
| 17 | 60.0 | 61.0 | 62.0 | 183.0 |
| 18 | 61.0 | 62.5 | 61.5 | 185.0 |

| Genotypes | Replication I | Replication II | Replication III | Total |
|-----------|---------------|----------------|-----------------|--------|
| 19 | 46.5 | 48.5 | 45.0 | 140.0 |
| 20 | 47.0 | 47.5 | 48.5 | 143.0 |
| 21 | 54.0 | 55.0 | 53.5 | 164.0 |
| 22 | 48.0 | 48.5 | 49.5 | 146.0 |
| 23 | 47.0 | 45.5 | 47.0 | 139.5 |
| 24 | 58.5 | 58.0 | 57.5 | 174.0 |
| 25 | 55.5 | 57.5 | 56.5 | 169.5 |
| Total | 1263.4 | 1267.8 | 1275.9 | 3807.1 |

Title:

Experiment No:

Date:

A. Correlation Factor: $\frac{\sum T^2}{N} = \frac{(3807.1)^2}{75} = 193253.46$

Total sum of squares = $\sum x^2 - CF = 196058.55 - 193253.46 = 2805.09$

Treatment sum of squares = $\frac{\sum T^2}{r} - CF = \frac{5878886.7}{3} - 193253.46 = 2708.59$

Replication sum of squares = $\frac{\sum R^2}{t} - CF = \frac{4831417.10}{25} - 193253.46 = 3.22$

Error = Total SS - Treat. SS - Rep. SS = 93.28

ANOVA table

| Source | df | SS | MS | F |
|-------------|-------------------|---------|--------|-------|
| Replication | $(r-1) = 2$ | 3.22 | 1.6 | |
| Treatment | $(t-1) = 24$ | 2708.59 | 112.86 | 38.18 |
| Error | $(t-1)(r-1) = 48$ | 93.28 | 1.94 | |
| Total | $(rt-1) = 74$ | 2805.09 | - | |

Environmental Variance = $\sigma_e^2 = 1.94$

Genotypic Variance = $\sigma_g^2 = \text{MS due to genotype} - \text{MS due to error}$

= $\frac{112.86 - 1.94}{3} = 36.97$

Phenotypic Variance = $\sigma_p^2 = \sigma_g^2 + \sigma_e^2 = 36.97 + 1.94 = 38.91$

Title:

Experiment No:

Date:

Environment coefficient of Variation =

$$ECV = \frac{\sigma_e}{\text{Grand mean}} \times 100 = \frac{\sqrt{1.94}}{50.76} \times 100 = 2.76\%$$

Genotypic coefficient of Variation =

$$GCV = \frac{\sigma_g}{\text{Grand mean}} \times 100 = \frac{\sqrt{36.97}}{50.76} \times 100 = 11.98\%$$

Phenotypic coefficient of Variation =

$$PCV = \frac{\sigma_p}{\text{Grand mean}} \times 100 = \frac{\sqrt{38.91}}{50.76} \times 100 = 12.29\%$$

Conclusion :-

The PCV and GCV of lint index are moderate. It means that the variability observed in 25 genotypes is moderate. The ECV is low. Therefore the influence of environment on lint index is low.

Regression analysis

A trial was conducted with 6 parents of maize crossed in a full dialled fashion. The cob length of 36 genotypes are given below. Analyze the data in Hayman approach & interpret the results.

| Genotype | Cob length (cm) | | | Total | Mean |
|------------------|-----------------|---------|----------|-------|-------|
| | Rep. I | Rep. II | Rep. III | | |
| $P_1 \times P_1$ | 9.21 | 8.46 | 8.23 | 25.92 | 8.64 |
| $P_1 \times P_2$ | 11.95 | 12.46 | 13.18 | 37.59 | 12.53 |
| $P_1 \times P_3$ | 17.21 | 15.99 | 16.21 | 49.41 | 16.47 |
| $P_1 \times P_4$ | 20.62 | 21.43 | 20.68 | 62.73 | 20.91 |
| $P_1 \times P_5$ | 18.63 | 17.98 | 16.55 | 53.16 | 17.72 |
| $P_1 \times P_6$ | 15.98 | 16.83 | 17.08 | 49.89 | 16.63 |
| $P_2 \times P_1$ | 17.36 | 17.21 | 16.19 | 50.76 | 16.92 |
| $P_2 \times P_2$ | 9.87 | 10.76 | 10.96 | 31.59 | 10.53 |
| $P_2 \times P_3$ | 11.73 | 12.34 | 11.49 | 35.76 | 11.92 |
| $P_2 \times P_4$ | 17.36 | 17.82 | 15.55 | 50.73 | 16.91 |
| $P_2 \times P_5$ | 13.26 | 12.82 | 11.06 | 37.14 | 12.38 |
| $P_2 \times P_6$ | 11.21 | 12.76 | 13.71 | 37.68 | 12.58 |
| $P_3 \times P_1$ | 10.93 | 11.98 | 13.84 | 36.75 | 12.25 |
| $P_3 \times P_2$ | 16.30 | 15.68 | 18.15 | 50.13 | 16.71 |
| $P_3 \times P_3$ | 11.28 | 12.10 | 11.24 | 34.62 | 11.54 |
| $P_3 \times P_4$ | 19.08 | 20.37 | 18.27 | 57.72 | 19.24 |
| $P_3 \times P_5$ | 11.92 | 12.63 | 12.50 | 37.05 | 12.35 |
| $P_3 \times P_6$ | 15.83 | 17.21 | 15.92 | 48.96 | 16.32 |
| $P_4 \times P_1$ | 18.36 | 17.98 | 15.17 | 51.51 | 17.17 |
| $P_4 \times P_2$ | 16.85 | 17.54 | 17.54 | 51.93 | 17.31 |
| $P_4 \times P_3$ | 11.82 | 10.89 | 11.13 | 33.84 | 11.28 |
| $P_4 \times P_4$ | 13.21 | 12.38 | 11.68 | 37.47 | 12.49 |
| $P_4 \times P_5$ | 11.21 | 12.37 | 11.49 | 35.07 | 11.69 |
| $P_4 \times P_6$ | 17.63 | 16.82 | 14.66 | 49.11 | 16.37 |
| $P_5 \times P_1$ | 17.63 | 18.82 | 18.42 | 54.87 | 18.29 |
| $P_5 \times P_2$ | 15.08 | 15.64 | 12.99 | 43.71 | 14.57 |
| $P_5 \times P_3$ | 14.63 | 15.21 | 15.22 | 45.06 | 15.02 |

| | | | | | |
|------------------|--------|--------|--------|---------|-------|
| $P_5 \times P_4$ | 17.21 | 16.12 | 17.01 | 50.34 | 16.78 |
| $P_5 \times P_5$ | 12.63 | 12.52 | 14.20 | 40.35 | 13.45 |
| $P_5 \times P_6$ | 16.93 | 15.62 | 16.71 | 49.26 | 16.42 |
| $P_6 \times P_1$ | 18.23 | 17.83 | 15.60 | 51.66 | 17.22 |
| $P_6 \times P_2$ | 15.82 | 16.21 | 17.05 | 49.08 | 16.36 |
| $P_6 \times P_3$ | 16.83 | 16.38 | 15.42 | 48.63 | 16.21 |
| $P_6 \times P_4$ | 21.32 | 19.68 | 21.79 | 62.79 | 20.93 |
| $P_6 \times P_5$ | 11.28 | 11.67 | 12.12 | 35.07 | 11.69 |
| $P_6 \times P_6$ | 13.08 | 12.83 | 11.35 | 37.26 | 12.42 |
| Total | 539.48 | 544.71 | 530.38 | 1614.60 | 14.95 |

A. Analysis of Variance for RBD

| Source | df | SS | MS | F |
|-------------|-----|---------|-------|-------|
| Replication | 2 | 2.94 | 1.47 | 1.81 |
| Genotype | 35 | 945.35 | 27.01 | 33.24 |
| Error | 70 | 56.70 | 0.81 | - |
| Total | 107 | 1004.99 | - | - |

Two-Way Table

| | P_1 | P_2 | P_3 | P_4 | P_5 | P_6 | Total | Mean |
|-------|-------|-------|-------|-------|-------|-------|--------|-------|
| P_1 | 8.64 | 14.73 | 14.36 | 19.04 | 18.01 | 16.93 | 91.71 | 15.29 |
| P_2 | | 16.53 | 14.32 | 17.11 | 13.48 | 14.46 | 84.63 | 14.11 |
| P_3 | | | 11.51 | 15.26 | 13.69 | 16.27 | 85.44 | 14.24 |
| P_4 | | | | 12.49 | 14.24 | 18.65 | 96.79 | 16.13 |
| P_5 | | | | | 13.45 | 14.06 | 86.73 | 14.49 |
| P_6 | | | | | | 12.42 | 92.79 | 15.47 |
| Total | | | | | | | 538.29 | 89.73 |

Estimates of Variances & Covariances

i) parental Mean = $\frac{1}{6} [8.64 + 10.53 + \dots + 12.42] = 11.51$

ii) Variance of parents - $V_p (V_{00}) = \frac{1}{P-1}$

$$\left[8.64^2 + 10.53^2 + \dots + 12.42^2 - \frac{69.07^2}{6} \right] = 2.95$$

iii) Variance of each array - V_x :

$$V_{x_i} = \frac{1}{P-1} \left[8.64^2 + 14.73^2 + \dots + 16.93^2 - \frac{91.71^2}{6} \right] = 13.90$$

$$V_{x_1} = 13.90$$

$$V_{x_4} = 6.68$$

$$V_{x_2} = 4.55$$

$$V_{x_5} = 3.07$$

$$V_{x_3} = 2.55$$

$$V_{x_6} = 5.04$$

iv) Mean of variance of the arrays $(V_i L_i)$ (or) $\bar{V}_x = 5.97$

v) Variance of the mean of arrays (V_{00}) (or)

$$V_{\bar{y}} = \frac{1}{P-1} \left[15.29^2 + 14.11^2 + \dots + 15.47^2 - \frac{89.73^2}{6} \right]$$

$$= 0.64$$

vi) Co-Variance of each array - W_x :

[Co-variance b/w a parent & offspring i.e., covariance of the array with non-descendant parent]

$$W_{01} = \frac{1}{P-1} \left[(-8.64 \times 8.64) + (14.73 \times 10.53) + \dots + \frac{(16.93 \times 12.42) - (91.71)(69.07)}{P} \right] = 6.01$$

$$W_{01} = 6.01$$

$$W_{04} = -2.86$$

$$W_{02} = 0.76$$

$$W_{05} = -2.36$$

$$W_{03} = 0.25$$

$$W_{06} = -1.11$$

Vii) Mean of covariance of the arrays (W_{01}) (or)

$$\bar{W}_x = 0.115$$

Variance & covariance of Arrays

| Parents | V_x | W_x |
|---------|-------|-------|
| 1 | 13.90 | 6.01 |
| 2 | 4.55 | 0.76 |
| 3 | 2.55 | 0.25 |
| 4 | 6.68 | -2.86 |
| 5 | 3.07 | -2.36 |
| 6 | 5.04 | -1.11 |
| Mean | 5.97 | 0.115 |

Test of assumptions of Roy's hypothesis

(i) t^2 (or) F test

$$\text{Variance of } V_x = \frac{1}{P-1} \left[13.90^2 + 4.55^2 + \dots + 5.04^2 - \frac{35.79^2}{P} \right] = 17.27$$

$$\text{Variance of } W_x = \frac{1}{P-1} \left[6.01^2 + 0.76^2 + \dots + (-1.11)^2 - \frac{0.69^2}{P} \right] = 10.32$$

Covariance of V_p & W_x

$$= \frac{1}{P-1} [(13.90 \times 6.0) + (4.55 \times 0.76) + \dots + (5.04 \times 1.11) - \frac{(35.79 \times 0.69)}{P}] = 10.31$$

$$t^2 = \frac{P-2}{4} \left[\frac{(\text{Var} \cdot V_x - \text{Var} \cdot W_x)^2}{(\text{Var} \cdot V_x \times \text{Var} \cdot W_x) - [\text{Cov} \cdot V_x \cdot W_x]^2} \right]$$

$$= \frac{4}{4} \left[\frac{(17.27 - 10.31)^2}{(17.27 \times 10.32) - (10.31)^2} \right] = 0.67$$

The table F value 4 & (P-2) degrees of freedom is 6.39. The calculated t^2 value is less than table F value. Hence, it is non-significant. The non-significance of t^2 value indicated the fulfillment of assumptions of Haysen.

(ii) Regression coefficient test

$$b = \frac{\text{Cov} \cdot V_x \cdot W_x}{\text{Var} \cdot V_x} = \frac{10.31}{17.27} = 0.597$$

$$SE_b = \sqrt{\frac{\text{Var} \cdot W_x - b \cdot \text{Cov} \cdot V_x \cdot W_x}{\text{Var} \cdot V_x (P-2)}} = \sqrt{\frac{10.32 - (0.597 \times 10.31)}{17.27 \times 4}}$$

$$= \sqrt{\frac{4.165}{69.08}} = 0.246$$

$$t = \frac{1-b}{SE_b} \quad (\text{or}) \quad \frac{b-0}{SE_b} = \frac{0.403}{0.246} \quad (\text{or}) \quad \frac{0.597}{0.246}$$

$$= 1.64 \quad (\text{or}) \quad 2.43$$

These 't' values are tested against 't' for P-2 degrees of freedom i.e. 2.776, since the calculated t-values, the assumptions of Haymen were fulfilled.

V_s - W_x graph

parabola limits

W_x for parabola

$$W_x = \sqrt{V_{s1} \times V_{o1}}$$

$$W_{x1} = \sqrt{13.90 \times 2.95} = 6.40$$

$$W_{x4} = 4.44$$

$$W_{x2} = 3.66$$

$$W_{x5} = 3.01$$

$$W_{x3} = 2.74$$

$$W_{x6} = 3.85$$

These W_x values are plotted in the graph (Y-axis) against V_s value (X-axis) to determine the external limits of parabola.

For drawing expected standard regression line of unit slope, the expected W_x values for given V_s values are worked out. The point of interception of the regression line with W_x ordinate i.e. 'a' is obtained as follows:

$$a = \bar{W}_x - b\bar{V}_s = 0.115 - (0.592 \times 5.97) = -3.45$$

The expected W_x values for given V_s values are obtained as follows:

$$Y = a + bX$$

$$h_x = a + bh_x$$

| V_x | h_x | V_x | h_x |
|-------|-------|-------|-------|
| 2 | -2.26 | 10 | 2.52 |
| 4 | -1.06 | 12 | 3.71 |
| 6 | 0.13 | 14 | 4.91 |
| 8 | 1.30 | 16 | 6.10 |

The h_x values are plotted in the graph against given values. Then a straight line passing through these points is drawn, which is known as regression line of unit slope. This regression line cuts the axis (Y-axis) at the point of 'a'. Then the parents are positioned along the regression line with corresponding V_x & h_x values.

Genetic Information from $V_x - h_x$ Graph

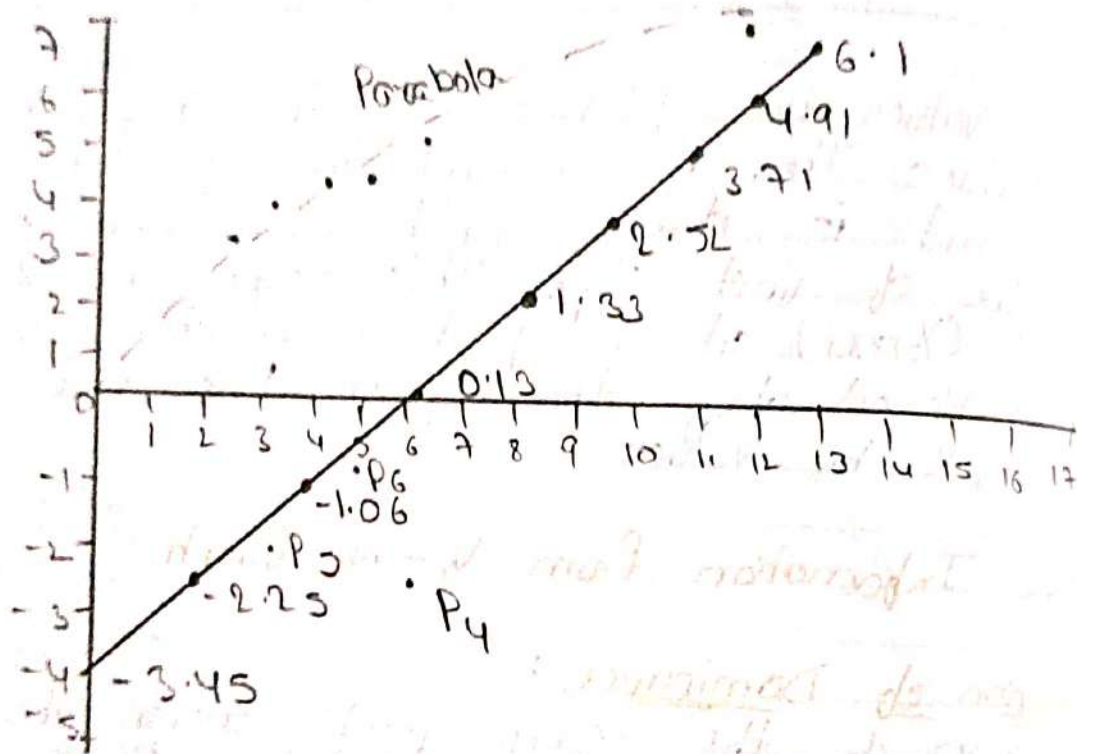
i) Direction of Dominance :

The order of the array points along the regression line throws light on the distribution of dominant & recessive alleles among the parents. These parents P_5, P_6, P_4, P_3 & P_2 appeared to possess more dominant alleles. Parent P_1 contains more of recessive alleles.

ii) Level of Dominance :

The intercept of regression line on the covariance ordinate (Y-axis) being below the origin, shows a clear cut case of over dominance.

(ii) The scattered array points on the regression line indicates diversity among parents.



$V_{x^2} - \bar{x}^2$ graph

Estimation of genetic components of variation

$$1) F = \frac{F.H.S.}{8} = \frac{0.81}{3} = 0.27$$

$$2) D = \frac{4}{7} (V_p + \bar{W}_x + V_x) = \frac{4}{7} (2.95 + 0.115 + 0.01) = 2.67$$

$$3) H_1 = V_p - 4 \bar{W}_x + 4V_x - [3(P-2)F/P]$$

$$= 2.95 - 4(0.115) + 4(5.92) - (12 \times 0.27/6) = 25.67$$

$$4) H_2 = 4V_x - 4V_x - 2F$$

$$= (4 \times 5.92) - 4(0.01) - (2 \times 0.27) = 20.75$$

$$5) F = 2V_p - 4\bar{W}_x - [2(P-2)F/P]$$

$$= (2 \times 2.95) - 4 \times 0.115 - [2(4)0.27/6] = 5.08$$

$$6) h^2 = [\text{izard mean} - \text{Mean of parents}]^2 - \left[\frac{4(P-1)F}{P^2} \right]$$

$$= 4(14.95 - 11.51)^2 - \left[\frac{20 \times 0.27}{36} \right] = 4 \times 11.82 - 0.15 = 47.49$$

Significance of genetic parameters

$$\text{Common multiplier} = S^2 = \frac{1}{2} [V_x \cdot W_x - V_x]$$

$$= \frac{1}{2} \left[\left[\frac{1}{P-1} \right] \sum (W_{x_i} - V_{x_i})^2 - \frac{(\sum W_{x_i} - V_{x_i})^2}{P} \right]$$

$$g^2 = 3.48$$

Specific Multiplier

$$D = \frac{(P^5 - 1P^4)}{P^5} = 1.17$$

$$H_1 = \frac{(P^5 + 4P^4 - 19P^3 + 4P^2)}{P^5} = 7.52$$

$$H_2 = \frac{(36P^4)}{P^5} = 6.0$$

$$H = \frac{(4P^5 + 20P^4 - 16P^3 + 16P^2)}{P^5} = 6.96$$

$$h^2 = \frac{(16P^4 + 16P^2 - 32P + 16)}{P^5} = 2.72$$

$$F = \frac{h^4}{h^3} = 0.17$$

SE = (Common Multiplier x Specific Multiplier)^{1/2}

SE Box

$$D = (3.48 \times 1.17)^{1/2} = 2.02 \quad H_1 = (3.48 \times 7.52)^{1/2} = 5.12$$

$$H_2 = (3.48 \times 6.00)^{1/2} = 4.57 \quad H = (3.48 \times 6.96)^{1/2} = 4.93$$

$$h^2 = (3.48 \times 2.72)^{1/2} = 3.08 \quad F = (3.48 \times 0.17)^{1/2} = 0.76$$

t Value Box $D = \frac{2.12}{2.02} = 1.05$

$$H_1 = \frac{25.63}{25.12} = 5.01$$

$$F = \frac{5.08}{4.93} = 1.03$$

$$E = \frac{0.29}{0.76} = 0.36$$

$$H_2 = \frac{20.75}{4.57} = 4.54$$

$$h^2 = \frac{17.14}{3.08} = 5.56$$

Table t value at error d.f. = 1.994

Hence, the estimates of H_1 , H_2 & h^2 are significant. Other estimates are not significant.

Genetic Ratios

$$1) \text{ Average degree of dominance} = \left[\frac{H_1}{D} \right]^2 = \sqrt{\frac{25.63}{2.12}} = 3.09$$

Since the average degree of dominance is more than 1, the character cob length in Maize is governed by over dominance. This was also already confirmed from $V_r = W_r$ graph.

2) proportion of alleles with positive & negative effects in parents:

$$= \frac{H_2}{4H_1} = \frac{20.75}{4 \times 25.63} = 0.20$$

Since, this ratio is less than 0.25, there is asymmetry of positive & negative alleles. There is unequal allelic frequency at all loci.

3) proportion of dominant & recessive alleles in parents

$$\frac{(4DH)^{\frac{1}{2}} + F}{(4DH)^{\frac{1}{2}} - F} = \frac{(4 \times 2.12 \times 25.63)^{\frac{1}{2}} + 5.08}{(4 \times 2.12 \times 25.63)^{\frac{1}{2}} - 5.08} = 1.88$$

Since, this ratio is more than 1, there is more of dominant alleles than recessive alleles in parents.

4) F_1 - covariance of additive & dominance effects in a single array.

$$P_1 = 2(2.95 - 0.115 + 5.97 - 6.01 - 13.9) - \left[\frac{2 \times 4 \times 0.27}{6} \right] = -22.57$$

$$P_2 = 2(2.95 - 6.115 + 5.97 - 0.27 - 4.55) - 0.36 = 6.63$$

$$P_3 = 11.65$$

$$P_5 = 15.83$$

$$P_4 = 9.61$$

$$P_6 = 9.39$$

The parent 1 is having negative F_1 value. Hence, it is having more of recessive alleles than dominant alleles. Other parents 2, 3, 4, 5 & 6 are having more of dominant alleles than recessive alleles. It was already confirmed by $V_0 - V_6$ graph also.

5) Heritability

Title:

Experiment No:

Date:

$$\text{Broad sense} = \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + F} = 0.96$$

$$\text{Real sense} = \frac{\frac{1}{8}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F + F} = 0.12$$

6) no. of genes controlling the characters & exhibit dominance

$$= \frac{h^2}{H^2} = \frac{47.14}{20.75} = 2.27$$

Method - 1

A total of six parents in sesame were crossed in diallel fashion following Method - 1. The no. of primary branches recorded on three replications in a RBD is given below. Work out the gene action and suggest suitable breeding method for improvement of no. of primary branches.

| Genotype | No. of Primary Branches | | | | |
|---------------------------------|-------------------------|---------|----------|-------|------|
| | Rep. I | Rep. II | Rep. III | Total | Mean |
| P ₁ x P ₁ | 3.8 | 4.0 | 4.8 | 12.6 | 4.2 |
| P ₁ x P ₂ | 3.8 | 3.0 | 2.8 | 9.6 | 3.2 |
| P ₁ x P ₃ | 2.6 | 2.4 | 2.5 | 7.5 | 2.5 |
| P ₁ x P ₄ | 3.9 | 3.7 | 3.2 | 10.8 | 3.6 |
| P ₁ x P ₅ | 3.3 | 4.2 | 3.9 | 11.4 | 3.8 |
| P ₁ x P ₆ | 3.9 | 4.8 | 4.5 | 13.2 | 4.4 |
| P ₂ x P ₁ | 3.4 | 3.2 | 2.7 | 9.3 | 3.1 |
| P ₂ x P ₂ | 2.9 | 3.6 | 3.4 | 9.9 | 3.3 |
| P ₂ x P ₃ | 4.3 | 4.6 | 4.0 | 12.9 | 4.3 |
| P ₂ x P ₄ | 2.3 | 3.0 | 3.1 | 8.4 | 2.8 |
| P ₂ x P ₅ | 3.0 | 3.2 | 2.5 | 8.7 | 2.9 |
| P ₂ x P ₆ | 3.3 | 3.9 | 4.2 | 11.4 | 3.8 |
| P ₃ x P ₁ | 2.6 | 2.9 | 2.6 | 8.1 | 2.7 |
| P ₃ x P ₂ | 3.6 | 4.2 | 4.5 | 12.3 | 4.1 |
| P ₃ x P ₃ | 2.8 | 3.4 | 2.8 | 9.0 | 3.0 |
| P ₃ x P ₄ | 4.2 | 4.1 | 4.6 | 12.9 | 4.3 |
| P ₃ x P ₅ | 2.6 | 3.1 | 3.3 | 9.0 | 3.0 |
| P ₃ x P ₆ | 3.3 | 3.8 | 3.7 | 10.8 | 3.6 |
| P ₄ x P ₁ | 3.2 | 3.5 | 3.5 | 10.2 | 3.4 |
| P ₄ x P ₂ | 3.2 | 2.8 | 3.0 | 9.0 | 3.0 |
| P ₄ x P ₃ | 3.9 | 4.1 | 4.6 | 12.6 | 4.2 |
| P ₄ x P ₄ | 3.3 | 3.4 | 4.1 | 10.8 | 3.6 |
| P ₄ x P ₅ | 4.3 | 4.8 | 4.7 | 13.8 | 4.6 |
| P ₄ x P ₆ | 3.7 | 4.2 | 4.4 | 12.3 | 4.1 |

Title:

Experiment No:

Date:

| | | | | | |
|---------------------------------|-------|-------|-------|-------|-------|
| P ₅ X P ₁ | 3.9 | 4.3 | 3.5 | 10.2 | 3.4 |
| P ₅ X P ₂ | 2.8 | 3.1 | 3.0 | 9.0 | 3.0 |
| P ₅ X P ₃ | 3.1 | 3.0 | 4.6 | 12.6 | 4.2 |
| P ₅ X P ₄ | 4.4 | 4.3 | 4.1 | 10.8 | 3.6 |
| P ₅ X P ₅ | 1.8 | 2.1 | 4.7 | 13.8 | 4.6 |
| P ₅ X P ₆ | 4.5 | 4.0 | 4.4 | 12.3 | 4.1 |
| P ₆ X P ₁ | 3.9 | 4.3 | 3.5 | 11.7 | 4.5 |
| P ₆ X P ₂ | 2.8 | 3.1 | 3.1 | 9.0 | 4.0 |
| P ₆ X P ₃ | 3.1 | 3.0 | 3.5 | 9.6 | 3.5 |
| P ₆ X P ₄ | 4.4 | 4.3 | 4.8 | 13.5 | 4.1 |
| P ₆ X P ₅ | 1.8 | 2.1 | 2.7 | 6.6 | 4.2 |
| P ₆ X P ₆ | 4.5 | 4.0 | 4.4 | 17.9 | 3.3 |
| Total | 124.4 | 132.3 | 133.9 | 390.6 | 130.2 |

A. CF = 1412.67

Analysis of variance for RBD

| Source of Variation | D.F. | SS | MS | F |
|---------------------|------|-------|-------|-------|
| Replication | 2 | 1.44 | 0.72 | 6.18 |
| Genotypes | 35 | 42.69 | 1.22 | 10.49 |
| Error | 70 | 8.14 | 0.116 | |
| Total | 107 | | | |

Two-way Table

| Genotypes | P ₁ | P ₂ | P ₃ | P ₄ | P ₅ | P ₆ | Total |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|-------|
| P ₁ | 4.2 | 3.2 | 2.5 | 3.6 | 3.8 | 4.4 | 21.7 |
| P ₂ | 3.1 | 3.3 | 4.3 | 2.8 | 2.9 | 3.8 | 20.2 |
| P ₃ | 2.7 | 4.1 | 3.0 | 4.3 | 3.0 | 3.6 | 20.7 |
| P ₄ | 3.4 | 3.0 | 4.2 | 3.6 | 4.6 | 4.1 | 22.9 |
| P ₅ | 3.9 | 3.0 | 3.2 | 4.5 | 2.2 | 4.3 | 21.1 |
| P ₆ | 4.5 | 4.0 | 3.3 | 4.1 | 4.2 | 3.3 | 23.6 |
| Total | 21.8 | 20.6 | 20.7 | 22.9 | 20.7 | 23.5 | 130.2 |

$$SS \text{ due to } hCA = \frac{1}{2P} \sum (Y_i + Y_j)^2 - \frac{r}{p^2} \sum Y_i^2$$

$$= \frac{1}{2 \times 6} [(21.7 + 21.8)^2 + \dots + (23.6 + 23.5)^2]$$

$$= \frac{2}{36} (130.2)^2 = 2.72$$

$$\text{SS due to SCA} = \left[\frac{1}{2} \sum \sum Y_{ij} (Y_{ij} + Y_{ji}) - \frac{1}{2P} \sum (Y_{i.} + Y_{.j})^2 + \frac{1}{P^2} Y_{..}^2 \right]$$

$$= \frac{1}{2} [4.2(4.2 + 4.2) + 3.2(3.2 + 3.1) + 3.1(3.1 + 3.2) + \dots + 3.3(3.3 + 3.3)]$$

$$= \frac{1}{2 \times 6} [(21.7 + 21.8)^2 + \dots + (23.6 + 23.5)^2 + \frac{1}{6 \times 6} (130.2)^2] = 11.36$$

$$\text{SS due to RCA} = \frac{1}{2} \sum \sum (Y_{ij} - Y_{ji})^2 [(3.2 - 3.1)^2 + (2.5 - 2.7)^2 + \dots + (4.3 - 4.2)^2] = 0.16$$

Analysis of Variance for Combining Ability

| Source | df | SS | MS | F |
|--------|----|-------|-----------|-------|
| InCA | 5 | 2.71 | 0.54 (Hg) | 14.09 |
| SCA | 15 | 11.24 | 0.76 (Ms) | 19.49 |
| RCA | 15 | 0.16 | 0.01 (Hg) | 0.28 |
| Error | 30 | 8.08 | 0.27 (Me) | - |

Genetic Components:

Model-1

$$\sum g_i^2 = \frac{Mg - Mc}{2P} = \frac{0.54 - 0.039}{12} = 0.042$$

$$\sum S_{ij}^2 = Ms - Mc = 0.76 - 0.039 = 0.722$$

The ratio of $\frac{\sum g_i^2}{\sum S_{ij}^2} = \frac{0.042}{0.722} = 0.058$

Since the ratio of GCA variance / SCA variance is less than unity (one), the no. of primary branches is governed by dominance gene action.

Estimation of Genetic Effects:

i) Gca effects of parents

$$g_i = \frac{1}{2P} (Y_i + Y_{ij}) - \frac{1}{P^2} Y_{..} = \frac{1}{2 \times 6} (21.7 + 21.8) -$$

$$\frac{1}{36} \times 150.2 = 0.01$$

$$P_1 = 0.01$$

$$P_4 = 0.20$$

$$P_2 = -0.22$$

$$P_5 = -0.19$$

$$P_3 = -0.17$$

$$P_6 = 0.31$$

Significance of Gca effects

$$SE g_i = \sqrt{\frac{P-1}{2P^2} Mc} = \sqrt{\frac{5}{72} \times 0.039} = 0.05$$

$$t = \frac{g_i}{SE g_i} \text{ Calculated 't' at } 1000 \times \text{d.f. } P = 1.999$$

ii) Sca effects of hybrids

$$S_{ij} = \frac{1}{2} (Y_{ij} + Y_{ji}) - \frac{1}{2p} (Y_{i\cdot} + Y_{j\cdot} + Y_{\cdot i} + Y_{\cdot j}) + \frac{1}{p^2} Y_{\cdot\cdot}$$

$$P_1 \times P_2 = \frac{1}{2} (3.2 + 3.1) - \frac{1}{2 \times 6} (21.7 + 21.8 + 20.2 + 20.6) + \frac{1}{6 \times 6} 130.2 = -0.26$$

$$P_1 \times P_3 = -0.26$$

$$P_2 \times P_3 = 0.97$$

$$P_3 \times P_5 = -0.22$$

$$P_1 \times P_4 = -0.86$$

$$P_2 \times P_4 = -0.70$$

$$P_3 \times P_6 = -0.21$$

$$P_1 \times P_5 = -0.33$$

$$P_2 \times P_5 = -0.32$$

$$P_4 \times P_5 = 0.87$$

$$P_1 \times P_6 = 0.36$$

$$P_2 \times P_6 = 0.19$$

$$P_4 \times P_6 = -0.03$$

$$P_1 \times P_6 = 0.52$$

$$P_3 \times P_4 = 0.60$$

$$P_5 \times P_6 = 0.46$$

Significance of sca effects

$$SE S_{ij} = \sqrt{\frac{(p-1)^2}{p^2} Me} = \sqrt{\frac{25}{36} \times 0.039} = 0.16$$

$$t = \frac{S_{ij}}{SE S_{ij}}$$

Calculated 't' at error df. = 1.994

Since R.A. variance is not significant, sca effects need not be worked out. The sca effects of the hybrids can be taken as such for their reciprocal crosses also.

The two parents viz; P_4 and P_6 recorded significantly positive sca effects. Hence, these two parents can be used in breeding programmes to improve

The no. of primary branches. The hybrids viz, $P_1 \times P_5$, $P_2 \times P_1$, $P_1 \times P_6$, $P_6 \times P_1$, $P_1 \times P_3$, $P_3 \times P_4$, $P_4 \times P_3$, $P_4 \times P_5$, $P_5 \times P_4$, $P_5 \times P_6$ and $P_6 \times P_5$, which showed positively significant sca effects are recommended for tetra-allelic breeding. The tria hybrids viz, $P_4 \times P_6$ and $P_6 \times P_4$ (whose parents having positively significant sca effects) are recommended for recombination breeding since their sca is not significant (absence of dominance).

Title: Diallel analysis - Griffing method - II Experiment No: 6
interpretation of results Date: 12-5-22

A total of eight parents in 3 rows were crossed in diallel fashion following method-II. The seed yield recorded on three replications in a RBD is given below. Work out the gene action and suggest suitable breeding method for improvement of seed yield. Suggest the suitability of parents & hybrids in different breeding programme.

| Genotypes | Rep. I | Rep. II | Rep. III | Total | Mean |
|------------------|--------|---------|----------|-------|-------|
| $P_1 \times P_1$ | 5.85 | 7.13 | 7.91 | 20.79 | 6.93 |
| $P_1 \times P_2$ | 10.34 | 9.65 | 10.64 | 30.63 | 10.21 |
| $P_1 \times P_3$ | 7.08 | 5.64 | 4.35 | 17.07 | 5.69 |
| $P_1 \times P_4$ | 10.69 | 10.98 | 12.89 | 34.56 | 11.52 |
| $P_1 \times P_5$ | 11.84 | 10.28 | 11.48 | 33.60 | 11.20 |
| $P_1 \times P_6$ | 8.63 | 10.23 | 8.71 | 27.57 | 9.19 |
| $P_1 \times P_7$ | 7.86 | 8.15 | 8.74 | 24.75 | 8.25 |
| $P_1 \times P_8$ | 8.62 | 7.48 | 6.63 | 22.73 | 7.51 |
| $P_2 \times P_2$ | 6.26 | 5.72 | 6.02 | 18.00 | 6.00 |
| $P_2 \times P_3$ | 11.83 | 12.14 | 12.14 | 36.11 | 12.04 |
| $P_2 \times P_4$ | 5.82 | 5.36 | 6.09 | 17.27 | 5.76 |
| $P_2 \times P_5$ | 10.68 | 11.03 | 11.62 | 33.33 | 11.11 |
| $P_2 \times P_6$ | 9.46 | 9.28 | 10.99 | 29.73 | 9.91 |
| $P_2 \times P_7$ | 4.26 | 5.18 | 5.80 | 15.24 | 5.08 |
| $P_2 \times P_8$ | 14.21 | 12.96 | 14.02 | 41.19 | 13.80 |
| $P_3 \times P_3$ | 4.22 | 5.10 | 4.99 | 14.31 | 4.77 |
| $P_3 \times P_4$ | 11.52 | 10.26 | 10.08 | 31.86 | 10.62 |
| $P_3 \times P_5$ | 7.21 | 6.04 | 7.21 | 20.46 | 6.82 |
| $P_3 \times P_6$ | 7.03 | 6.78 | 6.68 | 20.49 | 6.83 |
| $P_3 \times P_7$ | 4.03 | 4.72 | 4.83 | 13.58 | 4.53 |
| $P_3 \times P_8$ | 8.21 | 7.56 | 7.30 | 23.07 | 7.69 |
| $P_4 \times P_4$ | 4.21 | 5.02 | 4.93 | 14.16 | 4.72 |
| $P_4 \times P_5$ | 11.85 | 12.03 | 13.26 | 37.14 | 12.38 |

Title:

Experiment No:

Date:

| | | | | | |
|------------------|-------|-------|-------|-------|--------|
| $P_4 \times P_6$ | 11.21 | 11.68 | 12.48 | 35.37 | 11.79 |
| $P_4 \times P_7$ | 5.08 | 5.42 | 5.40 | 15.90 | 5.30 |
| $P_4 \times P_8$ | 6.82 | 6.41 | 5.83 | 19.08 | 6.36 |
| $P_5 \times P_6$ | 4.52 | 5.13 | 5.83 | 15.48 | 5.16 |
| $P_5 \times P_7$ | 13.23 | 14.68 | 13.19 | 41.10 | 13.70 |
| $P_5 \times P_8$ | 6.33 | 6.96 | 6.62 | 19.71 | 6.57 |
| $P_6 \times P_7$ | 12.63 | 13.28 | 15.37 | 41.28 | 13.76 |
| $P_6 \times P_8$ | 6.23 | 6.10 | 5.79 | 18.12 | 6.04 |
| $P_7 \times P_6$ | 8.23 | 9.21 | 8.66 | 26.10 | 8.70 |
| $P_7 \times P_8$ | 13.08 | 12.33 | 12.03 | 37.44 | 12.48 |
| $P_8 \times P_7$ | 7.02 | 7.56 | 6.03 | 20.61 | 6.87 |
| $P_8 \times P_8$ | 8.83 | 8.37 | 8.03 | 25.23 | 8.41 |
| $P_8 \times P_9$ | 5.38 | 6.21 | 5.78 | 17.39 | 5.79 |
| Total | - | - | - | 910.2 | 303.34 |

A. Analysis of Variance for RBD

| Source | df | SS | MS | F |
|-------------|-----|--------|-------|-------|
| Replication | 2 | 0.54 | 0.27 | 0.51 |
| Genotypes | 35 | 921.85 | 26.34 | 50.24 |
| Error | 70 | 36.69 | 0.52 | - |
| Total | 107 | 959.08 | - | - |

Two-way Table

| | P_1 | P_2 | P_3 | P_4 | P_5 | P_6 | P_7 | P_8 | Total | $\sum X_i + \sum Y_j$ |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|-----------------------|
| P_1 | 6.93 | 10.22 | 5.69 | 11.52 | 11.20 | 9.19 | 8.25 | 7.51 | 70.51 | 77.44 |
| P_2 | | 6.00 | 12.37 | 5.09 | 11.11 | 9.91 | 5.28 | 13.73 | 63.49 | 79.71 |
| P_3 | | | 4.79 | 10.64 | 6.82 | 6.84 | 4.53 | 7.69 | 41.7 | 64.16 |
| P_4 | | | | 6.72 | 12.38 | 11.79 | 5.30 | 6.36 | 40.55 | 79.52 |
| P_5 | | | | | 5.16 | 13.78 | 6.57 | 13.76 | 39.19 | 85.86 |
| P_6 | | | | | | 6.04 | 8.70 | 12.48 | 27.22 | 84.69 |
| P_7 | | | | | | | 6.87 | 8.41 | 15.28 | 60.78 |
| P_8 | | | | | | | | 5.79 | 5.79 | 81.52 |
| Total | | | | | | | | | 303.34 | - |

$Y_i = \text{row total} + \text{value of reciprocal crosses}$

$$SS \text{ due to GCA} = \frac{1}{p+2} \left[\sum (Y_i + Y_{ii})^2 - \frac{4}{p} Y^2_{..} \right]$$

$$= \frac{1}{10} \left[(77.44)^2 + \dots + (81.52)^2 - \frac{4}{8} (303.34)^2 \right]$$

$$= 60.28$$

$$SS \text{ due to SCA} = \sum \sum Y_{ij}^2 - \frac{1}{p+2} \sum (Y_i + Y_{ii})^2$$

$$+ \frac{2}{(p+1)(p+2)} Y^2_{..}$$

$$= (6.93)^2 + (10.22)^2 + (5.69)^2 + \dots + (8.41)^2 - \frac{1}{10}$$

$$\left[(77.44)^2 + \dots + (81.52)^2 \right] + \frac{2}{9 \times 10} (303.34)^2 = 247.01$$

Analysis of Variance for Combining Ability

| Source | df | SS | MS | F |
|--------|----|--------|------------|-------|
| GCA | 7 | 60.28 | 8.61 (Mg) | 49.28 |
| SCA | 28 | 247.01 | 8.82 (Ms) | 50.49 |
| Error | 70 | 36.70 | 0.175 (Me) | - |

Genetic Components:

Model - 1

$$\sum g_i^2 = \frac{Mg - Me}{(p+2)} = \frac{8.61 - 0.175}{10} = 0.84$$

$$\sum s_{ij}^2 = MS - Me = 8.82 - 0.175 = 8.65$$

$$\text{The ratio of } \frac{\sum g_i^2}{\sum s_j^2} = \frac{0.84}{8.65} = 0.10$$

Since the ratio of GCA variance / SCA variance is less than unity (one), the seed yield is Sesame is governed by dominance gene action.

Estimation of Genetic Effects:

i) GCA effects of parents

$$g_i = \frac{1}{p+2} \left[(X_i + Y_{ii}) - \frac{2}{p} Y_{..} \right]$$

$$P_1 = \frac{1}{10} \left[27.44 - \frac{2}{8} 303.34 \right] = 0.16$$

$$P_2 = 0.16$$

$$P_5 = 1.00$$

$$P_2 = 0.39$$

$$P_6 = 0.89$$

$$P_3 = 1.17$$

$$P_7 = -1.51$$

$$P_4 = -0.33$$

$$P_8 = 0.57$$

$$\sum g_i = 0$$

Significance of GCA effects

$$Stg_i = \sqrt{\frac{(p-1)Me}{p(p+2)}} = \sqrt{\frac{7 \times 0.175}{8 \times 10}} = 0.12$$

$$t = \frac{g_i}{Stg_i} \text{ calculated } t \text{ at error d.f.} = 1.904$$

∴

i) SCA effects of hybrids

$$S_{ij} = Y_{ij} - \frac{1}{P+2} (Y_i + Y_{i1} + Y_j + Y_{j1}) + \frac{2}{(P+1)(P+2)} Y$$

$$= P_1 \times P_2 - \frac{1}{P+2} (Y_1 + Y_{11} + Y_2 + Y_{21}) + \frac{2}{(P+1)(P+2)} Y$$

$$P_1 \times P_2 = 10.22 - \frac{1}{10} (77.44 + 79.71) + \frac{2}{9 \times 10} 303.34 = 1.25$$

$$P_1 \times P_3 = 1.25$$

$$P_1 \times P_4 = -1.73$$

$$P_1 \times P_5 = 3.26$$

$$P_1 \times P_6 = 1.61$$

$$P_1 \times P_7 = -0.28$$

$$P_1 \times P_8 = 1.17$$

$$P_1 \times P_9 = -1.65$$

$$P_2 \times P_3 = 4.72$$

$$P_2 \times P_4 = -0.39$$

$$P_2 \times P_5 = 1.29$$

$$P_2 \times P_6 = 0.21$$

$$P_2 \times P_7 = -2.03$$

$$P_2 \times P_8 = 4.35$$

$$P_3 \times P_4 = 3.71$$

$$P_3 \times P_5 = 1.44$$

$$P_3 \times P_6 = -1.30$$

$$P_3 \times P_7 = -1.22$$

$$P_3 \times P_8 = -0.14$$

$$P_4 \times P_5 = 3.28$$

$$P_4 \times P_6 = 2.81$$

$$P_4 \times P_7 = -1.29$$

$$P_4 \times P_8 = -2.30$$

$$P_5 \times P_6 = 3.39$$

$$P_5 \times P_7 = -1.35$$

$$P_5 \times P_8 = 3.76$$

$$P_6 \times P_7 = 0.89$$

$$P_6 \times P_8 = 2.60$$

$$P_7 \times P_8 = 0.92$$

Significance of SCA effects

$$SE_{Sij} = \sqrt{\frac{P(P-1)Mc}{(P+1)(P+2)}} = \sqrt{\frac{56 \times 0.175}{9 \times 10}} = 0.33$$

$$t = \frac{S_{ij}}{SE_{Sij}}, \text{ calculated } t \text{ at error d.f.} = 1.994$$

The four parents viz; P_2, P_5, P_6 and P_8 are crossed

Significantly positive gca effects. Hence, these four can be used in breeding programmes to improve seed yield per plant. The hybrids viz., $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_5$, $P_1 \times P_6$, $P_2 \times P_3$, $P_2 \times P_5$, $P_2 \times P_6$, $P_3 \times P_5$, $P_3 \times P_6$, $P_5 \times P_6$, $P_6 \times P_7$ and $P_7 \times P_8$, which recorded positively significant sca effects are recommended for heterosis breeding. The hybrid $P_3 \times P_6$ is recommended for decombination breeding, since its SCA effects is not significant.

A total of six parents in some were crossed in diallel fashion following Method III. The no. of primary branches recorded on three replications in a RBD is given below. Work out the gene action and suggest suitable breeding method for improvement of no. of primary branches. Suggest the suitability of parents & hybrids in different breeding programmes.

| Genotypes | No. of primary branches | | | | |
|---------------------------------|-------------------------|--------|---------|-------|------|
| | Rep I | Rep II | Rep III | Total | Mean |
| P ₁ × P ₂ | 3.8 | 3.0 | 2.8 | 9.6 | 3.2 |
| P ₁ × P ₃ | 2.6 | 2.4 | 2.5 | 7.5 | 2.5 |
| P ₁ × P ₄ | 3.9 | 3.7 | 3.2 | 10.8 | 3.6 |
| P ₁ × P ₅ | 3.3 | 4.2 | 3.9 | 11.4 | 3.8 |
| P ₁ × P ₆ | 3.9 | 4.8 | 4.5 | 13.2 | 4.4 |
| P ₂ × P ₁ | 8.4 | 3.2 | 2.7 | 9.3 | 3.1 |
| P ₂ × P ₃ | 4.3 | 4.6 | 4.0 | 12.9 | 4.3 |
| P ₂ × P ₄ | 2.3 | 3.0 | 3.1 | 8.4 | 2.8 |
| P ₂ × P ₅ | 3.0 | 3.2 | 2.5 | 8.7 | 2.9 |
| P ₂ × P ₆ | 3.3 | 3.9 | 4.2 | 11.4 | 3.8 |
| P ₃ × P ₁ | 2.6 | 2.9 | 2.6 | 8.1 | 2.7 |
| P ₃ × P ₂ | 3.6 | 4.2 | 4.5 | 12.3 | 4.1 |
| P ₃ × P ₄ | 4.2 | 4.1 | 4.6 | 12.9 | 4.3 |
| P ₃ × P ₅ | 2.6 | 3.1 | 3.3 | 9.0 | 3.0 |
| P ₃ × P ₆ | 3.3 | 3.8 | 3.7 | 10.8 | 3.6 |
| P ₄ × P ₁ | 3.2 | 3.5 | 3.5 | 10.2 | 3.4 |
| P ₄ × P ₂ | 3.2 | 2.8 | 3.0 | 9.0 | 3.0 |
| P ₄ × P ₃ | 3.9 | 4.1 | 4.6 | 12.6 | 4.2 |
| P ₄ × P ₅ | 4.3 | 4.8 | 4.7 | 13.8 | 4.6 |
| P ₄ × P ₆ | 3.7 | 4.2 | 4.4 | 12.3 | 4.1 |
| P ₅ × P ₁ | 3.9 | 4.3 | 2.5 | 11.7 | 3.9 |
| P ₅ × P ₂ | 2.8 | 3.1 | 3.1 | 9.0 | 3.0 |
| P ₅ × P ₃ | 3.1 | 3.0 | 3.5 | 9.6 | 3.2 |
| P ₅ × P ₄ | 4.4 | 4.3 | 4.8 | 13.5 | 4.5 |
| P ₅ × P ₆ | 4.5 | 4.0 | 4.4 | 12.9 | 4.3 |

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| | | | | | |
|---------------------------------|-------|-------|-------|-------|-------|
| P ₁ x P ₁ | 4.6 | 4.3 | 4.6 | 13.5 | 4.5 |
| P ₁ x P ₂ | 3.3 | 4.1 | 4.6 | 12.0 | 4.0 |
| P ₁ x P ₃ | 3.5 | 3.8 | 3.2 | 10.5 | 3.5 |
| P ₁ x P ₄ | 4.0 | 4.3 | 4.0 | 12.3 | 4.1 |
| P ₁ x P ₅ | 4.3 | 4.2 | 4.1 | 12.6 | 4.2 |
| Total | 106.8 | 112.9 | 112.1 | 331.8 | 110.6 |

A. Analysis of Variance for RBD

| Source | df | SS | MS | F |
|-------------|----|-------|------|-------|
| Replication | 2 | 0.73 | 0.37 | 3.10 |
| Genotypes | 29 | 33.46 | 1.15 | 10.71 |
| Error | 58 | 6.25 | 0.11 | |
| Total | 89 | 40.44 | | |

Two-way Table

| | P ₁ | P ₂ | P ₃ | P ₄ | P ₅ | P ₆ | Total |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|-------|
| P ₁ | - | 3.2 | 2.5 | 3.6 | 3.8 | 4.4 | 17.5 |
| P ₂ | 3.1 | - | 4.3 | 2.8 | 2.9 | 3.8 | 16.9 |
| P ₃ | 2.7 | 4.1 | - | 4.3 | 3.0 | 3.6 | 17.7 |
| P ₄ | 3.4 | 3.0 | 4.2 | - | 4.6 | 4.1 | 19.3 |
| P ₅ | 3.9 | 3.0 | 3.2 | 4.5 | - | 4.3 | 18.9 |
| P ₆ | 4.5 | 4.0 | 3.5 | 4.1 | 4.2 | - | 20.3 |
| Total | 17.6 | 17.3 | 17.7 | 19.3 | 18.3 | 20.2 | 110.6 |

$$SS \text{ due to } (CA) = \frac{1}{2(P-2)} \sum (Y_{i.} + Y_{.j})^2 - \frac{2}{n(n-2)} Y_{..}^2$$

$$= \frac{1}{2 \times 4} [(17.5 + 17.9)^2 + (16.9 + 17.3)^2 + \dots + (20.3 + 20.3)^2]$$

$$- \frac{2}{(4)} (110.6)^2 = 3.61$$

$$\begin{aligned}
 \text{SS due to SCA} &= \frac{1}{2} \sum \sum (Y_{ij} + Y_{ji}) - \frac{1}{2(p-2)} \\
 &\quad \sum (Y_i + Y_j)^2 - \frac{1}{(p-1)(p-2)} Y^2 \\
 &= \frac{1}{2} [(2 \cdot 2 + 3 \cdot 1)^2 + (2 \cdot 5 + 2 \cdot 7)^2 + \dots + (4 \cdot 3 + 4 \cdot 2)^2] \\
 &\quad - \frac{1}{2 \times 4} [(17 \cdot 5 + 17 \cdot 6)^2 + \dots + (20 \cdot 3 + 20 \cdot 2)^2] - \\
 &\quad \frac{1}{5 \times 4} (110 \cdot 6)^2 = 426.13
 \end{aligned}$$

$$\begin{aligned}
 \text{SS due to RCA} &= \frac{1}{2} \sum \sum (Y_{ij} - Y_{ji})^2 \\
 &= \frac{1}{2} [(2 \cdot 2 - 3 \cdot 1)^2 + (2 \cdot 5 - 2 \cdot 7)^2 + \dots + (4 \cdot 3 - 4 \cdot 2)^2] = 0.32
 \end{aligned}$$

Analysis of Variance of Combining Ability

| Source | df | SS | MS | F |
|--------|----|--------|------------|--------|
| GCA | 5 | 3.61 | 0.72 (Ms) | 20.11 |
| SCA | 9 | 426.13 | 47.35 (Ms) | 718.69 |
| RCA | 15 | 0.32 | 0.02 (Ms) | 0.59 |
| Error | 58 | 6.25 | 0.036 (Ms) | - |

Genetic components:

Model-1

$$\sum g_i^2 = \frac{Mg - Me}{2(p-2)} = \frac{0.72 - 0.036}{2 \times 4} = 0.086$$

$$\sum S_{ij}^2 = \frac{Mg - Me}{2} = \frac{47.35 - 0.036}{2} = 23.66$$

$$\frac{\sum g_i^2}{\sum S_{ij}^2} = \frac{0.086}{23.66} = 0.004$$

Since the ratio of GCA variance / SCA variance is less than unity, the no. of primary branches is governed by dominance gene action.

Estimation of genetic effects -

i) GCA effect of parents

$$g_i = \frac{1}{2P(P-2)} [P(Y_i + Y_j) - 2Y_{..}]$$

$$P_1 = \frac{1}{12 \times 4} [6(17.5 + 17.6) - 2 \times 110.6] = \frac{210.60 - 221.20}{48} = -0.22$$

$$P_1 = -0.22$$

$$P_4 = 0.22$$

$$P_2 = -0.33$$

$$P_5 = 0.07$$

$$P_3 = -0.19$$

$$P_6 = 0.45$$

$$\sum g_i = 0$$

Significance of GCA effects

$$Stg_i = \sqrt{\frac{(P-1)Me}{2P(P-2)}} = \sqrt{\frac{5 \times 0.036}{2 \times 6 \times 4}} = 0.061$$

$$t = \frac{g_i}{Stg_i} \text{ calculated } t \text{ at error d.f.} = 1.96$$

(ii) SCA effects of hybrids

$$S_{ij} = \frac{1}{2}(Y_{ij} + Y_{j.i}) - \frac{1}{2(P-2)}(Y_i + Y_i + Y_j + Y_j) + \frac{1}{(P-1)(P-2)} Y_{..}$$

$$P_1 \times P_2 = \frac{1}{2} (3.2 + 3.0) - \frac{1}{2 \times 4} (17.5 + 16.9 + 17.6 + 17.3) + \frac{1}{3 \times 4} 11.06$$

$$= 3.15 - 8.66 + 5.53 = 0.02$$

- | | | |
|--------------------------|--------------------------|--------------------------|
| $P_1 \times P_2 = 0.02$ | $P_2 \times P_3 = 1.03$ | $P_3 \times P_3 = -0.49$ |
| $P_1 \times P_3 = -0.68$ | $P_2 \times P_4 = -0.67$ | $P_3 \times P_6 = -0.41$ |
| $P_1 \times P_4 = -0.18$ | $P_2 \times P_5 = -0.47$ | $P_4 \times P_5 = 0.38$ |
| $P_1 \times P_5 = 0.32$ | $P_2 \times P_6 = 0.09$ | $P_4 \times P_6 = -0.26$ |
| $P_1 \times P_6 = 0.53$ | $P_3 \times P_4 = 0.53$ | $P_5 \times P_6 = 0.04$ |

Significance of SCA effects

$$SE_{Sij} = \sqrt{\frac{(P-3)M_e}{2(P-1)}} = \sqrt{\frac{3 \times 0.036}{2 \times 5}} = 0.11$$

$$t = \frac{S_{ij}}{SE_{ij}} \text{ - calculated 't' at error d.f = 1.96}$$

Since PCA variance is not significant, PCA effect not be worked out. The SCA effects of the hybrids can be taken as such for their reciprocal cross.

The two parents viz; P_4 & P_6 recorded positively significant GCA effect. Hence, these two parents can be used in breeding programmes to improve the root primary branches. The hybrid viz., $P_1 \times P_5$, $P_5 \times P_1$, $P_1 \times P_6$, $P_6 \times P_1$, $P_2 \times P_3$, $P_3 \times P_2$, $P_3 \times P_4$, $P_4 \times P_3$, $P_4 \times P_5$ & $P_5 \times P_4$ which recorded positively significant SCA effect are recommended for heterosis breeding. Though two parent (P_4 & P_6) recorded significant GCA effects, their hybrid recorded negatively significant SCA effects.

Title:

Experiment No:

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Hence, this hybrid is of no use. However, the hybrid $P_3 \times P_6$ (with non-significant SCA effects) could be used in combination breeding since at least one of the parents had positively significant GCA effects & the other parent with non-significant GCA effects.

A total of eight parents in maize were crossed in diallel fashion following method IV. The grain yield per plant (g) recorded on three replications in RBD is given below. Work out the gene action & suggest suitable breeding method for improvement of grain yield. Suggest the suitability of parents & hybrids in different breeding programmes.

| Genotype | Grain yield per plant (g) | | | | |
|---------------------------------|---------------------------|---------|----------|--------|--------|
| | Rep. I | Rep. II | Rep. III | Total | Mean |
| P ₁ × P ₂ | 88.60 | 96.80 | 105.72 | 291.12 | 97.04 |
| P ₁ × P ₃ | 72.36 | 82.72 | 78.86 | 233.94 | 77.98 |
| P ₁ × P ₄ | 146.32 | 128.37 | 124.75 | 409.44 | 136.48 |
| P ₁ × P ₅ | 97.63 | 102.78 | 95.21 | 295.62 | 98.54 |
| P ₁ × P ₆ | 102.73 | 118.64 | 112.62 | 333.99 | 111.33 |
| P ₁ × P ₇ | 98.72 | 105.31 | 101.92 | 306.00 | 102.00 |
| P ₁ × P ₈ | 144.84 | 135.64 | 121.73 | 402.21 | 134.07 |
| P ₂ × P ₃ | 86.45 | 97.17 | 99.24 | 282.86 | 94.32 |
| P ₂ × P ₄ | 108.32 | 120.68 | 121.16 | 350.16 | 116.72 |
| P ₂ × P ₅ | 98.34 | 86.78 | 91.51 | 276.63 | 92.21 |
| P ₂ × P ₆ | 126.32 | 110.84 | 129.59 | 366.75 | 122.25 |
| P ₂ × P ₇ | 143.73 | 129.64 | 121.64 | 404.01 | 134.67 |
| P ₂ × P ₈ | 103.42 | 116.84 | 115.59 | 335.85 | 111.95 |
| P ₃ × P ₄ | 119.34 | 130.07 | 103.78 | 353.19 | 117.73 |
| P ₃ × P ₅ | 112.68 | 98.40 | 99.82 | 310.90 | 103.63 |
| P ₃ × P ₆ | 118.32 | 131.37 | 117.18 | 366.87 | 122.29 |
| P ₃ × P ₇ | 131.64 | 148.76 | 153.28 | 433.68 | 144.56 |
| P ₃ × P ₈ | 161.40 | 156.78 | 147.06 | 465.24 | 153.08 |
| P ₄ × P ₅ | 98.30 | 102.68 | 113.66 | 314.64 | 104.88 |
| P ₄ × P ₆ | 118.76 | 103.24 | 120.27 | 342.27 | 114.09 |
| P ₄ × P ₇ | 104.64 | 112.78 | 93.67 | 311.09 | 103.69 |
| P ₄ × P ₈ | 152.28 | 136.37 | 156.25 | 444.90 | 148.30 |

| | | | | | |
|---------------------------------|--------|--------|--------|---------|---------|
| P ₂ x P ₆ | 121.62 | 113.70 | 131.62 | 377.94 | 125.98 |
| P ₃ x P ₇ | 111.54 | 125.32 | 118.04 | 355.20 | 118.40 |
| P ₄ x P ₈ | 109.72 | 113.20 | 87.31 | 310.23 | 103.41 |
| P ₅ x P ₇ | 132.78 | 152.87 | 160.14 | 446.79 | 148.93 |
| P ₆ x P ₈ | 111.24 | 99.72 | 101.73 | 312.69 | 104.23 |
| P ₇ x P ₈ | 115.23 | 110.71 | 126.83 | 352.77 | 117.59 |
| Total | - | - | - | 9785.13 | 3261.71 |

A. Analysis of Variance for RBD

| Source | df | SS | MS | F |
|-------------|----|----------|---------|-------|
| Replication | 2 | 7.14 | 3.57 | 0.04 |
| Genotypes | 27 | 29020.41 | 1074.83 | 12.75 |
| Error | 54 | 4551.10 | 84.28 | |
| Total | 83 | 33578.64 | - | - |

Two-way Table

| | P ₁ | P ₂ | P ₃ | P ₄ | P ₅ | P ₆ | P ₇ | P ₈ | Total | Y _i |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|---------|----------------|
| P ₁ | - | 97.04 | 77.98 | 136.48 | 98.54 | 111.33 | 102.00 | 134.07 | 754.44 | 757.44 |
| P ₂ | - | - | 94.72 | 116.72 | 92.21 | 122.25 | 134.67 | 111.95 | 672.12 | 769.16 |
| P ₃ | - | - | - | 117.73 | 103.65 | 122.29 | 144.56 | 153.08 | 641.31 | 813.61 |
| P ₄ | - | - | - | - | 104.88 | 114.09 | 105.03 | 149.30 | 472.30 | 513.22 |
| P ₅ | - | - | - | - | - | 125.48 | 118.40 | 103.41 | 347.29 | 477.07 |
| P ₆ | - | - | - | - | - | - | 148.97 | 104.23 | 253.16 | 349.10 |
| P ₇ | - | - | - | - | - | - | - | 117.59 | 117.59 | 321.19 |
| P ₈ | - | - | - | - | - | - | - | - | - | 372.63 |
| Total | - | - | - | - | - | - | - | - | 3261.71 | |

Y_i = row total + value of reciprocal crosses

$$SS \text{ due to GCA} = \frac{1}{P-2} \left[\sum Y_i^2 - \frac{4}{P(P-2)} Y_{..}^2 \right]$$

$$= \frac{1}{6} [757.44^2 + 769.16^2 + \dots + 872.63^2] - \frac{4}{7 \times 6} (3261.71) = 3077.74$$

$$\text{SS due to SCA} = \sum \sum y_{ij}^2 - \frac{1}{p-2} \sum y_i^2 + \frac{2}{(p-1)(p-2)} \sum y_i^2$$

$$= [97.04^2 + 77.98^2 + \dots + 117.59^2] - \frac{1}{6} [757.44^2 + \dots + 872.63^2] + \frac{2}{7 \times 6} (3261.71)^2$$

$$= 6595.76$$

Analysis of Variance for Combining Ability

| Source | df | SS | MS | F |
|--------|----|---------|-------------|-------|
| GCA | 7 | 3077.74 | 439.68 (Mg) | 15.65 |
| SCA | 20 | 6595.76 | 329.79 (Ht) | 11.74 |
| Errors | 34 | 4571.19 | 28.09 (Ht) | - |

Genetic components +

Model - 1

$$\sum g_i^2 = \frac{Mg - Mc}{(p-2)} = \frac{439.68 - 28.09}{6} = 68.60$$

$$\sum s_{ij}^2 = MS - Mc = 329.79 - 28.09 = 301.70$$

$$\text{The ratio of } \frac{\sum g_i^2}{\sum s_{ij}^2} = \frac{68.60}{301.70} = 0.23$$

Since the ratio of GCA variance / SCA variance is less than unity, the grain yield per plant in maize is governed by dominance gene action.

Estimation of heredit Effects.

i) GCA effects of parents

$$g_i = \frac{1}{P(P-2)} [PX_i + 2Y_{..}]$$

$$P_1 = \frac{1}{8 \times 6} [(8 \times 757.44) - (2 \times 3261.71)] = \frac{1}{48}$$

$$(6059.52 - 6523.42) = -9.66$$

$$P_1 = -9.66$$

$$P_5 = -11.39$$

$$P_2 = -7.71$$

$$P_6 = 5.61$$

$$P_3 = -0.30$$

$$P_7 = 9.29$$

$$P_4 = 4.63$$

$$P_8 = 9.53$$

$$\sum g_i = 0$$

Significance of GCA effects

$$SEg_i = \sqrt{\frac{(P-1) M_e}{P(P-2)}} = \sqrt{\frac{7 \times 28.09}{8 \times 6}} = 2.02$$

$$t = \frac{g_i}{SEg_i} \text{ calculated 't' at error d.f.} = 1.96$$

ii) SA effects of hybrids

$$S_{ij} = Y_{ij} - \frac{1}{P-2} (Y_i + Y_j) + \frac{2}{(P-1)(P-2)} Y_{..}$$

$$= P_1 \times P_2 - \frac{1}{P-2} (Y_1 + Y_2) + \frac{1}{(P-1)(P-2)} Y_{..}$$

$$P_1 \times P_2 = 97.04 - \frac{1}{6} (757.44 + 769.10) + \frac{2}{7 \times 6} (3261.71)$$

$$= 97.04 - 254.43 + 155.32 = -2.07$$

$$P_1 \times P_2 = -2.07$$

$$P_2 \times P_4 = 3.31$$

$$P_4 \times P_5 = -4.85$$

$$P_1 \times P_3 = -28.54$$

$$P_2 \times P_5 = -5.18$$

$$P_4 \times P_6 = -12.65$$

$$P_1 \times P_4 = 25.02$$

$$P_2 \times P_6 = 7.86$$

$$P_4 \times P_7 = -25.39$$

$$P_1 \times P_5 = 2.11$$

$$P_2 \times P_7 = 16.60$$

$$P_4 \times P_8 = 17.64$$

$$P_1 \times P_6 = -4.1$$

$$P_2 \times P_8 = -6.30$$

$$P_5 \times P_6 = 15.23$$

$$P_1 \times P_7 = -14.12$$

$$P_3 \times P_4 = -3.09$$

$$P_5 \times P_7 = 4.01$$

$$P_1 \times P_8 = 13.17$$

$$P_3 \times P_5 = -1.14$$

$$P_5 \times P_8 = -11.22$$

$$P_2 \times P_3 = -14.16$$

$$P_3 \times P_6 = 0.49$$

$$P_6 \times P_7 = 17.54$$

$$P_3 \times P_7 = 19.08$$

$$P_6 \times P_8 = -27.41$$

$$P_3 \times P_8 = 27.36$$

$$P_7 \times P_8 = -17.73$$

Significance of SCA effects

$$SE_{Sij} = \sqrt{\frac{(P-3) M_e}{(P-1)}} = \sqrt{\frac{5 \times 28.09}{7}} = 4.48$$

$$t = \frac{S_{ij}}{SE_{Sij}}$$

calculated 't' at error d.f = 2.005

The four parent viz; P_4 , P_6 , P_7 and P_8 recorded positively significant GCA effects. Hence, these four parents can be used in breeding programmes to improve grain yield. The hybrids viz, $P_1 \times P_4$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_7$, $P_3 \times P_8$, $P_4 \times P_8$, $P_5 \times P_6$ and $P_6 \times P_7$ which recorded positively significant SCA effects are recommended for heterosis breeding. The two hybrids viz $P_4 \times P_8$ and $P_6 \times P_7$ are recommended for recombination breeding. However, since the SCA effects of these hybrids are significant selection of superior plants should be postponed to later generation.

A total of 24 cotton hybrids obtained by LX Mating design were evaluated in an RBD with three replicans. The following are data on 2.5% span length in mm. Workout the mode of inheritance and suggest breeding method to improve span length. Estimate gca and sca effects and suggest suitability of the parents and hybrids for different breeding programmes.

| Hybrid | 2.5% Span length (mm) | | | | |
|---------------------------------|-----------------------|-------|-------|--------|------|
| | R1 | R11 | R111 | Total | Mean |
| L ₁ X T ₁ | 30.4 | 30.7 | 30.7 | 91.8 | 30.6 |
| L ₂ X T ₁ | 32.1 | 31.7 | 32.2 | 96.0 | 32.0 |
| L ₃ X T ₁ | 30.2 | 30.3 | 30.1 | 90.6 | 30.2 |
| L ₄ X T ₁ | 27.9 | 28.0 | 27.5 | 83.4 | 27.8 |
| L ₅ X T ₁ | 27.1 | 27.4 | 27.4 | 81.9 | 27.3 |
| L ₆ X T ₁ | 28.6 | 28.8 | 28.4 | 85.8 | 28.6 |
| L ₇ X T ₁ | 30.0 | 29.8 | 29.9 | 89.7 | 29.9 |
| L ₈ X T ₁ | 32.6 | 32.5 | 32.4 | 97.5 | 32.5 |
| L ₁ X T ₂ | 27.3 | 27.2 | 27.1 | 81.6 | 27.2 |
| L ₂ X T ₂ | 27.4 | 27.1 | 27.1 | 81.6 | 27.2 |
| L ₃ X T ₂ | 25.9 | 26.1 | 25.7 | 77.7 | 25.9 |
| L ₄ X T ₂ | 25.5 | 25.0 | 25.1 | 75.6 | 25.2 |
| L ₅ X T ₂ | 24.7 | 24.6 | 24.8 | 74.1 | 24.7 |
| L ₆ X T ₂ | 25.9 | 25.7 | 25.5 | 77.1 | 25.7 |
| L ₇ X T ₂ | 27.0 | 27.2 | 26.8 | 81.0 | 27.0 |
| L ₈ X T ₂ | 27.0 | 26.8 | 26.9 | 80.7 | 26.9 |
| L ₁ X T ₃ | 28.6 | 28.9 | 28.9 | 86.4 | 28.8 |
| L ₂ X T ₃ | 31.2 | 31.1 | 30.7 | 93.0 | 31.0 |
| L ₃ X T ₃ | 29.2 | 28.9 | 29.2 | 87.3 | 29.1 |
| L ₄ X T ₃ | 29.0 | 29.2 | 29.1 | 87.3 | 29.1 |
| L ₅ X T ₃ | 29.6 | 29.2 | 29.7 | 88.5 | 29.5 |
| L ₆ X T ₃ | 30.2 | 30.4 | 30.0 | 90.6 | 30.2 |
| L ₇ X T ₃ | 30.3 | 30.1 | 29.9 | 90.3 | 30.1 |
| L ₈ X T ₃ | 31.9 | 32.0 | 32.1 | 96.0 | 32.0 |
| Total | 689.6 | 688.7 | 687.2 | 2065.5 | |

Title:

Experiment No:

Date:

A. Correction Factor = $\frac{2065.5^2}{72} = 59254.02$
 Total SS = $39593.13 - CF = 339.10$
 Rep. SS = $59254.15 - CF = 0.12$
 Treat. SS = $59591.49 - CF = 337.46$
 Error SS = Total SS - Treat. SS - Rep. SS
 = $339.10 - 337.46 - 0.12 = 1.52$

ANOVA for RBD

| Source | df | SS | MS | F |
|-------------|----|--------|-------|--------|
| Replication | 2 | 0.12 | - | |
| Treatment | 23 | 337.46 | 14.67 | 444.76 |
| Error | 46 | 1.52 | 0.033 | |

Two-way table

| Testers lines | T ₁ | T ₂ | T ₃ | X _i |
|----------------|----------------|----------------|----------------|----------------|
| l ₁ | 91.8 | 81.6 | 86.4 | 259.8 |
| l ₂ | 96.0 | 81.6 | 93.0 | 270.6 |
| l ₃ | 90.6 | 77.7 | 87.3 | 255.6 |
| l ₄ | 83.4 | 75.6 | 87.3 | 246.3 |
| l ₅ | 81.9 | 74.1 | 88.5 | 244.5 |
| l ₆ | 85.8 | 77.1 | 90.6 | 253.5 |
| l ₇ | 89.7 | 81.0 | 90.3 | 261.0 |
| l ₈ | 97.5 | 80.7 | 96.0 | 274.2 |
| X _j | 716.7 | 629.4 | 719.4 | 2065.5 |

line SS = $\frac{259.8^2 + \dots + 274.2^2}{8 \times 3} - CF = \frac{534064.59}{24} - CF = 86.48$

$$\text{Testex SS} = \frac{716.7^2 + \dots + 719.4^2}{8 \times 1} - CF$$

$$= \frac{1497339.61}{328} - CF$$

$$= 218.45$$

$$\text{line} \times \text{Testex SS} = \text{Treat. SS} - \text{line SS} - \text{Testex SS}$$

$$= 337.46 - 86.48 - 218.45$$

$$= 32.53$$

ANOVA for combining Ability

| Source | df | SS | MS | | F |
|---------------------------|----|--------|--------|--------------------|--------|
| Treatment | 93 | 337.46 | | | |
| lines | 7 | 86.48 | 12.35 | (MS ₁) | |
| Testexs | 2 | 218.45 | 109.23 | (MS ₂) | 324.24 |
| line x Testex interaction | 14 | 32.53 | 2.32 | (MS ₃) | 331000 |
| Error | 46 | 1.53 | 0.033 | (MS ₄) | 704 |

$$\sigma^2_{hCA} = \frac{(MS_1 - MS_3) + (MS_2 - MS_3)}{2(1+1)}$$

$$= \frac{(12.35 - 2.32) + (109.23 - 2.32)}{3 \times 11}$$

$$= 3.54$$

$$\text{Additive genetic Variance } (\sigma_A^2) = 2 \times \sigma_{GCA}^2 = 2.08$$

$$\sigma_{SCA}^2 = \frac{MS_3 - MS_4}{8} = \frac{2.287}{3} = 0.76$$

$$\text{Dominance genetic Variance } (\sigma_D^2) = \sigma_{SCA}^2 = 0.76$$

Since additive genetic variance (σ_A^2) is several times higher than dominance genetic variance (σ_D^2), the trait 2.5% span length in cotton is governed by additive gene action. Therefore, simple selection techniques and recombination breeding followed by pedigree method of selection is suggested to improve 2.5% span length.

Combining Ability Effects:

i) General combining ability effects (GCA):

$$\text{GCA effects of lines } (g_i) = \frac{\sum x_{i..}}{8} - \frac{\sum x_{...}}{24}$$

$$\text{SE for GCA of lines} = \sqrt{\frac{EMS}{81}} = \sqrt{\frac{0.033}{9}} = 0.06$$

$$\text{GCA effects of testers } (g_j) = \frac{\sum x_{.j.}}{81} - \frac{\sum x_{...}}{24}$$

$$\text{SE for GCA of testers} = \sqrt{\frac{EMS}{81}} = \sqrt{\frac{0.033}{24}} = 0.04$$

$$\text{Calculated } t = \frac{\text{GCA}}{\text{SE GCA}} \quad \text{Table } t \text{ at } 46 \text{ d.f.} = 2.013$$

| parents Lines | GCA effects | t value |
|------------------|---|-----------------------|
| L ₁ | $\frac{259.8}{3 \times 3} - \frac{2065.5}{3 \times 8 \times 3}$ | $= \frac{0.18}{0.06}$ |
| | 0.18 | = 3.0 |
| L ₂ | 1.38 | 23.0 |
| L ₃ | -0.29 | 4.83 |
| L ₄ | -1.32 | 22.00 |
| L ₅ | -1.52 | 25.33 |
| L ₆ | -0.52 | 8.67 |
| L ₇ | 0.31 | 5.17 |
| L ₈ | 1.78 | 29.67 |
| Testers | | |
| T ₁ | $\frac{716.7}{3 \times 8} - \frac{2065.5}{3 \times 8 \times 3}$ | $= \frac{1.17}{0.04}$ |
| | 1.17 | = 29.25 |
| T ₂ | -2.46 | 61.75 |
| T ₃ | 1.29 | 32.25 |

$$\sum g_j \text{ (for lines)} = 0$$

$$\sum g_j \text{ (for testers)} = 0$$

ii) special combining ability effects (SCA):

$$\text{SCA effects of hybrids } (S_{ij}) = \frac{x_{ij}}{8} - \frac{x_{i.}}{8} - \frac{x_{.j}}{8} + \frac{x}{81}$$

$$\text{SE for SCA} = \sqrt{\frac{\text{EMS}}{8}} = \sqrt{\frac{0.033}{3}} = 0.11$$

$$\text{Calculated } t = \frac{\text{SCA}}{\text{SE SCA}} \quad \text{Table 1 at 46 d.f} = 2.01$$

| Hybrids | SCA effects | F-Value |
|----------------------|---|-----------------------|
| $L_1 \times \bar{T}$ | $\frac{91.8}{3} - \frac{259.8}{9} - \frac{216.7}{24}$ | $= \frac{0.56}{0.11}$ |
| | $+ \frac{2065.5}{3 \times 8 \times 3}$ | |
| | $= 0.56$ | $= 3.09$ |
| $L_1 \times T_1$ | 0.79 | 7.18 |
| $L_1 \times T_2$ | -1.36 | 12.36 |
| $L_2 \times T_1$ | 0.76 | 6.91 |
| $L_2 \times T_2$ | -0.41 | 3.73 |
| $L_2 \times T_3$ | 0.36 | 3.92 |
| $L_3 \times T_1$ | 0.63 | 5.73 |
| $L_3 \times T_2$ | -0.04 | 0.36 |
| $L_3 \times T_3$ | -0.59 | 5.36 |
| $L_4 \times T_1$ | -0.74 | 6.73 |
| $L_4 \times T_2$ | 0.29 | 2.64 |
| $L_4 \times T_3$ | 0.44 | 4.00 |
| $L_5 \times T_1$ | 1.04 | 9.45 |
| $L_5 \times T_2$ | -0.01 | 0.09 |
| $L_5 \times T_3$ | 1.04 | 9.45 |
| $L_6 \times T_1$ | -0.74 | 6.73 |
| $L_6 \times T_2$ | 0.01 | 0.09 |
| $L_6 \times T_3$ | 0.74 | 6.73 |
| $L_7 \times T_1$ | 0.23 | 2.45 |
| $L_7 \times T_2$ | 0.46 | 4.18 |
| $L_7 \times T_3$ | -0.19 | 1.73 |
| $L_8 \times T_1$ | 0.86 | 7.82 |
| $L_8 \times T_2$ | -1.11 | 10.09 |
| $L_8 \times T_3$ | 0.24 | 2.18 |

The parents L_1, L_2, L_3, L_6, T_1 and T_3 revealed positively significant ICA effects. Therefore these parents excelled others. A multiple crossing programme involving all these parents will result

in identification of superior genotypes with high 2.5% span length.

The hybrids $L_1 \times T_1$, $L_1 \times T_2$, $L_2 \times T_1$, $L_3 \times T_1$, $L_4 \times T_2$, $L_4 \times T_3$, $L_5 \times T_3$, $L_6 \times T_3$, $L_7 \times T_2$ and $L_8 \times T_1$, recorded possibly significant SCA effects. Therefore these hybrids are recommended for by-selection breeding. The hybrids with non-significant SCA effect (absence of dominance) and parents with significant GCA effects (presence of additive gene action) are useful in identification of superior segregants. Therefore, the hybrid $L_7 \times T_2$ (with non-significant SCA effects) and parents with significant GCA effects is recommended for recombination breeding with pedigree method of selection.

Title: Estimation of Heterosis and Inbreeding depression

Experiment No: 10

Date: 2-6-22

A total of 15 hybrids and their parents was evaluated in RBD with four replications. The following is the data on yield in gms. Work out the heterosis present on all the three bases and comment on the results. Assume P_3 is the standard check.

| Genotype | R _I | R _{II} | R _{III} | R _{IV} | Total | Mean |
|------------------|----------------|-----------------|------------------|-----------------|--------|--------|
| $P_1 \times P_6$ | 64.4 | 60.8 | 51.0 | 58.6 | 234.2 | 58.55 |
| $P_2 \times P_6$ | 91.8 | 89.2 | 98.8 | 92.7 | 372.5 | 93.13 |
| $P_3 \times P_6$ | 38.1 | 48.2 | 42.5 | 45.8 | 174.6 | 43.65 |
| $P_4 \times P_6$ | 54.1 | 55.6 | 62.7 | 61.7 | 234.1 | 58.53 |
| $P_5 \times P_6$ | 74.2 | 85.3 | 78.8 | 84.5 | 322.8 | 80.70 |
| $P_1 \times P_7$ | 86.9 | 81.4 | 75.8 | 70.4 | 314.5 | 78.63 |
| $P_2 \times P_7$ | 99.8 | 88.2 | 83.3 | 92.3 | 363.6 | 90.90 |
| $P_3 \times P_7$ | 109.2 | 102.3 | 108.2 | 104.5 | 424.2 | 106.05 |
| $P_4 \times P_7$ | 99.7 | 106.5 | 112.8 | 110.9 | 429.9 | 107.48 |
| $P_5 \times P_7$ | 105.2 | 106.7 | 97.9 | 111.4 | 421.2 | 105.3 |
| $P_1 \times P_8$ | 54.4 | 60.8 | 64.8 | 64.1 | 244.1 | 61.03 |
| $P_2 \times P_8$ | 53.9 | 48.3 | 50.6 | 54.6 | 207.4 | 51.85 |
| $P_3 \times P_8$ | 93.5 | 93.1 | 89.2 | 83.8 | 359.6 | 89.90 |
| $P_4 \times P_8$ | 81.4 | 79.8 | 82.8 | 83.7 | 327.7 | 81.93 |
| $P_5 \times P_8$ | 88.6 | 94.2 | 90.8 | 96.2 | 369.8 | 92.45 |
| P_1 | 64.4 | 56.2 | 62.9 | 59.3 | 242.8 | 60.70 |
| P_2 | 96.9 | 91.4 | 83.8 | 88.4 | 360.5 | 90.13 |
| P_3 | 95.8 | 99.3 | 96.2 | 99.4 | 390.7 | 97.68 |
| P_4 | 82.4 | 70.8 | 73.8 | 69.8 | 296.8 | 69.20 |
| P_5 | 81.5 | 72.8 | 89.8 | 83.7 | 327.8 | 81.95 |
| P_6 | 53.2 | 60.6 | 61.6 | 56.8 | 232.2 | 58.05 |
| P_7 | 92.2 | 99.7 | 90.2 | 99.4 | 381.5 | 95.63 |
| P_8 | 85.3 | 89.6 | 79.4 | 84.3 | 338.6 | 84.65 |
| Total | 1827.9 | 1840.8 | 1827.7 | 1855.7 | 7352.1 | 79.9 |

A.

$$\text{Correction Factor} = \frac{(7352.1)^2}{92}$$

$$= 587536.68$$

$$\text{Total SS} = 619820.41 - CF = 32283.73$$

$$\text{Replication SS} = 587539.69 - CF = 23.01$$

$$\text{Treatment SS} = 618232.94 - CF = 30696.26$$

$$\text{Error SS} = \text{Total SS} - \text{Rep. SS} - \text{Treat. SS} = 1564.46$$

ANOVA Table

| Source | df | SS | MS | F |
|-------------|----|----------|---------|-------|
| Replication | 8 | 23.01 | 2.87 | 0.32 |
| Treatment | 22 | 30696.26 | 1395.28 | 58.87 |
| Error | 66 | 1564.46 | 23.70 | |
| Total | 91 | | | |

Standard error:

$$\text{Relative heterosis (di)} = \sqrt{\frac{3}{24} EMS} = \sqrt{\frac{3}{8} 23.70} = 2.98$$

Heterobeltosis (dii) & standard heterosis (diii)

$$= \sqrt{\frac{2}{8} EMS} = \sqrt{\frac{2}{4} 23.70} = 3.44$$

Heterosis percent:

$$P_1 \times P_6 \text{ di} = \frac{\bar{F}_1 - \bar{MP}}{\bar{MP}} \times 100 = \frac{58.55 - 59.38}{59.38} \times 100 = -1.40$$

$$\text{dii} = \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100 = \frac{58.55 - 60.70}{60.70} \times 100 = -3.34$$

$$\text{diii} = \frac{\bar{F}_1 - \bar{SV}}{\bar{SV}} \times 100 = \frac{58.55 - 97.68}{97.68} \times 100 = -40.66$$

Similarly, for all hybrids heterosis percent was worked out.

Test of significance

$$t \text{ value for di} = \frac{\bar{F}_1 - \bar{MP}}{SE}$$

$$t \text{ value for dii} = \frac{\bar{F}_1 - \bar{BP}}{SE}$$

$$t \text{ value for diii} = \frac{\bar{F}_1 - \bar{SV}}{SE}$$

| t value | (di) | (dii) | (diii) |
|------------------|------------------------------|------------------------------|--------------------------------|
| $P_1 \times P_6$ | $\frac{-0.83}{2.98} = -0.28$ | $\frac{-2.15}{3.44} = -0.63$ | $\frac{-39.13}{3.44} = -11.38$ |

Similarly, t value for all hybrids was worked out. Tabulated t value at 5% d.f₆₆ = 1.997.

Heterosis percent

| Hybrid | Relative heterosis | t-value | Hetero-beltiosis | t-value | Standard heterosis | t-value |
|---------------------------------|--------------------|---------|------------------|---------|--------------------|---------|
| P ₁ x P ₆ | -1.40 | 0.28 | -3.54 | 0.63 | -40.06 | 11.38 |
| P ₂ x P ₆ | 25.70 | 6.39 | 3.33 | 0.87 | -4.66 | 1.32 |
| P ₃ x P ₆ | -43.95 | 11.49 | -53.31 | 15.71 | -53.31 | 15.71 |
| P ₄ x P ₆ | -8.02 | 1.71 | -15.42 | 3.10 | -40.08 | 11.38 |
| P ₅ x P ₆ | 15.29 | 3.59 | -1.53 | 0.36 | -17.38 | 4.94 |
| P ₁ x P ₇ | 0.59 | 0.15 | -17.78 | 4.94 | -19.50 | 5.54 |
| P ₂ x P ₇ | -2.13 | 0.66 | -4.95 | 1.38 | -6.94 | 1.97 |
| P ₃ x P ₇ | 9.71 | 3.15 | 8.57 | 2.43 | 8.57 | 2.43 |
| P ₄ x P ₇ | 30.41 | 8.41 | 12.39 | 3.44 | 10.03 | 2.85 |
| P ₅ x P ₇ | 18.59 | 5.54 | 10.11 | 2.81 | 7.80 | 2.22 |
| P ₁ x P ₈ | 16.03 | 3.91 | -27.90 | 6.87 | -37.32 | 10.65 |
| P ₂ x P ₈ | -40.67 | 11.93 | -42.47 | 11.13 | -46.92 | 13.32 |
| P ₃ x P ₈ | -1.39 | 0.43 | -7.96 | 2.26 | -7.96 | 2.26 |
| P ₄ x P ₈ | 6.50 | 1.68 | -3.21 | 0.79 | -16.12 | 4.38 |
| P ₅ x P ₈ | 10.98 | 3.07 | 9.21 | 2.77 | -5.35 | 1.52 |

Conclusion

The hybrids P₃ x P₇, P₄ x P₇ and P₅ x P₇ and exceeded other hybrids by recording significantly superior heterosis on all the three bases.

A total of 15 hybrids & their parents was evaluated in a RBD with four replications. The following is the data on yield in gms. Work out the heterosis percent on all the three bases and comment on the results. Assume P₃ is the standard check.

| Genotype | R1 | R11 | R111 | R1V | Total | Mean | F ₂ |
|---------------------------------|--------|--------|--------|--------|--------|---------|----------------|
| P ₁ × P ₆ | 64.4 | 60.8 | 51.0 | 58.0 | 234.2 | 58.55 | 58.90 |
| P ₂ × P ₆ | 91.8 | 89.2 | 98.8 | 92.7 | 372.5 | 93.13 | 60.5 |
| P ₃ × P ₆ | 38.1 | 48.2 | 42.5 | 45.8 | 174.6 | 43.65 | 72.5 |
| P ₄ × P ₆ | 54.1 | 55.6 | 62.9 | 61.7 | 234.1 | 58.53 | 55.2 |
| P ₅ × P ₆ | 74.2 | 85.3 | 78.8 | 84.5 | 322.8 | 80.70 | 49.1 |
| P ₁ × P ₃ | 76.9 | 81.4 | 75.8 | 70.4 | 314.5 | 78.63 | 64.5 |
| P ₂ × P ₃ | 99.8 | 88.2 | 83.3 | 92.7 | 363.6 | 90.90 | 75.3 |
| P ₃ × P ₃ | 109.2 | 102.3 | 108.2 | 104.5 | 424.2 | 106.05 | 94.2 |
| P ₄ × P ₃ | 99.7 | 106.5 | 112.5 | 110.9 | 429.9 | 107.48 | 89.1 |
| P ₅ × P ₃ | 105.2 | 106.7 | 99.9 | 111.4 | 423.2 | 105.7 | 72.5 |
| P ₁ × P ₃ | 54.4 | 60.8 | 64.8 | 64.1 | 244.1 | 61.03 | 60.1 |
| P ₂ × P ₃ | 58.9 | 48.3 | 50.6 | 51.6 | 209.4 | 51.85 | 49.3 |
| P ₃ × P ₃ | 98.5 | 92.1 | 89.2 | 83.8 | 359.6 | 89.90 | 54.2 |
| P ₄ × P ₃ | 81.4 | 79.8 | 82.8 | 83.7 | 327.7 | 81.93 | 62.5 |
| P ₅ × P ₃ | 88.6 | 94.2 | 90.8 | 96.2 | 369.8 | 92.45 | 84.3 |
| Total | 1195.2 | 1200.4 | 1189.7 | 1214.6 | 4800.2 | 1200.08 | 1002.2 |

$$\text{Inbreeding depression} = \frac{F_1 - F_2}{F_1} \times 100$$

$$P_1 \times P_6 = \frac{58.55 - 58.90}{58.55} = 0.058 \%$$

$$P_2 \times P_6 = \frac{93.13 - 60.5}{93.13} = 0.350 \%$$

$$P_3 \times P_6 = \frac{43.65 - 72.5}{43.65} = 0.66 \%$$

$$P_4 \times P_6 = \frac{58.53 - 55.2}{58.53} = 0.05 \%$$

$$P_5 \times P_6 = \frac{80.70 - 49.1}{80.70} = 0.39 \%$$

$$P_1 \times P_7 = \frac{78.63 - 64.5}{78.63} = 0.17 \%$$

$$P_2 \times P_7 = \frac{90.90 - 75.3}{90.90} = 0.17 \%$$

$$P_3 \times P_7 = \frac{106.05 - 94.2}{106.05} = 0.11 \%$$

$$P_4 \times P_7 = \frac{107.48 - 89.1}{107.48} = 0.17 \%$$

$$P_5 \times P_7 = \frac{105.3 - 72.5}{105.3} = 0.31 \%$$

$$P_1 \times P_8 = \frac{61.03 - 60.1}{61.03} = 0.01 \%$$

$$P_2 \times P_8 = \frac{51.85 - 49.3}{51.85} = 0.049 \%$$

$$P_3 \times P_8 = \frac{89.90 - 54.2}{89.90} = 0.39 \%$$

$$P_1 \times P_8 = \frac{81.93 - 62.5}{81.93} = 0.237$$

$$P_3 \times P_8 = \frac{92.45 - 84.3}{92.45} = 0.0887$$

$$\left[\frac{11200.05 - 1002.2}{11200.08} = 0.91 \right]$$

So, here I conclude that $P_2 \times P_6$ is having highest inbreeding depression, $P_3 \times P_6$ is having medium inbreeding depression and $P_1 \times P_8$ is having lowest inbreeding depression.

A total of 12 genotypes of sesame was evaluated in three environments in RBD with three replications. The following is the environment wise data on plant height (cm) worked out the stability parameters for different genotypes & comment on the results.

Environment - 1

| Genotype | Rep. I | Rep. II | Rep. III | Total | Mean |
|----------|--------|---------|----------|--------|-------|
| 1 | 108.8 | 104.6 | 97.1 | 310.5 | 103.5 |
| 2 | 71.2 | 76.4 | 77.7 | 225.3 | 75.1 |
| 3 | 103.4 | 99.6 | 95.9 | 297.9 | 99.3 |
| 4 | 96.8 | 88.4 | 89.3 | 274.5 | 91.5 |
| 5 | 75.4 | 82.7 | 82.8 | 240.9 | 80.3 |
| 6 | 82.1 | 84.2 | 85.7 | 252.0 | 84.0 |
| 7 | 86.7 | 91.9 | 97.4 | 276.0 | 92.0 |
| 8 | 85.0 | 92.4 | 85.4 | 262.8 | 87.6 |
| 9 | 69.4 | 61.2 | 65.0 | 195.6 | 65.2 |
| 10 | 92.2 | 88.7 | 98.4 | 279.3 | 93.1 |
| 11 | 81.4 | 87.6 | 76.7 | 245.7 | 81.9 |
| 12 | 98.2 | 106.0 | 108.4 | 312.6 | 104.2 |
| Total | 1050.6 | 1062.7 | 1059.8 | 3173.1 | |

Environment - 2

| Genotypes | Rep 1 | Rep. II | Rep III | Total | Mean |
|-----------|-------|---------|---------|-------|-------|
| 1 | 103.7 | 112.6 | 116 | 327.9 | 109.3 |
| 2 | 102.6 | 95.3 | 94.6 | 292.5 | 97.5 |
| 3 | 99.9 | 108.3 | 98.4 | 306.6 | 102.2 |
| 4 | 106.8 | 102.8 | 112.6 | 322.2 | 107.4 |
| 5 | 115.0 | 123.4 | 118.4 | 357.0 | 119.0 |
| 6 | 98.6 | 100.8 | 108.6 | 307.8 | 102.6 |
| 7 | 93.3 | 103.6 | 102.3 | 301.2 | 100.4 |

Title:

Experiment No:

Date:

| | | | | | |
|-------|--------|--------|--------|--------|-------|
| 8 | 92.6 | 98.6 | 89.3 | 280.5 | 93.5 |
| 9 | 82.4 | 88.8 | 89.8 | 261 | 87.0 |
| 10 | 97.6 | 104.3 | 92.7 | 294.6 | 98.2 |
| 11 | 75.9 | 74.8 | 79.7 | 230.4 | 76.8 |
| 12 | 107.7 | 104.2 | 113.6 | 325.5 | 108.5 |
| Total | 1176.1 | 1219.5 | 1211.6 | 3607.2 | |

Environment 3

| Genotype | Rep I | Rep. II | Rep. III | Total | Mean |
|----------|--------|---------|----------|--------|-------|
| 1 | 88.7 | 76.8 | 78.7 | 244.2 | 81.4 |
| 2 | 88.4 | 96.7 | 101.4 | 286.5 | 95.5 |
| 3 | 106.8 | 99.2 | 108.7 | 314.7 | 104.9 |
| 4 | 108.2 | 119.8 | 117.6 | 345.6 | 115.2 |
| 5 | 110.0 | 105.3 | 116.2 | 331.5 | 110.5 |
| 6 | 118.7 | 112.2 | 119.8 | 350.7 | 116.9 |
| 7 | 129.7 | 118.0 | 125.8 | 373.5 | 124.6 |
| 8 | 108.6 | 108.5 | 94.8 | 311.9 | 103.8 |
| 9 | 100.7 | 107.8 | 94.3 | 298.8 | 99.6 |
| 10 | 108.2 | 106.1 | 98.6 | 312.9 | 104.3 |
| 11 | 86.1 | 84.3 | 92.1 | 262.5 | 87.5 |
| 12 | 96.2 | 99.7 | 86.8 | 282.7 | 91.9 |
| Total | 1250.3 | 1223.7 | 1234.3 | 3708.3 | |

A. Analysis of variance for individual environments

| Source | df | E1 | | | E2 | | | E3 | | |
|-------------|----|---------|--------|------|---------|--------|------|---------|--------|------|
| | | SS | MS | F | SS | MS | F | SS | MS | F |
| Replication | 2 | 6.65 | 3.33 | - | 89.06 | 44.53 | - | 29.89 | 14.95 | - |
| Genotypes | 11 | 4449.93 | 404.54 | 18.1 | 4024.28 | 366.75 | 17.0 | 3305.89 | 482.35 | 14.4 |
| Error | 22 | 491.73 | 22.35 | - | 435.58 | 21.62 | - | 737.29 | 33.51 | - |
| Total | 35 | 4948.31 | - | - | 4549.94 | - | - | 6073.17 | - | - |

Since, in all the three environment the genotypes are

significantly different, all the three environment are used for pooled analysis.

Bartlett's test for homogeneity of variances $\chi^2 = 1.2037$

As the χ^2 value is non-significant at 5% level pooled analysis can be performed.

pooled Analysis

Two-way Table

| Genotype | E ₁ | E ₂ | E ₃ | Total | Mean |
|----------|----------------|----------------|----------------|--------|--------|
| 1 | 103.5 | 109.3 | 81.4 | 294.2 | 98.07 |
| 2 | 75.1 | 97.5 | 95.5 | 268.1 | 89.37 |
| 3 | 99.2 | 102.2 | 104.9 | 306.4 | 102.13 |
| 4 | 91.5 | 107.4 | 115.2 | 314.1 | 104.70 |
| 5 | 80.3 | 119.0 | 110.5 | 309.8 | 103.27 |
| 6 | 84.0 | 102.6 | 116.9 | 303.5 | 101.17 |
| 7 | 92.0 | 100.4 | 124.6 | 317.0 | 105.67 |
| 8 | 97.6 | 93.5 | 103.8 | 294.9 | 94.97 |
| 9 | 65.2 | 87.0 | 99.6 | 251.8 | 83.93 |
| 10 | 93.1 | 98.2 | 104.3 | 295.6 | 98.53 |
| 11 | 81.4 | 76.8 | 87.5 | 246.2 | 82.07 |
| 12 | 104.2 | 108.5 | 91.9 | 304.6 | 101.53 |
| Total | 1057.7 | 1209.4 | 1236.1 | 3496.2 | - |
| Mean | 88.14 | 100.20 | 103.01 | 291.35 | 97.12 |

$$CF = \frac{(3496.2)^2}{36} = 339530.29$$

$$\text{Table SS} = 103.5^2 + 109.3^2 + \dots + 91.9^2 - CF = 6093.94$$

$$\text{Genotype SS} = \frac{294.2^2 + \dots + 304.6^2}{3} - CF = 209.22$$

$$\text{Environment SS} = \frac{10.57 \cdot 7^2 + \dots + 12.36 \cdot 1^2}{12} - CF = 1497.23$$

$$\text{GxE interaction SS} = 6093.94 - 2092 - 1497.23 = 2504.49$$

$$\text{MS due to pooled error} = \frac{491.73 + 475.58 + 733.39}{22 + 22 + 22}$$

$$= \frac{1704.70}{66} = 25.83$$

The pooled analysis was done using the mean data of 3 replications. Therefore, the MS due to the pooled error calculated above is to be divided by 3.

$$\text{MS due to pooled error} = \frac{25.83}{3} = 8.61$$

pooled Analysis of Variance

| Source | df | SS | MS | F |
|-----------------|----|---------|--------|-------|
| Genotypes | 11 | 2092.22 | 190.20 | 1.62 |
| Environment | 2 | 1497.23 | 748.61 | 6.58 |
| GxE Interaction | 22 | 2504.48 | 113.84 | 13.22 |
| pooled error | 66 | 1704.70 | 8.61 | |
| Total | 35 | 6093.93 | - | - |

Since the GxE interaction is significant, the analysis may be produced further for estimating stability parameters by different models.

I. Stability factors

As the E_1 and E_2 has high & low mean, the ratio b/w these two environments were calculated.

For the Stability Factor:

| Genotype | $E_1 (LE)$ | $E_2 (HE)$ | SF = (HE/LE) |
|----------|------------|------------|----------------|
| 1 | 102.50 | 81.40 | 0.79 |
| 2 | 75.10 | 95.50 | 1.27 |
| 3 | 99.30 | 104.90 | 1.06 |
| 4 | 91.50 | 115.20 | 1.26 |
| 5 | 80.30 | 110.50 | 1.38 |
| 6 | 84.00 | 116.90 | 1.39 |
| 7 | 92.00 | 124.60 | 1.35 |
| 8 | 87.60 | 103.80 | 1.18 |
| 9 | 65.20 | 99.60 | 1.53 |
| 10 | 93.10 | 104.30 | 1.12 |
| 11 | 81.90 | 87.50 | 1.07 |
| 12 | 104.20 | 91.90 | 0.88 |
| Mean | 88.14 | 103.01 | |

Stable genotypes should have consistent performance in both high & low mean environment & SF should be equal to 1. Among the genotypes, genotype 3 & 11 recorded SF nearer to 1 than other genotypes. Hence the genotypes 3 & 11 are considered as stable genotypes than others.

Eberhart & Russel Model

i) Environmental index (I_j for each environment):

$$I_j = \frac{\sum_j Y_{ij}}{g} - \frac{\sum_i sY_{ij}}{ge}$$

$$I_1 \text{ for } E_1 = \frac{1057.7}{12} - \frac{3496.2}{36} = \frac{88.14 - 97.12}{3} = -0.98$$

$$T_2 \text{ for } t_2 = \frac{1202.4}{12} - \frac{3496.2}{36} = 2.08$$

$$T_3 \text{ for } t_3 = \frac{1236.1}{12} - \frac{3496.2}{36} = 5.89$$

2) Regression Coefficient (b_i for each variety):

$$b_i = \frac{\sum Y_{ij} T_j}{\sum T_j^2}$$

$$\sum Y_{ij} T_j \text{ for genotypes 1} = (103.5 \times -8.98) + (109.3 \times 3.08) + (81.4 \times 5.89) = -112.32$$

$$\sum T_j^2 \text{ for all genotypes} = (-8.98)^2 + (3.08)^2 + (5.89)^2 = 124.82$$

$$b_1 \text{ for Genotype 1} = \frac{-112.32}{124.82} = -0.90$$

$$b_1 \text{ for Genotype 2} = -0.90$$

$$b_2 \text{ for Genotype 2} = 1.52$$

$$b_3 \text{ for Genotype 3} = 0.34$$

$$b_4 \text{ for Genotype 4} = 1.51$$

$$b_5 \text{ for Genotype 5} = 2.38$$

$$b_6 \text{ for Genotype 6} = 2.01$$

$$b_7 \text{ for Genotype 7} = 1.75$$

$$b_8 \text{ for Genotype 8} = 0.91$$

$$b_9 \text{ for Genotype 9} = 2.16$$

$$b_{10} \text{ for Genotype 10} = 0.66$$

$$b_{11} \text{ for Genotype 11} = 0.14$$

$$b_{12} \text{ for Genotype 12} = -0.48$$

Note that $\bar{b} = 1.00$

3) Mean Square Deviation ($\bar{S}^2 d$) from linear regression for each variety;

$$S^2 d = \frac{\sum s_{ij}^2}{c-2} - \frac{S_e^2}{r}$$

$$\sum s_{ij}^2 = \left[\sum Y_{ij}^2 - \frac{Y_{i.}^2}{c} \right] - \frac{(\sum Y_{ij} I_j)^2}{\sum I_j^2}$$

$S_e^2 =$ No clue to pooled error

Genotype 1

$$\sum Y_{ij}^2 - \frac{Y_{i.}^2}{c} = 103 \cdot 5^2 + 109 \cdot 3^2 + 81 \cdot 4^2 - \frac{294 \cdot 9^2}{3}$$

$$= 29284.7 - 28851.2 = 433.49$$

$$\frac{(\sum Y_{ij} I_j)^2}{\sum I_j^2} = \frac{[(103 \cdot 5 \times -8.98) + (109 \cdot 3 \times 3.08) + (81 \cdot 4 \times 5.87)]^2}{124.82}$$

$$= \frac{(-112.32)^2}{124.82} = 101.12$$

$$\sum s_{ij}^2 = 433.49 - 101.12 = 332.37$$

$$\bar{S}^2 d = \frac{332.37}{1} - 8.61 = 323.76$$

Similarly, the $\bar{S}^2 d$ values for all the genotypes were estimated.

| Genotypes | $\bar{S}^2 d$ | Genotype | $\bar{S}^2 d$ |
|-----------|---------------|----------|---------------|
| 1 | 323.76 | 7 | 183.59 |
| 2 | 11.62 | 8 | 22.34 |
| 3 | -7.02 | 9 | 15.38 |

| | | | |
|---|--------|----|-------|
| 4 | -2.09 | 10 | 0.76 |
| 5 | 110.54 | 11 | 46.29 |
| 6 | 29.99 | 12 | 11.74 |

Analysis of Variance:

S.S. due to Environment + [Genotype x Environment]:

$$= \text{SS due to Env.} + \text{SS due to G} \times \text{E interaction}$$

$$= 1497.23 + 2504.49 = 4001.72$$

SS due to environment (linear) = SS due to environment from pooled analysis of variance table = 1497.23

SS due to Genotype x Environment (linear)

$$= \sum_i \left[\frac{\sum_j Y_{ij} I_j^2}{\sum_j I_j^2} \right] - \text{SS. due to environment (linear)}$$

$$= 3053.50 - 1497.23 = 1556.27$$

SS due to pooled deviation:

$$= \text{SS due to Env.} + (\text{Geno} + \text{Env}) - \text{SS due to Env. (linear)} - \text{SS due to Geno} \times \text{Env. (linear)}$$

$$= 4001.72 - 1497.23 - 1556.27 = 948.22$$

Analysis of Variance for Stability

| Source | df | SS | MS | F |
|---------------------|----|---------|-------------|------|
| Total | 35 | 6097.93 | 174.11 | |
| Genotype | 11 | 2099.22 | 190.20 (MS) | 2.41 |
| Env. + (Geno x Env) | 24 | 4011.72 | 166.74 | |
| Env. (linear) | 1 | 1497.23 | 1497.23 | |
| Geno x Env (linear) | 11 | 1536.27 | 141.48 (MS) | 1.79 |

| | | | | |
|-----------------|----|---------|--------------------------|-------|
| ooled deviation | 12 | 948.72 | 79.02 (MS _d) | |
| Genotype 1 | 1 | 332.37 | 332.37 | 38.6 |
| Genotype 2 | 1 | 90.23 | 90.23 | 9.35 |
| Genotype 3 | 1 | 1.59 | 1.59 | 6.18 |
| Genotype 4 | 1 | 6.52 | 6.52 | 0.76 |
| Genotype 5 | 1 | 119.15 | 119.15 | 13.84 |
| Genotype 6 | 1 | 38.60 | 38.60 | 4.48 |
| Genotype 7 | 1 | 192.20 | 192.20 | 22.32 |
| Genotype 8 | 1 | 30.95 | 30.95 | 3.79 |
| Genotype 9 | 1 | 21.99 | 21.99 | 2.55 |
| Genotype 10 | 1 | 9.37 | 9.37 | 1.09 |
| Genotype 11 | 1 | 54.90 | 54.90 | 6.38 |
| Genotype 12 | 1 | 120.35 | 120.35 | 13.98 |
| ooled error | 66 | 1704.70 | 8.61 | |

Stability parameters:

i) High Desirable mean:

$$\text{Grand mean} = \frac{2496.2}{36} = 69.34$$

$$SE_m = \sqrt{\frac{MS \text{ due to pooled deviation}}{t-1}} = \sqrt{\frac{79.02}{2}} = 6.29$$

$$CD = SE_m \times \sqrt{2} \times t \text{ at pooled error df} = 6.29 \times 1.414 \times 1.997 = 17.76$$

This CD may be used to decide ~~at~~ about the superiority of the mean of individual genotypes.

ii) Deviation from linear regression: ($S^2d = 0$):
The S^2d for all genotypes are already presented.
To test the deviation of individual genotype from

linear regression, the following F-test is used.

$$F = \frac{\sum S_{ij}^2 / e-2}{M.S. \text{ pooled error}}$$

The F value of individual genotypes are already present.

iii) Regression coefficient:

The regression coefficient (b_i) for all genotypes are already presented. To test the significance of b_i values the following test is used:

$$SE_{b_i} = \sqrt{\frac{MS \text{ due to pooled deviation of } i^{\text{th}} \text{ genotype}}{\sum T_j^2}}$$

where, MS due to pooled deviation of i^{th} genotype = $\frac{S_{ij}^2}{e-2}$

$$SE_{b_i} = \sqrt{\frac{332.37}{124.81}} = 1.62$$

Stable genotype

The regression coefficient needs to be checked for only those genotypes with non significant SE values i.e., stable genotypes.

The next step is to test the significance of b_i from zero.

$$t = \frac{b_i - 0}{SE(b_i)}$$

The calculated t value is to be compared with table t -value $n-2$ df where n is the no. of env.

If b_i is significant from zero, it can be concluded that the ~~t -value~~ particular genotype is responsive to the environment. This has to be followed by test of significance of b_i from the unity.

$$t = \frac{b-1}{SE(b)}$$

If b_i is significantly different from $b=1$, then the value need to be checked for whether $b > 1$ (or) $b < 1$. Acc to response of genotype to the env can be defined.

| Genotype | Mean | S ² d | b_i | SE(b_i) | $t = (b-0)/SE$ | $t = (b-1)/SE$ |
|----------|--------|------------------|-------|-------------|----------------|----------------|
| 7 | 105.67 | 183.60 | 1.75 | 1.24 | 1.41 ns | 0.60 ns |
| 4 | 104.70 | 7.09 | 1.51 | 0.23 | 6.61 ns | 2.24 ns |
| 5 | 103.27 | 110.54 | 2.38 | 0.98 | 2.44 ns | 1.41 ns |
| 3 | 102.13 | 7.02 | 0.34 | 0.11 | 2.98 ns | -5.88 ns |
| 12 | 101.53 | 111.74 | -0.47 | 0.98 | -0.48 ns | -1.50 ns |
| 6 | 101.17 | 29.99 | 2.01 | 0.56 | 3.62 ns | 1.82 ns |
| 10 | 98.53 | 0.77 | 0.65 | 0.27 | 2.39 ns | -1.26 ns |
| 1 | 98.67 | 323.77 | -0.90 | 1.62 | -0.35 ns | -1.16 ns |
| 8 | 94.99 | 22.34 | 0.91 | 0.50 | 1.82 ns | -0.18 ns |
| 2 | 89.37 | 11.63 | 1.52 | 0.40 | 3.77 ns | 1.28 ns |
| 9 | 83.93 | 13.38 | 2.16 | 0.42 | 5.15 ns | 2.77 ns |
| 11 | 82.67 | 46.29 | 0.14 | 0.66 | 0.21 ns | -1.30 ns |
| Mean | 97.12 | | | | | |

The genotypes 4, 3, 10, 2, & 9 deviated non-significantly from 0 (S²d:0). Hence they are stable. All these genotypes recorded $b=0$ & termed as non responsive to environment. Hence, these genotypes are suited to all env. Among these gen. 4, 3, 10, 8 & 2 are statistically on par. However, the genotype 4, 3 & 10 which are better than the grand mean may be recommended for all env.

title: Biparental mating NCD-I
their interpretations

Experiment No: 12

Date: 23-6-22

NCD-1 problem

In a random mating population of bajra, 24 full sib progenies were produced by crossing 12 random males each with 2 different random females. These 12 random males were treated as 3 sets with 2 replications. The mean data (in grain yield) of progenies of each full sib family is presented below. Estimate the gene action and suggest suitable breeding methodology for improvement of grain yield.

Grain Yield Per plant (g) in Bajra

| Set | Male | Rep. 1 | | Rep. 2 | | Total | | Total |
|-------------|-------|--------|--------|--------|--------|--------|--------|--------|
| | | Female | Female | Female | Female | Female | Female | |
| | | 1 | 2 | 1 | 2 | 1 | 2 | |
| I | 1 | 28.6 | 27.5 | 28.1 | 28.6 | 56.7 | 56.1 | 112.8 |
| | 2 | 40.4 | 31.7 | 48.9 | 34.2 | 98.3 | 66.0 | 164.3 |
| | 3 | 25.4 | 20.0 | 25.2 | 20.8 | 50.6 | 46.8 | 97.4 |
| | 4 | 42.5 | 37.7 | 40.8 | 30.4 | 83.3 | 68.1 | 151.4 |
| | Total | | 262.8 | | 257.1 | | | 519.9 |
| II | 1 | 34.9 | 33.6 | 32.8 | 30.8 | 67.7 | 64.4 | 132.1 |
| | 2 | 49.7 | 44.2 | 48.4 | 42.3 | 98.1 | 86.5 | 184.6 |
| | 3 | 46.4 | 48.3 | 45.0 | 49.7 | 91.4 | 98.0 | 189.4 |
| | 4 | 53.8 | 50.2 | 51.6 | 48.6 | 105.4 | 98.8 | 204.2 |
| | Total | | 361.1 | | 349.7 | | | 710.3 |
| III | 1 | 30.3 | 35.6 | 31.2 | 37.4 | 61.5 | 73.0 | 134.5 |
| | 2 | 26.8 | 24.2 | 23.6 | 25.6 | 50.4 | 49.8 | 100.2 |
| | 3 | 33.8 | 36.8 | 32.2 | 39.4 | 66.0 | 76.2 | 142.2 |
| | 4 | 48.3 | 40.2 | 46.2 | 38.6 | 94.5 | 78.8 | 173.3 |
| | Total | | 276.0 | | 274.2 | | | 550.2 |
| Grand Total | | | | | | | | 1780.4 |

A. $CF = \frac{1780.4}{48} = 660.39.00$

$$\text{Total SS} = 28 \cdot 6^2 + 27 \cdot 5^2 + \dots + 38 \cdot 6^2 = 70203.94 - CF = 4165.94$$

$$\text{Set SS} = \frac{519 \cdot 9^2 + 710 \cdot 3^2 + 350 \cdot 2^2}{16} = 67346.38 - CF = 1308.38$$

$$\text{Rep in sets SS} = \frac{262 \cdot 8^2 + \dots + 274 \cdot 2^2}{8} - CF - \text{Set SS}$$

$$= 67357.42 - 66038.00 - 1308.38 = 11.09$$

$$\text{Males in sets SS} = \frac{112 \cdot 8^2 + 164 \cdot 3^2 + \dots + 173 \cdot 3^2}{4} - CF - \text{Set SS}$$

$$= 69618.96 - 66038.00 - 1308.38 = 2272.58$$

Females in males in sets SS

$$= \frac{56 \cdot 7^2 + 56 \cdot 1^2 + \dots + 78 \cdot 8^2}{2} - CF - \text{Males in sets SS} - \text{Set SS}$$

$$= 70140.52 - 66038.00 - 2272.58 - 1308.38 = 521.61$$

Error SS = Total SS - Females in males in sets SS - Males in set SS - rep. in set SS - set SS

$$= 4165.94 - 521.61 - 2272.58 - 11.09 - 1308.38 = 52.28$$

~~ANOVA Table~~

| Source | df | SS | MS | Expectations of MS |
|--------------------------|----------------|---------|-------------|---|
| Sets | $(S-1) = 2$ | 1308.38 | 654.19 | |
| Rep in Set | $S(x-1) = 3$ | 11.09 | 3.69 | |
| Males in set | $S(m-1) = 9$ | 2272.58 | 252.51 (MS) | $\sigma_e^2 + \sigma_{\alpha}^2 + \sigma_{\beta}^2 + \sigma_{\gamma}^2$ |
| Females in males in sets | $9m(f-1) = 12$ | 521.61 | 43.47 (MS) | $\sigma_e^2 + \sigma_{\beta}^2$ |

Title:

Experiment No:

Date:

| | | | | |
|-------|----------------------------------|-------|-------------------------|--------------|
| Error | $S(\text{mf}-1)(\bar{y}-1) = 21$ | 52.78 | 2.49 (MS _e) | σ_e^2 |
| Total | $(S\text{mf} - 1) = 43$ | - | - | |

Genetic parameters:

$$\sigma_m^2 = \frac{MS_e - MS_f}{f \times r} = \frac{252.31 - 43.47}{2 \times 2} = 52.26$$

$$\sigma_f^2 = \frac{MS_e - MS_f}{r} = \frac{43.47 - 2.49}{2} = 20.49$$

$$\sigma_m^2 = \frac{1}{4} \sigma_D^2$$

$$\therefore \sigma_D^2 \text{ (Additive genetic variance)} = 4 \times \sigma_m^2 = 209.04$$

$$\sigma_f^2 = \frac{1}{4} (\sigma_D^2 + \sigma_H^2) \cdot 4\sigma_f^2 = \sigma_D^2 + \sigma_H^2$$

$$\sigma_H^2 \text{ (Dominance genetic variance)} = 4\sigma_f^2 - \sigma_D^2 = (4 \times 20.49)$$

$$- 209.04 = -127.08$$

Since the ratio of $\frac{\sigma_D^2}{\sigma_H^2}$ is more than 1, grain yield in bajra is governed by additive gene action. The pre dominance of additive gene action suggests that progeny selection could be used effectively to improve the population for grain yield. Moreover, an approach of combining the favourable additive genes present in both-sib progenies into a gene pool by developing composites (or) synthetics is suggested for yield improvement in bajra.

Title: Biparental mating NCD-II
& their interpretations

Experiment No: 13

Date: 23-6-22

NCD II - problem

In a random mating population of bajra, 20 full sib progenies were produced by crossing 5 random males each with 4 same random females. These 20 full sib family progenies were evaluated in an F₂ with 2 replications wise. Estimate the gene action & suggest suitable breeding methodology for improvement of grain yield.

Grain yield per plant (g) in Bajra

| Male | Rep ₁ | | | | Rep ₂ | | | | Rep ₃ | | | | Total |
|-------|------------------|----------|----------|----------|------------------|----------|----------|----------|------------------|----------|----------|----------|-------|
| | Female 1 | Female 2 | Female 3 | Female 4 | Female 1 | Female 2 | Female 3 | Female 4 | Female 1 | Female 2 | Female 3 | Female 4 | |
| 1 | 34.4 | 24.5 | 34.2 | 23.5 | 35.6 | 26.3 | 32.2 | 25.5 | 30.0 | 30.8 | 66.9 | 49.0 | 115.9 |
| 2 | 21.6 | 37.8 | 20.2 | 29.2 | 24.3 | 36.8 | 22.1 | 28.3 | 45.9 | 26.6 | 41.3 | 52.5 | 120.3 |
| 3 | 35.6 | 32.6 | 46.3 | 49.5 | 37.4 | 36.2 | 42.4 | 44.8 | 73.0 | 68.8 | 88.7 | 94.3 | 321.8 |
| 4 | 57.5 | 33.9 | 49.8 | 48.3 | 60.2 | 38.2 | 46.2 | 51.4 | 117.7 | 72.1 | 96.0 | 99.7 | 395.5 |
| 5 | 45.0 | 50.7 | 46.4 | 35.3 | 46.2 | 48.3 | 48.7 | 37.4 | 91.2 | 99.6 | 95.1 | 72.7 | 352.0 |
| Total | | | | 746.3 | | | | | 728.5 | 397.8 | 3653 | 381.7 | 1519 |

A. $CF = \frac{1524.8^2}{40} = 58125.38$

Total SS = $\frac{34.4^2 + 24.5^2 + \dots + 37.4^2}{8} - CF = \frac{62340.20}{8} - 58125.38 = 4214.82$

Rep. SS = $\frac{746.3^2 + 778.5^2}{20} - CF = \frac{5815130}{20} - 58125.38 = 25.92$

Male SS = $\frac{236.2^2 + \dots + 358.6^2}{8} - CF = \frac{60823.98}{8} - 58125.38 = 2698.60$

Female SS = $\frac{397.8^2 + \dots + 273.2^2}{10} - CF = \frac{58189.94}{10} - 58125.38 = 64.56$

$$\begin{aligned} \text{Male} \times \text{Female SS} &= \frac{70 \cdot 0^2 + 50 \cdot 8^2 + \dots + 72 \cdot 7^2}{2} - CF \\ &= 62268.13 - 58125.38 = 4142.75 \text{ (crude SS)} - \text{Male SS} - \\ &\quad \text{Female SS} \\ &= 4142.75 - 2698.60 - 64.56 = 1379.59 \end{aligned}$$

$$\begin{aligned} \text{Error SS} &= \text{Total SS} - \text{Rep. SS} - \text{Male} \times \text{Female crude SS} \\ &= 6214.82 - 25.92 - 4142.75 = 1046.15 \end{aligned}$$

ANOVA Table

| Source | df | SS | MS | Expectations of MS |
|---------------|---------------------|---------|---------------------------|--|
| Replication | $(r-1) = 1$ | 25.92 | | |
| Male | $(m-1) = 4$ | 2698.60 | 674.65 (MS ₁) | $\sigma_e^2 + 8\sigma_{mf}^2 + 8\sigma_m^2$ |
| Female | $(f-1) = 3$ | 64.56 | 21.52 (MS ₂) | $\sigma_e^2 + 8\sigma_{mf}^2 + 8\sigma_{mf}^2$ |
| Male x Female | $(m-1)(f-1) = 12$ | 1379.59 | 114.97 (MS ₃) | $\sigma_e^2 + 8\sigma_{mf}^2$ |
| Error | $(mff-1)(r-1) = 19$ | 1046.15 | 55.06 (MS ₄) | σ_e^2 |
| Total | $(mfr-1) = 39$ | 6214.82 | | |

Genetic parameters:

$$\sigma_m^2 = \frac{MS_1 - MS_3}{df} = \frac{674.65 - 114.97}{2 \times 4} = 69.96$$

$$\sigma_f^2 = \frac{MS_2 - MS_3}{2m} = \frac{21.52 - 114.97}{2 \times 3} = 9.35$$

$$\sigma_{mf}^2 = \frac{MS_3 - MS_4}{8} = \frac{114.97 - 55.06}{2} = 29.95$$

$$\sigma_m^2 = \frac{1}{4} \sigma_D^2 \cdot \sigma_f^2 = \frac{1}{4} \sigma_D^2$$

$$\begin{aligned} \therefore \sigma_D^2 &= \frac{4 \times \sigma_m^2 + 4 \sigma_f^2}{2} = \frac{(4 \times 69.96) + (4 \times 9.35)}{2} \\ &= \frac{279.84 + 37.4}{2} = 121.22 \end{aligned}$$

$$\sigma_m^2 = \frac{1}{4} \sigma_H^2$$

$$\therefore \sigma_H^2 = 4 \sigma_m^2 = 4 \times 56.27 = 225.08$$

Since the ratio of $\frac{\sigma_D^2}{\sigma_H^2}$ is less than 1 (0.54), the grain yield in bajra is governed by dominance gene action. The predominance of dominance gene action suggests that heterosis breeding could be used effectively to improve grain yield. However, since additive gene action is also present to a considerable extent along with dominance gene action, reciprocal recurrent selection would be useful to improve the population for grain yield.

Title: Biparental mating NCD-III & their inter pretations

Experiment No: 14

Date: 23-6-22

NCD-III problem:

An F_2 population was produced in Bajra by crossing two inbred lines 1 and 2. From F_2 , 12 individual plants (males) were selected randomly & back crossed to both the inbreds (females). Thus a total of 24 full sib families were obtained. These 24 full sib families were treated as three sets & evaluated in an RBD with two replications. The mean data (mean grain yield) of progenies of each full sib family is presented below. Estimate the gene action & suggest a suitable breeding methodology for improvement of grain yield.

Grain Yield per plant (g) in Bajra

| Set | Male | Rep 1 | | Rep 2 | | Total | | Total |
|-------------|-------|--------|--------|--------|--------|--------|--------|--------|
| | | Female | Female | Female | Female | Female | Female | |
| | | 1 | 2 | 1 | 2 | 1 | 2 | |
| I | 1 | 28.6 | 27.5 | 28.1 | 28.6 | 56.7 | 56.1 | 112.8 |
| | 2 | 49.4 | 31.7 | 48.9 | 34.3 | 88.3 | 66.0 | 164.3 |
| | 3 | 25.4 | 20.0 | 25.2 | 20.8 | 50.6 | 40.8 | 91.4 |
| | 4 | 42.5 | 37.7 | 40.8 | 30.4 | 83.3 | 68.1 | 151.4 |
| | Total | | 262.8 | | 252.1 | 288.9 | 231.0 | 519.9 |
| II | 1 | 34.9 | 37.6 | 32.8 | 30.8 | 67.7 | 64.4 | 132.1 |
| | 2 | 49.7 | 44.2 | 48.4 | 42.3 | 98.1 | 86.5 | 184.6 |
| | 3 | 46.4 | 48.3 | 45.0 | 49.7 | 91.4 | 98.0 | 189.4 |
| | 4 | 53.8 | 50.2 | 51.6 | 48.6 | 105.4 | 98.8 | 204.2 |
| | Total | | 361.1 | | 349.2 | 362.6 | 347.7 | 710.3 |
| III | 1 | 30.3 | 35.6 | 31.2 | 37.4 | 61.5 | 73.0 | 134.5 |
| | 2 | 26.8 | 24.2 | 23.6 | 25.6 | 50.4 | 49.8 | 100.2 |
| | 3 | 33.8 | 36.8 | 32.2 | 39.4 | 66.0 | 76.2 | 142.2 |
| | 4 | 48.3 | 40.2 | 46.2 | 38.6 | 94.5 | 78.8 | 173.3 |
| | Total | | 276.0 | | 274.2 | 272.4 | 277.8 | 550.2 |
| Grand Total | | | | | | | | 1780.4 |

Title:

Experiment No:

Date:

$$A. \quad CF = \frac{1780.4}{48} = 66038.00$$

$$\text{Total SS} = 28 \cdot 6^2 + \dots + 38 \cdot 6^2 = 70203.94 - CF = 4165.94$$

$$\begin{aligned} \text{Rep. in sets SS} &= \frac{262 \cdot 8^2 + \dots + 274 \cdot 2^2}{8} - CF - \text{set SS} \\ &= 67357.47 - 66038.00 - 1308.38 = 11.09 \end{aligned}$$

$$\begin{aligned} \text{Females (Inbred lines) in sets SS} &= \frac{288 \cdot 9^2 + 2310^2 + \dots + 277 \cdot 8^2}{8} \\ &\quad - CF - \text{set SS} \\ &= 67571.61 - 66038.00 - 1308.38 = 225.23 \end{aligned}$$

$$\begin{aligned} \text{Males in sets SS} &= \frac{112 \cdot 8^2 + 164 \cdot 3^2 + \dots + 173 \cdot 3^2}{4} - CF - \text{set SS} \\ &= 69618.96 - 66038.00 - 1308.38 = 2272.58 \end{aligned}$$

$$\begin{aligned} \text{Males x Females interactions in sets SS} &= \frac{56 \cdot 7^2 + 56 \cdot 1^2 + \dots + 7 \cdot 3^2}{2} \\ &\quad - CF - \text{Males in sets SS} - \text{Females in sets SS} - \text{sets SS} \\ &= 70140.57 - 66038.00 - 2272.58 - 225.23 - 1308.38 = 296.38 \end{aligned}$$

$$\begin{aligned} \text{Error SS} &= \text{Total SS} - \text{Males x Females int. in sets SS} - \text{Rep. in sets SS} - \text{set SS} \\ &= 4165.94 - 296.38 - 227.58 - 225.23 - 11.09 - 1308.38 \\ &= 52.58 \end{aligned}$$

ANOVA Table

| Source | df | SS | MS | Expectation set MS |
|--------|--------|----|----|--------------------|
| sets | (S-1)2 | | | |

| | | | | |
|------------------------------|---------------------|---------|-------------|-------------------------------|
| Rep in sets | $S(x-1) 3$ | | | |
| Females inset | $S(f-1) 3$ | | | |
| Males in sets | $S(m-1) = 9$ | 9272.58 | 252.51 (MS) | $\sigma_e^2 + 28\sigma_m^2$ |
| Males x Females int. in sets | $S(m-1)(f-1) = 9$ | 296.38 | 22.93 (MS) | $\sigma_e^2 + 8\sigma_{mf}^2$ |
| Error | $S(mf-1)(2-1) = 21$ | 52.28 | 2.49 (MS) | σ_e^2 |
| Total | $(S(mf) - 1) = 47$ | - | - | |

Genetic parameters

$$\sigma_m^2 = \frac{MS_1 - MS_2}{28} = \frac{252.51 - 2.49}{4} = 62.51$$

$$\sigma_{mf}^2 = \frac{MS_2 - MS_3}{8} = \frac{22.93 - 2.49}{2} = 15.22$$

$$\sigma_m = \frac{1}{4} \sigma_D^2$$

$$\therefore \sigma_D^2 \text{ (Additive genetic variance)} = 4 \times \sigma_m^2 = 4 \times 62.51 = 250.04$$

$$\sigma_{mf}^2 = \frac{1}{2} \sigma_H^2$$

$$\therefore \sigma_H^2 = 2 \times \sigma_{mf}^2 = 2 \times 15.22 = 30.44$$

Since the ratio of $\frac{\sigma_D^2}{\sigma_H^2}$ is more than 1 (8.21) the grain yield in bajra is governed by additive gene action. The predominance of additive gene action suggests that progeny selection could be used effectively to improve the population for grain yield. Moreover, an approach of combining the favourable additive gene present in the full-sib progenies into a gene pool by developing composites (CoS) synthetics is suggested for yield improvement in bajra.

QTL:

QTL - Quantitative trait locus, mapping is a genome wide inference of the relationship b/w genotype at various genomic locations & phenotype for a set of quantitative traits in terms of the number, genomic positions, effects and interaction of QTL.

Requirements for QTL Mapping:

Mapping population

Saturated linkage map

Phenotypic screening

Statistical package

Markers [$\leq 5\text{cm}$ from a gene (or) QTL]

procedure:

These are the salient requirements for QTL mapping:

1) Suitable mapping population

2) Dense marker linkage map for the species

3) Reliable phenotypic evaluation for the target trait

4) Appropriate software packages for QTL detection

4 mapping

QTL mapping is generally based on biparental populations, alternatively, natural population germplasm collection, and breeding lines can be used for linkage disequilibrium - based association mapping of QTLs. The general procedure for QTL linkage mapping is briefly summarized below:

1) As the first step, two homozygous lines having contrasting phenotypes for the trait(s) of interest are selected and crossed to develop a doubled haploid (DH) or recombinant inbred lines (RIL) population. The two homozygous lines used as parents should show a large difference for the target

and preferably, they should have been developed by divergent selection for the traits.

2) The mapping population is evaluated for the target trait in replicated trials conducted, preferably, over seasons & years. This is known as phenotyping.

3) The two parents of the mapping population are tested with a large no. of markers covering the entire genome, & polymorphic markers are identified. It is important that the polymorphic markers should cover the whole genome at a sufficient density.

4) All the individual lines of the mapping population are now analyzed using these polymorphic markers, this is termed as genotyping.

5) The marker genotype data are used to construct a framework linkage map for the population, which depicts the order of the markers & the genetic distances b/w marker pairs in terms of centi-morgans [cM].

6) Finally, the marker genotype & the trait phenotype data are analyzed to detect association phenotype. In simple terms, the plants are divided into separate groups on the basis of their marker genotype. For each of these groups, mean & variance for the trait phenotype, mean & variance for the traits phenotype are estimated & used for comparison b/w the groups. In case the genotype groups for a marker differ significantly for the traits of interest, it is concluded that concerned marker is associated with the trait, i.e., the marker is most likely linked to a QTL controlling the trait phenotype.

Method of QTL mapping:

1) Single-marker analysis:
Probability of QTL detection declines as the distance b/w a QTL & the marker increases. Two (or) more QTLs linked a single marker are detected as a single QTL; QTL location cannot be determined.

2) Simple Interval Mapping:
More powerful than single marker analysis, cannot separate two (or) more QTLs present in the same marker interval. QTL location is not accurate.

3) Complex Interval Mapping:
Minimizes the background effects of other linked QTLs.

4) Multiple Interval Mapping:
Mapping multiple QTLs & detects QTL x QTL interactions. The results from CIM & MIM are highly dependent on the genetic model used for QTL analysis, as well as marker co-factor selection for CIM.

Lod Score:

• The lod score is a measure of the strength of evidence for the presence of a QTL at a particular location.

• In interval mapping the lod score is \log_{10} of the ratio of probability that a QTL is present to the probability that a QTL is absent.

• For example, if the presence of a QTL is 1000 times more probable than its absence, then the lod score = 3, because \log_{10} of 1000 = 3.

Software's used for QTL mapping:

- R/qtl: basic & advanced QTL tools
- R/qtlbim: Bayesian Interval Mapping for Multiple QTLs
- R/qtlhot: QTL Hotspots & Causal Architecture
- R/qtlnet: Causal inference of QTL networks
- R/qtl yeast: QTL Analysis of Brem & Kruglyak yeast data.

Merits:

- It is to provide insights into whether differences of phenotype are primarily affected by a few loci with large effects, or by numerous loci, each with tiny effects.
- The primary purpose of QTL mapping is to localize chromosomal region that significantly affect the variation of quantitative traits in a population.

Limitations:

- Only allelic diversity that segregates b/w the parents of the particular cross can be assayed & second, the amt of recombination that occurs during the creation of RIL population places a limit.
- Limited to the genetic diversity present in the parents of your segregating population.