**Supplementary material**

**Statistical and biometrical analysis**

**A) Basic analysis**

**i. Mean:** Sample mean values were obtained for each character by sum of all the observations in a sample divided by their corresponding number. It was calculated by using the following formula.

Where,

Y = population mean

Yi = individual value

N = number of observations

**ii. Range:** It is the difference between lowest and highest values for each character and thus it is the measure of the spread of variation in a sample.

Range = X1 to Xn

Where,

X1 = lower limit

Xn = upper limit

**iii. Standard deviation:** It is the square root of variance. It is the best measure of variation in a population and is estimated with the help of following formula.

1. **Variance:** In all the populations, variance was computed for all the characters by using the formula.

Where,

Yi = individual value

Y = population mean

n = number of observations

1. **Standard error (Se):** It is the measure of uncontrolled variation in the present in a sample. Se is calculated by using the following formula.

Where,

SD = standard deviation (deviation of individual value from population mean)

n = number of observations in a sample

1. **Critical difference (C.D.):** S.E. of the difference between any two treatments means is C.D. It was calculated by using the following formula.

Where,

Where,

r = number of replications

EMS = error mean sum of square

t = critical value of t for a specified level of significance and error degree of freedom

1. **Coefficient of variation (CV):** For comparing the variability of two or more than two characters, coefficient of variation was calculated by using the formula given below:

Where,

S.D. = population standard deviation

= population mean

1. **Analysis of variance (ANOVA)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Source** | **d.f.** | **Expected values of M.S.S.** | **MSS** | **Calculated Value of (F)** |
| Replication | r-1 | MSSr (M1) | - | (M1/M3) |
| Genotype | g-1 | MSSg (M2) | e + g | - |
| Error | (r-1) (g-1) | MSSe (M3) | e | - |
| Total | (rg-1) | M1 + M2M3 | M1 + (M2/ M3) |  |

Where,

r = number of replications

g = number of genotypes

MSSr = mean sum of squares due to replication

MSSg = mean sum of squares due to genotypes

MSSe = mean sum of squares due to error

e = error of variance

g = genotypic variance

**B) Analysis of genetic parameters**

**i) Genotypic and phenotypic variance**

Genotypic and phenotypic variances were computed based on the expected mean sum of squares from the ANOVA table as follows.

Where,

g = genotypic variance

p = phenotypic variance

e = environmental variance

* + 1. **Genotypic and phenotypic coefficients of variations**

The genotypic coefficients of variations (GCV) and the phenotypic coefficients of variations (PCV) were calculated by the formula mentioned by Burton (1952).

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as follows.

|  |  |
| --- | --- |
| Less than 10 % | : Low |
| 10-20 % | : Medium |
| More than 20 % | : High |

* + 1. **Heritability (h2bs)**

The heritability estimates are used to measure the degree of correspondence between phenotypic value and breeding value. It is worked out by using the formula suggested by Lush (1949) and Burton and Devance (1953) and expressed in percentage according to Weber and Moorthy (1952).

The heritability percentage was categorized as low, moderate and high as given by Hanson *et al*. (1956).

|  |  |
| --- | --- |
| Less than 20 % | : Low |
| 20-50 % | : Medium |
| More than 50 % | : High |

* + 1. **Genetic advance (GA)**

Genetic advance (GA) was estimated as per the formula suggested by Johnson *et al.* (1955).

Where,

h2 = Heritability in broad sense

σp = Phenotypic standard deviation

K = Standard selection differential (2.06) at 5 per cent selection intensity

Genetic advance as per cent mean (GAM) was computed by the formula.



The genetic advance as per cent over mean was categorized as suggested by Johnson *et al*. (1955).

|  |  |
| --- | --- |
| Less than 10 % | : Low |
| 10-20 % | : Medium |
| More than 20 % | : High |