

A Genetic Analysis in *Pennisetum typhoides* (Stapf & Hubb)

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ABSTRACT

The results of genetic analysis of a set of diallel crosses in the pearl millet are discussed. A considerable degree of heritability in the characters panicle length and grain yield gives scope for improvement in these traits, through back crossing and selection.

INTRODUCTION

In an attempt to study the genetic components of certain characters of chosen inbreds in pearl millet, with an object of exploring the possibility of obtaining by suitable breeding methods, increased expressions of useful traits, for which each of these inbreds may have low values, a set of diallel crosses was undertaken and the results of the genetic analysis are presented and discussed.

MATERIALS AND METHODS

Six inbreds of *Pennisetum typhoides* which are of diverse origin were chosen for the study. These are listed below:

| S. No. | Type | Origin |
|--------|------------|------------|
| 1. | PT 826 / 4 | Salem |
| 2. | PT 834 / 3 | Bombay |
| 3. | PT 937 | Coimbatore |
| 4. | PT 952 | Pepsu |
| 5. | PT 956 | Nellore |
| 6. | J 104 | Jamnagar |

The first five of the above types were inbred for more than 20 generations while the sixth one was selfed for more than eight generations. They also represent a random sample of the germplasm collections maintained at the Millet Breeding Station, Coimbatore. The criteria taken by Mahadevappa and Ponnaiya (1966) regarding the suitability of their material for a diallel analysis hold good for the materials under the present study also. All the possible crosses among the six inbreds were made. The F_1 's along with their parents were raised in 1972 main season in a randomised block design with four replications. Five plants in every progeny in each replication were studied individually for plant height, number of tillers, head length and grain weight. The mean observations made on each of the characters studied were analysed separately. The method developed by Hayman (1954) and illustrated by Jinks (1954) and Askel and Johnson (1963) was used for the genetic analysis. The Wr-Vr graphs were prepared to test the adequacy of the additive dominance model and other

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assumptions for the material under study. Estimates of genetic parameters D , H_1 , H_2 , F and h^2 and the ratios $(H_1/D)^{\frac{1}{2}}$, h^2/H_2 , $\frac{1}{4}H_2/H_1$ and heritability were obtained and discussed.

RESULTS AND DISCUSSION

The results of graphic and genetic analysis are characterwise presented.

Plant height: the analysis of variance for this character (Table 1) revealed that the differences between the progenies are significant. The t^2 was 0.0002 disclosing that the data is valid for further analysis. The regression value of W_r - V_r graph (0.622) was significantly different from zero but not from unity showing the adequacy of additive dominance model for this character.

TABLE 1. Analysis of Variance

| Source | D. F. | Plant height | Number of tillers | Panicle length | Grain yield |
|----------|-------|--------------|-------------------|----------------|-------------|
| Variance | 29 | 1697.94 | 2.18 | 25.61 | 65.34 |
| Error | 87 | 128.55 | 1.78 | 3.33 | 30.54 |
| F | | 5.416** | 1.22 NS | 7.69** | 2.13* |

TABLE 2. Estimation of genetic components of variance

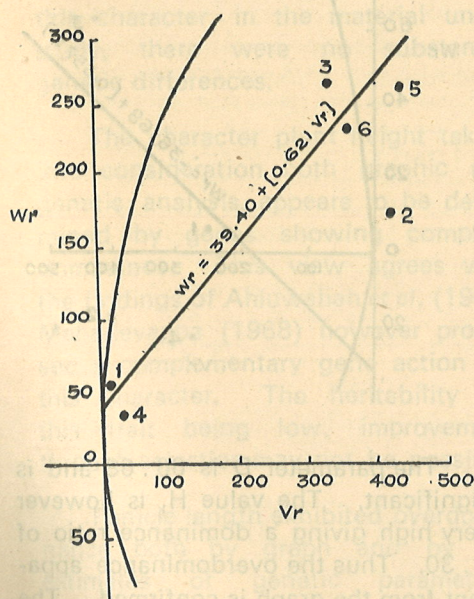
| Statistics | Plant height | Panicle length | Grain yield |
|---|-----------------|----------------|-----------------|
| Additive effect (D) | 478.92 ± 75.49 | 4.24 ± 1.29 | 66.68 ± 27.02 |
| Dominance effect (H ₁) | 750.68 ± 192.54 | 23.20 ± 3.29 | 1231.96 ± 69.06 |
| (H ₂) | 704.64 ± 171.71 | 15.20 ± 2.95 | 1194.80 ± 61.71 |
| Relative frequency of dominant and recessive alleles (F) | 374.84 ± 190.16 | 4.80 ± 3.27 | 8.52 ± 68.01 |
| Relative frequency of increasing and decreasing alleles H ₂ /4H ₁ | 0.23 | 0.16 | 0.24 |
| KD/KR | 1.90 | 1.52 | 1.03 |
| h ² /H ₂ | 3.95 | 4.32 | 2.81 |
| (H ₁ /D) ^½ | 1.21 | 2.30 | 4.30 |
| Heritability (Narrow) | 0.37 | 0.55 | 0.61 |

The W_r - V_r regression line intercepts the W_r axis a little above the origin showing near complete dominance exhibited by the parents (Fig 1). The array points 1 and 4 are very near the origin and to one another. The

parents of these arrays may therefore, be inferred to possess most of the dominant genes besides being closely related to one another. Array points 3, 5 and 6 are away from the origin and are close to one another indicating

that the corresponding parents possess the maximum number of recessive genes and are also closely related. Array point 2 stands apart from both the groups. Fig. 1

Fig.1 $W_r - V_r$ GRAPH FOR PLANT HEIGHT

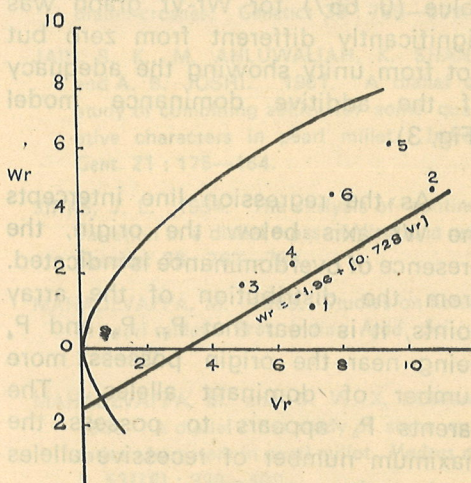


The parameter D is 478.92 and is significant. The estimate of H_1 is 750.68 and significant. The ratio $(H_1 / D)^{1/2}$ is 1.21 suggesting an over dominant trend. Studied together with the graph it can however be concluded that this character shows complete dominance. The high positive and significant value of F indicates a greater frequency of dominant alleles among the parents as also a high level of dominance. The ratio of h^2 / H_2 is 3.95 indicating that four groups of genes showing dominance might determine the expression of the character. The ratio of KD / KR is 1.90 showing

that there are more number of dominant genes over recessives. The non-significant correlation between $(W_r + V_r)$ and V_p (0.00067) indicates that dominance is ambidirectional. The heritability (0.37) for this character is low.

Panicle length: The analysis of variance for this character revealed significant differences between the progenies. The t^2 was 0.376 which permitted further analysis. The regression value (0.728) for $W_r - V_r$ graph significantly deviated from zero but not from unity. The regression line intercepts the covariance axis below the origin indicating over dominance (Fig. 2). The scattering of array points show that P_1 , P_8 and P_4 are relatively close to one another. Arrays P_2 , P_8 and P_6 form a group away from the origin and may therefore possess most of the recessive genes besides being closely related to one another. Fig. 2,

Fig.2 $[W_r - V_r]$ GRAPH FOR PANICLE LENGTH

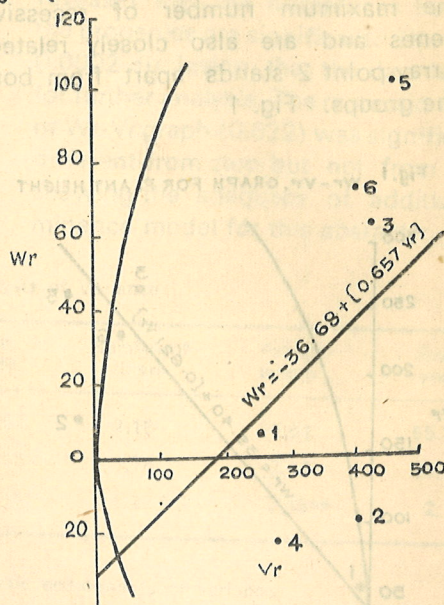


The parameter D is 4.24 and significant. The value for H_1 is 23.20. The dominance ratio, being 2.3, indicates over dominance. The estimate of F though positive is not significant, indicating equal frequency of dominant and recessive alleles in the parents. The ratio of $H_2/4H_1$, being 0.16, suggests an unequal distribution of positive and negative genes. The ratio of h^2/H_2 (4.32) indicates that four groups of genes showing dominance determine the expression of this character. The ratio KD/KR (1.52) taken together with the positive F suggests that the dominant genes are slightly more than the recessives. The correlation coefficient ($r=0.35$) between $(Wr+Vr)$ and Vp being not significant suggests that dominance might be ambidirectional. The heritability (0.55) for this character is considerable.

Grain yield: The differences between the progenies were highly significant. The t^2 was 0.087 and not significant. Therefore, further analysis of the data was made. The P value (0.657) for $Wr-Vr$ graph was significantly different from zero but not from unity showing the adequacy of the additive dominance model (Fig. 3).

As the regression line intercepts the Wr axis below the origin, the presence of overdominance is indicated. From the distribution of the array points, it is clear that P_1 , P_2 and P_4 being near the origin possess more number of dominant alleles. The parents P_5 appears to possess the maximum number of recessive alleles for the trait.

Fig.3 $[Wr-Vr]$ GRAPH FOR GRAIN YIELD



The parameter D is 66.68 and is significant. The value H_1 is however very high giving a dominance ratio of 4.30. Thus the overdominance apparent from the graph is confirmed. The F value is not significant indicating equal frequency of dominant and recessive alleles among the parents. The ratio of $H_2/4H_1$ (0.24) suggests an equal distribution of positive and negative genes among the parents. The ratio of h^2/H_2 is 2.81 indicating that three groups of dominant genes may determine the expression of the trait. The ratio of KD/KR (1.03) shows equal frequency of dominant and recessive genes.

The correlation coefficient between $(Wr+Vr)$ and Vp values (0.24) being not significant, indicates an ambidirectional dominance relationships.

The heritability was estimated to be 0.61 which is considerable for this trait.

Number of tillers: The differences among the progenies were not significant for the character number of tillers indicating that with reference to this character, in the material under study, there were no substantial genetic differences.

The character plant height taking into consideration both graphic and genetic analysis, appears to be determined by genes showing complete dominance. This view agrees with the findings of Ahluwalia et al. (1962) Mahadevappa (1968) however proposed a complementary gene action for this character. The heritability for this trait being low, improvement through selection may not be possible.

Panicle length exhibited overdominance both by graph and by the estimates of genetic parameters. However, there is a significant additive variability observed for this trait, which may allow improvement, to a certain extent through selection. Jain et al. (1961) observed partial dominance involved in this trait. Improvement in tillering through selection appears not possible in the present material as the differences among the arrays are not significant. For grain yield a high degree of overdominance was exhibited. Gupta and Singh (1971) also found considerable over dominance for this trait. Mahadevappa (1968) besides inferring additive gene action has also proposed complementary interaction for this character. The heritability however was considerable. The fairly

high heritability caused by significant additive genetic variance will therefore permit considerable improvement in grain yield through selection in the parent material.

The above findings disclose that besides utilisation of heterosis, improvement of the inbreds themselves through a systematic crossing and recurrent selection programme appears possible. Such improved inbreds will serve as superior parents for hybrids. Work has been initiated in this direction.

REFERENCES

- AHLUWALIAH, M., K. SHANKAR, S. K. JAIN and A. B. JOSHI. 1962. A diallel cross study of combining ability for some quantitative characters in pearl millet. *Indian J. Genet.* 22 : 45—53.
- ASKEL, R. and L. V. P. JOHNSON. 1963. Analysis of diallel cross. *Frontiers of Plant Sciences* 2 : 37—53.
- GUPTA, S. P., and T. H. SINGH. 1971. Genetic analysis of grain yield and its components in pearl millet. *Indian J. agric. Sci.* 41 : 324—8.
- HAYMAN, B. I. 1954. Theory and analysis of diallel crosses. *Genetics* 39 : 789—809.
- JAIN, S. K., M. AHLUWALIAH, K. SHANKAR and A. B. JOSHI. 1961. A diallel cross study of combining ability for some quantitative characters in pearl millet. *Indian J. Genet.* 21 : 175—184.
- JINKS, J. L. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica*. *Genetics* 39 : 767—788.
- MAHADEVAPPA, M. 1968. Studies on heterosis in pearl millet, *Proc. Indian Acad. Sci.*, 68 : 210—20.
- MAHADEVAPPA, M. and B. W. X. PONNAIYA. 1966. A diallel cross study of some quantitative characters in pearl millet. *Madras agric. J.*, 53(10) : 398—409.