Indian J. Genet., 50 (4): 338-341 (1990)

## CORRELATION, COMBINING ABILITY AND HETEROSIS STUDIES ON HUSK NUMBER AND SHANK LENGTH IN MAIZE

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(Received: March 14, 1989; accepted: October 7, 1989)

## ABSTRACT

The unexploited ear characters, viz., husk number and shank length were subjected to study along with other quantitative characters in all possible 100 crosses of 10 elite inbred lines. A strong negative association of these traits with yield and yield components emphasized the importance of these traits in the maize ideotype. The desirable combiners, the superior combinations and their contributions to heterosis were analysed and their implications are discussed.

Key words: Zea mays L., diallel, combining ability, heterosis, shank length, husk number.

Some of the rare quantitative characters like husk number and shank length of cob have not gained much importance in maize breeding programmes. From the evolutionary point of view, husks are modified leaf sheaths and shank a condensed side shoot which bears the cob at the tip. Allison and Watson [1] reported that contribution of husks to photosynthesis is negligible under normal conditions. The main reason for reduced sink capacity of maize is attributed to competition between vegetative and generative sink parts for photosynthates [2]. Hence there is a need to increase the partitioning efficiency of maize plants by manipulating vegetative sink traits. The study was, therefore, planned to know the nature of inheritance of these traits, their association with yield and yield contributing characters and to identify the good combiners and combinations of maize for these characters.

#### MATERIALS AND METHODS

A full diallel set of crosses involving ten parents was evaluated in randomized block design with four replications at the main research station, University of Agricultural Sciences, Dharwad, during kharif (rainy season) 1987. Observations were recorded on 10

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competitive random plants in each treatment for days to anthesis, days to silking, number of secondary tassel branches, tassel length, husk number, shank length, 100-grain weight, 100- grain volume, and grain yield per plant. Husk number was recorded by counting the number of husks covering the ear at the time of harvest and the shank length was measured from the base of its attachment to the stem to the base of the dehusked cob. The treatment means were subjected to combining ability analysis [3]. In addition, heterosis of F<sub>1</sub>s over midparent and genotypic and phenotypic correlations of husk number and shank length with various quantitative traits were worked out.

#### RESULTS AND DISCUSSION

Amongst the parents, Ant-5D had the lowest number of husks (9.9) and shortest shank (6.9 cm), while CM 111 exhibited the highest number of husks (15.6) and longest shank (12.4 cm). As regards the crosses, KUI 1411 x CM 110 had the lowest number of husks (7.4) and shortest shank (6.1 cm), whereas the cross KUI 1418 x CM 106 had the highest number of husks (14.4) and longest shank (13.8 cm). The occurance of a wide range of variability for both the traits highlighted the scope for selection among the parents and crosses for these traits. Since these characters have not been investigated or exploited for improvement, preliminary selection may be of great value.

The ANOVA of combining ability showed highly significant mean squares due to gca, sca and reciprocal effects for both traits (Table 1). Higher estimates of sca than those of gca variance indicates preponderance of nonadditive effects in the inheritance of these attributes. Kim and Brewbaker [4] also indicated the importance of both gca and sca variances for these traits. The significance of reciprocal effects indicated the need to take precaution while selecting the parents for hybrid production. Such reciprocal effects are attributable to effects of cytoplasm alone or due to different gene combinations under

| Source                            | d.f.     | Mean squares |                 |
|-----------------------------------|----------|--------------|-----------------|
|                                   |          | husk<br>No.  | shank<br>length |
| Gca                               | 9        | 3.11**       | 3.62**          |
| Sca                               | 45       | 3.00**       | 3.21**          |
| Reciprocal ef                     | fects 45 | 2.08**       | 1.23**          |
| Error                             | 297      | 0.10         | 0.10            |
| σ²g                               |          | 0.007        | 0.022           |
| σ <sup>2</sup> s                  |          | 1.594        | 1.713           |
| σ <sup>2</sup> g∕σ <sup>2</sup> s |          | 0.004        | 0.013           |

Table 1. ANOVA for combining ability

\*\*Significant at 1% level.

different cytoplasmic backgrounds when divergent genotypes are involved in crosses.

As regards gca effects, the parents Ant-5D, CM 105, KUI 1411 and KUI 1403 were good general combiners for both the traits (Table 2). Positive correlation between per se performance of the inbreds and their gca effects indicated the role of additive genetic effects in the inheritance of these traits.

Considerable variability was exhibited by F<sub>1</sub>s for sca along with reciprocal effects for both the traits mostly Table 2. Per se performance and gca effects of parents

| Inbreds  | Characters  |                |                   |                |  |
|----------|-------------|----------------|-------------------|----------------|--|
|          | husk number |                | shank length (cm) |                |  |
|          | per se      | gca<br>effects | per se            | gca<br>effects |  |
| CM 110   | 12.4        | -0.02          | 11.9              | 0.32**         |  |
| Ant-5D   | 9.9         | 0.32**         | 6.9               | 0.29**         |  |
| CM 106   | 10.8        | 0.16           | 10.2              | 0.26**         |  |
| CM 116   | 13.7        | 0.68**         | 12.2              | 0.38**         |  |
| CM 105   | 11.1        | -0.52**        | 7.0               | -0.38**        |  |
| CM 103   | 13.7        | 0.07           | 9.4               | 0.42**         |  |
| CM 111   | 15.6        | 0.03           | 12.4              | 0.60           |  |
| KUI 1411 | 13.3        | -0.27**        | 11.7              | -0.30**        |  |
| KUI 1418 | 12.7        | 0.57**         | 7.6               | 0.03           |  |
| KUI 1403 | 13.2        | -0.37**        | 12.3              | -0.14          |  |

\*\*\*Significant at 5 and 1% levels, respectively.

in negative (desirable) direction. Heterosis over midparent (MP) ranged from 25.4 (Ant-5D x KUI 1411) to -26.4% (CM 103 x CM 111) for husk number and from 57.8 (Ant-5D x CM 105) to -30.5% (CM 116 x CM 111) for shank length. Significant MP heterosis was exhibited by 26 and 33 out of 45 in F1 in respect of husk number and shank length, respectively. Six out of the 26 heterotic F1s for husk number, were 6 good x good, 14 good x poor, and 6 poor x poor combinations. Similarly, for shank length, 9, 15 and 9 F1s were good x good, good x poor and poor x poor combinations, respectively. Most of the crosses showed significant negative heterosis, which is a desirable feature. The majority of the heterotic crosses having good x poor combiners indicate the role of combining ability diversity, in addition to

genetic diversity in realising heterosis. This finding is in line with the earlier observation in pearl millet [5].

Majority of the superior heterotic crosses had either highly significant sca effects or reciprocal effects, or both, indicating the importance of nonadditive genetic effects and maternal effects in their inheritance. Some of the heterotic crosses involving good x good combinations of parents, viz. CM 105 x KUI 1403 (husk number) and CM 105 x CM 103 and Ant-5D x CM 103 (shank length), showed insignificant sca and reciprocal effects, indicating the involvement of additive x additive type of interactions causing heterosis [6].

Phenotypic and genotypic correlations were found to be in perfect agreement with each other and the higher magnitude of the latter indicated the masking effect of the environment on genotypic correlations. The tassel characters, viz., number of secondary branches and tassel length, which showed strong negative association with husk number, indicated the probable competition between the terminally placed tassel and the axially placed ear for nutrients at early stages of ear development under the influence of apical dominance [2]. The traits 100-grain volume and weight, which showed negative correlation with husk number and shank length, indicated that husks consume considerable amount of dry matter, resulting in limited sink size. Similarly, the negative correlation of husk number and shank length with yield indicated that, even though a few husks are essential for protection against insects etc., too many husks and lengthy shank may adversely affect yield. The present finding is in accordance with the earlier observations in maize [7]. Logically, too many husks may be a burden for the developing ear since it diverts (wastes) considerable amount of dry

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| Table 3. Genotypic and phenotypic correlations of |  |  |  |  |  |  |
|---|--|--|--|--|--|--|
| husk number and shank length with various         |  |  |  |  |  |  |
| quantitative traits                               |  |  |  |  |  |  |

| Characters        | Husk<br>number | Shank<br>length |
|-------------------|----------------|-----------------|
| Days to an thesis | -0.45          | 0.76            |
| Days to anthesis  | (-0.18)        | (-0.16)         |
| Days to silking   | -0.52          | 0.65            |
| ,                 | (-0.21)*       | (-0.17)         |
| No. of secondary  | -0.35          | -0.30           |
| tassel branches   | (27)**         | (0.15)          |
| Tassel length     | -0.61          | -0.02           |
| -                 | (0.22)*        | (0.14)          |
| Husk number       |                | 0.97            |
|                   |                | (0.56)**        |
| 100-grain weight  | -0.30          | 0.57            |
|                   | (0.15)         | (0.17)          |
| 100-grain volume  | 0.37           | -0.35           |
| -                 | (0.16)         | (0.12)          |
| Grain yield/plant | 0.27           | -0.32           |
|                   | (0.20)*        | (0.19)*         |

matter which otherwise would have been accumulated in the grains. Similarly, if shank is too long, it may bend well before grain filling and cause obstruction in the movement of food materials into the grains. The correlation coefficients help in inferring that there is a need to reduce the number of husks and length of the shank which, in turn, helps in increasing the partitioning efficiency of the present day maize cultivars. Although some more supporting physiological investigations are needed to confirm the precise mechanism of this effect on grain yield, the maize ideotype may however be characterized by fewer husks, short and erect shank, besides several other architectural traits of physiological and genetic importance.

Figures in parentheses indicate phenotypic correlations.

\*,\*\*Significant at 5 and 1% levels, respectively.

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