INHERITANCE OF QUALITY ATTRIBUTES IN OKRA
[ABELMOSCHUS ESCULENTUS (L.) MOENCH]

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ABSTRACT
An experiment was conducted to study the gene action and inheritance of quality attributing
traits in okra. Six generations of two crosses of okra (Punjab-8 x Arya Dhanlaxhmi and Punjab-8 x
Pusa sawani) were derived and evaluated for protein content, total minerals and mucilage content.
F1 means of both the crosses surpassed both of their corresponding parental means suggesting over
dominance for protein content, total minerals and mucilage content except for mucilage content in
cross Punjab-8 x Pusa Sawani. Evidence of epistasis was detected for all the traits. Both fixable and
non-fixable gene effects govern the inheritance for all the traits except for mucilage content in cross
Punjab-8 x Pusa Sawani. Dominance gene effects were found to contribute more substantially in the
inheritance of these traits along with the presence of duplicate type of epistasis. Therefore, genetic
improvement of okra with respect to these attributes in this material can be made through pure line
breeding or inbred development.

Key words: Gene effects, Inheritance, Okra, Quality.

Okra (Abelmoschus esculentus (L.) Moench) commonly known as lady’s finger or bhindi is an
important spring-summer vegetable crop grown for fresh market and processing. It contains
carbohydrate, protein, minerals, iodine and vitamin C in large quantities (Adeboye and Oputa, 1996).
Hence, it plays a vital role in human diet. Medically okra mucilage has found application as a plasma
replacement or blood volume expander. Industrially, okra mucilage is usually used to glace certain papers
and also useful in confectionary among other uses (Markose and Peter, 1990).

Before undergoing any breeding programme for specific objective, it is necessary to the breeder
to have significant knowledge regarding the nature of inheritance of various traits in terms of additive
and non-additive genetic variance, which could help in planning the hybridization and selection produce
effectively. The genetic information available so far needs further elaboration for effective implementation
of breeding programme. Therefore, the present investigation was undertaken to determine the
inheritance pattern of protein content, total minerals and mucilage content of okra, so that inference could
be utilized in forming the breeding programme accordingly.

The experimental material comprised of two F1’s of okra viz. Punjab-8 x Arya Dhanlaxhmi,
Punjab-8 x Pusa Sawani. These two F1’s were sown along with their respective parents during
summer 2009 at Punjab Agricultural University, Ludhiana. Some flowers from each cross was self
pollinated to produce F2’s and other back crossed with both the parents (Pc, Pi) in order to obtain back
cross (Bc, Bi) seeds, respectively. Moreover, the parents were again crossed to produce the seeds of
F1 hybrids because the earlier produced seeds of F1 hybrids were utilized for production of back crosses
and F2 generations’ seed. The parental lines of both the crosses were selfed to produce parental seed.
Seeds of all the six generations namely, Pc, Pi, F1, F2, B, and Bi were harvested separately. The six basic
sets of generations namely, Pc, Pi, F1, F2, B, and Bi were sown in rainy season of the same year (2009),
using randomized block design (RBD) with three replications. Both the crosses were treated as
separate experiment i.e. the randomization was done within crosses and between rows. The distance
between row to row and plant to plant was maintained as 45 x 30 cm. The crop was raised by using recommended package of practices for cultivation of vegetables. The observations were recorded on 10 selected fruits per replication to estimate the protein content, total minerals and mucilage content. For each character, \( P_1 \) was higher scoring parent than \( P_2 \). So whom so ever may be higher mean among parents (\( P_c, P_i \)) should be treated as \( P_1 \) for scaling and joint scaling tests. Similarly for backcrosses (\( B_c, B_i \)), \( B_i \) and \( B_c \) generations were obtained after crossing with \( P_i \) and \( P_c \) respectively.

Scaling test of Mather (1949) and joint scaling test of Cavalli (1952) were applied to detect the non-allelic interactions and gene effects respectively. First the three-parameter model has fitted to estimate the genetic parameters. On the other hand, three-parameter model was inadequate, than adequacy of best-fit model could be tested which having maximum significant genetic parameters and least non-significant chi-square value.

Protein estimation was carried out through Kjeldahl method.

### Total minerals (%) was calculated as follow:

Empty crucible was weighed and then 1.0 g dry powder was added. It was ignited on the heater to remove fumes and then kept in muffle furnace at 50\(^\circ\)C overnight. The furnace was switched off, crucible cooled and weighed.

\[
\text{% Ash} = \frac{W_2 - W_1}{W} \times 100
\]

- \( W = \) Weight of sample (g)
- \( W_1 = \) Weight of empty crucible (g)
- \( W_2 = \) Weight of empty crucible + ignited sample (g)

### Mucilage content (%) was calculated as follow:

Twenty grams of the sample was taken and 100 ml of distilled water added. After keeping it for 24 hrs, it was filtered through muslin cloth and to the filtrate 50 ml of ethanol was added and stirred it on magnetic stirrer for 15 min. It was filtered through pre-weighed filter paper and kept in the oven at 60\(^\circ\)C for drying. After drying, the material was again weighed along with filter paper.

\[
\text{Calculation} = \frac{W_2 - W_1}{W} \times 100
\]

- \( W_2 = \) Weight of filter paper along with material after drying (g)
- \( W_1 = \) Weight of pre-weighed filter paper (g)
- \( W = \) Weight of sample (g)

### Protein content

In both the crosses, \( F_1 \) means surpasses both of their corresponding parental means indicating over dominance for the character (Table-1). The \( F_2 \) means were lower than their corresponding \( F_1 \) means in both the crosses indicating some degree of inbreeding depression. \( B_c \) means were higher than their corresponding \( B_i \) means in both the crosses, as the recurrent parent involved in \( B_c \)'s which had higher mean than that of recurrent parent involved in corresponding \( B_i \)'s (Table 1).

Significant estimation of scaling test ‘B’ and ‘C’ in both the crosses for this character indicating the presence of epistasis (Table-2). Moreover, the significant chi-square value for additive-dominance model also indicating the presence of epistasis and this suggested that simple additive-dominance model was inadequate to explain the total genetic variation.

After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the additive (\( d \)) and dominance (\( h \)) gene effects were significant in both the crosses. The magnitude of dominance (\( h \)) gene effects were more than the additive (\( d \)) effects in both the crosses but negative sign of (\( h \)) indicates the dominance of decreaser alleles.

Among the epistatic effects, all the three types of gene interactions were significant in both the crosses (Table-2). Thus, in these crosses the adequacy of the best fit model could not be tested for the digenic interactions. The magnitude of dominance x dominance (\( l \)) gene effects were higher than other two types of interactions in these crosses, which indicated that dominance x dominance (\( l \)) gene effects were more important followed by additive x additive (\( i \)), additive x dominance (\( j \)) gene effects. The negative sign of additive x additive (\( i \)) effects in both the crosses indicated dissociated gene pair. Moreover, opposite signs of dominance (\( h \)) and dominance x dominance (\( l \)) effects in both the crosses showed the presence of duplicate type of epistasis. Thus, it can be concluded that protein content (%) is mainly governed by dominant gene effects though epistasis was also detected. So, the
further breeding improvement for protein content in this material could be achieved through Pure line breeding and selection methods.

**Total minerals**

The $F_2$ mean of cross Punjab-8 x Arya Dhanlaxhmi lied in between its parental means, it skewed too much towards the better parental ($P_i$) mean and was almost equal to it, indicating complete dominance for the character whereas in the cross Punjab-8 x Pusa Sawani, $F_1$ mean surpasses both of their corresponding parental means indicating over dominance for the character (Table-1). In both the crosses, $F_2$ means were lower than their corresponding $F_1$ means indicating some degree of inbreeding depression. $B_c$ means were higher than their corresponding $B_i$ means in both the crosses, indicating their behaviour as per expectation (Table-1).

The significance of one or all of the A, B and C scaling test in both the crosses clearly indicated the presence of all three type of non-allelic gene interactions for the character (Table-2). Moreover, the significant chi-square value for additive-dominance model in both the crosses also confirms the presence of epistasis (i.e. failure of additive-dominance model). After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the additive ($a$) and dominance ($h$) gene effects were significant in both the crosses. Moreover, the magnitude of dominance gene effects was more than that of additive gene effects in both the crosses which confirm that dominance gene effects were found to contribute substantially in the inheritance of total minerals.

Among the epistatic effects, all the three types of gene interactions i.e. ($i$), ($j$) and ($l$) were found significant in both the crosses (Table-2). Thus, in these crosses, the adequacy of the best fit model could not be used for the digenic interactions. The magnitude of dominance x dominance ($l$) gene effects were higher than other two types of interactions in these crosses, which indicated that dominance x dominance ($l$) gene effects were more important followed by additive x additive ($i$), additive x dominance ($j$) gene effects. Moreover, opposite signs of dominance ($h$) and dominance x dominance ($l$) effects in both the crosses showed the presence of duplicate type of epistasis. The negative sign of additive x additive ($i$) effects in both the crosses indicated dissociated gene pair. Thus, it can be concluded that total minerals is mainly governed by dominant gene effects. Similar results were also reported by Arora and Ghai (2007) and Arora, et al. (2007). Pure line breeding or selection can be done for further improvement due to presence of duplicate type of epistasis along with the significant dominant gene effects.

**Mucilage content**

In cross Punjab-8 x Arya Dhanlaxhmi, the $F_1$ mean lied in between its corresponding parental means, but lower than the corresponding mid parental mean, suggesting incomplete dominance whereas the $F_1$ mean of cross Punjab-8 x Pusa Sawani surpasses both of their corresponding parental means indicating over dominance for the character (Table-1). The $F_2$ means were lower than their corresponding $F_1$ means in both the crosses indicating some degree of inbreeding depression. In cross Punjab-8 x Arya Dhanlaxhmi, $F_2$ mean was as per expectation, whereas in cross Punjab-8 x Pusa Sawani, $F_2$ mean surpasses its both parental means indicating transgressive segregants in $F_2$. On
**TABLE 2:** Estimates of gene effects based on scaling, joint scaling tests and genetic components in the best fitting model in different crosses.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Protein content (%)</th>
<th>Total mineral content (%)</th>
<th>Mucilage content (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Punjab x Anjana</td>
<td>Punjab x Pusa Sawani</td>
<td>Punjab x Anjana</td>
</tr>
<tr>
<td></td>
<td>Dhanashmi</td>
<td>Dhanashmi</td>
<td>Dhanashmi</td>
</tr>
<tr>
<td><strong>A</strong></td>
<td>-0.06 ± 0.04</td>
<td>0.06 ± 0.03</td>
<td>0.11 ± 0.05</td>
</tr>
<tr>
<td><strong>B</strong></td>
<td>-0.20 ± 0.04**</td>
<td>-0.31 ± 0.06**</td>
<td>-0.37 ± 0.04**</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>0.27 ± 0.07**</td>
<td>0.20 ± 0.08**</td>
<td>0.16 ± 0.11</td>
</tr>
<tr>
<td><strong>Joint Scaling Test</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>m</td>
<td>1.0 ± 0.01**</td>
<td>0.9 ± 0.01***</td>
<td>1.2 ± 0.01**</td>
</tr>
<tr>
<td>[d]</td>
<td>0.2 ± 0.01**</td>
<td>0.2 ± 0.01**</td>
<td>0.4 ± 0.01**</td>
</tr>
<tr>
<td>[h]</td>
<td>0.3 ± 0.02**</td>
<td>0.2 ± 0.02**</td>
<td>0.2 ± 0.02**</td>
</tr>
<tr>
<td>$\chi^2_{(df,1)}$</td>
<td>62.98***</td>
<td>45.49***</td>
<td>87.68***</td>
</tr>
<tr>
<td>m</td>
<td>1.5 ± 0.07**</td>
<td>1.4 ± 0.08**</td>
<td>1.6 ± 0.11**</td>
</tr>
<tr>
<td>[d]</td>
<td>0.13 ± 0.01**</td>
<td>0.19 ± 0.01**</td>
<td>0.29 ± 0.01**</td>
</tr>
<tr>
<td>[h]</td>
<td>-1.1 ± 0.19**</td>
<td>-1.0 ± 0.22**</td>
<td>-0.91 ± 0.25**</td>
</tr>
<tr>
<td>[i]</td>
<td>-0.55 ± 0.07**</td>
<td>-0.48 ± 0.08**</td>
<td>-0.42 ± 0.11**</td>
</tr>
<tr>
<td>[l]</td>
<td>0.15 ± 0.05**</td>
<td>0.29 ± 0.07**</td>
<td>0.48 ± 0.04**</td>
</tr>
<tr>
<td>[l]</td>
<td>0.84 ± 0.12**</td>
<td>0.74 ± 0.14**</td>
<td>0.69 ± 0.15**</td>
</tr>
<tr>
<td>$\chi^2_{(df,1)}$</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

* *, **Significant at 5% and 1% level, respectively.
the other hand, B_i means were higher than their corresponding B_c means in both the crosses, as the recurrent parent involved in B_i's which had higher mean mucilage content than that of the recurrent parent involved in B_c's (Table-1).

The significance of one or all of the A, B and C scaling test in both the crosses clearly indicated the presence of non-allelic gene interactions for the character (Table-2). Significant chi-square value for additive-dominance model indicating the presence of epistasis and this suggested that simple additive-dominance model was inadequate to explain the total genetic variation for mucilage content in both the crosses. After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the dominance (h) and additive (d) gene effects were significant in both the crosses. However, the magnitude of dominance gene effects was more than that of additive gene effects in both the crosses which confirm that dominance gene effects were found to contribute substantially in the inheritance of mucilage content (%).

Among the epistatic effects, in cross Punjab-8 x Arya Dhanlaxhmi, all the three types of gene interactions were significant (Table-2). Therefore, the adequacy of the best fit model could not be tested for the digenic interactions in this cross. The magnitude of dominance x dominance (l) was more than the other interaction parameters. Moreover, opposite signs of dominance (h) and dominance x dominance (l) effects showed the presence of duplicate type of epistasis. Pure line breeding and inbred development could be effective for improvement of the character under this situation.

However, in cross Punjab-8 x Pusa Sawani only one interaction parameter was significant in the six-parameter model, out of three interaction parameters. The non-significant interaction parameters i.e additive x dominance and dominance x dominance were eliminated and the remaining four parameters were re-estimated along with testing the adequacy of the model using chi-square test. The four parameter model m, [d], [h], [i] was tested and observed to be best fit model (Table-2). This model showed significant estimates of additive x additive (i) gene effect for this character but its negative sign indicated dissociated gene pair. Selection could be effective for improvement of this character in this material. Similar results were also reported by Arora and Ghai (2007) and Arora, et al. (2007).

REFERENCES


