ASSOCIATION PATTERN AMONG YIELD AND ITS RELATED ATTRIBUTES IN PEAS (PISUM SATIVUM L.)

Mudassar Iqbal*, Ikram Bashir**, Muhammad Iqbal, Kashif Nadeem, Amir Lateef, Saeed Ahmad Shah Chishti and Shahid Niaz*

ABSTRACT

A study was conducted at Vegetables Research Institute, AARI, Faisalabad, Faisalabad during the year 2011-12 to evaluate the genetic inconsistency and character relationship of ten normal season pea accessions (Climax, FS-2187, Pea-09. 9800-10, GRW-45, KQP-5180, Winner, Green Arrow, Ambassador and 6173). The trial was sown in triplicate randomized complete block design. Data were recorded for days to 50 percent flowering, 100-seed weight, yield per plot, plant height, pods per plant, pod length, seeds per pod and pod width. The data were subjected to analysis of variances using the Statistix 8.1. The results revealed significant differences for all traits studied. Maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was shown by yield per plot (29.26% and 40.34%) against minimum by plant height (8.78 and 10.15). The broad sense heritability ranged from 54 percent for yield per plot to 99 percent for days to 50 percent flowering. Genetic advance varied from 13.30 percent for plant height to 45.05 percent for 100-seed weight. Correlation coefficient analysis showed positive and significant association among yield per plot, plant height and number of seeds per pod while pod width was highly significantly and positively associated with 100-seed weight. It is concluded that these attributes worked as selection criteria for the development of high yielding lines for normal season of plantation in Punjab.

KEYWORDS: Pisum sativum.; association pattern; accessions; genotypic coefficient; yield; Pakistan.

INTRODUCTION

Pea (Pisum sativum L.) is an essential winter vegetable relating to the family Papiliomaceae. It is an important vegetable used as fresh as well as dry in Pakistan. Pea crop was grown on an area of 15836 hectares during the year 2011-12 in the country (2). Punjab shared 73 percent in area and 72 percent in production during the reported year. Peas provide evenhanded diet in mixture with wheat, rice and other cereals. It is a cheapest source of protein

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among all vegetables. This crop is grown under a wide range of environment, from central to southern Punjab and different regions of other provinces.

For a successful breeding programme, variability for a particular trait is very important. For this purpose knowledge of polygenic variation which may be phenotypic genotypic or environment, gives information about the nature and magnitude of variability for desired trait (11).

Correlation studies give information about relationship between any two attributes. The findings of genetic diversity and its association with other traits are helpful for facilitating proficient germplasm collection, its management and exploitation (12). Presence of genetic inconsistency is vital for any breeding programme that gives opening for selection of desirable material. In selection procedure correlation study plays a vital role because correlation between traits affects the selection method considerably and provides the breeder a direction to find the required traits (7).

The present study was conducted to discover the pea lines having greater inconsistency and character relationship for yield in our local environment.

MATERIALS AND METHODS

This study was conducted at Vegetables Research Institute, AARI, Faisalabad, Pakistan during the year 2011-12. Ten pea varieties/lines (Climax, FS-2187, Pea-09, 9800-10, GRW-45, KQP-5180, Winner, Green Arrow, Ambassador and 6173) were sown on 18.11.2011 in RCBD with three replications. Plot size was 12m² (6.0 x 2.0m). The distance between plants was 10 cm and row to row distance was kept as 1.25m. All agronomic practices were followed to raise better crop. The data were recorded on days to 50 percent flowering, 100-seed weight (green), yield per plot, plant height, pods per plant, seeds per pod, pod length and pod width. Variability in these traits was estimated as suggested by Steel and Torrie (14). Genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were estimated as advised by Burton (4) and Allard (1).

RESULTS AND DISCUSSION

Phenotypic coefficient of variation (PCV) was maximised for yield per plot (40.34%) followed by number of pods per plant (30.20%) and 100-seed weight (26.27%) (Table 1). The lowest value was recorded for plant height (10.15%). Genotypic coefficient of variation (GCV) for yield per plot (29.26%). was highest, followed by 100-seed weight (26.01%). Minimum GCV value
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was recorded number of pods per plant (22.40%) and plant height (8.78%) (Table 1). Days to 50 percent flowering, 100-seed weight, yield per plot, plant height, number of pods per plant, pod length, number of seeds per pod and pod width showed greater values of PCV than their corresponding GCV values. It indicated that variation was not only due to the genotypes but also influenced by environmental factors, so these traits may be misleading in selection procedure in early pea lines.

Table 1. Estimates of genetic parameters for different attributes in peas.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Mean</th>
<th>Coefficient of variation (%)</th>
<th>Heritability (%)</th>
<th>Genetic advance (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>PCV</td>
<td>GCV</td>
<td>(h² B.S)</td>
<td></td>
</tr>
<tr>
<td>Days to 50% flowering</td>
<td>69.60</td>
<td>17.56</td>
<td>17.55</td>
<td>0.99</td>
</tr>
<tr>
<td>100-seed weight (g)</td>
<td>50.98</td>
<td>26.27</td>
<td>26.01</td>
<td>0.97</td>
</tr>
<tr>
<td>Yield per plot</td>
<td>7.44</td>
<td>40.34</td>
<td>29.26</td>
<td>0.54</td>
</tr>
<tr>
<td>Number of pods per plant</td>
<td>18.70</td>
<td>30.20</td>
<td>22.40</td>
<td>0.55</td>
</tr>
<tr>
<td>Pod length (cm)</td>
<td>9.23</td>
<td>11.92</td>
<td>9.91</td>
<td>0.69</td>
</tr>
<tr>
<td>Number of seeds per pod</td>
<td>7.45</td>
<td>10.60</td>
<td>9.10</td>
<td>0.73</td>
</tr>
<tr>
<td>Pod width (cm)</td>
<td>1.71</td>
<td>10.95</td>
<td>9.83</td>
<td>0.80</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>79.58</td>
<td>10.15</td>
<td>8.78</td>
<td>0.74</td>
</tr>
</tbody>
</table>

h² B.S = Broad sense heritability.

All morphological traits showed (Table 1) high heritability in broad sense (54 to 99%) which indicated the small environmental influence. However, for improvement, selection for these traits is not a good choice, as additive, dominant and epistatic variances affect genetic variance which is the base of broad sense heritability. The highest value of genetic advance was observed for 100-seed weight (45.05%), yield per plot (38.16 %) and days to 50 percent flowering (30.69 %). It showed that these characters were controlled by additive genes, so selection for these traits would be a turning point for a successful breeding programme but plant height (13.30 %) showed minimum genetic advance revealing that this trait was governed by non-additive genes. This study showed that characters such as 100-seed weight, yield per plot and number of pods per plant gave high values for GCV accompanied by heritability and genetic advance. This also showed that these characters were more likely influenced by additive gene effects. Maximum GCV with high heritability and high genetic advance gave the plant breeder a better insight to select better genotypes for yield as observed by earlier scientists (4, 5, 8, 10, 13).

Correlation revealed the association of different traits among themselves, to find the traits suitable for breeding programme. In general, GCV was greater than corresponding PCV (Table 2.).

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Table 2.  Genotypic coefficient correlation for different traits in peas.

<table>
<thead>
<tr>
<th></th>
<th>Days to 50% flowing</th>
<th>100 seed weight</th>
<th>Yield/plot</th>
<th>Pods/ plant</th>
<th>Pod length</th>
<th>Seeds/pod</th>
<th>Pod width</th>
</tr>
</thead>
<tbody>
<tr>
<td>100 seed weight</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yield/plot</td>
<td></td>
<td>0.70*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pods/ plant</td>
<td>0.19</td>
<td>-0.36</td>
<td>-0.13</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pod length</td>
<td>0.17</td>
<td>0.78</td>
<td>0.87*</td>
<td>-0.10</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Seeds/pod</td>
<td>-0.16</td>
<td>0.33</td>
<td>0.67*</td>
<td>-0.31</td>
<td>0.58</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pod width</td>
<td>-0.21</td>
<td>0.91**</td>
<td>0.61</td>
<td>-0.22</td>
<td>0.58</td>
<td>0.18</td>
<td></td>
</tr>
<tr>
<td>Plant height</td>
<td>0.19</td>
<td>-0.10</td>
<td>0.05</td>
<td>-0.59</td>
<td>-0.15</td>
<td>0.24</td>
<td>-0.07</td>
</tr>
</tbody>
</table>

It indicated a strong inherent association among differences traits under study. The correlation coefficient of variation revealed that there was a positive and significant relationship between yield per plot with 100-seed weight (0.70*), while other characters had non-significant relationship. This showed that increased 100-seed weight might provide a chance to improve yield per plot. Pod length and number of seed per pod had significant positive association with yield per plot (0.87* and 0.67*) which indicated that as pod length and number of seed per pod increased, yield per plot also increased. Correlation analysis indicated that pod width was highly significant and had positive relationship with 100-seed weight which showed that an increase in pod width will also increase the yield. Genotypic coefficient correlation also showed that plant height and number of pods per plant were non-significantly correlated with yield which revealed that there were no association between these traits.

CONCLUSION

Study concludes that seeds per pod and pod length stand significant and positive association with yield per plot. So these traits could be used as selection tool for yield improvement in pea lines.

REFERENCES

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