ESTIMATION OF GENETIC VARIABILITY AND CORRELATION ANALYSIS IN FIELD PEA (PISUM SATIVUM L.) GENOTYPES

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Received-12.01.2017, Revised-23.01.2017

Abstract: An experiment was undertaken to study genetic variability and correlation analysis in 20 genotypes of pea (Pisum sativum L.) on the experimental field at Department of Genetics and Plant Breeding, Rajasthan College of Agriculture during Rabi, 2014. The genotypes were tested under irrigation condition in randomized block design with three replications. Analysis of variance revealed significant differences for six characters studied among the genotypes. The per se mean performance of various genotypes exhibited wide range of variation for most of the traits studied. According to mean performance of various traits viz. seed yield per plant, days to maturity and pod per plant, seed per pod was found superior for selection. The highest genotypic coefficient of variation was observed primary branches per plant followed by seed yield per plant, pod per plant, and seed per pod. Heritability estimates (broad sense) were found to be high for days to maturity followed by yield per plant, seed per pod, and pod per plant. High expected genetic advance coupled with high heritability estimates were recorded for seed yield per plant and days to maturity. The both genotypic and phenotypic levels for pod per plant and seed per pod were significantly correlated with seed yield/plant. Heritability coupled with high genetic advance and correlation also useful tool in predicting the effect in selection of best genotypes for future hybridization in yield improvement programme of pea.

Keyword: GCV, PCV, Heritability, Genetic advance, Correlation

INTRODUCTION

Field pea (Pisum sativum L.) is one of the world’s oldest domesticated crops. Its area of origin and initial domestication lies in the Mediterranean, primarily in the Middle East. The pea (Pisum sativum L.) is an important vegetable crop due to its high nutritive value. The most important tasks for a pea breeding are development of high yielding varieties with stable productivity, with sufficiently good resistance to disease and unfavorable environmental conditions, increases in protein content essential amino acids and favorable ration among them (Tiwari et al., 2001). Its improvement is based mainly on exploiting the natural sources of germplasm by means of selection or hybridization followed by selection. Genetic variability is considered as an important factor which is essential prerequisite for crop improvement program for obtaining high yielding progenies (Tiwari & Lavanya, 2012). The evaluation of genetic variability is important to know the source of genes for a particular trait within the available germplasm. The heritable variances give a clue for possible improvement of the character under study. Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. The higher the heritable variation, the greater will be the possibility of fixing the character by selection methods (Sharma et al 2003). The natural selection over years operated towards increasing the potentiality for survival and wider adoption at the cost of yield traits. A great extent of variability has been observed in different agronomic characters of pea with respect to plant height, days to flowering, pod length, and seed weight (Pallavi et al., 2013). The research work in this study aims at studying genetic variability and heritability of some traits in pea (Pisum sativum) which may help to select suitable genotypes for future breeding programs. Correlation studies provide an opportunity to study the magnitude and direction of association of one character with another. It is important for a plant breeder to find out which of the characters are correlated with yield to bring about genetic improvement in crop plants. Rathi et al (2007) Hence, an experiment was conducted to study the genetic variability, correlation and path coefficients among yield and yield component traits in pea. Character association studies are also helpful while making selection in the field for increasing seed yield. The present investigation was therefore, undertaken to eliminate appropriate plant type for selection so as to improve the seed yield accordingly in view the interrelation between traits and heritability.

Experimental material and method

The experimental material for the present investigation from the Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, India. The experiment was conducted in randomized block design at Field Experimentation Centre, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture during Rabi, 2014. All recommended agronomic and plant protection practices were followed to raise a good crop. Material consisting of twenty genotypes with one check of pea was sown in four rows per plots of 4 m length with three
replications. Row-to-row and plant-to-plant distance was maintained at 45 cm and 15 cm respectively. Recommended agronomic practices and plant protection measures were followed to raise a good crop. After eliminating the border plants, observations were recorded on five randomly selected plants from each plot on six quantitative characters viz. Days to 50% flowering, Primary branches per plant, pods per plant, seeds per pod, days to maturity and seed yield per plant. The mean, range and standard deviation for each character have been calculated and analysis of variance for each of the character was performed. The mean square (MS) at error and phenotypic variances were estimated as per Johnson et al. (1955). Genotypic and phenotypic co-efficient of variation was calculated by the formula suggested by Burton (1952), Broad sense heritability was estimated (defined by Lush 1949) and given the formula, suggested by Hanson et al. (1956) and Johnson et al. (1955). The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson et al. (1955). Genotypic and phenotypic correlation coefficients were measured with the formula suggested by Johnson et al. (1955)

RESULT AND DISCUSSION

The success of any breeding programme lies upon the thorough knowledge of genetic variability, heritability and type of gene action involved in the inheritance of improvement of desirable characters. The analysis of variance showed significant differences among the genotypes for different characters were studied, showing the great amount of genetic variability present among the genotypes (Table. 1). Thus, success of genetic enhancement is attributed to the magnitude and nature of variability present for a specific character.

Per se mean performance of genotypes

The per se mean performance of various genotypes exhibited wide range of variation for most of the traits studied (Table 2). Despite that some traits showed more variation like as days to maturity (120-140days), seed yield per plant (71.50-172.85g), days to 50% flowering (55-79 days), pods/plant (18.26-42.13), primary branches per plant (4.15-11.05) and seed per pod (3.56-5.36) etc. indicates sufficient variation among the genotypes for the traits studied. The mean value for grain yield was found 125.41g with standard error of 10.49. This reflected that there is greater opportunity to improve the yield and its related traits in pea.

Genotypic and phenotypic variance

Phenotypic variance was higher than the genotypic variances for all the characters thus indicating the influence of the environmental factors on these traits. The genotypic and phenotypic variations were obtained for different characters, and they are presented in Table 2. Genotypic and phenotypic coefficients of variation was high in case of seed yield per plant (539.63, 870.06), days to flowering (25.96, 33.03) pod per plant (23.94, 35.60), showing the presence of high amount of variation. Moderate genotypic and phenotypic coefficient of variation were found in primary branches per plant (3.06,4.44) and days to maturity (21.17,29.70) Lowest genotypic and phenotypic coefficient of variation estimate was found in a seed per pod (0.18, 0.27).

Genotypic and Phenotypic Coefficient of Variation

The GCV and PCV provide a measure to compare the variability present in the traits. GCV and PCV were classified as suggested by Burton (1952). Phenotypic coefficient of variation (PCV) was slightly higher in magnitude than the genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors on these traits as revealed in Table 2. PCV and GCV were high for primary branches per plant (23.45, 28.27) followed by seed yield per plant (18.52, 23.52) and pod per plant (18.81, 22.94). Tiwari and Lavanya (2012) also reported High GCV and PCV estimates recorded for seed yield per plant, whereas heritability estimates were found high for days to 50% flowering and for days to maturity and high excepted genetic advance as per cent of mean was recorded for seed yield per plant. The other characters were showing moderate GCV and PCV estimates viz., seed per pod (8.78,10.61) and days to flowering (7.28,8.21). Low values (less than 10%) for days to maturity (3.56, 4.21) Ahmad et al. (2014) also gave the high genotypic and phenotypic coefficient of variation for branches /plant, seed yield per plant and pods/plant. Similar results were found by Yadav et al. (2009) in field pea where seed yield and pod per plant were showing high and significant positive GCV and PCV. Lavanya et al.(2010) also recorded that high GCV and PCV estimates for seed yield per plant. Heritability estimates were ranged lowest from days to maturity (0.62) to highest for days to flowering (0.79).

Table 1. Analysis of variance for quantitative traits in pea genotypes.

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Characters</th>
<th>Mean sum of squares</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Replication (d.f.= 2)</td>
<td>Treatments (d.f.= 19)</td>
</tr>
<tr>
<td>1</td>
<td>Days to Flowering</td>
<td>0.600</td>
<td>84.947**</td>
</tr>
</tbody>
</table>
The estimates of mean, range and genetic variability for seed yield and its component in field pea.

Table 2. The estimates of mean, range and genetic variability for seed yield and its component in field pea.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Range</th>
<th>Mean±SEM</th>
<th>Vg</th>
<th>Vp</th>
<th>GCV</th>
<th>PCV</th>
<th>h²</th>
<th>GA</th>
<th>GA as % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to Flowering</td>
<td>55.0-79.0</td>
<td>70.00±1.53</td>
<td>25.96</td>
<td>33.03</td>
<td>7.28</td>
<td>8.21</td>
<td>0.79</td>
<td>9.30</td>
<td>13.29</td>
</tr>
<tr>
<td>Primary Branches/ Plant</td>
<td>4.15-11.05</td>
<td>7.45±0.67</td>
<td>3.06</td>
<td>4.44</td>
<td>23.45</td>
<td>28.27</td>
<td>0.69</td>
<td>2.99</td>
<td>40.07</td>
</tr>
<tr>
<td>Pods/ Plant</td>
<td>18.26-42.13</td>
<td>26.01±1.97</td>
<td>23.94</td>
<td>35.60</td>
<td>18.81</td>
<td>22.94</td>
<td>0.67</td>
<td>8.26</td>
<td>31.77</td>
</tr>
<tr>
<td>Seeds/ Pod</td>
<td>3.56-5.36</td>
<td>4.86±0.16</td>
<td>0.18</td>
<td>0.27</td>
<td>8.78</td>
<td>10.61</td>
<td>0.68</td>
<td>0.73</td>
<td>14.95</td>
</tr>
<tr>
<td>Days to Maturity</td>
<td>120-140</td>
<td>129.30±1.68</td>
<td>21.17</td>
<td>29.70</td>
<td>3.56</td>
<td>4.21</td>
<td>0.62</td>
<td>8.00</td>
<td>6.19</td>
</tr>
<tr>
<td>Seed Yield/ Plant</td>
<td>71.50-172.83</td>
<td>125.41±10.4</td>
<td>539.6</td>
<td>870.0</td>
<td>18.52</td>
<td>23.52</td>
<td>0.71</td>
<td>37.6</td>
<td>30.05</td>
</tr>
</tbody>
</table>

Table 3. Genotypic and phenotypic correlation for quantitative traits in pea.

<table>
<thead>
<tr>
<th>Character</th>
<th>Days to Flowering</th>
<th>Primary Branches/ Plant</th>
<th>Pods/ Plant</th>
<th>Seeds/ Pod</th>
<th>Days to Maturity</th>
<th>Seed Yield/ Plant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to Flowering</td>
<td>1.000</td>
<td>0.093</td>
<td>-0.288</td>
<td>0.200</td>
<td>0.709**</td>
<td>-0.105</td>
</tr>
<tr>
<td>Primary Branches/ Plant</td>
<td>1.000</td>
<td>0.181</td>
<td>-0.271</td>
<td>0.114</td>
<td>0.436*</td>
<td>-0.129</td>
</tr>
<tr>
<td>Pods/ Plant</td>
<td>1.000</td>
<td>0.024</td>
<td>-0.072</td>
<td>0.249</td>
<td>0.010</td>
<td></td>
</tr>
<tr>
<td>Seeds/ Pod</td>
<td>1.000</td>
<td>0.143</td>
<td>-0.052</td>
<td>0.056</td>
<td>-0.131</td>
<td></td>
</tr>
<tr>
<td>Days to Maturity</td>
<td>1.000</td>
<td>0.00</td>
<td>-0.114</td>
<td>-0.416*</td>
<td>0.825**</td>
<td></td>
</tr>
<tr>
<td>Seed Yield/ Plant</td>
<td>1.000</td>
<td>0.00</td>
<td>-0.047</td>
<td>-0.059</td>
<td>0.859**</td>
<td></td>
</tr>
</tbody>
</table>

G-genotypic, P-phenotypic

Vg- Genotypic variance, Vp phenotypic variance, GCV-Genotypic coefficient of variation, PCV-phenotypic correlation coefficients, h²- heritability broad sense, GA – genetic advance

Heritability and genetic advance

The moderate heritability were found in seed yield per plant (0.71), primary branches per plant (0.69), seed per pod (0.68) and pods per plant (0.67). Nawab et al. (2008) also shown the high heritability of days to 50% flowering and yield (kg/ha). The highest estimates of heritability shown here is due to a little influence of environment. The highest value of genetic advance were obtained for seed yield per plant (37.69), days to flowering (9.30), pods per plant (8.26) and genetic advance as percentage of mean were found for primary branches per plant (40.07), pods per plant (31.77) and seed yield per plant (30.05). It reveals that these characters were governed by additive genes and selection for improvement in these traits would be beneficial. The minimum value of genetic advance for seed per pod (0.73) and as percent of mean for days to maturity (6.19) shown that this trait was being governed by non additive genes action.

Genotypic and Phenotypic Correlation

The estimates of genotypic and phenotypic correlation coefficients between different characters of pea genotypes are presented in (Table 3). The genotypic correlation coefficients in most of cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. In some cases, phenotypic correlation coefficients were higher than genotypic correlation indicating suppressing effect of the environment.
which modified the expression of the characters at phenotypic level. In present investigation were found significant and highly positive with seed yield per plant at both genotypic and phenotypic levels for pod per plant (0.825**, 0.859**) and seed per pod (0.478**, 0.405**). Rai et al. (2006) observed same result that the yield/plant is showing a positive and significant association of with pods/plant. The genotypic and phenotypic character of days to flowering was shown negative correlation with seed yield per plant. The genotypic characters of primary branches per plant shown positive correlation (0.010) but phenotypic negatively correlated (-0.131) with seed yield per plant. In case of days to maturity genotypic was found negatively correlation (-0.233) but phenotypic was found positive correlation (0.081) with seed yield per plant. Tiwari and Lavanya (2012) also reported similar characters like number of branches/plant, pod length, pods/plant, seeds/pod and seed index recorded high positive and significant correlation with seed yield, suggesting their potential use in field pea improvement. In case of correlation coefficients studies for genotypic and phenotypic, the genotypic coefficient values are higher than the phenotypic correlation coefficients value for almost all the characters either it is in positive or negative direction shows that the strong associations between the characters present in (Table 3.). Here the environment played a minor role in the modification of the expression of the genes. Govardhan et al. (2013) were also recorded that grain yield/plant is positively correlates with pods/plant and negatively correlated with days to maturity. Parihar et al. (2014) also observed that correlation studies exhibited that seed yield had positive significant correlation with most of the traits.

REFERENCES


