

Research Article

Estimates of Genetic Components of Variation for Earliness and Yield Traits in Garden Pea (*Pisum sativum* L.)

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Abstract

A study of fifty five F₁ hybrids of garden pea (*Pisum sativum* L.) in a half diallel set involving eleven parents were conducted in a Randomized Block Design with three replications. Over-dominance was found for all the characters which indicated predominance of non-additive gene action for the inheritance of these characters. The positive value of F in all the characters showed preponderance of dominant alleles in parents. Dominance effect (H) was found to be higher than additive effect (D) for all characters except plant height & days to 50% flowering and average degree of dominance was more than one for all the characters, confirmed the predominant role of non-additive gene action. For all traits narrow sense of heritability was less than 50% except plant height and days to 50% flowering, which suggests the preponderance of non-additive gene action and commercial exploitation of recombinant breeding for improvement of these characters.

Keywords: Gene action, *Pisum sativum*, earliness, yield

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Introduction

Garden pea (*Pisum sativum* L.) is an annual herbaceous legume vegetable belonging to the family Fabaceae. Pea is grown for both fresh green pods and dried seed throughout the world. It is used as pulse or in soup, canned, processed or dehydrated form. The seeds are rich source of protein (23–25%), digestible starch (50%), soluble sugars (5%), fiber, minerals and various kind of vitamins [1].

Development of high yielding varieties mainly depends upon genetically superior parents, coupled with suitable breeding methodology. To formulate any breeding method, it is imperative to have knowledge of gene action involved in inheritance of various traits. Since yield is a complex and polygenically inherited trait, knowledge of gene action or pattern of inheritance of different quantitative traits including yield will be helpful to formulate the suitable breeding method to be applied for achieving the desired objectives in the improvement of garden pea. Selection and hybridization are the most important methods for crop improvement. The success of selection mainly depends upon the extent of genetic variability exist in a particular crop. Therefore, a higher genetic base should be utilized for faster and higher magnitude of success. Utilization of divergent germplasm in hybridization creates such broad genetic base.

A detailed knowledge about the magnitude and nature of genetic variation in a specific population is of prime importance for prediction of the most effective breeding programme. In spite of exhibiting considerable amount of genetic diversity with respect to different characters, little attention has been given for improvement of this crop. Hayman (1954) [2] and Griffings (1956) [3] offered an excellent mean of obtaining information on magnitude and direction of dominance and over-dominance besides the nature and extent of gene action involved in the inheritance of quantitative traits. Hence, an attempt was made to investigate the gene action (inheritance pattern) of yield and yield attributing traits.

Materials and Methods

The present investigation was carried out during winter season of 2014-15 and 2015-16 at research farm of Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi. Eleven genetically diverse inbreds of garden pea viz, Arkel, VRP-6, AP-3, Pusa Pragati, GP-17, VRP-7, VP-233, GP-473, Arka Ajit, IP-3 and GP-6 were

crossed in a 11 x 11 half-diallel mating scheme [3]. The resulting 55 F₁ hybrids along with 11 parental lines were evaluated in a randomized block design with three replications. The plot size was kept as two rows of 4 m length for each genotype keeping plant spacing 45 × 10 cm apart. The recommended fertilizer (40:60:40 as NPK) doses and cultural practices were followed to raise a good crop. The observations were recorded for nine pod yield traits based on 10 sample plant and the average were computed for the characters such as plant height (cm), node bearing first flower, pod length (cm), days to 50% flowering, number of pods per plant, number of seeds per pod, average pod weight (g), shelling percentage (%) and pod yield per plant (g). The components of variances were estimated following diallel method of numerical approach given by Hayman (1954) [2]. The estimates of average degree of dominance [(H₁/D)^{1/2}] '0' denotes no dominance, 0 to 1 partial dominance; 1 complete dominance and > 1 over dominance. The maximum values of H₂/4 H₁ shall be 0.25 when u = v = 0.05. If the relative frequency of dominant and recessive genes [(4D H₁)^{1/2} + F/ (4D H₁)^{1/2} - F] in parents is equal to 1, it reflects equal proportion i.e. symmetrical distribution of dominant and recessive genes (u = v = 0.5). Any deviation from 1 shows asymmetry of distribution (u ≠ v) as > 1 refers to excess of dominant genes and minority of recessive genes (u > v) and <1 means minority of dominant genes and excess of recessive (u < v).

Results and Discussion

The estimates of genetic components of variation and various statistical parameters for different characters were represented in **Table 1**.

Table 1 Estimates of genetic components of variation and various statistical parameters for different characters

| Genetic parameters | Plant height | Node bearing first flower | Days to 50% flowering | Number of pods per plant | Pod length | Pod width | Number of seeds per pod | Pod weight | Shelling percentage | Yield per plant |
|---|----------------|---------------------------|-----------------------|--------------------------|-------------|-------------|-------------------------|-------------|---------------------|-----------------|
| D (Additive effect) | 158.71**±29.96 | 0.86±0.43 | 168.25**±14.10 | 9.12*±3.23 | 1.31*±0.54 | 0.06**±0.02 | 0.47**±0.11 | 0.81**±0.28 | 19.46**±4.50 | 250.48*±110.68 |
| F (Gene distribution) | 75.90*±33.23 | 1.26 ±0.98 | 153.06**±15.64 | 1.29±7.39 | 2.08*±1.24 | 0.07**±0.06 | 0.53*±0.26 | 0.99±0.65 | 23.15**±11.87 | 264.16±252.94 |
| H ₁ (Dominance effect) | 81.76**±14.54 | 4.10**±0.89 | 127.62**± 6.85 | 40.53**±6.66 | 6.24**±1.12 | 0.38**±0.05 | 1.24**±0.23 | 2.03**±0.58 | 72.09**±10.70 | 662.89**±228.04 |
| H ₂ | 118.24**±25.19 | 3.55**±0.75 | 94.38**±11.86 | 37.33**±5.60 | 4.65**±0.94 | 0.35**±0.04 | 1.01**±0.20 | 1.65**±0.49 | 59.26**±9.00 | 502.86**±191.70 |
| H ² | 7.45±16.85 | 3.17**±0.50 | 75.44**±7.93 | 13.58**±3.74 | 0.74±0.63 | 0.53**±0.03 | 0.33**±0.13 | 0.03±0.36 | 6.42±6.02 | 437.57**±128.23 |
| E (Environmental effect) | 4.22±4.20 | 0.29*±0.12 | 2.18±1.98 | 1.48±0.93 | 0.19±0.17 | 0.01±0.01 | 0.19**±0.03 | 0.06±0.08 | 6.44**±1.50 | 27.78± 31.95 |
| (H ₁ /D) ^{1/2} | 1.39 | 2.18 | 1.15 | 2.11 | 2.18 | 2.56 | 1.62 | 1.59 | 1.92 | 1.63 |
| (H ₂ /4H ₁) | 0.19 | 0.22 | 0.14 | 0.23 | 0.19 | 0.23 | 0.20 | 0.20 | 0.21 | 0.19 |
| [(4DH ₁) ^{1/2} + F / (4DH ₁) ^{1/2} - F] | 2.00 | 2.01 | 3.19 | 1.07 | 2.14 | 1.60 | 2.06 | 2.26 | 1.89 | 1.96 |
| (h ² / H ₂) | 0.06 | 0.89 | 0.80 | 0.36 | 0.16 | 1.51 | 0.33 | 0.02 | 0.11 | 0.87 |
| Heritability % (ns) | 55.06 | 17.76 | 58.29 | 16.81 | 21.04 | 13.77 | 24.11 | 38.73 | 20.66 | 32.94 |

* & ** Significant at 5% and 1% probability, respectively.

With respect to plant height, the data indicated that the estimates of D, F, H₁ and H₂ were highly significant whereas h² and E were non significant. The value of D was more than H₁, exhibiting additive gene action. The positive F value indicated more prevalence of dominant alleles in parents. The mean degree of dominance (H₁/D)^{1/2} was 1.39, indicating over-dominance. The proportion of genes with positive and negative effects (H₂/4 H₁) in parents was 0.19, denoting asymmetry at loci showing dominance. The proportion of dominant and recessive genes [(4DH₁)^{1/2} + F/ (4DH₁)^{1/2} - F] in parents was 2.00 whereas the number of genes (h²/ H₂) which controlled the character and exhibit dominance was 0.06. Narrow sense heritability was medium to high (55.06%), thus showing preponderance of additive gene action.

For node bearing first flower, the estimated value of H₁, H₂ and h² were highly significant and E was significant while other parameters viz. D and F were non-significant. The estimated value of H₁ was greater than D which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance (H₁/D)^{1/2} being 2.18 showed over-dominance. The proportion of genes with positive and negative effects (H₂/4H₁) was 0.22, which denotes asymmetry at loci. The proportion of dominance and recessive genes [(4DH₁)^{1/2} + F/ (4DH₁)^{1/2} - F] was 2.01 whereas the number of group of genes exhibiting dominance and controlling character was 0.89. The narrow sense heritability (17.76%) indicated the non-additive type of gene action for expression of this character.

The genetical parameters like D, H_1 , H_2 , h^2 and F were significant while E was non-significant for days to 50% flowering. The value of H_1 was lesser than D, indicating the presence of additive gene action. The positive value of F indicated that the dominant alleles were more frequent in parents. The mean degree of dominance $(H_1/D)^{1/2}$ being 1.15 exhibited over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) was noted 0.14, indicating asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ in the parents was 3.19 whereas the number of dominant group of genes (h^2 / H_2) was 0.80. Medium value of narrow sense heritability (58.29%) showed preponderance of additive type of gene action for this trait. These results for earliness characters were in similar with findings of Sharma *et al.* (2003) [4] and Singh and Singh (1989) [5].

The genetic component of variation for number of pods per plant *viz.* D, H_1 , H_2 and h^2 were highly significant whereas estimate of E and F were non-significant. The value of H_1 was more than D which showed more prevalence of dominant genes. The positive value of F suggested predominance of dominant alleles in the parents. The degree of dominance $(H_1/D)^{1/2}$ was 2.11, revealing the role of over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) was 0.23 exhibiting dominance. The proportion of dominant and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ was 1.07 whereas the number of group of genes (h^2 / H_2) which showed dominance was 0.36. Narrow sense heritability (16.81%) indicated non-additive gene action. These results for fruit characters were also similar with the findings of Rastogi (1988) [6] and Singh *et al.* (1986) [7].

The parameters like H_1 , H_2 were highly significant, D and F were significant only while h^2 and E were non-significant for pod length. The value of D was lesser than H_1 representing presence of non-additive genes. The mean degree of dominance $(H_1/D)^{1/2}$ was 2.18 exhibited over-dominance. The value of $H_2/4H_1$ was 0.19 indicating asymmetry at loci which shows dominance. The proportion of dominant and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ in the parents was 2.14 whereas the number of dominant group of genes (h^2/H_2) was 0.16. Narrow sense heritability (21.04%) showed preponderance of non-additive type of gene action for this important trait.

For pod width estimates of D, H_1 , H_2 , h^2 and F were highly significant whereas E was non-significant. The value of H_1 was greater than D, suggesting the presence of dominant alleles in parents. The positive F value indicated more prevalence of dominant alleles in parents. The mean degree of dominance $(H_1/D)^{1/2}$ being 2.56 indicated over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) was 0.23, showing dominance. The proportion of dominant and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ in the parents was 1.60, while the group of dominant genes (h^2 / H_2) was 1.51. Narrow sense heritability being low (13.17%), indicated the control of the trait by non-additive gene action.

The estimates of genetic component of variation for number of seeds per pod, *i.e.*, D, H_1 , H_2 and h^2 were highly significant while F was significant only. The value of H_1 was more than D, which signify that dominant genes were more than additive genes. The environmental influence (E) on the inheritance of this was significant. The positive F value indicated more prevalence of dominant alleles in parents. The mean degree of dominance $(H_1/D)^{1/2}$ was >1 (1.62) indicating the role of over-dominance for this trait. The proportion of genes with positive and negative effects ($H_2/4 H_1$) in the parents was < 0.25 (0.20), denoting asymmetry at the loci showing dominance. The proportion of dominant and recessive gene as indicated by $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ was 2.06 while the group of genes, which controlled the characters (h^2 / H_2) and exhibited dominance was 0.33. Narrow sense heritability being 24.11% showed preponderance of non-additive gene action.

For pod weight, the estimated value of D, H_1 and H_2 were highly significant while other parameters, *viz.* h^2 , E and F were non-significant. The estimated value of D was less than H_1 which revealed that non-additive genes were more than additive genes. Positive value of F indicated predominance of dominant alleles. The mean degree of dominance $(H_1/D)^{1/2}$ being 1.59 showed over-dominance. The proportion of genes with positive and negative effects ($H_2/4 H_1$) was 0.20, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ was 2.26 whereas number of group of genes exhibiting dominance and controlling character was 0.02. The narrow sense heritability (38.73%) indicated the non-additive type of gene action for expression of this character.

Sood and Kalia (2006) [8] also observed prevalence of overdominance for most of the traits. Non-additive gene action appeared to be more predominant for the inheritance of most characters studied. Low to medium narrow sense heritability indicated presence of non-additive gene action for most of the traits studied except for pod yield in the F_1 crosses. The proportion of genes with positive and negative effects ($H_2/4 H_1$) was 0.20, which denotes asymmetry at loci. The proportion of dominance and recessive genes $[(4D H_1)^{1/2} + F / (4D H_1)^{1/2} - F]$ was 2.26 whereas number of group of genes exhibiting dominance and controlling character was 0.02. The narrow sense heritability (38.73%) indicated the dominant type of gene action for expression of this character.

The estimates of D, F, H_2 , H_1 and E were highly significant and h^2 was non-significant for shelling percentage while the value of D was less than H_1 , exhibiting role of non-additive gene action. The positive value of F showed preponderance of dominant alleles for this trait in parents. The mean degree of dominance $(H_1/D)^{1/2}$ was 1.92

indicating the over dominance. While the proportion of genes with positive and negative effects ($H_2/4H_1$) in parents was found to be 0.21 denoting asymmetry at loci showing dominance. The proportion of dominant and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ in parents was 1.89 whereas the number of genes (h^2/H_2) which controlled the character and exhibit dominance was 0.11. Narrow sense heritability was 20.66% showed predominance of non-additive gene action.

Results pertaining to components of genetic variation for total yield per plant revealed that estimate of D, H_1 , H_2 and h^2 were highly significant while other parameters *viz.* E and F were non-significant. The value of H_1 was greater than D, indicating the presence of more dominant genes than additive ones. The positive value of F showed preponderance of dominant alleles for this trait in parents. The value of $(H_1/D)^{1/2}$ was higher (1.63) indicating over-dominance. This showed that there was possibility of an exceed dominance effect on population. Similar results had been reported by Snoad and Arthur (1974) [9], Ceyhan *et al.*, (2008) [10] and Rana and Gupta (1994) [11]. The proportion of genes with positive and negative effects ($H_2/4 H_1$) in parents was found to be 0.19 (less than 0.25), which denoted asymmetry at loci showing dominance. The proportion of dominance and recessive genes $[(4DH1)^{1/2} + F / (4DH1)^{1/2} - F]$ was 1.96. The number of group of genes (h^2/ H_2) exhibiting dominance and controlling the character was 0.87. Low to medium values of narrow sense heritability (32.94%) indicated that non-additive gene action played an important role in inheritance of this trait.

Conclusion

The results of present investigation showed dominance and over-dominance gene actions for all quantitative traits in garden pea. Average degree of dominance was more than 1 and narrow sense heritability was found to be less than 0.5 for all the characters except days to 50% flowering suggesting the preponderance of non-additive gene action. Thus, the predominance of non-additive gene action for most of the important yield contributing characters suggested the importance of hybrid breeding to get higher yield advantage in garden pea.

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