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Assessment of gene action for yield and its contributing traits in Pea (*Pisum sativum* L.)

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Abstract
The present experiment was carried out to assess gene action in fifty-four genotypes comprising fourteen parents and their forty crosses. Analysis of variance exhibited significant differences among the genotypes for all the traits under studied. The data was collected for various morphological characters associated with yield and its contributing traits. Estimates of additive variance (δ^2A) were lower than dominant variance (δ^2D) for different attributes except *viz*., TSS Brix %, green pods per plant, branches per plant, pod length, pod weight and pod diameter indicating that the presence of additive gene action. The dominance variance (δ^2D) was higher than additive variance (δ^2A) for characters except *viz*., days to first flowering, days to 50% flowering, days to first green pod picking, pod yield per plant, plant height and number of seeds per pod was indicated as non-additive gene action.

Keywords: Gene action, heterosis, pea (*Pisum sativum* L.) and variance

Introduction
Pea (*Pisum sativum* L. 2n=2x=14) is one of the most important annual herbaceous and popular winter vegetable crops that belongs to the family Fabaceae (Leguminosae) and sub-family Papilionaceae grown all over the world. All legume crops including pea is originated in Central Asia whereas, Asia Minor is the secondary centre of origin.
Due to their high protein content, advantageous amino acid composition, and low trypsin inhibitor levels, peas can provide the essential nutrients to a variety of age groups (Aysh *et al.,* 2015) [5]. Pea protein is high in lysine and other necessary amino acids but deficient in sulphur-containing cysteine and methionine. (Ceyhan and Avci, 2005) [7].
Garden pea has high nutritive value, particularly proteins, 7.2g per 100 g of an edible portion (Singh, 2007) [7] and other health-building substances like carbohydrates, calcium and phosphorous. Peas are a good human food that may be eaten as a vegetable or in soup. During times of scarcity, a large volume of peas is canned, frozen, or dehydrated for consumption. It is eaten as a grain legume as well as a vegetable and is known as field pea and vegetable pea, respectively
The choice of parents for use in hybridization programmes and the suitable breeding method for the genetic development of certain quantitative traits are both aided by knowledge of gene activity in plant breeding (Sharma *et al.,* 2013) [16]. Therefore, to choose the ideal parents for hybridization and enhance the existing cultivars, knowledge of combining ability and the nature of gene effects is required. There is some information on the additive and non-additive effects related to yield and qualities that influence yield, but it depends on the region, the genetic material involved, and the specific environmental factors.

Materials and Methods
Fifty-four pea genotypes were carried out using a Randomized Block Design (RBD) with three replications during *rabi* season, 2021-22 and 2022-23 at the Horticulture Research Centre of the Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut-250110 (U.P.), The following key traits were recorded for days to first flowering, days to 50% flowering, days to first green pod picking, plant height, branches per plant, green pod per

plant, pod weight, pod length, pod diameter, number of seeds per pod, TSS Brix % and pod yield per plant. All the agronomical practices were taken during the cropping season. The genetic components of variation were calculated by the methods suggested by Jinks and Hayman (1954) [10], Hayman (1954) [10] and Aksel and Johnson (1963) [3].

Genetic component and their magnitude

$$\text{Cov. Half sib (line)} = \frac{M_f - M_{fm}}{rm}$$

$$\text{Cov. Half sib (tester)} = \frac{M_m - M_{fm}}{rf}$$

$$\text{Cov. Half sib (average)} = \frac{1}{r(2fm - f - m)}\left[\frac{(f-1)M_f + (m-1)M_m}{f + m - 2} - M_{fm}\right]$$

$$\text{Cov. F.S. (average)} = \frac{(M_f - M_e) + (M_m - M_e) + (M_{fm} - M_e)}{3r} +$$

$$\frac{6r\,\text{Cov. H.S. (average)} - r(f + m)\,\text{Cov. H.S. (average)}}{3r}$$

Where,
M_f = Mean squares due to lines (females)
M_m = Mean squares due to testers (males)
M_{fm} = Mean squares due to line × tester interactions
M_e = Mean squares due to error
r = Number of replications
f = Number of lines
m = Number of testers

$$\text{gca variance } (\sigma^2 gca) = \text{Cov. H.S. (average)} = \left[\frac{1+F}{4}\right]\sigma^2 A$$

Therefore,
Additive genetic variance ($\sigma^2 A$) = 2 Cov. H.S. (average), if F = 1 and ($\sigma^2 A$) = 4 Cov. H.S. (average), If F = 0

$$\text{sca variance } (\sigma^2 sca) = \frac{(M_{fm} - M_e)}{r}$$

$$\sigma^2 sca = \left[\frac{1+F}{2}\right]^2 \sigma^2 D$$

Therefore,
Dominance variance ($\sigma^2 D$) = σ^2 sca with F = 1, and $\sigma^2 D$ = $4\sigma^2 sca$, if F = 0
Where,
F = Inbreeding coefficient

Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines (\%)} = \frac{\text{S.S. (lines)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of testers (\%)} = \frac{\text{S.S. (testers)}}{\text{S.S. (crosses)}} \times 100$$

$$\text{Contribution of lines × testers} = \frac{\text{S.S. (lines x testers)}}{\text{S.S. (crosses)}} \times 100$$

Results and Discussion
Genetic components and their magnitude
The estimates of GCA and SCA variance, predictability ratio, average degree of dominance, narrow heritability and proportional of lines, testers and lines x testers are given in Table-1.

The estimates of $\delta^2 g$ due to males were found to be higher than $\delta^2 g$ due to females for TSS Brix % (1.58), number of seeds per pod (0.18) and pod weight (0.13) a comparison of relative magnitude of these expressed to focus that additive gene action. However, the $\delta^2 g$ due to females showed higher than the $\delta^2 g$ due to males for plant height (32.61), pod yield per plant (24.68), days to first green pod picking (6.18), days to first flowering (4.68), days to 50% flowering (4.36), green pod per plant (0.57), branches per plant (0.39), pod length (0.14) and pod diameter (0.01) which indicated that the predominance role of additive gene action.

The estimates of $\delta^2 s$ were found to be higher than the $\delta^2 g$ (pooled) for all the characters except days to first flowering (6.59), days to 50% flowering (5.49), days to first green pod picking (5.38). In reference to estimates of additive variance ($\delta^2 A$) was lower than dominant variance ($\delta^2 D$) for different attributes except viz., TSS Brix % (0.126), green pods per plant (0.061), branches per plant (0.044), pod length (0.023), pod weight (0.019) and pod diameter (0.0008) indicating that presence of additive gene action. The dominance variance ($\delta^2 D$) was higher than additive variance ($\delta^2 A$) for characters except viz., days to first flowering (6.587), days to 50% flowering (5.490), days to first green pod picking (5.382), pod yield per plant (4.643), plant height (4.358) and number of seeds per pod (0.099) was indicated as non-additive gene action. The pedigree approach of breeding may be better suitable for utilizing additive genetic variance to improve such traits. Similar results for many of these characteristics were also investigated by Brar et al. (2012) [6], Kumar et al. (2016) [11], Devi et al. (2017) [9], Nageshwar et al. (2018) [14], Tampha et al. (2018) [20], Suchitra et al. (2022) [18].

Average degree of dominance exhibited partial dominance for green pods per plant (0.99), branches per plant (0.91), pod weight (0.86) and pod diameter (0.35). However, over dominance was observed for days to first flowering (4.00), days to 50% flowering (3.78), days to first green pod picking (3.23), number of seeds per pod (2.66), pod yield per plant (1.24) and plant height (1.15). The mean degree of dominance was greater found unity for all traits under study. The predictability ratio was observed less than unity for all characters. Narrow sense heritability was observed for branches per plant (29.43%) followed by TSS Brix % (27.44%), pod length (24.00%), plant height (23.48%), pod diameter (18.33%), green pods per plant (17.72%), pod yield per plant (17.31%), pod weight (16.27%), number of seeds per pod (6.45%), days to 50% flowering (4.59%), days to first flowering (4.44%) and days to first green pod picking (4.17%). These results, when applied to a number of characters, closely matched by Brar et al. (2012) [6], Suman et al. (2017) [19], Abdulla, S. M. S. (2018) [1] and Kumar et al. (2021) [13].

Proportional contribution of lines, testers and line x tester for all the characters under study revealed that the proportional contribution of lines for all the characters range varied from 79.64% (plant height) to 5.10% (TSS Brix %). The highest contribution of lines was recorded for plant height (79.64%) followed by branches per plant (74.00%), green pods per plant (73.36%), pod diameter (71.36%), pod yield per plant (64.23%), days to first green pod picking (58.35%), pod length (55.51%), days to 50% flowering (53.62%), days to first flowering (52.10%), pod weight (44.12%), number of seeds per pod (11.28%) and TSS Brix % (5.10%). The proportional contribution of testers for all the characters range varied from 94.15% (TSS Brix %) to 0.79% (days to first green pod picking). The highest contribution of testers was observed for TSS Brix % (94.15%) followed by number of seeds per plant (55.16%), pod weight (43.52%), pod length (43.35%), pod yield per plant (21.55%), pod diameter

(19.10%), branches per plant (17.86%), green pods per plant (14.29%), plant height (9.09%), days to first flowering (3.80%), days to 50% flowering (3.57%) and days to first green pod picking (0.79%). The proportional contribution of line x tester for all the characters range varied from 44.10% (days to first flowering) to 0.75% (TSS Brix %). The highest contribution of line x tester was found for days to first flowering (44.10%) followed by days to 50% flowering (42.81%), days to first green pod picking (40.86%), number of seeds per pod (33.55%), pod yield per plant (14.22%), pod weight (12.36%), green pods per plant (12.35%), plant height (11.27%), pod diameter (9.55%), branches per plant (8.13%), pod length (1.14%) and TSS Brix % (0.75%). Similar result was also reported earlier by Santra and Chaudhary (2012) [15], Dalia *et al.* (2013) [8], Suman *et al.* (2017) [19], Kumar *et al.* (2017) [12], Abdulla, S. M. S. (2018) [1], Askandar *et al.* (2018) [4], Tampha *et al.* (2018) [20] and Ahmed *et al.* (2022) [2].

Table 1: Estimate of genetic components and their magnitude for 12 quantitative characters in Pea (*Pisum sativum* L.)

Components	DFF	DFPF	DFGPP	PH (cm)	BPP	GPPP	PW (g)	PL (cm)	PD (mm)	NSPP	TBP	PYPP (g)
$\sigma^2 A$	0.413	0.384	0.515	3.271	0.044	0.061	0.019	0.023	0.0008	0.014	0.126	2.998
$\sigma^2 D$	6.587	5.490	5.382	4.358	0.036	0.060	0.014	-0.030	0.0001	0.099	-0.145	4.643
$\sigma^2 g$ (female)	4.68	4.36	6.18	32.61	0.39	0.57	0.10	0.14	0.01	0.00	0.07	24.68
$\sigma^2 g$ (male)	-0.17	-0.16	-0.62	4.04	0.11	0.13	0.13	0.13	0.00	0.18	1.58	9.95
$\sigma^2 g$ (pooled)	1.22	1.13	1.32	12.20	0.19	0.25	0.12	0.14	0.00	0.13	1.15	14.16
$\sigma^2 s$ (sca)	6.59	5.49	5.38	4.36	0.04	0.06	0.01	-0.03	0.00	0.10	-0.15	4.64
Average Degree of Dominance	4.00	3.78	3.23	1.15	0.91	0.99	0.86	-	0.35	2.66	-	1.24
Predictability ratio	0.06	0.07	0.09	0.43	0.55	0.50	0.57	-3.05	0.89	0.12	-6.44	0.39
% contribution (line)	52.10	53.62	58.35	79.64	74.00	73.36	44.12	55.51	71.36	11.28	5.10	64.23
% contribution (tester)	3.80	3.57	0.79	9.09	17.86	14.29	43.52	43.35	19.10	55.16	94.15	21.55
% contribution (L x T)	44.10	42.81	40.86	11.27	8.13	12.35	12.36	1.14	9.55	33.55	0.75	14.22
Narrow sense heritability (%)	4.44	4.59	4.17	23.48	29.43	17.72	16.27	24.00	18.33	6.45	27.44	17.31

DFF= Days to first flowering DFPF= Days to 50% flowering DFGPP= Days to first green pod picking PH= Plant height (cm) BPP= Branches per plant GPPP= green pods per plant PW=Pod weight (g) PL= Pod length (cm) PD= Pod diameter (mm) NSPP= Number of seeds per pod TBP= TSS Brix % PYPP= Pod yield per plant (g)

Conclusion
The studied indicated that all the traits showed significant genotypic differences. Genetic analysis showed that all the traits studied are controlled by the additive type of gene action except *viz.*, TSS Brix %, green pods per plant, branches per plant, pod length, pod weight and pod diameter. Presence of additive gene action in traits like days to first flowering, days to 50% flowering, days to first green pod picking, pod yield per plant, plant height and number of seeds per pod suggested early selection for improvement.

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