Genetic Investigation in Garden Pea for Yield and Quality Characters

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Authors' contributions

This work was carried out in collaboration among all authors. Author GKL, designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors PK and Devaraju managed the analysis of the study. Authors YK, VS and ANR managed the literature searches. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

An experiment was conducted to determine the magnitude of genetic variability, heritability and genetic advance as per cent over mean among twenty-two genotypes of garden pea using five quantitative and eight qualitative characters. The results of ANOVA showed significant differences among the genotypes for all the characters, indicating a wide spectrum of variability among the

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genotypes. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV). The high value of GCV and PCV was recorded for the weight of 10 green pods, the weight of seeds 10 green pods, Chlorophyll-A and Chlorophyll-B. All the characters showed a high magnitude of heritability in a broad sense (>60%), ranging from 86.68% (Pod yield per hectare) to 99.60% (Chlorophyll-A). Further, high heritability coupled with high genetic advance as per cent of mean (>20%) was observed for all the characters except firmness, suggesting that these characters are genetically controlled by additive (heritable) gene action and can be utilized for garden pea improvement through selection. This study has five promising genotypes: 'Arka Apoorva, ''Arka Sampoorna, ''Arka Tapas,''IIHR-570' and 'IIHR-684' which have been identified for higher yield, which can be utilized for further crop improvement program.

1. INTRODUCTION

Garden pea (*Pisum sativum* L.) 2n=14 is a major leguminous vegetable crop whose cultivation is confined to temperate and subtropical areas of the world. It is grown for its tender pods, foliage, and immature and mature seed. It has several health-benefiting properties as it is a rich source of protein ranging from 23 – 33%, minerals, vitamins and antioxidants. In addition, pea remains are a nutritious feed for animals and offer poor farmer families additional benefits. It also plays an important role in modern agricultural systems as it enhances soil structure and provides breaks for disease control [1]. Developing genotypes that offer a high genetic potential for seed or fodder yield is one of the fundamental directions for pea breeding. Genotypes for a particular agro ecological zone may be targeted. Genetic potential is best exploited in the environments for which certain genotypes have been established. Therefore, there is an urgent need to identify new genotypes with high genetic yield potential for pea germplasm improvement.

In order to achieve an effective crop breeding program, genetic variability in peas is still highly needed because the diversity of a crop determines the selection efficiency to improve it. Absolute variability in various characters cannot be decisive in determining which character shows the maximum degree of variability. Moreover, relative values of phenotypic and genotypic variation coefficients give a reliable idea of the extent of variability in the population. This way, the overall variation needs to be divided into genetic and nongenetic components and standardized by obtaining phenotypic and genotypic variability coefficients. The greater the variability in the initial genetic material, the better the chance of selecting the desirable type [2]. The variability available in the population can be partitioned into heritable and non-heritable components. The higher the heritable variation, the greater the possibility of fixing the characters by selection methods [3]. This study was, therefore, carried out to identify the potential pea genotype with a distinct genetic variability to improve the pea genotypes further.

2. MATERIALS AND METHODS

The present evaluation of garden pea genotypes for their variability was conducted at the research field unit of ICAR-Krishi Vigyan Kendra, Babbur farm, Hiriyur comes under the Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka-577 225 during *Rabi* season 2021-22. The experimental materials consisting of twenty-two genotypes and their sources from where they were procured given in Table 1. The experiment was laid out in RCBD with two replications. Seeds of twenty-two genotypes were directly sown in the field and a spacing of 60×10 cm was maintained. All recommended cultural practices were adopted uniformly to ensure a healthy crop stand. After eliminating border and unhealthy plants, observations were recorded on five randomly selected plants in each genotype per replication. Furthermore, observations were recorded on thirteen characters viz., the weight of 10 green pods (g), the weight of seeds 10 green pods (g), Shelling percentage, Pod yield per hectare (t/ha), Test weight (g), Chlorophyll-A (mg/g), Chlorophyll-B (mg/g), Total Chlorophyll (mg/g), firmness (lbs.), Dehydration ratio, Drying duration (min.), Per cent recovery and Rehydration ratio. The mean values were subjected to statistical analysis to work out ANOVA for all the characters, as suggested by Panse and Sukhatme [4].

2.1 Estimation of Genetic Parameters

2.1.1 Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated according to Burton and De Vane [5] based on an estimate of genotypic and phenotypic variance.

a) The genotypic coefficient of variation (GCV)

$$\text{GCV \%} = \frac{\sigma g}{\bar{x}} \times 100$$

b) The phenotypic coefficient of variation (PCV)

$$\text{PCV \%} = \frac{\sigma p}{\bar{x}} \times 100$$

Where,

$\bar{x}$ = Grand mean
r = number of replications
σg = Genotypic standard deviation
σp = Phenotypic standard deviation

PCV and GCV were classified [6] as mentioned below

0 – 10 % = Low
>10 – 20 % = Moderate

>20 % and above = High

2.1.2 Heritability (h^2 broad sense)

As indicated below, the broad sense heritability (h^2) was estimated following the formula suggested by Weber and Moorthy [7].

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 (%) = Heritability (Broad sense)
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

Heritability was categorized [8] as mentioned below

0 – 30 % = Low
>30 – 60 % = Moderate
>60 % and above = High

$$GA = h^2 \times \sigma p \times k$$

Where,

k = Selection differential at 5 per cent selection intensity
h^2 = heritability in the broad sense
σp = Phenotypic standard deviation

Table 1. List of garden pea genotypes used in the study

Sl. No.	Name of the genotypes	Source
1	Magadi Local	Magadi, Ramanagar
2	Arka Priya	ICAR-IIHR, Bangalore
3	Arka Karthik	ICAR-IIHR, Bangalore
4	Arka Pramodh	ICAR-IIHR, Bangalore
5	Arka Tapas	ICAR-IIHR, Bangalore
6	Arka Apoorva	ICAR-IIHR, Bangalore
7	Arka Chaitra	ICAR-IIHR, Bangalore
8	Arka Ajit	ICAR-IIHR, Bangalore
9	Arka Uttam	ICAR-IIHR, Bangalore
10	Arka Sampoorna	ICAR-IIHR, Bangalore
11	Arkel	ICAR-IARI, New-Delhi
12	IIHR-570	ICAR-IIHR, Bangalore
13	IIHR-671	ICAR-IIHR, Bangalore
14	IIHR-684	ICAR-IIHR, Bangalore
15	IIHR-688	ICAR-IIHR, Bangalore
16	IIHR-758	ICAR-IIHR, Bangalore
17	IIHR-766	ICAR-IIHR, Bangalore
18	IIHR-774	ICAR-IIHR, Bangalore
19	IIHR-775	ICAR-IIHR, Bangalore
20	AFA-10	Ashoka seeds, Bangalore
21	PS-101	Nutech seeds, New-Delhi
22	GS-10	Golden seeds, Bangalore

2.1.3 Genetic Advance (GA)

Genetic advance for each character was predicted by the formula given by Johnson et al. [9].

2.1.4 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent over mean was worked out as suggested by Johnsonet al. [9].

$$\text{GAM} = \frac{\text{GA}}{\bar{\text{x}}} \times 100$$

Where,

GA = Genetic advance
$\bar{\text{x}}$ = General mean

The Genetic advances as per cent of mean (GAM) were categorized as suggested by Johnson et al. [9] and are mentioned below:

0 – 10 % = Low
>10 – 20 % = Moderate
>20 % and above = High

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance was conducted to eliminate the variation due to causes other than genotypes from total variation. The ANOVA (Table 2) revealed highly significant variation among the genotypes for all the thirteen characters under study. This might be due to their genetic makeup and various places they have collected, suggesting a considerable variation among the genotypes. The existence of variability is critical for crop improvement programs and the magnitude of variability for a specific character determines the success of genetic improvement of a particular character. Similar to the present findings, wide variation for various characters was recorded by Ali and Ahmed [10-12]. However, the analysis of variance by itself is not enough and conclusive to explain all the inherent genotypic variance in the genotypes.

3.2 Mean Performance of 22 Genotypes of a Pea for Yield and Quality Characters

Further, the data obtained from the mean performance study (Table 3) also showed a highly significant difference indicating the existence of sufficient variability for all the characters among the genotypes investigated. The results revealed that the maximum weight of the green pod was observed in 'Arka Pramodh' (49.22g) and lowest in 'Magadi local' (16.03g), the weight of the seeds of ten green pods varied from 'Magadi local' (8.05 g) to 'Arka Pramodh' (23.58 g) and the highest shelling per cent was observed in 'Arka Tapas' (54.88 %) and lowest in 'IIHR-671'(28.85 %). Regarding pod yield per hectare, 'IIHR-766'was recorded to be the lowest (4.05 t/ha) and 'Arka Apoorva' yielded the highest (8.01t/ha). In addition, the Test weight of seeds varied from 'Magadi local' (15.34g) to 'Arka Karthik' (24.00g). Chlorophyll-A content varied from 'IIHR-758' (0.38 mg/g) to 'Arka Chaithra' (1.42 mg/g), chlorophyll- B varied from 'IIHR-758' (0.10 mg/g) to 'Arka Chaithra' (0.35 mg/g) and total chlorophyll content varies from 'IIHR-758' (0.48 mg/g) to'Arka Chaithra' (1.72 mg/g). The genotype 'Arka Pramodh' was recorded with maximum firmness (2.70 lbs.), whereas; the minimum value was observed with genotype 'IIHR-758' (2.16 lbs.). The maximum and the minimum dehydration ratio was recorded by the genotype 'Arka Chaitra'(3.32) and 'Arka Sampoorna'(2.50), respectively. The genotype 'Arka Ajit'was recorded with maximum drying duration (299.49 min), whereas; the minimum value was observed with genotype 'Arka Chaitra'(223.78 min). Similarly, the highest per cent recovery was observed withgenotype Arka Ajit (39.48 %), while IIHR-775 showed the lowest per cent recovery (29.92 %). In addition, the rehydration ratio ranged from 'Arka Chaitra' (1.57) to 'IIHR-671' (2.68).Similar findings were reported by Asha [13] indicating variability among the genotypes for most of the characters under study.

3.3 Genetic Components of Variation for Yield and Quality Parameters

Variability among twenty-two pea genotypes for all the thirteen characters measured in terms of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance are given in Table 4. In the present study magnitude of GCV for all the characters was less than the corresponding PCV indicating the influence of environmental components on the character expression. However, this difference between GCV and PCV was relatively small, specifying that genetic factors than environmental causes more highly controlled the expression of characters. Thus, the selection could be based

Table 2. Analysis of variance for 13 characters in Pea (*Pisum sativum* L.)

Source of variation/ characters	DF	Yield parameters					DF	Quality parameters							
		WTP	WSTP	S%	PYH	TW		Chl-A	Chl-B	TC	F	DR	DD	PR	RR
Replication	1	0.0580	0.0040	1.0230	0.1440	0.18	-	-							
Treatments (Genotypes)	21	108.531**	27.151**	68.509**	2.706**	8.97**	21	0.088**	0.005**	0.106**	0.043**	0.115**	1058.458**	16.81**	0.141**
Error	21	1.968	0.197	3.853	0.193	0.39	22	0.0002	0.0001	0.001	0.002	0.003	44.463	0.76	0.004

** Significant @ 1% level, DF- Degrees of Freedom, WTP- Weight of 10 Green Pods (g), WSTP- Weight of Seeds 10 Green Pods (g), S%- Shelling Percentage, PYH-Pod Yield per Hectare (t/ha), TW- Test Weight (g), Chl-A- Chlorophyll-A (mg/g), Chl-B- Chlorophyll-B (mg/g), TC- Total Chlorophyll (mg/g), F- Firmness (lbs), DR- Dehydration Ratio, DD- Drying Duration (min.), PR- Percent Recovery, RR- Rehydration Ratio

Table 3. Mean performance of 22 genotypes of a pea for 13 characters

Genotypes	WTP	WSTP	S%	PYH	TW	Chl-A	Chl-B	TC	F	DR	DD	PR	RR
Magadi Local	16.03	8.05	50.22	4.56	15.34	0.90	0.19	1.15	2.40	2.69	282.95	36.79	2.28
Arka Priya	37.22	15.86	42.52	7.51	21.00	1.19	0.25	1.41	2.59	2.75	272.04	35.87	2.63
Arka Karthik	33.58	16.78	49.87	6.15	24.00	1.04	0.25	1.28	2.30	2.91	256.81	33.91	2.42
Arka Pramodh	49.22	23.58	47.86	7.14	23.59	1.23	0.30	1.49	2.70	2.55	297.08	39.07	2.03
Arka Tapas	36.02	19.80	54.88	7.78	19.93	1.06	0.24	1.27	2.30	2.66	280.46	36.94	2.37
Arka apoorva	39.16	15.78	40.21	8.01	19.33	1.01	0.26	1.22	2.53	2.62	284.29	37.71	2.50
Arka Chaitra	23.09	10.34	44.56	5.65	20.08	1.42	0.35	1.72	2.28	3.32	223.78	30.09	1.57
Arka Ajit	34.82	18.18	52.13	6.78	23.24	0.74	0.20	1.04	2.43	2.51	299.49	39.48	2.33
Arka uttam	30.01	16.26	54.05	6.67	17.18	1.13	0.26	1.35	2.45	2.71	277.33	36.38	2.57
Arka Sampoorna	34.06	14.19	41.55	7.95	20.05	1.09	0.23	1.31	2.37	2.50	299.38	39.15	2.11
Arkel	30.30	13.18	43.36	6.20	18.96	1.12	0.27	1.37	2.48	2.79	269.41	35.30	2.19
IIHR-570	26.60	9.94	37.18	7.72	18.15	1.16	0.23	1.38	2.61	2.54	299.29	39.00	2.40
IIHR-671	28.16	8.18	28.85	6.48	16.15	1.09	0.19	1.28	2.24	3.07	241.68	31.89	2.68
IIHR-684	39.22	16.64	42.33	7.67	18.65	1.19	0.22	1.39	2.38	2.80	268.81	35.51	2.18
IIHR-688	30.14	13.74	45.45	4.19	18.50	1.04	0.27	1.27	2.39	2.70	275.62	36.28	2.18
IIHR-758	46.94	18.18	38.67	7.41	19.05	0.38	0.10	0.48	2.16	2.61	289.00	38.00	2.10
IIHR-766	30.06	13.38	44.37	4.05	20.50	1.12	0.24	1.34	2.57	2.62	289.47	37.75	2.11
IIHR-774	32.86	14.42	43.77	5.93	20.55	1.14	0.20	1.33	2.40	2.79	269.82	35.41	2.63
IIHR-775	29.82	14.18	47.42	6.02	20.00	1.04	0.24	1.25	2.66	3.30	226.76	29.92	2.65
AFA-10	33.87	15.60	45.94	6.50	20.36	0.85	0.18	1.09	2.28	2.59	292.10	38.18	2.15
PS-101	38.82	16.38	42.11	6.66	19.45	0.88	0.18	1.12	2.38	3.12	239.37	31.35	2.56
GS-10	40.38	17.42	43.07	7.29	20.04	0.84	0.19	1.07	2.61	2.91	256.31	33.88	2.44

Genotypes		WTP	WSTP	S%	PYH	TW	Chl-A	Chl-B	TC	F	DR	DD	PR	RR
Mean		33.65	15.00	44.56	6.56	19.73	1.03	0.23	1.25	2.43	2.77	272.33	35.81	**2.32**
Range	Minimum	16.03	8.05	28.85	4.05	15.34	0.38	0.10	0.48	2.16	2.50	223.78	29.92	1.57
	Maximum	49.22	23.58	54.88	8.01	24.00	1.42	0.35	1.72	2.70	3.32	299.49	39.48	2.68
S.Em ±		0.99	0.31	1.39	0.31	0.44	0.01	0.01	0.03	0.04	0.04	4.72	0.62	0.04
CD	@5%	2.92	0.92	4.08	0.91	1.29	-							
	@1%	-					0.04	0.03	0.11	0.14	0.15	18.80	2.45	0.18

Table 4. Coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for 13 characters in pea

Sl. No.	Characters	GCV (%)	PCV (%)	Heritability in a broad sense (%)	Genetic advance	Genetic advance as per cent over a mean (%)
1	Weight of 10 green pods (g)	21.69	22.09	96.44	4.77	43.88
2	Weight of seeds of 10 green pods (g)	24.47	24.65	98.56	7.51	50.05
3	Shelling percentage	12.76	13.50	89.35	11.07	24.85
4	Pod yield per hectare (t/ha)	17.09	18.36	86.68	2.15	32.78
5	Weight of 100 seeds (g)	10.50	10.96	91.76	4.09	20.72
6	Chl-A (mg/g)	20.42	20.47	99.60	0.55	53.80
7	Chl-B (mg/g)	22.14	22.41	97.60	0.13	57.75
8	Total (mg/g)	18.25	18.50	97.30	0.60	47.52
9	Firmness (lbs)	5.86	6.20	89.20	0.36	14.62
10	Dehydration ratio	8.55	8.76	95.30	0.61	22.04
11	Drying duration (min.)	8.27	8.62	91.90	57.00	20.93
12	Per cent recovery	7.91	8.28	91.34	87.99	245.71
13	Rehydration ratio	11.27	11.60	94.50	0.67	28.92

on phenotypic performance offering scope for crop improvement. High magnitude of GCV and PCV (>20 %) were observed for the weight of ten green pods, the weight of seeds of ten green pods, chlorophyll-A and chlorophyll-B. This reveals that the influence of environment on these characters is negligible and the role of genotypic performance for the full expression of the phenotype. These findings are by Ali and Ahmed [10],13-15]. The above findings depict that they are least affected by the environment and hence relied upon in improving these parameters by selection. Further, estimating heritability may be feasible to determine the amount of heritable variation and the degree to which a character is transmitted from parent to offspring.

Heritability estimates provide a guide for the breeder's selection procedure for the improvement of these traits under a given environment. In the present study, the magnitude of broad sense heritability ranged from 86.68% (Pod yield per hectare) to 99.60% (Chlorophyll-A) and high heritability (> 60%) was shown by all the thirteen characters under study. Heritability value alone does not indicate the genetic progress that would result from selecting the best individuals, as it includes both additive and non-additive gene action. In a broad sense, high heritability estimates would be a reliable selection tool if accompanied by genetic advances. High heritability coupled with high genetic advance as per cent of mean (>20%) was observed for all the characters except firmness, indicating the presence of additive gene action. The character firmness showed high heritability associated with moderate genetic advance due to its low GCV value. The reported results are in agreement with the findings of Johnson et al. [9-12].

4. CONCLUSION

The estimates of the mean sum of squares due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material. Hence, during selection, attention must be given to these traits to improve pod yield. Traits with high GCV and PCV indicate greater diversity for these traits and their further improvement through selection. High heritability coupled with high genetic advance was observed for most of the characters suggesting the preponderance of additive genes. It also indicated a higher response for selecting high-yielding genotypes, as additive gene actions

govern these characters. The five promising genotypes which have been identified for higher yield they can be utilized for further crop improvement program.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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