Assessment of Genetic Variability, Heritability and Genetic Advance in Garden pea (*Pisum sativum* L.)

Abstract

Genetic variability estimation was conducted in ten genotypes of peas during 2021-22. Analysis variance was highly significant for all characters studied except plant spread. The highest genotypic and phenotypic co-efficient of variation was recorded for pod yield per plant (15.3 ,16.97) followed by seed yield per plot (13.91 ,18) and lowest was recorded for days to 1st flowering (3.56,3.63) high heritability with genetic advance as per cent of mean was recorded as yield per plant (81,28.4) and pod yield per plant (59,22.1) and lowest was recorded for plant height (0.6,1.72). this study indicates that emphasis should be given to these characters for yield improvement.

Keywords: Genetic variability, GCV, PCV, Heritability, Genetic Advance, Pea

Introduction

Field pea (*Pisum sativum* L.), a legume crop, belongs to the Leguminosae family and contains a high amount of protein including amino acids, especially lysine. Beans are considered to be the most nutritious part of the human diet because they contain 42.65% carbohydrates, 27.8% protein and iron (Fe), sodium (Na) phosphorus (P), potassium (K), and some other important elements. Field pea has multifaceted uses as food, feed and fodder. The residues provide nutritious food for cattle and dairy cows and thus provide an additional benefit to poor farming families. Field peas are cultivated mainly for green beans and seeds are used as vegetables. Mature seeds can be used to make 'dal' or 'chapati' and other value-added goods such as 'fried dal'. As a legume, the field has a unique ability to fix atmospheric nitrogen through symbiosis. It may have originated in South Asia but it is one of the most important herbaceous vegetables in Bangladesh. Field peas with an annual production of 1,35,34,166 tons are one of the most produced pulses crops in the world. Major pea producing countries include Canada, the Russian Federation, China, Ukraine, India, USA, France, Australia, Ethiopia and Germany. The success of the breeding program depends on the amount of genetic variability available for absorption and the extent to which the desirable characters are heritable.

Collection, preservation and evaluation of germplasm are key information for any breeder to initiate a breeding program for crop improvement. Heritability acts as a predictive tool in expressing the reliability of phenotypic traits and thus high heritability traits can aid in the effective selection of specific characters and create future breeding programs. The analysis of the relationship helps in evaluating the existing relationship between the yield and its components. The study of genetic variability and interrelationships is of great value in the selection of the preferred characters of field pea genotypes to increase seed yield and quality. Genetic diversity is available in multivariate analysis, multiple statistical tools such as Euclidean clustering and principal component analysis (PCA). Multivariate analysis is an important tool for estimating genetic divergence in the populations of several workers. The principal component analysis is an adaptive data analysis technique that is used to effectively visualize similarities and differences between genotypes and to identify the quantitative characters that contribute the highest towards genetic divergence. To meet the present demand, there is an essential germplasm evaluation for the genetic improvement of pea to develop desired high yielding genotypes. Thus, the present study was conducted to identify higher genotypes based on genetic variability and association between yield and yield-related traits and to identify genetically different genotypes using PCA for further different breeding programs in the development of high yielding field pea varieties.

Materials and methods

The experiment was carried out at Crop Research Centre, School of Agriculture, ITM University, Gwalior, Madhya Pradesh. The experimental material comprised of ten genotypes which were collected from different source. The experiment was laid out in randomized block design (RBD) with three replications. The whole investigation was done under the scientific management practices. During study, observations for plant height (cm), plant spread, number of branches per plant, days to first flowering, days to 50 % flowering, days to first picking, number of pods per plant, number of seeds per pod, pod length (cm), pod width (cm), weight of 100 seeds, pod yield per plant (g), pod yield per plot, T.S.S and protein (Ali khan, 1973) were recorded on five randomly selected plants from each treatment. The genotypic and phenotypic coefficients of variation were calculated as per the method was suggested by Burton and Devane (1953). Heritability in broad sense and expected genetic advance on the basis of percent of mean were worked out according to the method advocated by Robinson *et al.*, (1953) and Johnson *et al.*, (1955), respectively.

Results and discussion

The Analysis of Variance (ANOVA) for different traits showed that mean sum of squares due to genotypes exhibit significant differences for most of the traits under observation at 1% probability level except for pod length which was significant at 5% probability level and plant height which was non significant at both levels of (Table 1). It shows large amount of genetic variability among pea genotypes.

Table: 1 Analysis of variance of 13 characters in garden pea genotypes

S. No.	Characters	Mean of sum square		
		Replication DF=2	**Treatment DF=2**	**Error DF=13**
1	Plant height	130.86	108.2	90.63
2	Plant spread	204.25	124.62	85.99
3	Days to first flowering	0.73	13.6**	0.18
4	Days to50% flowering	0.16	21.192**	0.04
5	Number of branches per plant	0.6	0.35	0.45
6	Number of pods per plant	1.68	5.04	2.05
7	Number of seeds per pod	0.08	1.3**	0.13
8	Pod length	0.36	0.14	0.35
9	Pod width	0.25	0.695**	0.14
10	Days to1st picking	1.23	7.88	4.04
11	Weight of 100 seeds	0.3	23.8**	3.28
12	Pod Yield per plant	655.84	1044.55**	74.11
13	Pod yield per plot	0.181	0.269**	0.05

** Level of significance at 5%

Mean of sum squares in ANOVA revealed high variability among 10 genotypes for all the characters (except number of branches per plant) at 5%level of probability (table1).

The mean performance of various genotypes has also showed good range of variability for various characters , which were studied in present investigation (table1) the range recorded for plant height (93.6-52.8), plant spread (100-59), days to 1st flowering (64.2-55.4), days to 50% flowering (70.2-60.2), number of branches per plant (7.6-5) number of pods per plant (23.6-16.6), number of seeds per pod (8.6-6), pod length (5.2-3.6), pod width(7.7-5.3) weight of 100 seeds (34-19), days to 1st harvest (79-70), yield per plant (160-72) and pod yield per plot (2.6-1.3). The characters under investigation were analysed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percent of mean (Table 2). It was observed that magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters under study which is an indicator of additive effect of the environment on the expression of the trait. It is also observed that the low range between PCV and GCV so it reveals that these traits have low sensitivity to environmental effects and it is reducible. Similar findings were also reported by Katoch *et al.,* (2016), Siddika *et al.,* (2013), Kumar *et al.,* (2013) and Ahmad *et al.,* (2013).

Genotypic coefficient of variation (GCV) ranged from (1.54-15.3), higher magnitude of GCV was recorded pod yield per plant (15.3), pod yield per plot (13.91), weight of 100 seeds (8.95). similar findings were recorded by (Naveen Kumar Jaiswal, G. Roopa Lavanya) (Archi Gupta 2020). (D. Satish, Abdul Karim2019) plant height (3.4), plant spread (4.65) , days to 1st flowering (3.56) , days to 50% flowering(4.2) , number of branches per plant (2.94), number of pods per plant (4.8) , number of seeds per pod (8.87) , days to 1st harvesting (1.54), weight of 100 seeds(8.95)pod length(5.89), pod width(6.58), pod yield per plant(15.3), pod yield per plot (13.91). High values of GCV is an indication of high genetic variability among the genotypes and thus the scope for improvement of these characters through simple selection would be better.

Phenotypic coefficient of variation (PCV) ranged from (3.63-18) higher magnitude of PCV was recorded pod yield per plot (18), pod yield per plant (16.97), plant height (13.81) similar findings were recorded by (Naveen Kumar Jaiswal, G. Roopa Lavanya) (Archi Gupta 2020). (D. Satish, Abdul Karim 2019) plant height (13.81), plant spread (12.89), days to 1st flowering (3.63), days to 50% flowering (4.21), number of branches per plant (10.23) number of pods per plant (8.42), number of seeds per pod (10.28), pod length (11.78), pod width (8.8), weight of 100 seeds (10.93), days to 1st harvest (3.14), pod yield per plant (16.97), pod yield per plot (18).

Heritability (bs) ranges from (99-0.6) higher magnitude of heritability was recorded in days to 50% flowering (99) similar findings were recorded by (Hafiz Bashir Ahmad, Salsabeel Rauf , Ch. Muhammad Rafiq) estimates of heritability of characters plant height (60) ,plant spread (13) , days to 1st flowering (96) , days to 50% flowering (99), number of branches per plant (0.6) , number of pods per plant (32) , number of seeds per pod (74),pod length (25), pod width (55) , days to 1st harvesting (24) , weight of 100 seeds (67), pod yield per plant (81), pod yield per plot (59). Similar findings were recorded by hafiz Bashir Ahmad (2014) and Naveen Kumar Jaiswal (2014).

Genetic advance ranged from (33.4 to 0.43) estimates of genetic advance was recorded as plant height (1.22), plant spread (2.66), number of branches per plant (0.12) , days to 1st flowering (4.27), days to 50% flowering (5.45) , number of pods per plant (1.17),number of seeds per plant (1.11) , pod length (0.07), pod width (0.66) , days to 1st harvesting (1.14) , weight of 100 seeds (4.36),pod yield per plant (33.41) pod yield per plot (0.43). Similar findings were recorded by Archi Gupta (2013) and Suraj Lathura (2020)

Genetic advance as percentage of mean ranged from 1.72 to 28.4 for plant height, yield per plot the estimates of genetic advance as percentage of mean was recorded as plant height (1.72), plant spread (3.46), number of branches per plant (3.02), days to 1st flowering (7.19), days to 50%flowering (8.63), number of pods per plant (5.65), number of seeds per pod (15.76) weight of 100seeds (15.1), days to 1st picking (1.55), pod length (36.8), width (10.14), yield per plant (28.4), yield per plot (22.1). Similar findings were recorded by Archi Gupta (2013), AsfakunsiddikaA.K.M.AminulIslam (2013) and Suraj Lathura (2020).

Table 3: Estimates of genetic parameters for growth, earliness, yield and quality parameters in garden pea genotypes

Characters	Grand mean	Range min	Range max	GCV	PCV	Heritability %	Genetic advance	Genetic advance as % of mean
Plant height	71.12	93.6	52.8	3.4	13.81	60	1.22	1.72
Plant spread	77.09	100	59	4.65	12.89	13	2.66	3.46
No. of branches/plant	6.36	7.6	5	2.94	10.23	0.6	.0.12	3.02
Days to first flowering	59.38	55.4	64.2	3.56	3.63	96	4.27	7.19
Days to 50% flowering	63.14	70.2	60.2	4.2	4.21	99	5.45	8.63
Days to first picking	73.46	79	70	1.54	3.14	24	1.14	1.55
Weight of 100 seeds	28.9	34	19	8.95	10.93	67	4.36	15.11
No. of pods per plant	20.75	23.6	16.6	4.8	8.42	32	1.17	5.65
No. of seeds per pod	7.04	8.6	6	8.87	10.28	74	1.11	15.76
Pod length	4.52	5.2	3.6	5.89	11.78	0.6	0.07	36.8
Pod width	6.5	7.78	5.35	6.58	8.8	55	0.66	10.14
Pod yield per plant	117.49	160	72	15.3	16.97	81	33.41	28.44
Pod yield per plot	1.94	2.6	1.3	13.91	18.05	59	0.43	22.1

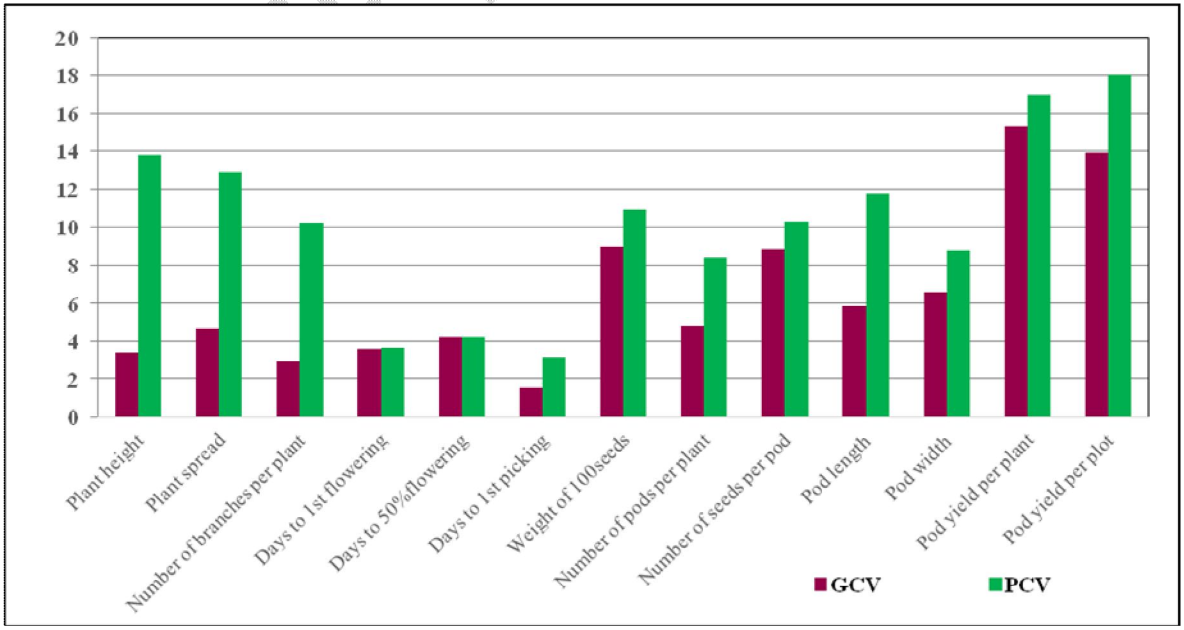

Fig. 1 Estimates of GCV and PCV for 13 characters in pea.

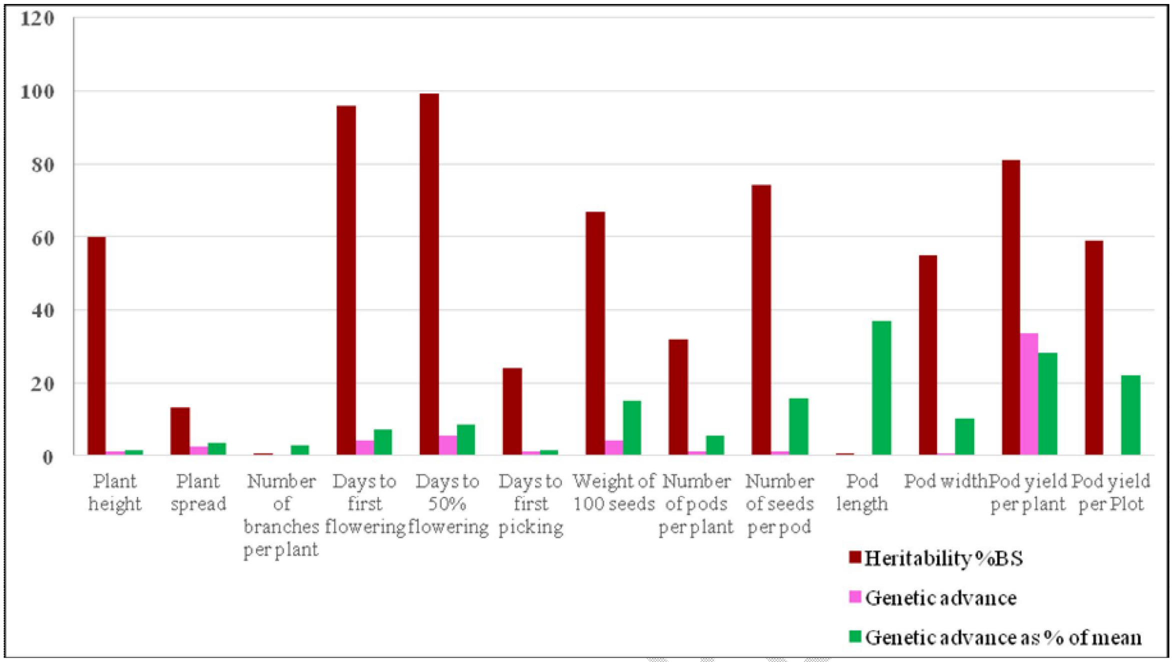

Fig. 2 Estimates of Heritability, Genetic Advance and Genetic Advance (%) mean for 13 characters in pea.

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