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

Abstract

Ten pea genotypes had their heritability evaluated in 2021 and '22. Except for the proliferation of plants, change analysis has a substantial impact on all other factors. Unit yield per plant (15.3,16.97) had the highest genotypic and phenotypic co-effective of variety, followed by seed yield per plot (13.91,18.00), and very long time to first bloom (3.56, 3.63) had the lowest; high heritability with hereditary development according to penny of mean was recorded for yield per plant (81.00, 28.4) and case yield per plant (59.00, 22.10), and very long time to first bloom (3.63) had the lowest (0.6, 1.72). According to the results of this research, highlighting these features may significantly boost production.

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

Introduction

The leguminous plant known as field pea (Pisum sativum L.) is a member of the pea family and a rich source of protein and amino acids, notably lysine. In addition to 42.65 percent carbs, 27.8 percent protein, iron (Fe), sodium (Na), phosphorus (P), and potassium (K), beans also include a number of other essential nutrients. The field pea has several purposes, including as food, feed, and fodder. An further advantage for low-income farming households is that the leftovers may be fed to cattle and dairy cows. The field pea, being a legume, is able to symbiotically fix atmospheric nitrogen.

In India, it is produced largely as a winter vegetable in the plains of North India. On 433.6 thousand acres, Indian farmers produce 3868.6 million metric tons of legumes, which have a production rate of 8.9 kg per hectare. In Madhya Pradesh the total area under pea cultivation is 56.1 thousand hectares with the production of 472.2 thousand metric tons annually at productivity of 8.4 tons per hectare (Economic survey, 2020-21). One of the world's most abundant crops, field peas account for 1,35,34,166 tons of yearly output, making them a major source of pulses. Several nations, including Canada, Russia, China, Ukraine, India, the United States, France, Australia, Ethiopia, and Germany, are major producers of peas.

To what degree the intended traits are heritable and how much genetic diversity is accessible to be absorbed are the two most important factors in determining the effectiveness of the breeding effort. In order to begin a breeding program for crop improvement, a breeder must have access to crucial knowledge on the collection, preservation, and assessment of germplasm. Since heritability serves as a forecasting tool in expressing the dependability of phenotypic features, characteristics with a high heritability may aid in the effective selection of certain characters and the creation of future breeding programs. Taking a closer look at the factors that affect yield provides a more realistic picture of the current state of affairs. Pea germplasm evaluation for genetic improvement towards production of desirable high yielding genotypes is essential for satisfying present demand. Therefore, identifying desirable genotypes based on genetic variability and link between yield and yield-related factors, and identifying genetically different genotypes using PCA, are crucial for use in various breeding projects aiming to create high-yielding field pea varieties. Understanding the genetic variability of field pea and the interactions between its many components is crucial for selecting genotypes with desired features such as increased seed yield and improved quality. This study set out to quantify the factors that contribute most to the wide range of genetic diversity across 10 different genotypes by looking at heritability, genetic progress, and genetic progress as a percentage of the mean.

Materials and Methods

The research was done in Gwalior, Madhya Pradesh, India, at the Crop Research Center of ITM University. Ten distinct genotypes of nursery peas were employed in the study, each of which came from a unique geographic region. A total of three different tests were conducted using a randomized block design (RBD). Procedures for conducting these tests were followed throughout. Five plants were selected at random from each treatment group, and their height, width, number of branches, days to first bloom, days to 50% bloom, days to first picking, number of cases per plant, number of seeds per unit, case length (cm), case width (cm), weight of 100 seeds, unit yield per plant (g), case yield per plot, total soluble solids (TSS), and protein content were all measured and recorded (Ali khan, 1973). We used a procedure suggested by Burton and Devane to determine the genotypic and phenotypic coefficients of variety (1953). The techniques proposed by Robinson et al., (1953) and Johnson et al., (1955) were used to determine the overall heritability and the heritable development as a percentage of the mean.

Results and discussion

The Analysis of Variance (ANOVA) for each trait revealed statistically significant differences between genotypes at the 1% probability level for all traits except for case length (basic at the 5% probability level) and plant level (not statistically significant at either of these two levels) (Table 1). There is a great deal of natural variation among pea genotypes, as seen by here.

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%

The analysis of variance (ANOVA) revealed significant variation across 10 genotypes for all features (excluding plant branching) at the 5% level of probability, as measured by the mean of total squares (table 1).

In addition, the average display of genotypes has shown a fair amount of variation for the several features that were the focus of the present study (table 1). Records were kept of the following: plant height (93.6-52.8), plant width (100-59), days until first bloom (64.2-55.4), days until half bloom (70.2-60.2), number of branches per plant (7.6-5), number of cases per plant (23.6-16.6), number of seeds per unit (8.6-6), unit length (5.2-3.6), case width (7.3-5.3), weight of 100 seeds (34.1-19), days until first reap (79-70), yield per plant (160-73), and yield per (2.6-1.3). Genotypic variation (GCV), phenotypic variation (PCV), heritability (in the broadest sense), and genetic drift (expressed as a percentage of the mean) were all analyzed for the features under investigation (Table 2). The phenotypic coefficient of variation (PCV) was found to be larger than the genotypic coefficient of variation (GCV) for all of the analyzed features, suggesting a more substantial effect of environmental factors on final product quality. The poor correlation between PCV and GCV also shows how vulnerable these attributes are to environmental changes and how easily they may be altered. Katoch et al. (2016), Siddika et al. (2013), Kumar et al. (2013), and Ahmad et al. (2015) all reported on findings that were similar (2013).

The range of the genetic diversity index (GCV) was from 1.54 to 15.3. Unit yield per plant (15.3), case yield per plot (13.91), and weight per 100 seeds all stayed at their larger original GCV sizes (8.95). Level of plant (3.40), spread of plant (4.65), days until first bloom (3.56), days until half flowering (4.2), number of branches (2.94), number of cases (4.8), number of seeds per unit (8.87), days until first harvest (1.54), weight of 100 seeds (8.95), case length (5.89), case width (6.58), case yield per plant (15.3), unit yield per plot (13.91). Several researchers, including Naveen Kumar Jaiswal (2013), G. Roopa Lavanya (2012), Archi Gupta (2020), and D. Satish, Abdul Karim (2017), have made findings that are similar (2019). A large GCV on the plus side indicates considerable genetic variation across the genotypes, suggesting that basic selection may be able to foster more improvement in these traits.

Changes in the phenotypic coefficient of variation (PCV) ranged (3.63-18) Case yield per plot (18), unit yield per plant (16.97), and plant level PCV sizes were all found to be larger than average (13.81). (Naveen Kumar Jaiswal, G. Roopa Lavanya) have made similar findings (Archi Gupta 2020). (D. Satish & Abdul Karim 2019) Case yield per plant (16.97), unit yield per plot (13.81), days to first reap (3.14), plant height (13.81), plant width (12.89), days to first bloom (3.63), days to half bloom (4.21), number of branches per plant (10.23), number of units per plant (8.42), number of seeds per case (10.28), unit length (11.78), case width (8.8), weight of 100 seeds (10.93), days to first reap (3.14). (18).

Increases in heritability (bs) may be shown between (99-0.6) Heritability in terms of days to half bloom was maintained at a larger scale (99). Heritability was determined for a wide range of plant characteristics, including height (60 cm), width (13 cm), days to first bloom (96), days to half bloom (99), number of branches per plant (0.6 cm), number of units per plant (32 cm), number of seeds per case (74), unit length (25 cm), unit width (55 cm), days to first reaping (24 cm), weight of 100 seeds (67 cm), unit yield per plant (81 cm), and case yield per plot (81 cm) (59). Both Hafiz Bashir Ahmad (2014) and Naveen Kumar Jaiswal (2017) reported findings that were similar (2014).

Changes in the hereditary component ranged from (33.4 to 0.43). Plant height (1.22), width (2.66), number of branches per plant (0.12), days to first bloom (4.27), days to half bloom (5.45), number of units per plant (1.17), number of seeds per plant (1.11), case length (0.07), unit width (0.63), days to first harvest (1.14), weight of 100 seeds (4.36), pod yield per plant (33.41), and unit yield per plot were all recorded as part of the evaluations of genetic development (0.43). Archi Gupta (2013) and Suraj Luthara (2017) both produced similar findings (2020).

The average height and production of plants per plot grew from 1.72 to 28.4 during the course of generations. Plant height (1.72), plant width (3.46), branch count (302), days to first bloom (7.19), days to 50% flowering (8.53), case count (5.65), seed count (15.76), seed weight (100.0) per 100 seeds (15.1), days until first picking (1.55), case length (36.8), width (10.14), yield per plant (28.4), and yield per plot (28.3) were all evaluated as means for hereditary development (22.1).Similar findings were recorded by Archi Gupta (2013), AsfakunsiddikaA.K.M.Aminulislam (2013) and Suraj Luthara (2020).

Table 2: 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

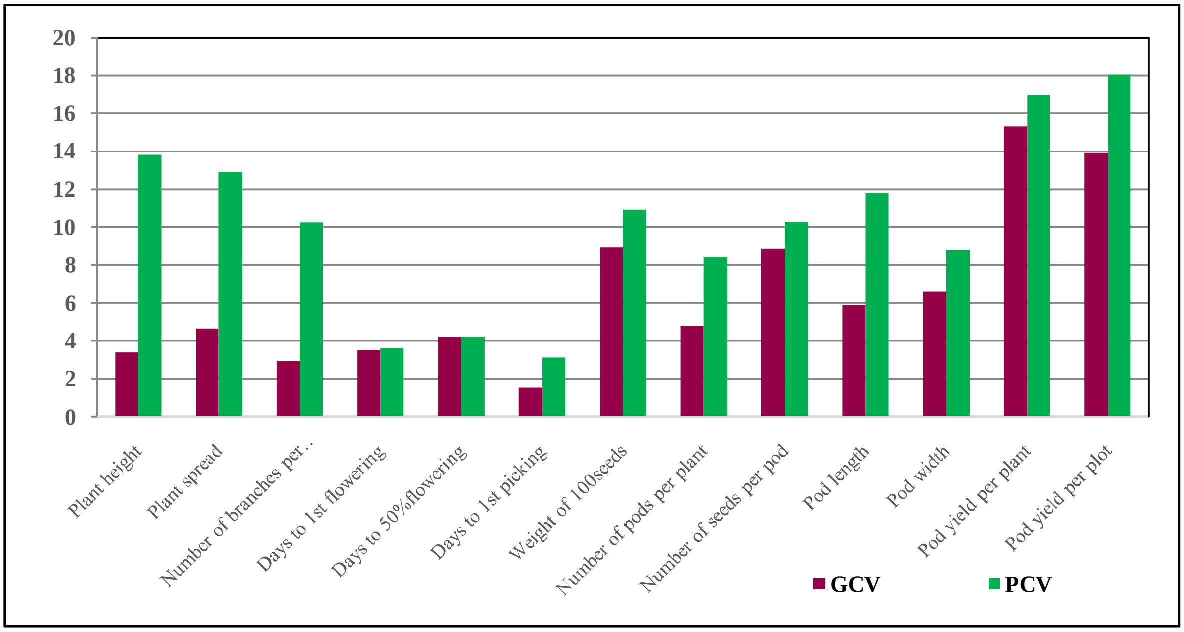

Fig 1: Estimates of GCV and PCV for 13 characters in pea.

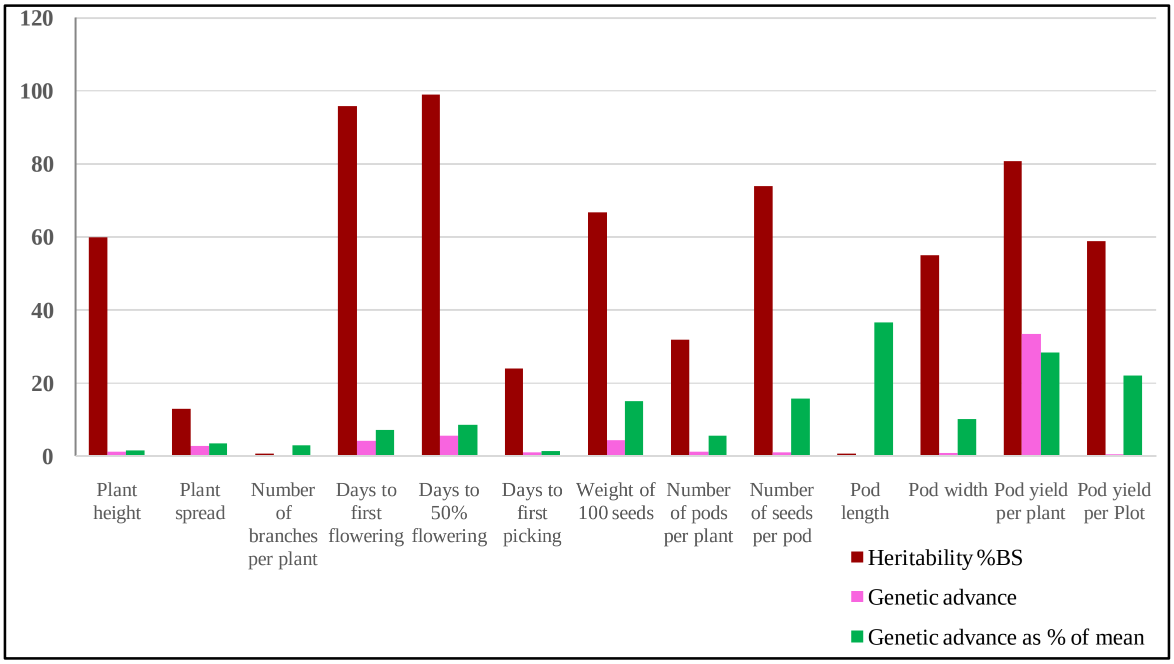

Fig 2: Estimates of Heritability, Genetic Advance and Genetic Advance (%) mean for 13 characters in pea.

Conclusion

Based on the mean exhibition of 10 garden pea genotypes, it is concluded that the genotype Nupandyan was best in terms of yield per plant, trailing behind Global G-10 and Swarna Mukti.

There was a large amount of variance found between the genotypes, according to the research. The maximum GCV and PCV were found for character seed yield per plot, with strong Heritability and Genetic Advance also showing additive gene activation.

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