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RESEARCH ARTICLE

Studies on the variability parameters in pea

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Abstract

Forty elite pea accessions were evaluated at Agriculture research Institute Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan during 2016 winter season. Highly significant genotypic differences were recorded for all the traits which implies that there is a considerable amount of variation present among genotypes for each character. The phenotypic variance was more than genotypic variance, and also the phenotypic coefficient of variation was higher than genotypic coefficient of variation which indicates more role of environment on the studied traits. Estimates of heritability were higher for almost all traits, except number of branches plant^{-1}. Moderate value of genetic advance was observed for grain yield plant^{-1} and the remaining traits recorded least value of genetic advance. High heritability along with high genetic advance indicated the prevalence of additive gene effects. Thus, the selection program based on these traits would be more effective in improving yield parameters of pea. The additive genetic variance in appearance of these characters can be useful in hybridization and selection for higher pod yield in pea

Key words: Genetic variability, heritability, genetic advance, pea, variation

Introduction

In Pakistan Pea is an important pulse crop mostly grown in Punjab and KPK provinces and play a major role in the economy of farmers. Pea is cultivated for different purposes in Pakistan because their pods seeds, and foliage all are used professionally, in any case of other constraints in pea production, the diseases are most important element which influence the production of pea. In Pakistan, pea is cultivated on an area of 22.8 thousand hectares and whole production of 118.5 thousand metric tons (FAO 2017). For its improvement of pea occurrence of towering variability in pea crop is much importance. A broad choice of variability in any crop always gives the good chances of selecting desired types which could be utilized in breeding (Vavilov, 1951). Genetic and phenotypic variance helps breeder to understand the actual potential. Heritability is the segment of phenotypic variation which is transmitted from parent to progeny. The higher the heritable difference, the superior will be the opportunity of fixing the character by selection methods. For this reason, an effort was make to estimate genetic variability, heritability and genetic advance of some character in the available germplasm of pea which may help to select suitable genotypes for future breeding programs.

Material and methods

The experiment was conducted at the experimental area of Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan during winter season 2016 to study genetic variability, heritability and genetic advance for some quantitative traits in pea under agro climatic condition of D.I. Khan. The experimental materials were comprised of 40 pea accessions along with 3 check varieties, *viz*., Meteor, Leader and 9800-10. These accessions were sown on ridges. The experiment was laid out in 4 blocks. Each block was consisted of 13 rows. 4 meter plot length was kept and width 60 cm or 0.6 meter, and the distance between 30 cm plants to plant with augmented block design. The data was recorded on the different parameters such as grain pod yield plant^{-1}, number of pods plant^{-1}, number of branches plant^{-1}, seed weight pod^{-1}and grain yield plant^{-1}. All the calculated data were entered to analysis of variance techniques as suggested the method of Singh and Chaudhary (1985). Genotypic and phenotypic inter-relationship between prametrs was esimate from analysis of variance. Broad sense heritability was calculated the following formula suggested by Falconer (1989) and LSD test was utilized when ANOVA showed significant differences among the accessions.

Results and discussion

Per se performance of pea accessions

Analysis of variance showed significant variation among the accessions for number of branches plant^{-1}. It ranged from 3.30 to 11.30 and with mean value of 5.24 (Table 1 and 2). The highest number of branches plant^{-1} (11.3) was observed in accession number 29782. The accession 29769 also showed more branches plant^{-1} (9.6). While the accessions 29771, 29963, and 29979 showed the least number of branches plant^{-1} (3.3). The mean value of check variety Meteor was more than the other two varieties Leader and 9800-10. Khan *et al.,* (2013) elucidated same result for number of branches plant^{-1}. Green pod yield plant^{-1} showed significant variation and ranged from 5.83-18.30. Mean value for this parameter was 10.14. The check variety Leader showed highest green pod yield plant^{-1} which was 16.9, the variety 9800-10 recorded 12.9 mean value and the Meteor variety recorded low mean value i.e. 7.8. Sharma *et al.*, (2011) observed highly significant variation for green pod yield plant^{-1} which supports our findings. For number of pods plant^{-1} among different pea accessions significant variation observed. This variation was ranged from 9.00 to 58.60 with the mean value was 33.80. Less number of pods plant^{-1} were exhibited by accession 29946 i.e. 9. Whereas, the accessions 29771, 29782, 29793 and 29820 presented maximum number of pods plant^{-1} which were 58.6, 58.5, 57.8 and 56.7 respectively with small difference from one another. The check variety Meteor depicted mean value of 18.6, Leader 23.5 and variety 9800-10 possessed mean value 21.5. Bashir *et al.*, (2014) observed highly significant variances for the number of pods plant^{-1}. Highly significant variability for seed weight pod^{-1} was observed in various 40 pea accessions. Range of variation for this parameter was ranged from 1.10 to 4.86 and the mean value recorded 2.45. Highest value was recorded from accession 29946 i.e. 4.9, two accessions 29784 and 29945 stood at second position with the value of 3.9. While three accessions 29765, 29771 and 29793 noticed to have same least seed for weight pod^{-1} which is 1.1. The mean value of check variety Meteor was 1.9, Leader was 3.2 and 9800-10 variety was 2. Natalia *et al.*, (2016) reported significant variances which supports our findings. For grain yield plant^{-1} expressed highly considerable differences in various 40 pea accessions. Average data ranged from 18.30 –

558.20g for grain yield plant^{-1} with average value of 155.41g. The accessions 29824 recorded least grain yield plant^{-1} i.e. 18.3g. The accession 29820 presented maximum grain yield plant^{-1} which was 558.2g and the accession 29789 also recorded second highest grain yield plant^{-1} i.e. 517.9g. These results were supported by finding of Natalia *et al.,* (2016). Hence, it can be noted that adequate variability is present based on *per se* performance of the pea accessions.

Variability parameters

For number of branches plant^{-1} the values of genotypic variance and phenotypic variance were 0.1 and 0.2 respectively (Table 3). The estimates of genotypic coefficient of variation (GCV) was low recording a value of 6.3% and estimates of phenotypic coefficient of variation (PCV) was also low 9.2% recorded for number of branches plant^{-1}. Low GCV with less PCV values showed the modest role of environment on the expression of this character. Bashir *et al.,* (2014) found similar result to that of present findings for given parameter. Merely heritability is not adequate for the selection of best genotypes but with expected genetic advance, it is more reliable. The heritability (h^2_{BS}) value for branches plant^{-1} was observed as 47.8 % and expected genetic advance value was 9.0%. In this parameter moderate value of heritability and low expected genetic advance (EGA) were recorded. Similar results for number of branches plant^{-1} were noted by Bashir *et al.,* (2014). For grain pod yield plant^{-1} the genotypic variance (GV) and phenotypic variance (PV) values revealed were 19.8 and 22.4 respectively. Genotypic coefficient of variation and phenotypic coefficient of variation observed values were 43.9% and 46.6% respectively. These values are comparatively higher. Minor difference in GCV and PCV values revealed that this trait was less affected by environmental fluctuations. Same result of PCV and GCV were elucidated by Garima and Lavanya (2012). The recorded values of heritability and genetic advance were 88.5% and 85.1% for the grain pod yield plant^{-1}. Greatest value with small difference in heritability and genetic advance were found. High heritability along with more genetic advance indicated that additive type of gene action hence, selection may be carried out in early generation. Similar result of heritability and genetic advance were reported by Garima and Lavanya (2012). For number of pods plant^{-1} the values of genotypic variance and phenotypic variance were 171.4 and 178.4 respectively. The genotypic coefficient of variation value was 39.4% and phenotypic coefficient of variation was 40.2%. For this parameter high value of PCV and GCV were observed. Bashir *et al.,* (2014) indicated similar results to present finding. Heritability estimates were 96.1% EGA was 79.6%. For this parameter greater value of heritability with high EGA were observed. Earlier researcher Natalia *et al.,* (2016) reported similar results. For seed weight pod^{-1} the value of genotypic variance was 0.4 and phenotypic variance was 0.5 respectively. Value of GCV was 26.1% and PCV was 29.7%. Highest value of GCV and PCV were presented for the given parameter. Similar result of PCV and GCV were recorded by Bashir *et al.,* (2014) for seed weight pod^{-1}. Estimates of heritability for seed weight pod^{-1} were 77.4% with 47.7% expected genetic advance. High value of heritability along with high (EGA) was indicated by seed weight pod^{-1}. Natalia *et al.,* (2016) reported similar result of heritability and genetic advance. For grain yield plant^{-1} GV and PV were 407.8 and 455.5 respectively. The value of GCV was 12.9% and PCV was 15.0%. For grain yield plant^{-1} moderate values of GCV as well as PCV were noticed. Natalia *et al.,* (2016) witnessed same results of GCV and PCV for grain yield plant^{-1}. Broad sense heritability and expected genetic advance were 89.5% and 25.3% respectively. High heritability with moderate value of expected genetic advance was recorded for this parameter. Bashir *et al.,* (2014) and Katore and Navale (2018) elucidated high heritability with more expected genetic advance for grain yield plant $^{-1}$. Such information will help to recognize the promising maize accessions which could be used for breeding programme and to develop pea varieties suitable for Dera Ismail Khan, KPK, Pakistan.

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Table 1: Analysis of variance

Characters	Blocks (df = 3)	Checks (variety) (df = 2)	Error (df = 6)	CV (%)
Number of branches plant^{-1}	0.01^{NS}	0.54*	0.12	33.22
Green pod yield plant^{-1}	2.02^{NS}	81.71**	2.59	30.58
Number of pods plant^{-1}	338.35^{NS}	521.08**	7.02	11.44
Seed weight pod^{-1}	0.19^{NS}	1.76**	0.12	35.03
Grain yield plant^{-1}	140.12^{NS}	1677.90**	48.03	90.06

***, ** Significant at $p \leq 0.05$ and $p \leq 0.01$, N.S. = Non-significant, CV = Coefficient of variation**

Table 2: *Per se* performance of pea accessions

Accession	No. of branches plant^{-1}	Green pod yield plant^{-1}	Number of pods plant^{-1}	Seed weight pod^{-1}	Grain yield plant^{-1}
29765	9.0	7.6	28.5	1.1	99.9
29768	6.0	13.2	29.5	1.5	141.4
29769	9.6	11.4	50.2	1.8	361.8
29771	3.3	6.5	58.6	1.1	58.3
29773	6.0	6.7	36.7	2.8	356.5
29776	4.0	13.1	21.1	1.9	130.6
29778	5.3	11.7	20.6	2.1	131.9
29779	3.6	13.7	25.3	1.9	159.5
29782	11.3	6.9	58.5	1.3	284.9
29784	4.0	15.7	32.0	3.9	441.8
29785	4.3	7.8	24.3	1.6	51.0
29786	5.3	7.5	21.3	2.5	210.6
29787	5.0	8.3	29.1	2.4	270
29789	7.6	8.1	38.2	3.3	517.9
29790	5.0	10.3	37.1	3.5	465.8
29793	4.0	7.1	57.8	1.1	21.1
29814	4.3	12.4	17.5	1.4	71.9
29818	4.3	10.4	16.3	3.2	36.2
29819	4.6	7.2	17.7	1.5	23.5
29820	8.0	10.6	56.7	2.4	558.2
29824	4.0	7.3	14.9	2.2	18.3
29826	3.6	8.9	20.7	3.1	194.5
29829	7.0	12.0	34.1	2.9	232.5
29830	3.6	10.9	15.5	3.4	124.3
29833	6.6	7.6	32.6	2.2	272.2
29836	6.3	7.8	26.4	1.7	127.1
29837	5.3	8.6	14	1.9	53.9
29839	7.0	8.3	35.5	2.7	205.3
29841	6.3	10.1	33.3	2.5	214
29843	5.3	9.8	30.4	1.4	149.1
29945	3.6	10.6	31.3	3.9	93.5
29946	3.6	10.3	9.0	4.9	39.3
29957	3.6	11.1	15	3.8	37.4
29958	4.0	11.6	16.5	3.4	92.6
29963	3.3	5.8	44.1	1.8	35.1
29973	5.3	9.1	13.3	3.3	43.0
29979	3.3	8.5	17.3	2.0	45.1
29985	3.6	6.0	49.0	1.8	36.8
29987	6.3	9.4	19.9	2.7	74.1
29992	5.3	6.9	39.6	3.1	506.0
Meteor	4.5	7.8	18.6	1.9	105.3
Leader	3.8	16.9	23.5	3.2	100.6
9800-10	3.8	12.9	21.5	2.6	67.7
Range	3.30-11.30	5.83-18.30	9.00-58.60	1.10-4.86	18.30-558.20

Table 3: Variance component for yield and yield contributing traits in pea

Traits	**Vg**	**Ve**	**Vp**	**GCV**	**PCV**	**H_2bs**	**GA**
No.of branches plant^{-1}	0.1	0.1	0.2	6.3 %	9.2 %	47.8 %	9.0 %
Green pod yield plant^{-1}	19.8	2.6	22.4	43.9 %	46.6 %	88.5 %	85.1 %
No. of pods plant^{-1}	171.4	7.0	178.4	39.4 %	40.2 %	96.1 %	79.6 %
Seed weight pod^{-1}	0.4	0.1	0.5	26.1 %	29.7 %	77.4 %	47.4 %
Grain yield plant^{-1}	407.5	48.0	455.5	12.9 %	15.0 %	89.5 %	25.3 %

Where, Vg: genotypic variance; Vp: phenotypic variance; GCV: genotypic coefficients of variation; PCV:phenotypic coefficients of variation H2BS: broad sense heritability; GA: genetic advance as percent of mean