Studies on genetic variability, divergence and association of characters in grass pea

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ABSTRACT

Grass pea (Lathyrus sativus L.) (2n=14), can be treated as an "insurance crop" because of its credible yields when other crops fail due to prolonged drought and flood condition. The present investigation was carried out during winter season of 2018-19 with 20 different genotypes of grass pea at the Regional Research Sub-Station, Chakdah, Nadia,West Bengal in Randomized Complete Block Design (RCBD) with three replications. Observation has been recorded on eight yield attributing traits to evaluate the genetic variability among the grass pea lines and to assess correlation between yield and yield attribute traits. Result reflected adequate variability on yield and yield attributing characters among the tested genotypes. High to moderate heritability (%) coupled with high to moderate genetic advance was observed for plant height (cm), days to 50 % flowering, number of pods plant^{-1}. The estimates of genotypic (GCV) and phenotypic (PCV) coefficient of variation for number of seeds pod^{-1}, number of branches, seed yield plant^{-1} (g) exhibited higher differences which indicated that environment play a key role in influencing the expression of these characters. Plant height, number of pods plant^{-1}, number of seeds pod^{-1}exhibited positive and significant correlation with seed yield plant^{-1} (g) at both genotypic and phenotypic levels. Genotypic path co-efficient analysis revealed that during selection greater emphasis should be given on number of pods plant^{-1}, number of seeds pod^{-1} and 100 seed weight (g) for improvement of seed yield. D^2 analysis of the present study resulted in five clusters among which maximum inter cluster distance was found between Cluster V and I (14.755). So, the genotypes from these two clusters might be used as parents in the hybridization programme to generate breeding material with high diversity to get encouraging results.

Keywords: Correlation, grass pea, genetic variability, heritability, path analysis.

Grass pea (*Lathyru ssativus* L.), a self-pollinated grain legume crop of fabaceae family is a versatile crop mainly used as a food grain for human consumption and also as forage and grain purpose for livestock feed. Originating in South Europe and Western Asia, this legume is mainly distributed and grown in India, Nepal, Bangladesh, Pakistan and Ethiopia for food, feed and fodder purpose to meet the nutritional and protein demand of the resource poor vulnerable section. Grass pea is a highly nutritious crop. Seeds are a source of 351 cal energy and having 58% carbohydrate, 28-32% protein, 0.6% fat and 3g minerals 100g^{-1} of seeds (Yang and Zhang, 2005). Seeds of grass pea also contain a high amount of L-homoarginine, which acts as a precursor for lysine in higher animals (Talukder, 2012). Despite of having all these qualities, this legume remains neglected because of its neurotoxin factor "â -N- Oxalyl-L-á, â-diamino propionic acid (BOAA or ODAP)" which is supposed to be a probable causative factor of a neurological disorder, "lathyrism" in human beings by excessive consumption of grass pea grains for prolonged periods. However, previous research confirmed that grass pea varieties having ODAP content lower than 0.2% is safe for human consumption (Yan *et al*., 2006). Hardy

and penetrating root systems of this crop enables to be grown in areas that are prone to drought and flood (Patto *et al.*, 2006). Unfortunately, still this crop is in infancy with relatively less research effort directed towards improvement of this grain legume, and it remains as an orphan crop. Research works have been primarily initiated in India, Bangladesh, Canada and Ethiopia for genetic improvement of this crop which is gaining importance nowadays with the growing concerns of climate change.

In systematic plant breeding programme three basic strategies are having paramount importance. Firstly, generating adequate genetic variability followed by selection and utilization of the promising material to be deployed in hybridization programme to evolve promising lines. Knowledge of heritability in the selection based improvement programmes reflects the degree of transmissibility of a character in subsequent generations. Genetic gain under selection is the representation of genetic advance and depends on genetic variability, selection intensity and heritability which specifies the mode of gene action in the expression of traits and further helps in choosing the constructive breeding strategies. In breeding programme, the degree

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and direction of relationship between independent characters are appraised through correlation coefficient and path analysis. Keeping these in view, the present study aimed to comprehend the genetic variability and association between yield attributing traits in grass pea which will furnish the premise for selection to improve the productivity of this crop.

MATERIALS AND METHODS

The present study was carried out during winter season of 2018-19 with 20 different genotypes of grass pea which were selected on the basis of yield attributing traits and previously reported information regarding low ODAP content and grown at the Regional Research Sub-Station, Chakdah, Nadia, West Bengal (23°5.3´N, 83°5.3´E & 9.75m) in Randomized Complete Block Design (RCBD) with three replications.The experimental plot consisted of 3 m long row and spacing between rows and plants were 30 cm and 15 cm respectively. The standard package of practices was followed to raise the crops. Data were recorded considering five randomly selected plants from each plot to measure plant height (cm), days to 50% flowering, days to maturity, number of branches plant[-1], number of pods plant[-1], number of seeds pod[-1],100-seed weight (g) and seed yield plant[-1] (g).

The total variations among genotypes for different yield attributing traits were tested for significance by 'F' test using analysis of variance, to decipher the 'F' values from the table (Fisher and Yates, 1953) the mean square values were tested, against the error mean squares. Phenotypic ($\acute{o}^2$p) and genotypic variance ($\acute{o}^2$g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were estimated using standard procedure (Singh and Chaudhary, 1995). Heritability was estimated according to the formulae insinuated by Singh and Chaudhary (1995). Genetic advance was appraised by the formula of Allard (1960) and correlation coefficient was calculated as per the formula suggested by Johnson *et al.* (1955) and Al. Jibouri *et al.* (1958). Path coefficient analysis was carried out according to the method of Dewey and Lu (1959). Mahalanobis' (1936) D[2] statistic was used for assessing the genetic divergence between populations. D[2] analysis was done using the programme GENRES. Clustering of D[2] values were done using Tocher's method as described by Rao (1952) and inter and intra cluster distances were estimated by formula given by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the twenty grass pea genotypes for all the eight characters under study. The mean sum of square values due to genotypes for all the above characters was highly significant which indicated genetic variability among the experimental materials (Table 1). From the values of coefficient of variation, it was observed that variability was highest in seed yield plant[-1] (g) followed by number of pods plant[-1] and number of branches plant[-1]. Considerable amount of variability for seed yield plant[-1] (g) (Sharma *et al.*, 2001), number of pods plant[-1] (Pandey *et al.*, 2000) and number of branches plant[-1] (Islam *et al.*, 1989) have been reported earlier.

Mean performances of twenty genotypes for eight characters were represented in table 2. Considering the performance of the genotypes for important yield attributing characters including seed yield plant[-1] (g) it was observed that the genotypes *viz.* IG-64842, IG-114559, IFLA-1426, IG-65912 and Mahateora were promising.

The estimation of PCV (Table 3) ranged from 6.65% indays to maturity to 54.14% in case of seed yield plant[-1] (g) and for GCV it was 4.23% in days to maturity to 49.62% in seed yield plant[-1] (g). GCV and PCV were high (>20%) for seed yield plant[-1] (g), number of pods plant[-1], 100 seed wt (g), moderate (10-20%) for plant height, number of seeds pod[-1], number of branches plant[-1], days to 50% flowering and low (<10%) for days to maturity. Similar results for high GCV and PCV for seed yield plant[-1] (g) (Barpete *et al.*, 2015) number of pods plant[-1] (Islam *et al.*, 1989), 100 seed wt (g) (Sharma *et al.*, 2001). The estimates of GCV and PCV value for number of pods plant[-1], number of seeds pod[-1], number of branches plant[-1], seed yield plant[-1] (g) exhibited higher differences which indicated the greater role of environmental factor influencing the expression of these characters. Very low differences between GCV and PCV were observed in case of plant height, 100 seed wt (g) indicating low sensitivity towards environment and greater role for genetic factors influencing the expression of these characters. Similar findings were also reported by previous studies (Nanda, 2000, Kumar and Dubey, 2001, Parihar *et al.*, 2015). Estimation of heritability in broad sense were very high for 100 seed weight (g) (95.20 %), plant height (cm) (87%), seed yield plant[-1] (g) (84.00%), days to 50 % flowering (74%), number of pods plant[-1] (77.80%). Previously, some researchers reported high heritability for 100-seed weight (Kumar and Dubey, 2001, Kumari and Prasad, 2005), days to 50% flowering and plant height (Singh and Dhillon, 2004), number of pods plant[-1] (Nanda, 2000), seed yield plant[-1] (g) (Ranjan *et al.*, 2007). The estimates of genetic advance as per cent mean were high for plant height (cm), days to 50 % flowering, number of pods plant[-1], number of seeds pod[-1], 100 seed weight (g), seed yield plant[-1] (g). Presence of high genetic advance for plant height, days to flowering and number of pods plant[-1] were also suggested by Kumar and Dubey (2001). Low genetic advance as per cent of mean were estimated in case of days to maturity. Heritability used in combination with genetic advance gives better information for selection

Table 1: Analysis of variance (ANOVA) for eight quantitative characters in grass pea

Source	DF	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of pods plant[-1]	No. of seeds pod[-1]	100 seed wt (g)	No. of branches plant[-1]	Seed yield plant(g)[-1]
Rep	2	1720.88	23.22	24.25	16.47	0.22	0.36	6.62	1.58
Tret	19	451.56**	154.85**	102.77**	199.86**	0.82**	13.90**	1.52**	29.07**
Eror	38	21.48	16.25	33.69	17.36	0.18	0.23	0.61	1.73

*, **: Significant at P=0.05 and 0.01, respectively

of best individuals than the heritability alone (Johnson *et al.*, 1955). High to moderate estimates of heritability accompanied with high to moderate genetic advance for plant height (cm), days to 50 % flowering, number of pods plant[-1] were indicated that these characters was influenced predominantly by additive gene action and in such case selection will be rewarding.

Genotypic and phenotypic correlation coefficient has been presented in table 4. It was observed that seed yield plant[-1] (g) was found to be significantly and positively correlated with plant height (cm), number of pods plant[-1], number of seeds pod[-1] at both genotypic and phenotypic level which indicated the importance of these characters for yield improvement. Similar correlation of seed yield plant[-1] with plant height (cm) (Pandey *et al.*, 2000; Kumariand Prasad, 2005), number of pods plant[-1] (Jiban and Mehra, 2001; Das and Kundagrami, 2002) reported earlier.

From the genotypic path analysis (Table 5) on the basis of the direct effect, it could be stated that number of pods plant[-1] exhibited the highest positive direct effect towards seed yield plant[-1] (g). Number of seeds pod[-1] and 100 seed weight (g) exhibited moderate direct effect and plant height (cm), days to 50% flowering exhibited low direct effect on seed yield plant[-1]. This finding indicated that the selection for these characters was likely to bring about an overall improvement in seed yield plant[-1] directly. On the other hand, low negative direct effect was exhibited by days to maturity, number of branches plant[-1]. Present study was in accordance to the findings of Zode *et al.* (1999), Urga *et al.* (2005), Sammour *et al.* (2007) and Talukadar (2009). So, it was suggested for improving seed yield plant[-1] (g) in grass pea the plant should be having large number of pods plant[-1] and seeds pod[-1] along with high seed index value. The residual effect in genotypic path coefficient (0.027) indicated that the eight characters included in this study explain decent percentage of variation in seed yield in this grain legume.

The genotypes of grass pea under study were distributed into five clusters (Fig. 1) based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to the same cluster had an average smaller D^2 values than those belonging to different clusters. Cluster I constituted by a maximum number of genotypes (9) followed by Cluster III (4), Cluster IV (4), Cluster II (2), Cluster V (1).

D^2 analysis is considered as the most effective method to measure the forces of differentiation at two levels namely, intra cluster and inter cluster levels and the present study revealed that the average intra cluster distance varied from 7.464 in CLUSTER I to 10.042 in CLUSTER IV (Fig. 2). The maximum inter cluster distance was found between cluster V and I (14.755) followed by cluster V and II (13.995), cluster IV and I (13.217), cluster IV and II (12.911), cluster IV and III

Table 2: Mean performance of twenty genotypes for eight quantitative characters in grass pea

Genotypes		Plant height (cm)	Days to 50% flowering	Days to maturity	No. of pods plant⁻¹	No. of seeds pod⁻¹	100 seed wt (g)	No. of branches plant⁻¹	Seed yield plant(g) ⁻¹
GP-94		87.25	51.67	106.67	27.67	3.00	6.76	4.50	5.62
GP-79		95.41	56.67	109.33	29.67	2.67	7.89	5.97	5.93
PUSA-24		76.08	59.00	116.00	29.33	3.00	5.62	4.47	4.11
MAHATEORA		70.20	62.67	104.33	33.00	3.67	6.96	5.83	7.68
IFLA-274		90.78	62.33	112.00	28.33	2.67	8.88	5.33	6.18
IG-117145		91.58	64.67	120.33	16.67	4.00	9.12	5.87	5.75
IG-66241		77.63	63.00	112.33	11.00	2.67	6.18	4.37	2.08
IG-64862		71.16	61.67	110.67	11.33	3.00	11.86	5.60	3.85
IFLA-143		93.57	66.67	114.33	11.67	2.67	11.13	5.80	3.35
IFLA-2475		86.34	64.67	114.67	30.00	3.33	7.91	6.07	6.71
IFLA-2460		89.57	61.33	111.67	32.00	3.00	7.07	5.40	6.76
IG-64847		73.28	65.33	115.33	22.00	2.33	8.20	6.00	3.71
IG-114559		104.89	90.00	127.00	28.67	4.00	11.00	4.13	11.61
IFLA-2341		76.19	62.67	110.67	23.33	3.67	6.54	4.80	5.33
IG-65912		88.90	69.00	127.33	19.33	4.00	11.16	5.13	7.85
BL-14-1		78.13	62.67	113.33	19.33	2.67	7.08	3.70	3.34
IFLA-1426		90.59	62.33	108.67	29.00	3.00	11.57	5.60	9.24
IG-64861		54.01	62.67	110.00	11.33	2.67	11.81	5.37	3.62
IG-114974		100.14	60.33	110.67	17.00	3.00	9.96	4.87	3.92
IG-64842		96.74	65.00	111.33	36.67	3.67	11.50	4.37	15.02
Mean		84.62	63.72	113.33	23.37	3.13	8.91	5.16	6.08
Range	Max	104.89	90.00	127.33	36.67	4.00	11.86	6.07	15.02
	Min	54.01	51.67	104.33	11.00	2.33	5.62	3.70	2.08
CV%		5.48	6.33	5.12	17.83	13.60	5.35	15.12	21.65
SEm(±)		3.78	3.29	4.74	3.40	0.35	0.39	0.64	1.08

Table 3: Phenotypic and genotypic coefficients of variability, heritability and genetic advance for eight quantitative characters in Grass pea

Characters	Grand Mean	Range		Heritability (%)	Coefficient of variation %		Genetic advance	Genetic advance as percent of mean
		Min	Max		GCV	PCV		
Plant height	84.62	104.89	54.01	87.00	14.15	15.17	23.00	27.18
Days to 50% flowering	63.72	90.00	51.67	74.00	10.67	12.40	12.04	18.90
Days to maturity	113.33	127.33	104.33	40.60	4.23	6.65	6.30	5.56
No. of pods.plant^{-1}	23.37	36.67	11.00	77.80	33.38	37.84	14.17	60.64
No. of seeds.pod^{-1}	3.13	4.00	2.33	54.00	14.73	20.05	0.70	22.34
100 seed wt (g)	8.91	11.86	5.62	95.20	23.96	24.55	4.29	48.15
No. of branches.plant^{-1}	5.16	6.07	3.70	33.30	10.69	18.52	0.66	12.79
Seed yield.plant(g)$^{-1}$	6.08	15.02	2.08	84.00	49.62	54.14	5.70	93.70

Table 4: Genotypic(G) and Phenotypic (P) correlation coefficient for eight quantitative characters in Grass pea

Characters		Days to 50% flowering	Days to maturity	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed wt.(g)	No. of branches plant^{-1}	Seed yield plant(g)$^{-1}$
Plant height	G	0.333	0.433	0.339	0.378	0.195	-0.186	0.517*
	P	0.297	0.267	0.37	0.236	0.184	-0.038	0.485*
Days to 50% flowering	G		0.742**	-0.02	0.577**	0.430	-0.297	0.472*
	P		0.736**	0.031	0.351	0.373	-0.073	0.37
Days to maturity	G			-0.236	0.670**	0.306	-0.309	0.229
	P			-0.051	0.292	0.218	-0.06	0.161
No. of pods.plant^{-1}	G				0.336	-0.282	-0.196	0.715**
	P				0.206	-0.229	0.135	0.679**
No. of seeds.pod^{-1}	G					0.175	-0.255	0.653**
	P					0.174	0.011	0.591**
100 seed wt (g)	G						0.215	0.371
	P						0.164	0.367
No. of branches.plant^{-1}	G							-0.265
	P							0.008

Table 5: Genotypic path coefficient analysis of eight characters on seed yield

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of pods plant⁻¹	No. of seeds pod⁻¹	100 seed wt (g)	No. of branches plant⁻¹	Seed yield. plant(g)⁻¹
Plant height	0.05	0.039	-0.044	0.239	0.1	0.103	0.03	0.517*
Days to 50% flowering	0.017	0.117	-0.075	-0.014	0.152	0.228	0.048	0.472*
Days to maturity	0.022	0.087	-0.101	-0.167	0.177	0.162	0.05	0.229
No. of pods.plant⁻¹	0.017	-0.002	0.024	0.706	0.089	-0.15	0.031	0.715**
No. of seeds.pod⁻¹	0.019	0.067	-0.068	0.237	0.264	0.093	0.041	0.653**
100 seed wt (g)	0.01	0.05	-0.031	-0.199	0.046	0.529	-0.034	0.371
No. of branches.plant⁻¹	-0.009	-0.035	0.031	-0.138	-0.067	0.114	-0.16	-0.265

Note : Residual=0.0269

*,**: Significant at P=0.05 and 0.01, respectively

Bold figure indicate direct effects

(11.826), and so on and this indicated a considerable amount of divergence within and between clusters. Selection of genotypes from distant clusters as a parent would be favourable for gaining recombinants with high heterotic effect. So, genotypes from clusters V (IG-64861), cluster I (GP-94, GP-79, PUSA-24, MAHATEORA, IFLA-274, IG-117145, IG-66241, IFLA-2475, IFLA-2460) and cluster II (IFLA-2341, BL-14-1) might be utilized as parents in the hybridization programme to generate superior breeding material. Previously, genetic diversity assessment of global germplasm set through utilizing morphological (Granati *et al.*, 2003; Infantino *et al.*, 1994) and biochemical (Chowdhury and Slinkard, 2000) markers revealed a wide genetic diversity among the accessions collected from distant geographic areas of grass pea. The genotypes identified in the present study will be valuable treasure trove for future grass pea breeding programme.

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