Biological Forum – An International Journal 13(1): 736-745(2021)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Estimation of Variability for Wide Hybridization between Grasspea and Pea

Rita Chopkar*, Abhinav Sao, H. C. Nanda, Sunil Nair and A.K. Sarawgi
Department of Genetics and Plant Breeding,
College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.

(Corresponding author: Rita Chopkar)*

(Received 10 March 2021, Accepted 20 May, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: The experiment was comprised of 55 crosses of wide hybrids of grasspea intergeneric with pea genotypes and interspecific crosses with three species viz., *sativus*, *cicera* and *odoratus* of grasspea. The analysis of variance revealed highly significant for eleven characters out of fourteen characters at 1% level of significance The remaining three characters viz., Number of primary branch per plant, pod length and pod breadth showed significant only at 5 % level of significance. The highest PCV and GCV was recorded for ODAP content (84.29, 84.19), Days to maturity (54.18, 53.40), seed yield per plant (53.24 , 52.73), seeds per plant (52.44 , 52.27), Pods per plant (45.91, 45.64), seed index (44.09, 43.94), Secondary branch per plant (36.27, 35.37), seeds per pod (32.14, 31.69), Pod length (26.43, 26.39) and Primary branch per plant (23.72, 21.53), high heritability coupled with high genetic advance as percent of mean was recorded for the characters ODAP estimation (99.75 %, 97.64), Seeds per plant (99.34%, 94.31), Seed Index (99.30 %, 90.19) Days to 50 percent flowering (99.06 %, 34.21), Seed yield (98.11 %, 94.59), Seeds per pod (97.18 %, 64.34), Days to maturity (97.14 %, 95.42), Pod length (99.71%, 54.29), Days to first flowering (99.18 %, 36.18), Pods per plant (98.85 %, 93.48), Pod breadth (98.55 %, 35.88), Secondary branch per plant (95.15 %, 71.67) and Primary branch per plant (82.33%, 40.23), it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effectives for crop improvement.

Keywords: Grasspea, genetic variability, heritability, genetic advance, wide hybridization, seed yield.

INTRODUCTION

Grasspea (*Lathyrus sativus* L.) is a pulse crop that belongs to the family Papilionaceae and sub-family Fabaceae. Grasspea economically, represent the second most important family of crop plants after the grass family. Among the grain legumes are some of mankind's earliest crop plants, whose domestication parallelled that of cereals: Soybean in China; faba bean, lentil, chickpea and pea in the Fertile Crescent of the Near East and so on. It is economically important as food (pulse), fodder, forage, ornamental crops, and even in traditional medicine mainly *viz.*, *L. sativus*, *L. cicera*, and *L. odoratus* (Patto and Rubiales, 2014). It is a robust crop considered one of the most resilient to climate changes and to be survival food during drought-triggered famines. The hardy penetrating root system allows the cultivation of grass pea in various soil types, including marginal ones. Grass pea can serve a variety of purposes, such as animal feed and fodder, but also as human food, thanks to 18–34% and 17% of protein content in seeds and mature leaves, respectively (Rizvi *et al*., 2016). Wide crossing or distant hybridization has been used in the genetic improvement of crop plants by developing useful variability for breeding populations in crop. It is an effective means of transferring desirable genes into cultivated plants from related wild or cultivated species and genera. In world 95.98 metric tonnes production,23.24 metric tonnes in India which contributing around 24.21 percentage share with first rank of the total pulse production (Annon., 2019). The pulse area coverage in year 2018-19 in Chhattisgarh 0.74 million ha contributes 2.56 percent of country whereas for production Chhattisgarh 0.54 million tonnes contributes 2.29 percent production in the country with yield of 722 Kg/ha. The main limitation of this crop is the presence of the toxin β-L-oxalys-2,3 diaminopropionic acid (β-L-ODAP) in its seeds during reproductive stage and green tissues in vegetative stage which can cause paralysis in humans if grasspea is consumed upto 30 percent over long periods for 3 to 4 months.

The yield being a complex trait is influenced by many other important yield contributing characters controlled by polygene and also environment factors. Therefore, in these characters, observed variability is the sum total of hereditary effects of concerned genes in addition to the influence of the environment. The success of most crop improvement programmes largely depends upon the genetic variability and heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding scheme to be used for improvement purpose. The phenotypic variability and heritability of character to a large extent determine the rate of genetic advance. Hence, it is essential to partition the overall variability into the heritable and non-heritable components in order to determine the most effective breeding procedure (Christov, 2013).

MATERIALS AND METHODS

The present study was conducted at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.) during *Rabi* 2018-19 for making crosses and its evaluation of generation advance for phenotypic data under managed and favorable field condition. The present research work was conducted at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.) Raipur in situated mid- eastern part of Chhattisgarh state and located at 21º16″ N Latitude and 81º 36″ E longitude with an altitude of 298.56 meters above the mean sea level. In rabi season all the parents were grown and evaluated during 2017-18 in a Randomized Completely Block Design (RBD) with two replications. Each genotype was grown in 2m length with 30 cm row distance and 10 cm plant distance. The materials used under study are seventeen grasspea genotypes from which three popular varieties of *Lathyrus sativus* L. viz., Mahateora Ratan and Prateek with eleven germplasm lines with low ODAP content, one genotype of *Lathyrus odoratus* and two germplasm lines of *Lathyrus cicera* and seven pea genotypes from which four popular varieties with three germplasm lines of field pea.

At reproductive stage make all possible crosses were made. Out of fifty five crosses four crosses in which interspecific crosses i.e. different species of grasspea *Lathyrus sativus, Lathyrus odoratus*, *Lathyrus cicera* and fifty one intergeneric crosses i.e. making crosses between different species of grasspea (*Lathyrus* species) with pea (*Pisum sativum*). Tagged all the possible crosses with cross name, date of crossing etc (Alvarez and Guzmán, 2018).

In second year all crosses were evaluated for yield and its related agronomical characters. The second phase of experimentation grown the first filial generation of 55 crosses with 24 parents grown I Rabi 2018 in RCBD design with two replications in 2m length and row distance 30 cm and plant distance of 10 cm. The agronomical characters were recorded for parents and crosses with five plants in each replication. The fourteen agronomical characters viz., Days to first flowering (number of days), days to 50% flowering, days to maturity, plant height (cm), Number of primary branch per plant, Number of Secondary branches per plant, Number of pods per plant, Number of seeds per pod, Number of seeds per plant, Pod Length (cm), Pod Breadth (cm), Seed Index (100 seed weight), Seed yield per plant and ODAP content (β-N-Oxalyl-L-α, β-Diaminopropionic Acid) used under study for recording the observation (Arslan *et al.*, 2020).

The mean data of five plants in each replication were selected for observation were statistically analysed and described by method given by Panse and Sukhatme (1967) for finding overall total variability present in the plants under study for each character and for all the populations. PCV and GCV were calculated by using the formula given by Burton (1952) and estimation of PCV and GCV recorded according to Sivasubramanian and Menon (1973) viz., low (0 to 10%), moderate (10 to 20%), high (more than 20%). The estimation of heritability was done as per the formula given by Hanson *et al*. (1956) and genetic advance was calculated by method given by Johnson *et al*., (1955) and also were classified into low, moderate and high as follows: low (0 to 10%), moderate (10 to 20%) and high (more than 20%).

RESULTS AND DISCUSSION

A. Analysis of Variances

The analysis of varicance for all the fourteen agronomical characters of seventy nine genotypes (55 crosses and 24 parents) on Rabi-2018 with on quality character were studied. The analysis of variance showed a wide range of variation and significant difference for all the traits under research work with the sufficient amount of variability. The quantitative mean sum of square due to replication were non significant for all the traits under studied. The result were presented in Table No.1 for all agronomical quantitative traits. All the characters showed highly significant at 1% level of significance except for the characters viz., Number of primary branch per plant, pod length and pod breadth. These three character showed significant only at 5 % level of significance.

B. Assessment of Genetic parameter of variability

1. Phenotypic coefficient of variability (PCV) and Genotypic coefficient of variability (GCV). Information on the nature and magnitude of genetic variability is of immense significant for initiating any breeding programme. Further the presence of variability in the base material ensures better chances of selection for desirable plant types. In the present study intimates' the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the quantitative characters (Table 2) but fortunately the difference between the variability was relatively very small for all the agronomical traits, it indicating that these characters were less influence by the environment and it is desirable for further selection.

Similar findings were reported by Abate *et al.*, (2018) and Rubiales *et al.*, (2020)

In the study the highest PCV and GCV was recorded for ODAP content (84.29, 84.19), Days to maturity (54.18, 53.40), seed yield per plant (53.24, 52.73), seeds per plant (52.44, 52.27), Pods per plant (45.91, 45.64), seed index (44.09, 43.94), Secondary branch per plant (36.27, 35.37), seeds per pod (32.14, 31.69), Pod length (26.43, 26.39) and Primary branch per plant (23.72, 21.53). The quantitative characters showed high PCV and GCV indicating the presence of considerable genetic variability and less influence of environment on the expression on this traits. The similar findings were also reported by Jeberson *et al.*, (2018) for traits number of primary branches/ plant, number of pods / plant, biological yield/plant, seed yield/plant, number of primary branches/plant and Gour *et al* (2018) similar finding observed in pea for characters number of primary branches/plant, number of secondary branches/plant, plant height, number of node/plant, number of effective node/plant, pod bearing length, number of pod/plant, number of effective pod/plant, number of seed/plant, biological yield, biological yield/plant, seed yield/plant.

The moderate PCV and GCV were recorded for Days to first flowering (17.71, 17.64), Pod breadth (17.68, 17.55), Days to 50 percent flowering (16.76, 16.68) and The similar finding were also observed by Jeberson *et al.*, (2018) for the characters 100 Seed Weight, plant height, Harvest Index, number of pods/plan. The similar findings also observed by Gour *et al.*, (2018) in pea for characters Day to first flower opening, days to 50% flowering, 100 seed weight, HI, total sugar, non-reducing sugar and ash. The only one character plant height recorded low PCV and GCV (8.6, 8.59).

2. Heritability (Broad sense). Heritability is a measure of extent of phenotypic variation caused by the action of genes. The major function of heritability estimates is to provide information on transmission of characters from parents to their progeny in next generation.

Agronomical Characters: High heritability was recorded for all the fourteen characters under study viz., ODAP estimation (99.75%), Pod Length (99.71 %), Seeds per plant (99.34 %), Seed Index (99.30 %), Days to first flowering (99.18%), Days to 50% flowering (99.06), Pods per plant (98.85%), Pod Breadth (98.55%), seed Yield (98.11 %), Seeds per pod (97.18%), Days to Maturity (97.14%), Secondary branch per plant (95.15 %), Plant Height (89.17%) and Primary branch per plant (82.33 %). Similar findings were also reported by Abate *et al* (2018) for characters biological yield, plant height, number of primary branches per plant, 100 seed weight and by Jeberson *et al* (2018) for characters seed yield per plant, number of pods per plant and pod length. The similar finding also found by Lavanya *et al.*, (2010) in characters number of pods per plant and weight of 100 seed, suggesting their effective use during selection. Seed yield per plant, plant height, biological yield, harvest index, number of pods per plant except days to maturity.

3. Genetic advance as percent of mean for quantities traits:

Genetic advance as percent of mean highest for character ODAP content (97.64), Days to maturity (95.42), Seed yield (94.59), Seeds per plant (94.31), Pods per plant (93.48), Seed Index (90.19), Secondary branch per plant (71.67), Seeds per pod (64.34), Pod Length (54.29), Primary branch per plant (40.23), Days to first flowering (36.18), Pod breadth (35.88) and Days to 50% flowering (34.21) while moderate value was recorded for the character Plant height (17.66).

4. Heritability (broad sense) and genetic advance as percent of mean:

Heritability and genetic advance as percent of mean are important criteria for selection. Heritability with genetic advance as percent of mean are more powerful for predicting the genetic gain under selection. From the result, high heritability coupled with high genetic advance as percent of mean was recorded for the characters ODAP estimation (99.75 %, 97.64), Seeds per plant (99.34%, 94.31), Seed Index (99.30 %, 90.19) Days to 50 percent flowering (99.06 %, 34.21), Seed yield (98.11 %, 94.59), Seeds per pod (97.18 %, 64.34), Days to maturity (97.14 %, 95.42), Pod length (99.71%, 54.29), Days to first flowering (99.18 %, 36.18), Pods per plant (98.85 %, 93.48), Pod breadth (98.55 %, 35.88), Secondary branch per plant (95.15 %, 71.67) and Primary branch per plant (82.33%, 40.23), it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effectives for crop improvement. Similar findings were reported by Singh *et al.*, (2017) for characters plant height, number of pods/plant and pod length, Jeberson *et al.*, (2018) for biological yield, number of primary branches per plant, 100 seed weight and seed yield/plant. The similar result also found in other crops by Ullah *et al.*, (2019) in pea, Lavanya *et al.*, (2010) in field pea, Khandait *et al.*, (2016) in cowpea.

High heritability coupled with moderate genetic advance as percent of mean was reported in character plant height (89.17, 17.66) indicating importance of both additive and non additive gene action. Ghosh and Khan (2018) and Lavanya *et al.*, (2010) also reported the similar findings for the different agronomical characters.

C. Agronomical characters

1: Days to first flowering: Out of 55 crosses the cross EC 356344 x Mahateora showed minimum days to first flowering 42.80 days to maximum days 90.95 in cross L.O × Ratan with a overall mean 57.49 days and in parents genotype EC 356344 with minimum days 50.25 while maximum days 74.35 in genotype Ambika. The cross with minimum days for first flowering required less number of days as compare to its female parent.

2 Days to 50 % flowering: This observation ranges from 54.50 days in cross Ambika × Prateek to 109.85 days in cross *L. odoratus* . × IC 294285 with an overall mean 69.96 days while in parents it ranged from 57.10 days in cross Indira Matar_1 to 105.20 days in cross *L. odoratus*. In cross viz., Ambika × Prateek with minimum days to 50 % flowering recorded early flowering as compare to its female and male parent Ambika and Prateek with 77.35 days and 61.05 days respectively .

3. Days to maturity: From 55 crosses this observation ranged from 98.45 days in cross Ambika × Prateek to 141.35 days in cross *L. odoratus* × IC 294285 with overall mean 109.61 days. The cross with very early maturing in 98.45 days as compare to parent Ambika and Prateek with 120.15 and 101.30 days respectively. In parents ranges from minimum 96.05 days in parent EC 356344 to maximum 120.15 days in parent Ambika (Shujaat *et al*., 2019).

4 Plant Height (cm): Plant height varied from minimum height 37.60 cm in cross IC 142851 × Indira Matar-1 to 136.55 cm in cross Ambika × Mahateora with an overall mean 75.39 cm. In parents plant height ranged from 42.75 cm in IC 142990 to 132.50 cm in Indira Matar-1.

5. Number of Primary branch per plant: This observation varied from 2.54 in cross IC 142991 × Paras to 6.32 in cross IC 142857 × Indira Matar-1 with a mean value of 3.97. It is varied from 2.43 in parent IC 142878 to 4.08 in parent Mahateora.

6. Number of Secondary branch per plant: From 55 crosses minimum secondary branch per plant 4.81 in cross IC 142991 × Paras to 17.07 in cross IG 64869 × Shubhra with a mean of 8.15. From 24 parents minimum value 5.02 in IC 142991 to maximum 8.57 in parent IC 294285. In cross with minimum value also showed minimum for female parent.

7 Number of Pods per plant: This observation ranged from 6.76 pods per plant in cross IC 142991 × Paras to 65.93 in cross IC 142857 × Paras with a mean value of 30.66 In parental population minimum with 11.13 in *L. odoratus* to 36.16 in EC 356344.

8. Number of seeds per pod: The observation varied from 1.74 seeds per pod in cross EC 243834 × Mahateora to 5.54 in cross IC 142991 × Indira Matar-1 and overall mean 3.94. For parents 4.00 seeds per pod in genotype IC 142782 to 8.14 maximum Indira Matar-1.

9. Number of seeds per plant : In this observation 9.11 seed per plant in cross IC 142991 × Paras to 250.75 seeds in cross L.O. x Indira Matar-1 with a mean value 114.30 and in parents it varied from 51.78 seed per plant in Ratan to 183.27 in parent IC 294285.

10: Pod length: The observation varied from 2.15 cm in EC 356344 × Prateek to 6.13 cm in cross Ambika × Prateek while in parent ranged from 2.52 cm in parent Ratan to 5.10 cm in parent Indira Matar-1 with an overall mean 3.53 cm**.**

11. Pod breadth: In this observation crosses ranged from 0.71 in cross IC 142857 × Paras to 1.84 cm in Ambika × Ratan with an overall mean overall mean 0.99 while in 0.85 cm in parents IC 142851 to 1.22 cm in Paras and Ambika.

12. Seed Index : It varies from 2.34 in cross IG 64869 × Shubhra to 25.03 in cross Indira Matar-1 × Ratan while in parents ranged from 5.22 in genotype IC 142857 to 10.29 in genotype Indira Matar-1 with an overall 8.15.

13. Seed yield: In this observation ranged from 1.91 g in cross IC 142991 × Paras to 26.89 g in cross IC 142991 x Indira Matar-1 both crosses with common female parent IC 142991 while in parents 3.94 g in genotype IC 142881 to 16.31g in genotype Indira Matar-1 (Table 3 and Table 4 and Fig. 1).

14. ODAP (β N oxalyl α β di-amino propionic acid): The neurotoxin content varied from 0.0207 in cross Ambika × Prateek to 0.6619 in cross Ratan × Indira Matar-1 while 0.0815 in parent Mahateora to 0.1566 in parent IC 142851.

Table 1: Analysis of variance (ANOVA) for agronomical character.

Sr. No.	**Characters**	**Replication (df=1)**	**Treatment (df=78)**	**Error (df=78)**
1	Days to first flowering (DFF)	4.37	206.48**	0.84
2	Days to 50% flowering (DF)	5.17	273.74**	1.29
3	Days to Maturity (DM)	1.26	177.43**	0.26
4	Plant Height (PH)	10.28	1620.17**	23.53
5	Number of Primary branch per plant (PB/pl)	0.81	1.62*	0.15
6	Number of Secondary branch per plant (SB/pl)	1.66	17.05**	0.43
7	Pod per plant (P/pl)	15.28	394.06**	2.27
8	Seed per pod (S/pod)	0.001	3.16**	0.04
9	Seed per plant (S/pl)	47.15	7161.72**	23.66
10	Pod length PL (cm)	0.0004	1.74*	0.002
11	Pod breadth PB (cm)	0.0007	0.062*	0.0004
12	Seed Index (SI)	0.355	25.75**	0.089
13	Seed Yield (SY)	2.65	41.97**	0.400
14	ODAP content	0.000001	0.05**	0.000006

Note : *and ** represent significant levels at 5% (1.454) and 1% (1.702) respectively.

Fig. 1. Variation in crosses with their respective parents. **A**. Ratan × Indira Marar-1, **B**. Mahateora × Ambika, **C**. Prateek × Indira Matar-1, **D**. IC 142991 × Indira Matar-1, **E**. *Lathyrus odoratus* × Indira Matar-1, **F**. Mahateora × Ambika **G**. IG 64869 × Shubhra, **H**. IG 64975 × Paras

Table 2: Genetic parameters of variation for yield and its related characters.

Sr. No.	Character	Mean	Range		PCV(%)	GCV(%)	h^2 (%)bs	GA as % of mean	CD (5%)	CV	SEm	SEd
			Min	Max								
1	DFF	57.49	42.10	92.30	17.71	17.64	99.18	36.18	1.83	1.60	0.65	0.92
2	DF(50%)	69.96	53.80	110.50	16.76	16.68	99.06	34.21	2.26	1.63	0.80	1.14
3	DM	109.61	98.30	141.50	8.60	8.59	89.17	17.66	1.01	0.46	0.36	0.51
4	PH	52.91	6.50	106.50	54.18	53.40	97.14	95.42	9.66	9.17	3.43	4.85
5	PB/pl	3.97	2.21	6.34	23.72	21.53	82.33	40.23	0.79	9.97	0.28	0.40
6	SB/pl	8.15	4.34	18.66	36.27	35.37	95.14	71.67	1.30	8.00	0.46	0.65
7	P/pl	30.66	6.00	79.54	45.91	45.64	98.85	93.48	3.00	4.92	1.07	1.51
8	S/pod	3.94	1.55	5.67	32.14	31.69	97.18	64.35	0.42	5.40	0.15	0.21
9	S/pl	114.30	8.70	385.46	52.44	52.27	99.34	94.31	9.68	4.26	3.44	4.86
10	PL	3.53	2.15	6.13	26.43	26.39	99.71	54.29	0.10	1.42	0.04	0.05
11	PB	0.99	0.70	1.86	17.68	17.55	98.55	35.88	0.04	2.13	0.01	0.02
12	SI	8.15	2.31	25.04	44.09	43.94	99.30	90.19	0.60	3.68	0.21	0.30
13	SY	8.65	1.68	27.42	53.24	52.73	98.11	94.59	1.26	7.32	0.45	0.63
14	ODAP	0.19	0.02	0.66	84.29	84.19	99.75	97.64	0.03	0.42	0.01	0.02

Table 3: Mean performance of agronomical characters for hybrids.

Cross	DFF	DF	DM	PH	PB/pl	SB/pl	P/pl	S/pod	S/pl	PL	PB	SI	SY	ODAP
Ratan × Indira Matar-1	59.75	68.65	106.40	61.50	5.18	11.95	47.72	2.48	116.52	2.95	0.94	6.28	8.60	0.6619
Ratan × Ambika	52.75	67.70	104.70	63.00	4.38	14.01	60.22	3.31	195.25	2.98	0.90	6.39	13.90	0.1662
RGRLS 212-2xIindira Matar-1	56.05	70.40	110.45	53.70	3.37	6.80	20.72	3.23	65.75	2.86	0.89	9.26	6.17	0.2108
Prateek × Indira Matar-1	53.45	64.60	102.70	45.05	3.18	6.15	18.78	3.32	60.72	2.94	0.86	11.26	6.62	0.1583
Prateek × Ambika	52.30	61.80	101.85	45.60	4.33	10.79	40.79	3.77	151.96	2.95	0.93	4.60	5.34	0.1357
Mahateora × Ambika	51.05	63.25	105.30	52.45	3.36	5.83	23.86	4.87	108.79	3.06	0.82	4.50	5.26	0.3155
Mahateora × Indira Matar-1	51.90	62.60	109.40	50.14	4.49	6.64	25.09	3.44	86.48	3.01	0.81	5.35	4.42	0.3005
L.O. × Ambika	53.85	70.75	108.60	97.35	3.23	5.96	14.62	4.43	57.15	4.41	1.03	10.28	6.39	0.0518
L.O. × Indira Matar-1	82.15	104.35	135.50	91.45	4.96	11.84	50.57	4.98	250.75	4.98	0.99	4.49	11.42	0.1986
L.O. × IC 294285	87.70	109.85	141.35	85.60	4.17	4.98	13.31	4.48	58.12	5.15	0.98	15.32	9.40	0.0527

IG 64869 × Shubhra	66.00	83.25	121.55	53.65	5.74	17.07	47.77	2.13	85.08	3.01	0.96	2.34	8.64	0.3474
IG64975 × Paras	61.85	85.55	121.35	58.70	5.20	14.45	24.92	4.38	102.11	3.95	1.23	3.36	8.13	0.1676
Mahateora × Shubhra	51.70	72.35	109.45	47.05	4.35	10.03	38.28	4.62	166.08	4.12	0.95	4.25	6.58	0.3586
IC 142991 × Shubhra	53.90	74.25	111.40	51.56	4.04	12.85	52.24	3.68	189.85	3.13	0.86	4.49	8.26	0.3206
IC 142991 × Paras	55.00	74.35	112.50	49.84	2.54	4.81	6.76	1.76	9.11	2.63	0.86	19.41	1.91	0.4825
IC 142991 × Indira Matar-1	52.00	74.80	115.55	48.65	4.42	8.99	37.24	5.54	235.28	5.25	1.08	12.85	27.16	0.0574
IC 142991 × Ambika	52.95	72.95	114.60	53.35	5.30	9.09	37.84	2.37	88.20	3.08	0.95	8.29	8.01	0.3127
IC 142990 × Indira Matar-1	52.05	62.10	110.20	52.50	4.23	14.93	62.41	3.54	177.01	3.41	0.90	6.36	12.01	0.2517
IC 142881 × Shubhra	55.20	64.55	103.85	50.12	4.28	7.74	28.87	3.38	90.90	2.78	0.87	3.41	3.13	0.5474
IC 142881 × Indira Matar-1	43.05	64.75	106.70	43.25	5.40	8.88	34.27	3.68	124.87	2.96	0.86	4.78	6.40	0.4187
IC 142881 × Paras	43.00	62.30	103.45	42.65	3.43	7.96	33.36	3.19	109.12	3.01	0.86	7.51	8.31	0.4174
IC 142881 × Ambika	53.20	62.75	105.40	47.35	5.32	8.99	34.11	3.16	101.84	3.13	1.06	8.60	9.70	0.3705
IC 142878 × Paras	52.10	63.40	105.40	56.85	3.95	7.78	27.78	3.39	88.93	2.76	0.88	7.49	6.95	0.3117
IC 142878 × Indira Matar	52.85	68.20	106.60	55.80	5.44	8.16	34.43	3.10	108.54	2.37	0.88	6.36	7.62	0.2826
IC 142857 × Paras	53.25	64.55	105.30	48.35	3.42	15.18	65.93	3.19	199.95	2.93	0.71	5.39	10.42	0.3474
IC 142857 × Indira Matar-1	52.80	64.30	103.65	51.35	6.32	12.06	51.67	3.79	142.37	3.96	0.81	7.17	10.88	0.3873
IC 142857 × Ambika	54.05	62.60	105.45	42.10	4.53	11.96	51.71	3.09	154.46	3.08	0.97	7.29	11.15	0.2456
IC 142855 × Indira Matar-1	60.80	72.50	115.55	54.35	5.32	10.98	46.25	4.16	189.77	3.02	0.92	5.79	11.03	0.2085
IC 142851 × Paras	53.95	68.25	103.40	49.70	5.30	8.43	30.17	3.57	106.17	3.11	0.94	5.20	5.87	0.2413
IC 142851 × Indira Matar-1	55.20	70.00	105.25	37.60	3.87	5.87	19.77	3.14	55.97	3.24	0.89	5.60	3.53	0.4657
IC 142843 × Shubhra	52.95	69.05	105.35	43.70	5.46	10.11	23.73	2.63	64.25	3.12	0.91	12.33	8.98	0.2207
IC 142782 × Indira Matar-1	53.30	66.25	104.45	38.60	4.54	10.68	38.84	3.27	123.36	3.01	0.96	6.21	7.19	0.2447

IC 142782 × Ambika	50.10	55.10	102.70	63.52	3.95	9.80	35.11	3.40	113.80	2.55	0.85	6.72	8.23	0.2076
Ambika × IG 64869	48.80	60.40	101.60	115.70	3.97	6.88	28.44	2.70	74.41	5.03	1.06	7.50	6.09	0.2165
Ambika × L.O.	50.00	58.85	107.25	122.47	4.26	5.92	24.17	3.13	70.83	4.96	0.98	9.29	6.87	0.0753
Ambika × Mahateora	51.00	62.75	105.60	136.55	4.18	8.11	35.31	3.57	110.91	2.48	1.13	7.48	8.82	0.1329
Ambika × Prateek	47.10	54.50	98.45	113.85	4.88	10.89	44.81	4.49	193.01	6.13	1.35	11.06	21.85	0.0207
Ambika × Ratan	50.95	66.05	107.50	118.23	4.14	10.39	38.85	4.15	153.98	5.16	1.84	6.25	9.93	0.0846
IC 294285 × Mahateora	47.85	66.20	105.55	117.65	4.90	8.69	33.95	3.90	147.34	4.12	1.11	11.63	15.44	0.0250
Indira Matar-1 × Ratan	51.00	68.55	111.40	124.42	3.90	9.86	35.97	4.15	151.29	5.03	1.04	25.03	23.94	0.1747
Paras × IG 64869	53.00	66.55	109.55	94.05	4.27	10.75	43.84	3.18	135.73	4.76	1.44	6.57	8.71	0.2587
Paras × Mahateora	55.00	68.35	106.40	112.03	4.14	11.65	42.69	3.59	152.45	3.63	1.34	6.72	10.08	0.1935
Shubhra × Mahateora	53.05	66.25	106.30	95.24	4.06	10.00	42.31	3.29	126.42	3.13	1.22	6.59	8.57	0.5056
Shubhra × Prateek	52.35	66.25	109.85	125.80	4.01	6.01	22.15	3.01	52.87	2.86	1.01	10.57	6.03	0.4783
Shubhra × Ratan	55.25	78.00	113.70	112.45	3.90	5.32	20.19	2.18	39.05	3.16	0.99	13.34	4.92	0.0377
EC 243834 × L.O.	52.70	63.15	106.25	109.40	4.15	11.46	52.81	3.36	186.34	4.32	1.24	5.86	10.59	0.0353
EC 243834 × Mahateora	51.00	61.85	104.75	108.60	4.07	5.91	20.19	1.74	28.60	3.04	0.95	15.55	4.70	0.0297
EC 243834 × Prateek	49.70	62.75	106.00	102.56	4.82	10.91	48.19	3.79	186.50	3.96	0.85	8.69	15.90	0.2747
EC 356344 × Mahateora	42.80	63.20	106.95	81.60	3.94	9.98	41.53	3.63	153.68	2.88	0.92	8.47	13.14	0.0377
EC 356344 × Prateek	44.55	63.05	106.00	109.51	4.14	6.85	28.32	3.40	86.76	2.15	0.95	11.03	9.64	0.0443
L.O × Ratan	90.95	108.45	137.95	85.63	5.84	8.91	33.12	2.74	92.29	6.01	1.48	8.15	7.76	0.0353
L.O. × RGRLS 212-2	86.00	101.15	135.65	103.50	4.25	5.77	15.62	3.82	57.62	5.36	0.85	11.01	6.24	0.5877
L.O. × IG 64975	88.20	102.80	136.90	106.40	3.80	5.74	26.31	1.77	45.26	4.65	0.91	16.05	7.87	0.5173
L.O. × IG 64869	83.95	104.75	138.00	89.50	3.95	4.97	20.17	3.58	67.01	5.35	0.94	5.74	3.90	0.0287
IC 142846 × Paras	57.55	70.70	107.95	58.78	4.04	5.30	17.62	3.37	50.10	3.15	0.88	10.91	5.99	0.1883

Table 4: Mean performance of agronomical characters of parents.

Parents	DFF	DF	DM	PH	PB/pl	SB/pl	P/pl	S/pod	S/pl	PL	PB	SI	SY	ODAP
Mahateora	56.60	63.50	103.15	56.95	4.08	6.15	14.67	4.10	56.58	3.06	0.92	9.46	5.38	0.0815
Prateek	54.10	61.05	101.30	42.80	3.13	6.31	18.62	4.08	74.97	2.92	0.91	8.69	6.72	0.0886
Ratan	58.60	64.30	106.00	52.70	2.90	5.62	12.67	4.15	51.78	2.52	0.91	9.18	4.30	0.0874
RGRLS 212-2	65.90	72.00	112.90	56.45	3.05	5.34	16.12	4.05	64.33	2.85	0.92	8.31	5.24	0.0927
IC 142782	58.15	67.75	105.00	68.45	3.06	5.46	22.11	4.00	87.28	2.74	0.86	6.83	5.91	0.1205
IC 142843	59.55	65.80	107.05	44.05	3.25	5.89	20.18	4.08	80.42	3.04	0.85	6.50	5.20	0.0834
IC 142846	58.25	64.95	104.95	61.70	2.61	5.93	20.63	4.12	83.54	3.06	0.92	6.40	5.27	0.1455
IC 142851	62.50	68.10	108.00	43.80	3.20	5.19	21.12	4.13	80.05	3.07	0.85	6.28	4.88	0.1566
IC 142855	64.70	74.05	114.05	55.80	3.17	5.66	20.18	4.12	81.53	3.23	0.85	8.52	5.92	0.1443
IC 142857	59.25	64.85	105.25	50.00	2.87	5.81	22.17	4.18	84.55	3.48	0.99	5.22	4.96	0.1324
IC 142878	62.45	70.95	109.00	53.85	2.43	5.60	24.12	4.07	85.89	2.75	0.96	6.35	6.54	0.0914
IC 142881	61.00	68.80	106.90	47.40	3.02	5.42	16.18	4.09	62.05	2.82	0.99	6.39	3.94	0.1316
IC 142990	62.30	67.80	107.85	42.75	2.56	5.27	23.67	4.21	88.49	3.07	0.95	6.57	5.34	0.1304
IC 142991	67.05	75.80	116.05	57.30	2.70	5.02	18.67	4.13	65.73	3.53	0.97	7.49	5.18	0.1226
L.odoratus	65.05	105.20	112.15	93.60	2.60	5.44	11.13	7.09	76.20	4.34	1.02	7.32	5.12	0.1103
IG 64975	62.50	67.80	108.00	73.85	2.43	5.32	14.17	5.24	72.95	3.57	1.17	8.45	5.68	0.0963
IG 64869	64.30	70.15	109.95	69.65	2.61	5.89	16.67	4.90	82.09	3.02	0.97	6.60	5.24	0.0923
Indira Matar_1	53.30	57.10	97.85	132.50	3.42	5.60	20.12	8.14	160.25	5.10	1.05	10.29	16.31	0.00
Ambika	74.35	77.35	120.15	129.70	3.60	5.34	23.12	7.87	178.96	4.77	1.22	9.65	16.25	0.00
Shubhra	54.75	64.30	101.15	126.05	3.36	5.40	24.12	7.57	176.39	2.93	1.06	9.33	16.11	0.00
Paras	63.15	72.60	111.00	119.40	3.61	5.64	25.12	7.19	174.43	4.13	1.22	8.28	14.26	0.00
EC 356344	50.25	57.15	96.05	112.50	3.09	8.15	36.16	5.16	176.16	2.68	1.09	6.45	11.49	0.00
EC 243834	54.60	62.60	100.25	113.80	3.20	8.00	32.17	5.32	162.93	2.97	1.06	6.35	10.53	0.00
IC 294285	54.45	61.90	100.15	120.50	3.25	8.57	36.11	5.20	183.27	3.91	1.05	6.84	12.76	0.00
Overall Mean	**57.49**	**69.96**	**109.61**	**75.39**	**3.97**	**8.15**	**30.66**	**3.94**	**114.30**	**3.53**	**0.99**	**8.15**	**8.65**	**0.1926**

Note: DFF-Days to first flowering (Days), **DF-**Dats to 50% flowering (Days), **DM**-Days to maturity (days), **PH**-Plant Height (cm), **PB/pl-** Number of primary branches per plant, **SB/pl**-Number of secondary plants per plant, **P/pl-** Number of Pods per plants, **S/pod**-Number of seeds per pod, **S/pl-** number of seeds per plant, **PL**-Pod length (cm), **PB**-Pod breadth (cm), **SI-** Seed Index, **SY**-Seed yield per plant, **ODAP-** β N oxalyl α β di-amino propionic acid.

CONCLUSION

The analysis of variance showed a wide range of variation and significant difference for all the traits under research work with the sufficient amount of variability. The highest PCV and GCV was recorded for ODAP content, Days to maturity, seed yield per plant, seeds per plant, Pods per plant, seed index, Secondary branch per plant, seeds per pod, Pod length and Primary branch per plant. The genetic variability showed less influence of environment on the expression on traits. The heritability was recorded higher for all the fourteen characters. High heritability coupled with high genetic advance as percent of mean was recorded highest for the characters ODAP estimation followed by Seeds per plan, Seed Index, Days to 50 percent flowering, Seed yield, Seeds per pod, Days to maturit, Pod length, Days to first flowering, Pods per plant, Pod breadth, Secondary branch per plant and Primary branch per plant, it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effectives for crop improvement. The maximum yield 26.89 gm per plant obtained by cross IC 142991 × Indira Matar-1 and low ODAP content was minimum (0.0207) in cross Ambika × Prateek while seed index was maximum in cross. 25.03 in cross Indira Matar-1 x Ratan.

ACKNOWLEDGEMENT

Authors are thankful to the Director, Research Services, Indira Gandhi Krishi Vishwavidyalaya, Raipur Chhattisgarh for constant encouragement and support. I also thankful to the Director Research Farm IGKV, Raipur for providing field and all necessary support during the conduction of experiment with valuable package of practices.

REFERENCES

Abate Alemu, Mekbib Firew, Fikre Asnake and Ahmed Seid (2018). Genetic Variability and Heritability in Ethiopian Grasspea (*lathyrus sativus* l.) Accessions *Ethiop. J. Crop Sci.*, *6*(2) pp 79-94.

Anonymous, (2019). State of Indian Agriculture 2019-20 Printed and published by Directorate of Economics and Statistics, Ministry of Agriculture, Government of India. New Delhi.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. *6th int. Grassland Cong*., **1**: 277-283.

Ghosh, Argha and Khan, Safiuddin Ahmed (2018). Determination of optimum sowing time of grass pea based on yield variation as affected by varied dates of sowing in new alluvial zone of West Bengal. *Int. Jour. of Agri., Environ. and Biotech*., **11**(1): 11-16.

Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. *Agronomy journal*, **48**(6), 268-272.

Jeberson, M.S., Gonmei, R., Kumar, Manish, Shashidhar, K.S., Singh, N.B. and Sharma, Ph Ranjit (2018). Genetic variability, heritability, correlation coefficient and path analysis in *Lathyrus* for yield and its related contributes under NEH condition. *Journal of Pharmacognosy and Phytochemistry,* **7**(6): 1806-1809.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetics and environment variability in soybean. *Agronomy Journal, 47* pp. 314–318.

Khandait, Ramnarayan, Jain, P.K., Prajapati, Sunil and Solanki Pritibala (2016). Genetic variability studies of diverse cowpea *(Vigna unguiculata* L.) genotypes. *Journal of Functional and Environmental Botany,* **6**(2) pp: 114-122

Lavanya, G. Roopa, Singh Dheerendra and Vinoth R. (2010). Genetic Variability, Character Association and Component Analysis in Field pea, *Pisum sativum var. arvense. Madras Agric. J*., **97**(10-12): 329-331.

Panse, V. G., & Sukhatme, P. V. (1967). Statistical methods for agricultural workers ICAR Publication. *New Delhi*, *259*.

Rizvi, A. H., Sarker, A., & Dogra, A. (2016). Enhancing grass pea (*Lathyrus sativus* L.) production in problematic soils of South Asia for nutritional security. *Indian J. Genet. Plant Breed*, **76**, 583-592.

Rubiales Diego, Emeran Amero A. and Flores Fernando (2020). Adaptation of Grass Pea (*Lathyrus sativus*) to Mediterranean Environments. *Journal of Agronomy,* **10** (1295): 1-12.

Singh Prabhat Kumar, Sadhukhan R. and Kumar Adyant (2017). Correlation studied on several quantitative traits in induced mutagenic population of grasspea (*Lathyrus sativus* L.). *Int. J. Curr. Microbiol. App. Sci.,* **6**(10): 612-619

Sivasubramanian, S. and Madhava Menon P., (1973). Genotypic and phenotypic variability in Rice. *Madras Agriculture Journal,* **60**, pp. 1093–1096.

Ullah, S., Batool, S., Mohibullah, M., Noreen, J., Khan, M., Ali, S. Farjad Sikandar Saddozai, Hammad Sikandar Saddozai, and Muhammad Amin, (2019). Studies on the variability parameters in pea. *J. Genetics Genomics Plant Breed*, **3**(1), 17-22.

Vaz Patto, M. C., & Rubiales, D. (2014). Lathyrus diversity: available resources with relevance to crop improvement–L. sativus and L. cicera as case studies. *Annals of botany*, **113**(6), 895-908.

Alvarez, J. B., & Guzmán, C. (2018). Interspecific and intergeneric hybridization as a source of variation for wheat grain quality improvement. *Theoretical and applied genetics*, **131**(2), 225-251.

Arslan Mehmet, Arslan Merve, Aksu Elcin, Uzun Bulent and Yol Engin (2020). Genotyping of Low β-ODAP Grass Pea *Lathyrus sativus* L.) Germplasm with EST-SSR Markers. *Journal of Brazilian Archives of Biology and Technology*, **63***:* e20190150.pp:1-13.

Christov, M. (2013). Contribution of interspecific and intergeneric hybridization to sunflower breeding. *Helia*, **36**(58), 1-18.

How to cite this article: Chopkar, R., Sao, A., Nanda, H.C., Nair, S. and Sarawgi, A.K. (2021). Estimation of Variability Analysis for Wide Hybridization between Grasspea and Pea. *Biological Forum – An International Journal*, **13**(1): 736-745.