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**Varsha Kanwar**

M.Sc. Scholar, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

**Krishna Tandekar**

Scientist, ACRIP on MULLaRP Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

**Rashmi Sai**

M.Sc. Scholar, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

**Vinita Singh Kanwar**

M.Sc. Scholar, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

**Lalit Kumar Singh**

M.Sc. Scholar, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

**Corresponding Author:**

**Varsha Kanwar**

M.Sc. Scholar, Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh, India

## Genetic variability analysis for and yield attributing traits in a germplasm accession of grasspea (*Lathyrus sativus* L.)

**Varsha Kanwar, Krishna Tandekar, Rashmi Sai, Vinita Singh Kanwar and Lalit Kumar Singh**

### Abstract

Grasspea (*Lathyrus sativus* L.) is considered an "insurance crop" due to its credible yields during drought and flood conditions. This study investigated the genetic variability among grasspea accessions during the *Rabi* season of 2022-23 using thirty-six genotypes with two checks. Observation was carried on fourteen yield-related characteristics are used to assess genetic variability. Analysis conclude that all characters were highly significant except days to maturity and days to 50% flowering, indicating the genotypes under test have enough variability. All traits had PCV values larger than GCV values, showing the impact of environment on the way characters are expressed. The biological yield/plant, pod bearing length, seed yield/plant, no. of pods/plant, no. of effective pods/plant, harvest index, ODAP content and hundred seed weight all showed high heritability along with high genetic advance, indicating additive gene action and the potential for selection to increase seed yield.

**Keywords:** Variability, genetic advance, heritability, phenotypic, genotypic, grasspea

### Introduction

Grasspea (*Lathyrus sativus* L.) is a grain legume crop that is self-pollinated and has chromosomal number  $2n=14$ . It is a member of the Fabaceae family. This resilient crop is mostly utilised as a grain for human use, along with fodder as animal feed. In order to fulfil the dietary needs of the vulnerable population who live in areas with few resources for food and nutrition, this legume which has its origins in South Europe and Western Asia is primarily farmed and supplied in India, Nepal, Bangladesh, Pakistan and Ethiopia for food, feed and fodder.

A very nutrient dense crop is grasspea. According to Yang and Zhang (2005) [20], 100 g of seeds contains 3g of minerals, 58% of which are carbohydrates, 28-32% of which are proteins and 0.6% of which are fat. In grasspea seed, there contains a lot of L-homoarginine, which is a precursor to lysine in higher animals (Talukdar, 2012) [17]. Despite having all of these advantages this legume is still not widely used since it contains the neurotoxin " $\beta$ -N oxalyl-L-di-amino propionic acid ( $\beta$ -ODAP)". It is considered to be a potential contributor to the neurological disorder known as "lathyrism" in people. Overindulging in grasspea grains for extended periods of time is the cause of this. Studies indicate that humans may safely eat grasspea cultivars with ODAP concentration less than 0.2% according to Yan *et al.* (2006) [19]. In systematic plant breeding efforts the fundamental strategies are critical. It develops an appropriate degree of genetic variation initially, then chooses and exploits promising material to build future lines. The degree of a character's transmissibility to next generations can be determined by understanding heredity in selection-based development projects. Genetic progress is represented by genetic gain under selection, which is dependent on heritability, genetic diversity and selection intensity. Heritability outlines the process of gene activity in the manifestation of traits, which assists in the selection of advantageous breeding approaches.

### Methods and Materials

The present study was conducted during *Rabi* season, 2022-23 with thirty-six genotypes of grasspea which were selected based on features that contribute to yield. The experiment was conducted at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, CoA, IGKV, Raipur (21°16' N latitude & 81°31' E longitude) in Alpha Lattice Design with 2 replications.

The experimental plot had 30 cm between rows spacing and 15 cm between plants spacing. Five plants that were selected at random from each plot were evaluated for plant height (cm), days to 50% flowering, days to maturity, number of primary branches/plant, number of pods/plant, number of seeds/pod, number of effective pods, pod bearing length (cm), biological yield/plant (g), harvest index (%), protein content (%), ODAP (%), 100 seed weight (g) and seed yield/plant (g).

### Statistical analysis

Analysis of variance was performed as per the procedure provided by Patterson and Williams, 1976. In accordance with Burton (1952) [2], phenotypic and genotypic coefficients of variation were calculated. According to the formulae suggested by Hanson *et al.* (1956) [4], heritability was estimated. According to the formulas suggested by Johnson *et al.* (1955) [6], genetic advance has been assessed. According to the classification made by Johnson *et al.* (1955) [6], the range of genetic advance above the mean was categorised as low (0–10%), moderate (11–20%), and high (20% and above).

### Results and Discussion

With regard to the fourteen yield-attributing features listed in Table 1, an ANOVA was conducted. All traits were highly significant according to analysis of variance (ANOVA), with the exception of time of maturity and time of 50% flowering, suggesting that all of the genotypes have enough variation and that there is huge scope for improvement in all of the traits. Similar findings were reported by Singh *et al.* (2012) [15], Parihar *et al.* (2015) [11], Ullah *et al.* (2019) [18], Abate *et al.*

(2018) [1] and Dowlatshah *et al.* (2021) [3]. The phenotypic coefficient variance were larger than the genotypic coefficient variance for all of the characteristics studied, confirming that character expression is greatly influenced by the environment, as Ullah *et al.* (2019) [18] discovered. The no. of effective pods/plant (31.48, 31.8) had the highest genotypic and phenotypic coefficient of variation, followed by seed yield/plant (29.91, 30.69), no. of pods/plant (25.11, 25.4) and biological yield/plant (21.5, 21.97).

Heritability represents the percentage of transfers of characteristics from one generation to another generation. High heritability means that additive gene activity predominates in the expression of traits and may be increased by choosing specific plants (Rashwan (2010) [14], Makeen *et al.* (2007) [10]). The highest heritabilities were seen in the following variables *viz.*, no. of effective pods/plant (98%), no. of pods/plant (97.7%), ODAP % (97.3%), seed yield/plant (95%), pod bearing length (94%), biological yield/ plant (92.7%), no. of seeds/pod (84.3%), HI (81.8%), hundred seed weight (78.9%), primary branches/plant (77.7%), plant height (72.7%) and protein (61.2%). Similar result obtained by Jesberson *et al.* (2018) [5], Kumar and Dubey (2010) [7], Ranjan *et al.* (2007) [13] for primary branches/plant and seed yield/plant.

Genetic advance as percent of mean was found high for the characters namely ODAP (%) (82.12) followed by no. of effective pods/plant (64.2), seed yield/plant (60.04), no. of pods/plant (51.13), biological yield/plant (41.96), pod bearing length (33.56), harvest index (27.09) and hundred seed weight (21.69).

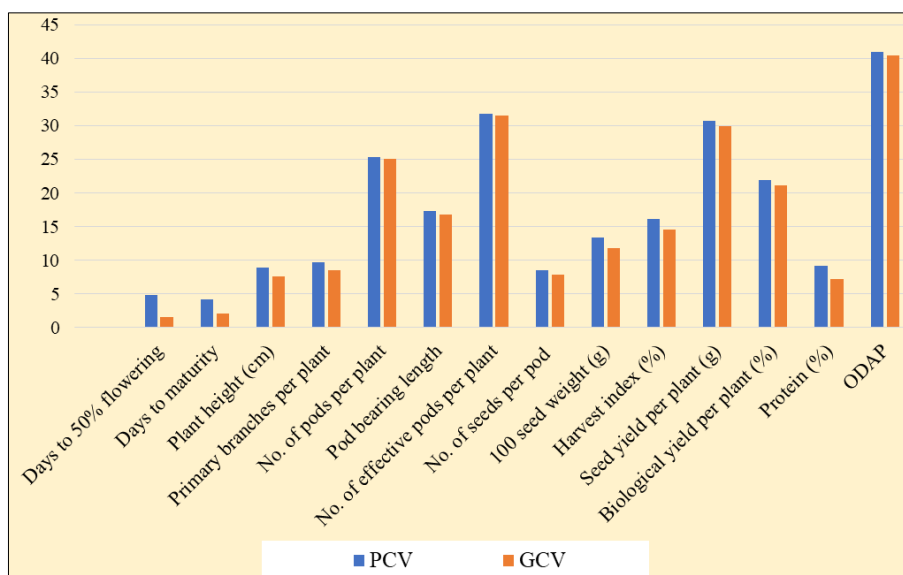
**Table 1:** ANOVA for yield and its relative characters in grasspea germplasm+

S. No.	Source of Variation	Replication	Treatment	Error
	DF	1	35	35
Mean sum of square				
1	Time of 50% flowering (days)	0.065	8.437	6.847
2	Time of maturity (days)	4.239	22.303	13.897
3	Height of plant (cm)	0.069	29.885 **	4.718
4	Primary branches/plant	0.043	0.285 **	0.036
5	No. of pods/plant	0.052	30.713 **	0.352
6	Pod bearing length (cm)	1.448	28.380 **	0.877
7	No. of effective pods/plant	0.084	35.235 **	0.353
8	No. of seeds/pod	0	0.142 **	0.012
9	100 seed weight (g)	0.046	2.673 **	0.316
10	Harvest index (%)	3.056	84.121 **	8.439
11	Seed yield/ plant (g)	0.139	2.333 **	0.06
12	Biological yield/ plant (g)	0.004	6.494 **	0.245
13	Protein content (%)	0.008	9.796 **	2.356
14	ODAP content (%)	0.001	0.020 **	0

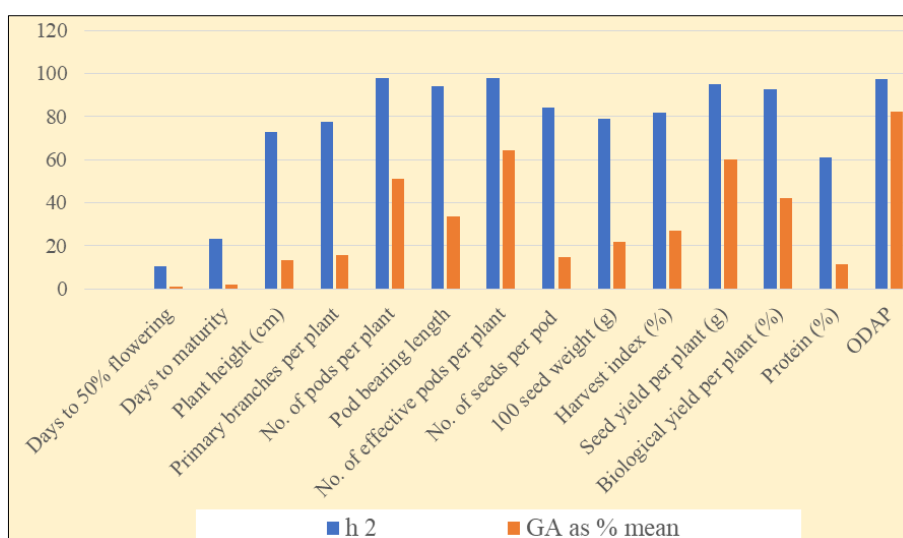
(\*\* Shown at 1% significant level)

**Table 2:** Estimates of genetic variability for yield attributing characters of grasspea genotypes

S. No.	Characters	Mean	Range		GCV	PCV	h <sup>2</sup>	GA	GA as % mean
			Min.	Max.					
1	Time of 50% flowering (days)	57.31	54.0	63.0	1.56	4.82	10.4	0.59	1.03
2	Time of maturity (days)	100.36	93.0	108.0	2.04	4.24	23.2	2.04	2.03
3	Height of plant (cm)	46.78	36.0	59.4	7.58	8.89	72.7	6.23	13.32
4	Primary branches per plant	4.13	2.4	5.8	8.56	9.71	77.7	0.64	15.54
5	No. of pods per plant	15.52	6.4	34.2	25.11	25.4	97.7	7.94	51.13
6	Pod bearing length (cm)	22.01	10.4	31.6	16.85	17.37	94	7.41	33.65
7	No. of effective pods per plant	13.27	3.6	34.0	31.48	31.8	98	8.52	64.2
8	No. of seeds per pod	3.24	2.4	4.0	7.87	8.57	84.3	0.48	14.89
9	100 seed weight (g)	9.16	7.0	11.8	11.86	13.35	78.9	1.99	21.69
10	Harvest index (%)	42.30	11.4	62.7	14.54	16.08	81.8	11.46	27.09
11	Seed yield per plant (g)	3.56	1.2	9.4	29.91	30.69	95	2.14	60.04
12	Biological yield per plant (g)	8.36	4.4	16.4	21.15	21.97	92.7	3.51	41.96
13	Protein content (%)	26.87	22.2	32.8	7.18	9.18	61.2	3.11	11.57
14	ODAP content (%)	0.24	0.010	0.410	40.42	40.98	97.3	0.20	82.12



**Fig 1:** Bar diagram for GCV and PCV values for seed yield and its contributing characters



**Fig 2:** Bar diagram showing h<sup>2</sup> and GA as % of mean for seed yield and its contributing characters

The high heritability coupled with high GA found for biological yield/plant, pod bearing length, seed yield/plant, No of pods/plant, no. of effective pods, harvest index (%), ODAP content and hundred seed weight. This indicates that these traits are controlled by additive gene action so, the improvement in yield could be achieved through the selection of these traits. Similar results were conducted by several authors by Tadesse and Bekele (2003) <sup>[16]</sup>, Kumari and Maiti (2016) <sup>[8]</sup>, Abate *et al.* (2018) <sup>[1]</sup> for biological yield/plant, pod bearing length (cm), no. of pods/plant and ODAP content (%), Mahapatra *et al.* (2020) <sup>[9]</sup> for no. of pods/plant and Ranjan *et al.* (2007) <sup>[13]</sup> concluded for seed yield/plant. High heritability coupled with high GA is an essential genetic aspect for selection of any genotype that consent superior capability of selection by sorting out environmental effect from entire variability. Similar finding by Johnson *et al.* (1955) <sup>[6]</sup>, Ullah *et al.* (2019) <sup>[18]</sup> and Abate *et al.* (2018) <sup>[1]</sup>.

### Conclusion

From entire study we can conclude that considerable genetic variability was found among the genotypes for all the characters under investigation. For all of the traits, the

genotypic coefficient of variance was smaller than the phenotypic coefficient of variation, indicating the effect of environmental influences. In regard to biological yield per plant, seed yield per plant, number of pods per plant, number of effective pods per plant and harvest index (%), strong heritability and high genetic advance were demonstrated. Selection for these traits will thus help to increase seed yield.

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