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ORIGINAL ARTICLE

Genetic variability study for green biomass attributing traits in  
Sunnhemp [*Crotalaria juncea*(L.)]

Desai Tarjani B.\*, Madhu Bala and Patel R. K.

Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural  
University, Navsari, 396450, Gujarat, India

\*Corresponding Author: Email - [desaitarjani311@gmail.com](mailto:desaitarjani311@gmail.com)

ABSTRACT

*Crotalaria juncea* L. (2n=16) is an important Indian originated fiber crop. The analysis of variance revealed significant genotypic differences for all thirteen characters under study. A wide range of variability was observed for different traits indicating the scope for selection of suitable initial breeding material for further improvement. The highest genotypic coefficient of variation was observed for root nodules per plant followed by fresh weight of root nodules per plant. The high heritability were observed for days to 50 % flowering, fresh weight of root nodules per plant, dry weight of root nodules per plant, root nodules per plant, fresh weight of plant and leaf length. Genetic advance expressed as percentage of mean were found high for root nodules per plant, fresh weight of root nodules per plant, dry weight of root nodules per plant, fresh weight of plant and days to 50 % flowering, indicating presence of additive gene action for these traits, so more emphasis should be given to these characters as far as selection procedure is concerned. High heritability with high genetic advance as per cent of mean were observed for root nodules per plant, fresh weight of root nodules per plant, dry weight of root nodules per plant, fresh weight of plant and days to 50 % flowering compared to other traits. Hence, priority should be given to these traits in formulating selection strategies on the basis of these traits to realize better green biomass by selection.

**Key words:** Sunnhemp, Green manuring, Variability

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INTRODUCTION

Sunnhemp (*Crotalaria juncea* L.) is a plant of sub-order papilionaceae of the order Fabaceae is an annual shrub cultivated as multipurpose legume especially for its fine fibre in many countries including India. The sunnhemp crop is native to India. Sunnhemp as a fibre and green manuring crop is cultivated in all states of India. It is the producer of sunnhemp fibre followed by Bangladesh and Brazil. Species of this genus are wide spread throughout tropical, sub-tropical and to a lesser extent in temperate countries.

Sunnhemp generally reported to be self-incompatible plant. Cross pollination is extensive and self-pollination occurs only after the stigmatic surface has been stimulated by insect or some other means [8]. Sunnhemp is the one of the important fibre crop of India, where it is grown for green manuring and fibre purpose. It is also considered as the king of green manuring crops which adds about 40 to 60 kg nitrogen per hectare into the soil [12].

During the past few years intensive research work has been initiated in India to improve the green biomass as well as quality of fibre. It is well known that yield is a very complex character and it is the result of interaction of number of factors inherent to plants and the environment in which it is grown. Therefore, it becomes difficult for plant breeders to evaluate and select for this complex polygenic character directly. The improvement in yield and its components depends on the nature and magnitude of genetic variability present in the population. The genetic variability in conjunction with total variability can be used in predicting the gain for a given selection intensity.

The fundamental goal in any crop improvement programme is to increase the yield potential of the crop. A successful breeding programme for yield improvement through phenotypic selection is mainly dependent on the nature and magnitude of variation in the available material and part played by the environment in the expression of the plant characters i.e. phenotype. This required the partitioning of the overall variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genetic coefficient of variation, heritability and genetic advance.

## MATERIAL AND METHODS

The present investigation was carried out using thirty genotypes of sunnhemp collected from various locations throughout the country. The thirty genotypes were sown in randomized block design at research farm of Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari during late kharif 2017. A spacing of 30 cm between rows and 10 cm between plants within the row was maintained. Two guard rows surrounded the experiment to avoid damage and border effects. Data was collected from five randomly selected plants tagged from each accession. Analysis of variance was carried out as per standard procedure [11]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) [3], heritability [1], genetic advance [5], were estimated.

## RESULT AND DISCUSSION

The analysis of variance showed that the genotypes under study differed significantly among themselves for all the thirteen characters. Similar results for most of the characters were also reported by Qamar *et al.* [13], Rao *et al.* [14], Venkatesan *et al.* [19], Bakshi and Ghoshdastidar [2], Reddy *et al.* [16], Kumar *et al.* [7], Ojo *et al.* [10]. Wide variability facilitates the better chances of improvement. The mean, range, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance as per cent of mean for all the characters are presented in Table 1. The magnitude of PCV was higher than that of GCV for all the traits. The highest genotypic coefficient of variation was observed for root nodules per plant followed by fresh weight of root nodules per plant. The moderate amount of variation was observed for dry weight of root nodules per plant, fresh weight of plant, days to 50 % flowering and leaf length. While stem diameter, internodes per plant and plant height, leaf area, C:N ratio, root length and primary branches per plant had the lower coefficients of variation. Similar results were also obtained by Rao *et al.* [14] for number of nodules per plant, leaf area and dry weight of root nodules per plant and Dev *et al.* [4] for primary branches per plant.

The highest value of PCV was observed for root nodules per plant, fresh weight of root nodules per plant and leaf area. The moderate value of PCV was observed for dry weight of root nodules per plant, fresh weight of plant, primary branches per plant, leaf length, stem diameter, days to 50 % flowering, root length and internodes per plant. While plant height had the lowest PCV. Similar results were also obtained by Rao *et al.* [14] for number of nodules per plant, leaf area and dry weight of root nodules per plant, Rathi and Dhaka [15] for primary branches per plant, Joshi *et al.* [6] for branches per plant and Dev *et al.* [4] for primary branches per plant.

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of characters is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedure. In the present study, high heritability estimates were observed for days to 50 % flowering and was followed by fresh weight of root nodules per plant, dry weight of root nodules per plant, root nodules per plant, fresh weight of plant and leaf length. Less influence of environmental effects on the characters leads to high heritability estimates. This also suggested that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be more reliable. Similar observations were reported by Rao *et al.* [14] for leaf area, root nodules per plant and dry weight of root nodules per plant, Yadav *et al.* [20], Kumar *et al.* [7], Malik *et al.* [9], Tiwari & Lavanaya [18] for days to 50 % flowering, Ojo *et al.* [10] for root nodules per plant and days to 50 % flowering. High heritability for all the characters studied indicated the preponderance of additive gene effects. Therefore, further improvement through individual plant selection on the basis of these traits would be possible. Whereas, lower heritability values indicated little scope for improvement. The heritability estimates were found to be moderate for C:N ratio, root length and plant height.

Genetic advance is the deviation in the characters of selected population over the base population. If the value of genetic advance is more than there will be good progress over population mean. Heritability and genetic advance are important parameters. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Hence, heritability values

used in conjunction with the genetic advance would be more reliable than heritability alone [5] which will be helpful in forming selection procedures.

High heritability with high genetic advance as per cent of mean were observed for root nodules per plant, fresh weight of root nodules per plant, dry weight of root nodules per plant, fresh weight of plant and days to 50 % flowering compared to other traits. Hence, priority should be given to these traits in formulating selection strategies on the basis of these traits to realize better green biomass yield by selection. Similar results were also reported by Yadav *et al.* [20] and Saroj *et al.* [17] for days to 50 % flowering. Thus results indicated the substantial contribution of additive genetic variance in the expression of these characters and could be improved through individual plant selection.

The result revealed low heritability coupled with low genetic advance as percent mean for internodes per plant, primary branches per plant, stem diameter and leaf area. The character leaf length showed high heritability coupled with moderate genetic advance as percent of mean. High heritability accompanied with moderate genetic advance as percent of mean indicated that genotypes under study were diverse with immense genetic potential and further improvement in the trait is possible by adopting simple selection technique.

Moderate heritability coupled with low genetic advance as percent of mean was observed for the characters plant height and root length and moderate genetic advance as percent of mean for C:N ratio. It indicated that the character is highly influenced by environmental effects and selection would be ineffective.

**Table 1: Mean, range, variability parameter, heritability and genetic advance for different traits in sunnhemp**

Parameters	Mean	Range	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	GCV%	PCV%	Heritability (%)	Genetic Advance (% Mean)
Days to 50 % flowering	67.82	50.00-85.00	75.39	69.31	6.08	12.28	12.80	91.94	24.25
Plant height (cm)	156.18	146.00-168.33	70.69	23.72	46.96	3.12	5.38	33.56	3.72
Internodes per plant	36.54	31.33-42.67	18.28	3.53	14.75	5.14	11.70	19.32	4.66
Primary branches per plant	3.75	3.00-4.33	0.47	0.07	0.40	7.28	18.25	15.91	5.98
Stem diameter (cm)	2.47	2.03-2.87	0.13	0.02	0.10	6.15	14.38	18.30	5.42
Leaf length (cm)	9.59	6.67-12.00	2.27	1.38	0.89	12.24	15.72	60.69	19.65
Leaf area (cm <sup>2</sup> )	6.72	5.33-8.33	1.84	0.30	1.55	8.11	20.20	16.12	6.71
Root length (cm)	32.39	27.00-39.33	14.68	6.01	8.67	7.57	11.83	40.93	9.97
C:N ratio	24.86	22.47-30.70	7.03	4.08	2.95	8.12	10.66	57.99	12.74
Root nodules per plant	10.38	4.67-14.00	6.39	5.26	1.13	22.10	24.36	82.29	41.30
Fresh weight of root nodules per plant (g)	2.68	1.59-3.47	0.32	0.29	0.03	20.13	21.26	89.63	39.25
Dry weight of root nodules per plant (g)	1.09	0.64-1.31	0.04	0.04	0.01	17.54	19.03	84.91	33.28
Fresh weight of plant (g)	66.88	50.33-85.67	159.17	124.06	35.10	16.65	18.86	77.95	30.29

**CONCLUSION**

In conclusion the analysis of variance revealed the presence of sufficient variability among the all genotypes for different characters. Maximum range of variation indicated the presence of wide variation for the characters. The values of phenotypic coefficient of variation were slightly higher than genotypic coefficient of variation indicating the less influence of environmental factors in most of the characters. The high estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for root nodules per plant, fresh weight of root nodules per plant, dry weight of root nodules per plant, fresh weight of plant and days to 50 % flowering may be attributed to the

preponderance of additive gene action and these traits possess high selective value. Hence, emphasis should be focused on selection to improve biomass production in sunnhemp.

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#### AUTHOR CONTRIBUTIONS

All author equally contributed to the research.

#### CONFLICT OF INTEREST

There is no conflict of interest.

#### ETHICAL APPROVAL

This article does not contain any studies with human participants or animals performed by any of the authors.

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