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Genetic variability studies in cowpea genotypes

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Abstract

An experiment was conducted with forty one genotypes in *rabi* season of 2019-20 at research and education farm, Department of Agriculture Botany, College of Agriculture, Dapoli. Observations were recorded on fourteen characters *viz.*, days to initiation of flowering, day to 50 per cent flowering, days to maturity, plant height at maturity (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length 100 seed weight, dry matter yield per plant, seed yield per plant, harvest index (%), protein content (%) and iron content (ppm). A wide range of variation exhibited for yield and yield attributing traits among the progenies under study. In general PCV was higher in magnitude than GCV. The analysis of variance revealed significant variation among the genotypes for all the characters studied. The estimates of mean sum of squares showed comparatively wide range of variation for the characters Iron content, dry matter yield per plant and plant height at maturity while the lowest variation was recorded for number of primary branches per plant. Appreciable heritability values were observed for the characters under study. Highest heritability estimates were recorded for the character, iron content, dry matter yield per plant, plant height at maturity, days to initiation of flowering and days to 50% flowering. The lowest heritability estimate recorded in number of seeds per pod, pod length, hundred seed weight and number of primary branches per plant.

Keywords: Variability, GCV, PCV, heritability

Introduction

Pulses are economically cheaper and vital source of protein, vitamins and minerals in Indian diet. Cowpea (*Vigna unguiculata* (L.) Walp) $2n=22$ is one of the most widely adapted; drought-tolerant, versatile, and nutritious grain legume crop. Cowpea, a self-pollinating plant species that belongs to the family Fabaceae, is cultivated worldwide (Mahe *et al.* 1994; Musvosvi, 2009) [12]. It is native to India (Vavilov, 1949) [18] but tropical and central Africa is also considered as secondary centre of origin.

It is an important legume crop in eastern, southern, central and western Africa (Emongor, 2007) [4]. It is a highly nutritious legume crop (Kay, 1979) [8]. The seeds contain small amounts of β -carotene (precursor of vitamin A), thiamine, riboflavin, niacin, folic acid and ascorbic acid (Kay, 1979; Tindall, 1983) [8, 17]. It is a major source of inexpensive protein in human diets with grains containing about 23–25% protein (Bressani, 1985; Gupta 1988) [2], 1.8% fat and 60.3% carbohydrates and it is a rich source of calcium and iron (Gupta, 1988). Cowpea leaves and immature pods are also consumed as a green vegetable (Singh *et al.* 2002) [16].

Materials and Methods

The present investigation was carried out at Research and Education Farm, College of Agriculture, Dapoli, Dist. Ratnagiri during the period *rabi* season of 2019-20. The experiment was conducted in Randomized Block Design with two replications. The seed was dibbled at 30 cm X 20 cm distance. Each plot had 2.0 m \times 1.5 m area with 5 rows per genotypes. Each row contains 10 plants thus there were 50 plants per population, constitute 100 plants in two replications. The total fertilizer dose applied @ 25 Kg N: 50 Kg P₂O₅ per hectare. Out of which half dose of nitrogen in the form of urea was applied at the time of sowing and remaining dose nitrogen was applied one month after sowing. An recommended package of practices were carried out as and when required so as to maintain good stand of crop as per the standard recommendations.

Analysis of variance was performed following the standard procedure given by Panse and Sukhatme (1967) [13]. The phenotypic and genotypic coefficients of variation (PCV, GCV) were computed as per method described by Burton and Devane (1953) [3]. Heritability in broad sense estimated for various character by the formulae suggested by Lush (1949) [10] and genetic advance was calculated in percent by the formula suggested by Johnson *et al.* (1955) [7].

Result and Discussion

Analysis of variance

The mean sum of square due to genotypes was found significant for all the fourteen quantitative characters under study. Significant variation was observed among the genotypes for all the characters under study. The genotypic and error mean sum of squares were further used for analysis of genotypic and phenotypic variances.

Mean performance of genotypes

Mean performance of various genotypes exhibited wide range of variation for most of the traits studied. But some traits showed more variation like as iron content (25.10 to 157.52 ppm), plant height at maturity (19.21 to 46.79 cm) and seed yield per plant (20.98 to 37.54 g) indicates sufficient variation among the genotypes for the above traits. The genotypes IC-614758 followed by AKP-1264 and PGCP-27 were observed as best performance in the all genotypes studied. These had highest seed yield per plant and also maximum yield attributing characters. The genotype CPD-31 had maximum seed weight; CP-13 had maximum number of seed per pod, while CP-25 had the maximum number of pods per plant. The genotype Phule vithai had highest protein content, CPD-219 had highest iron content and CPD-220 had minimum plant height. The genotype Konkan sadabahar had early maturing.

Phenotypic and Genotypic coefficient of variations (PCV and GCV)

The estimates of genetic parameters are given in table 2. The genotypic coefficients of variation for all characters studied were lesser than phenotypic coefficient of variation indicating masking effects of environment. The highest phenotypic coefficient of variability was recorded for iron content (36.18%), plant height at maturity (24.72%), number of primary branches per plant (23.14%). The highest genotypic coefficient of variability was recorded for iron content (36.17%), plant height at maturity (24.57%), number of branches per plant (19.83%) and seed yield per plant (16.22%). Similar results were found by Sharma *et al.* (2017) [15], Joghthane *et al.* (2017) [6], Mohammad *et al.* (2019) and Shanko *et al.* (2014) [14].

Heritability and Genetic advance

Heritability in broad sense ranged from 68.11 per cent for number of seeds per pod to 99.93 per cent for iron content. High heritability recorded by the character *viz.*, iron content (99.93%), dry matter yield per plant (98.90%), plant height at maturity (98.12%), seed yield per plant (97.40%), days to initiation of flowering (96.2%), days to 50% flowering (95.51%) as compared to other characters.

The minimum heritability was recorded by the character number of seeds per pod (68.11%), pod length (71.51%), hundred seed weight (71.95%) and number of primary branches per plant (73.45%). Similar results were reported Sharma *et al.* (2017) [15], Joghthane *et al.* (2017) [6], Innuwa *et al.* (2012) [15] for these characters.

The genetic advance was from 1.19 to 68.90. Iron content (68.90) showed the highest estimate of genetic advance where minimum magnitude of genetic advance was observed in characters number of branches per plant (1.19) followed by hundred seed weight (1.86), number of pods per plant (2.41), pod length (2.49), protein content (3.40), harvest index (5.70), days to initiation of flowering (8.01) and days to 50% flowering (9.06). The moderate estimates of genetic advance were recorded by characters *viz.*, plant height at maturity (14.98), days to maturity (14.64) and dry matter yield per plant (16.03). High genetic advance as per cent of mean was recorded in pod length and seed yield per plant by Khan *et al.* (2015) [9]. High genetic advance as per cent of mean was recorded in plant height at maturity and days to maturity by Shanko *et al.* (2014) [14].

Conclusion

The analysis of variance revealed significant variation among the lines for all the characters studied. In general, phenotypic coefficient of variation was higher in magnitude over the respective genotypic coefficient of variation for all the characters. High estimates PCV and GCV were observed in iron content and plant height at maturity.

Table 1: Analysis of variance for 14 quantitative characters.

Sr. No	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to initiation of flowering	0.1127	32.0996**	0.6214
2.	Days to 50% flowering	0.6269	41.4862**	0.9533
3.	Days to maturity	0.0517	103.9773**	0.9877
4.	Number of primary branches per plant	0.2469	1.0775**	0.1649
5.	Number of pods per plant	0.1409	4.2114**	0.5854
6.	Pod length (cm)	0.0126	4.9186**	0.8169
7.	Number of seed per pod	0.0001	3.3877**	0.6426
8.	Plant height at maturity (cm)	0.1046	107.6114**	0.6218
9.	Hundred seed weight (g)	0.2458	2.7183**	0.4435
10.	Seed yield per plant (g)	0.3783	40.7169**	0.5352
11.	Dry matter yield per plant (g)	0.0169	123.2447**	0.6814
12.	Harvest index (%)	0.2265	19.1306**	1.3880
13.	Protein content (%)	0.1854	7.7966**	0.8981
14.	Iron content (ppm)	0.5184	2239.87**	0.7382

Table 2: Estimates of genetic parameters for 14 quantitative characters in cowpea.

Sr No.	Characters	PCV (%)	GCV (%)	ECV (%)	H ² bs (%)	GA	GAM (%)
1.	Days to initiation of flowering	8.05	7.90	1.57	96.2	8.01	15.96
2.	Days to 50% flowering	7.62	7.44	1.61	95.51	9.06	14.99
3.	Days to maturity	8.67	8.59	1.19	98.12	14.64	17.54
4.	Number of primary branches per plant	23.14	19.83	11.92	73.45	1.19	35.01
5.	Number of pods per plant	7.87	6.84	3.89	75.59	2.41	12.26
6.	Pod length (cm)	12.86	10.88	6.86	71.51	2.49	18.95
7.	Number of seeds per pod	12.37	10.21	6.98	68.11	1.99	17.35
8.	Plant height at maturity (cm)	24.72	24.57	2.65	98.85	14.98	50.34
9.	Hundred seed weight (gm)	9.92	8.41	5.25	71.95	1.86	14.70
10.	Seed yield per plant (g)	16.43	16.22	2.64	97.40	9.11	32.98
11.	Dry matter yield per plant (g)	10.07	10.01	1.05	98.90	16.03	20.52
12.	Harvest index (%)	9.46	8.80	3.48	86.47	5.70	16.86
13.	Protein content (%)	10.82	9.64	4.92	79.34	3.40	17.69
14.	Iron content (ppm)	36.18	36.17	0.92	99.93	68.90	74.49

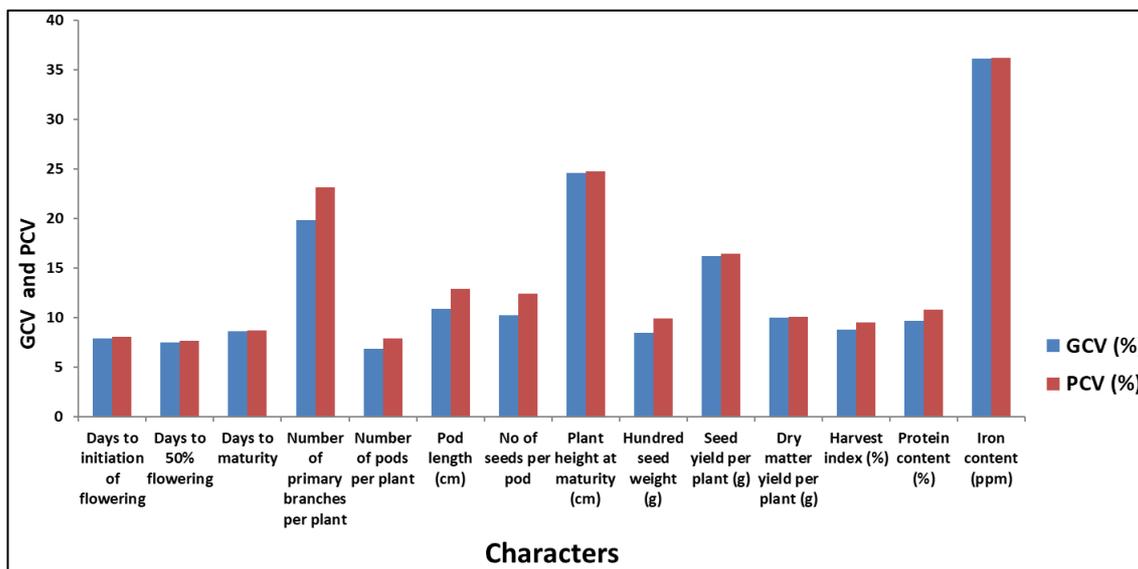


Fig 1: Genotypic and phenotypic coefficient of variation for yield contributing characters

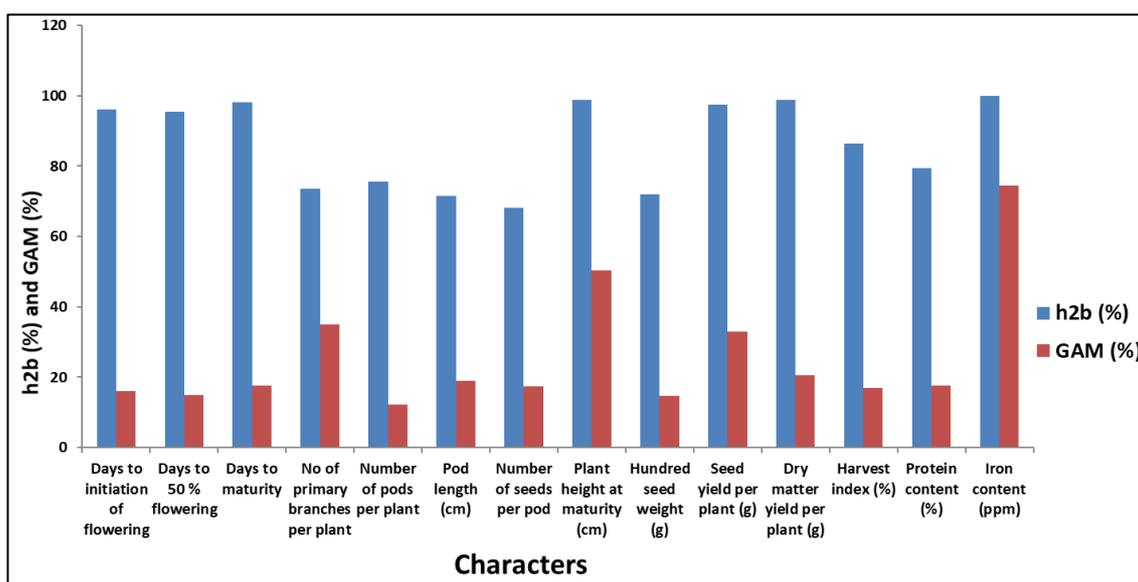


Fig 2: Heritability and genetic advance as percentage of mean for yield contributing characters in cowpea

References

- Anonymous. FAO, FAOSTAT. Food and Agriculture Organization of the United Nations, Rome, Italy 2017.
- Bressani R. Nutritive value of cowpea. In: Singh SR, Rachie KO (eds), Cowpea research, production and utilisation. Chichester: John Wiley and Sons 1985, 353-359.
- Burton GW, De Vane EH. Estimating heritability in tall Fesche (*Festuca arundinaceae*) from replicated clonal material. Agron. J 1953;45:478-481.
- Emongor V. Gibberellic acid (GA3) influence on vegetative growth, nodulation and yield of cowpea (*Vigna unguiculata* (L.) Walp.). Journal of Agronomy 2007;6:509-517.
- Inuwa AH, Ajeigbe HA, Muhammed SG, Mustapha Y. Genetic variability and heritability of some selected cowpea [*Vigna unguiculata* (L.) Walp.] lines 2012.
- Jogdhande S, Kale VS, Nagre PK. Correlation and Path Analysis Study in Cowpea [*Vigna unguiculata* (L.) Walp.] Genotypes. Int. J. Curr. Microbiol. App. Sci 2017;6(6):3305-3313.
- Johnson HW, Robinson HF, Comstock PE. Estimate of genetic and environmental variability in soybeans. Agron J 1955;47:314-318.
- Kay DE. Food legumes. London: Tropical Development and Research Institute 1979.
- Khan Hasan KP, Vishwanatha, Sowmya HC. Study of genetic variability parameters in cowpea (*Vigna unguiculata* (L.) Walp.) germplasm lines. The Bioscan, international quarterly journal of life science 2015;10(2):747-750.
- Lush JC. Heritability of quantitative characters in farm animals. Proceeding of 8th Congress Hereditas 1949;28:356-375.
- Mohammed A, Fikre A. Correlation and path coefficient analysis among seed yield and yield related traits of Ethiopian chickpea (*Cicer arietinum* L.) landraces. Acta agriculturae Slovenica 2018, 111-3.
- Musvosvi C. Morphological characterisation and interrelationships among descriptors in some cowpea genotypes. J. Afri. Crop Sci 2009;9:501-507.
- Panse VG, PV Sukhatme. Statistical method for agricultural workers, 4th Edn., ICAR, New Delhi 1985.

14. Shanko D, Andargie M, Zelleke H. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.) Res. in Pl. Bio 2014;4(2):21-26.
15. Sharma M, Sharma PP, Hemlata Sharma, Meghawal DV. Genetic variability in cowpea (*Vigna unguiculata* L. Walp.) germplasm lines. Journal of pharmacognosy and phytochemistry 2017;6(4):1384-1387.
16. Singh BB, Ehlers JD, Sharma B, Freire -filho FR. Recent progress in cowpea breeding: In: Fatokun CA, Tarawali SA, Singh BB, Kormawa PM, Tamo M (eds), Challenges and opportunities for enhancing sustainable cowpea production. Ibadan: International Institute of Tropical Agriculture 2002, pp 22-40.
17. Tindall HD. Vegetables in the tropics. London: Macmillan Press 1983.
18. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Ed. K. S. Tranil, chester, Roland Press Company, New York 1995.