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Assesment of genetic of coefficient (PCV, GCV), heritability and genetic advance for leaf yield and its component characters of Chench (*Corchorus acutangulus* Lam.)

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Abstract

Investigation was comprised of 46 chench (*Corchorus acutangulus* Lam.) indigenous genotypes exhibited wide spectrum of variation for various agronomic and morphological characters collected from three agroclimatic zones of Chhattisgarh India. The experiment was laid out in Randomized Complete Block Design (RBCD) with three replication during Kharif 2015 at Horticultural Instructional and Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) to identify diverse genotypes. The genotypes were employed for the assessment of genetic variability, heritability and genetic advance for analysis. Variance revealed that sufficient genetic variation has been created for seed yield and its attribute for taking different biometrical analyses. Relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. The analysis of variance revealed that the high genotypic and phenotypic coefficient of variation was recorded for Number of branches plant, fresh weight of plant, dry weight of plant. High heritability coupled with high genetic advance was observed for number of branches per plant, test weight, yield kg per plot, petiole length, plant height, fresh weight of leaves, days to 50 % flowering, dry matter %, root weight, leaf width, duration of the crop, leaf stem ratio and internodal length the lesser influence of environment in expression of these traits and prevalence of additive gene action in their inheritance hence, amenable of simple selection.

Keywords: Chench, GCV, PCV, heritability, genetic advance

Introduction

Leafy vegetable not only provide food quantity but also make significant contribution to the population nutrition throughout the year. In India, the leaves of a large number of wild and cultivated plants are used as leafy vegetables. Green leafy vegetables are rich source of vitamins such as beta carotene, ascorbic acid, folic acid and riboflavin as well as minerals such as iron, calcium and phosphorous. They also contain an immense variety of bioactive non-nutritive health promoting compounds such as antioxidants and phytochemicals, which provide health benefits beyond basic nutrition.

Chench (*Corchorus acutangulus* Lam.) is one of the unexploited and underutilized leafy vegetable and also know as vegetable jute in India. In Chhattisgarh, it is popularly known as Chench Bhaji and belongs to the family Tiliaceae. Chench is an annual herb, green leaves along with tender petiole and soft stem from a wide range of plants are consumed as a leafy vegetable. The 100 g of fresh edible portion of chench bhaji contain is water (81.4 g), energy (58 kcal), protein (5.1 g), fat (1.1 g), carbohydrate (8.1 g), fibre (1.6 g), Ca (241 mg), P (83 mg), Fe (7.2 mg) and ascorbic acid (80 mg) (Gopalan *et al*., 2004) [5]. The bitterness in Corchorus Leaves is due to Corchorin Glycosides. Green leafy vegetables are good source of folic acid and antioxidant properties. The roots and leaves are said to cure gonorrhea and urethral discharge the seeds are stomachic and used in pneumonia. The plant is said to possess anticancer antipyretic, anticonvulsant, stomachic and digitalis glycoside like action whereas, leaves and arial parts of *Corchorus acutangulus* Lam. possess antibacterial potential (Patel, 2011) [12]. Moreover, Corchorus is known to contain high levels of iron and folate which are useful for the prevention of anaemia (Steyn *et al*., 2001) [21].

The characters for which variability is present should be highly heritable for the success of crop improvement programme as progress due to selection depends on heritability,

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selection intensity and genetic advance of the character. Heritability and genetic advance estimates for different targeted traits help to apply appropriate breeding methodology in the crop improvement programme.

Biometrical techniques are useful to the plant breeder in the assessment of genetic variability present in a population by range, variance, standard deviation, coefficient of variation analysis measure the mutual relationship between various plant characters and determine the component characters on which selection can be based for genetic improvement in yield and other characters. Path coefficient, measure the direct and indirect contribution of independent variables on dependent variables. PCA is a technique which identifies plant traits that contribute most of the observed variation within a group of genotypes. The tool has a practical application in the selection of parent lines for breeding purposes.

Material and Methods

The experimental material for the study comprised of 46 genotypes collected from three agroclimatic zones of Chhattisgarh and laid in Randomized Complete Block Design (RBCD) with three replications at the Horticultural Instructional and Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) lies between 21°16’ N latitude and 81°36’ E longitude with an altitude of 289.56 meters above the mean sea level. The experiment was conducted during Rabi season 2015-16. The soil properties like organic carbon (%) 0.60, Available N (kg ha^{-1}) 275.00, Available P (kg ha-1) 16.75 and Available K (kg ha^{-1}) 303.00 Soil Reaction pH 7.09 and Electrical conductivity (n mh cm^{-1}) 0.19 was observed in the site of experiment. The seeds were sown in 20 cm apart between rows and 15 cm within the row. Standard agronomic practices and plant protection measures were taken as per schedule. Test weight was recorded before sowing of crop. The following genetic parameters were estimated for the character having significant mean square due to the germplasm.

Estimation of genetic parameter of variation

1. Mean

Mean of the character was estimated by summing up of all the observation and dividing the sum by the number of observation.

$$\overline{X} = \frac{Xi}{N}$$

Where,

ΣXi = Summation of all the observation,

N = Number of observations

2. Range

Range is the differences between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotype.

Estimation of heritability

Heritability in broad sense (h^2 bs) defined as the proportion of the genotypic variance to the total variance (phenotypic) was calculated as per the formula suggested by Burton and De Vane (1953) [4].

$$h^2bs\ \% = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Where,

h^2 (bs) = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The broad sense heritability estimates were classified as low (<50%), moderate (50-70%) and high (<70%) as suggested by Robinson (1966) [15].

Estimation of coefficients of variation

The coefficient of variation for different characters was estimated by formula as suggested by Burton (1952) [3].

$$PCV\ (\%) = \frac{\sqrt{\sigma 2p}}{\overline{X}} \times 100$$

$$GCV\ (\%) = \frac{\sqrt{\sigma 2g}}{\overline{X}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Mean of character

$\sqrt{\sigma 2g}$ = Genotypic variance

$\sqrt{\sigma 2p}$ = Phenotypic variance

The estimates of genotypic and phenotypic coefficient of variance were classified as low (less than 10 %), moderate (10 to 20%) and high (more than 20 %) as suggested by Sivasubramanium and Madhavamenon (1973) [20].

Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The expected advance was calculated by the formula given by Johnson *et al.* (1955) [6] as described below.

$$GA = K.h^2.\sigma_p$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having value of 2.06 at 5% level of selection intensity.

h^2 = Heritability of the character

σ_p = Phenotypic Standard deviation

The genetic advance as percentage of mean was estimated as per the below formula

$$\text{Genetic advance as percent of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

The magnitude of genetic advance as percent of mean was categorized as high (more than 20%), moderate (20-10%) and low (less than10%).

Result and Discussion

Variability is a pre requisite for any breeding programme aimed at improving the yield and other characters. Thus, it is imperative to have information on both genotypic and phenotypic coefficients of variation. The information on phenotypic coefficient of variation and heritability are help full in prediction of the possible genetic advance by selection of genotypes for a character. Looking to the importance variability parameters *viz*., GCV, PCV, Heritability and Genetic Gain were studied.

The analysis of variance indicated that the mean sum of square due to genotypes were highly significant for all the studied characters. Significant mean sum of squares due to leaf yield and attributing characters revealed existence of considerable variability in material studied for improvement of various traits.

The highest leaf yield quintal per hectare was recorded in genotype IGCB-2013-23 (55.42 q/ha) followed by IGCB-2015-9 (53.58 q/ha) and IGCB-2015-14 (52.58 q/ha). Maximum number of leaves per plant recorded in genotype IGCB-2015-13 (18.23) followed by IGCB-2015-15 (18.03) and IGCB-2015-14 (17.80). Highest number of branches per plant recorded in genotypes IGCB-2015-9 (14.90) followed by ICGB-2015-14 (14.00) and IGCB-2015-33 (13.47). Maximum plant height was recorded in the genotype IGCB-2015-8 (42.82 cm) followed by IGCB-2015-14 (41.59 cm), IGCB-2013-23 (40.59 cm) and IGCB-2015-2 (39.85 cm.).

Maximum internodal length is recorded in IGCB-2015-1 (1.67 cm) followed by ICGB-2015-12 (1.65) and IGCB-2015-10 (1.61 cm). Maximum fresh weight recorded in genotypes IGCB-2015-10 (12.37 g) followed by IGCB-2015-9 (11.61) and IGCB-2015-8 (10.96). Highest harvest index recorded in genotypes genotype IGCB-2013-16 (52.58 %) followed by IGCB-2013-6 (48.53 %) and IGCB-2015-19 (45.28 %). Maximum leaf stem ratio recorded in genotypes IGCB-2013-8 (1.31) followed by IGCB-2013-8 (1.04) and IGCB-2013-6 (0.78). Maximum fiber content recorded in genotypes IGCB-2013-19 (12.01 %) followed by IGCB-2015-21 (11.58 %) and IGCB-2015-7 (11.50 %). Maximum root length is recorded in IGCB-2013-15 (18.68 cm) followed by IGCB-2013-16 (16.58 cm) and IGCB-2013-20 (14.95 cm). Maximum dry matter % recorded in genotypes IGCB-2015-9 (40.48 %) followed by IGCB-2015-6 (33.18 %) and IGCB-2015-12 (32.80 %). Minimum crop duration was recorded in the genotype IGCB-2015-10 (27.33 days) which was followed by IGCB-2015-11 (29.66 days) and IGCB-2013-25 (29.66 days). Maximum test weight was recorded in IGCB-2013-14 (3.35 g) followed by IGCB-2013-21 (3.32 g) and IGCB-2013-10 (3.26 g).

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Sivasubramanian and Madhavamenon (1973) [20]. Genotypic and phenotypic coefficients of variation of different characters are presented in Table 2. High magnitude of genotypic as well as phenotypic coefficient of variations were recorded for traits viz., Number of branches plant-1 (42.87 and 44.06 %), fresh weight of plant (36.86 and 39.84 %), dry weight of plant (30.28 and 40.43 %), dry matter % (29.40 and 31.95 %), root weight (28.74 and 31.29 %), leaf stem ratio (27.08 and 31.32 %), petiole length (26.22 and 28.20 %) and leaf width (25.42 and 28.59 %), suggested the substantial improvement on chench through selection for these traits. Moderate GCV and PCV were recorded for yield kg per plot (18.77 and 19.59 %), leaf length (15.36 and 18.88 %), test weight (14.81 and 15.30 %), root length (14.11 and 17.34 %), plant height (14.06 and 14.79 %), stem girth (13.09 and 18.26 %), harvest index (12.02 and 20.01 %), duration of the crop (11.75 and 13.09%), fiber content (10.91 and 13.58%), number of leaves per plant (10.14 and 13.60 %) and internodal length (10.06 and 11.68 %). Suggested existence of considerable variability in the population. Selection for these traits may also be given the importance for improvement programme. Characters like Stem girth (8.89 and 9.63 %) had low genotypic and phenotypic coefficient of variation. Similar findings were also reported earlier by Varalakshmi and Reddy (1994) [22], Revanappa and Madalgeri (1998) [14], Anuja and Mohideen (2007a) [1] and Venkatesh *et al*. (2014b) [24].

In the present investigation high magnitude of heritability was recorded for most of characters. The highest heritability was recorded for the characters number of branches per plant (94.65 %), test weight (93.67 %), yield kg per plot (91.76 %), plant height (90.42 %), petiole length (86.48 %), fresh weight of plant (85.57 %), days to 50 % flowering (85.11 %), dry matter % (84.67 %), root weight (84.39 %), duration of the crop (80.57 %), leaf width (79.05. %), leaf stem ratio (74.75 %) and internodal length (74.16 %).

Table 1: Analysis of variance for leaf yield and its component characters in Chench

S. No.	Characters	Mean sum of square		
		Replication	**Treatment**	**Error**
	(df)	**2**	**45**	**90**
1	Plant height	2.096	63.782**	2.176
2	No. of leaves per plant	3.162	9.519**	2.005
3	Leaf length	0.938	2.506**	0.365
4	Leaf width	0.269	1.252**	0.102
5	Petiole length	0.148	1.306**	0.065
6	Stem girth	0.02	0.227**	0.055
7	No. of branches per plant	2.02	40.230**	0.745
8	Root weight	0.04	0.318**	0.018
9	Root length	0.733	10.623**	1.543
10	Fresh weight of plant	0.796	18.236**	0.97
11	Dry weight of plant	0.119	0.454**	0.094
12	Internodal length	0.003	0.065**	0.007
13	Dry matter %	3.372	86.533**	4.925
14	Days to 50% flowering	3.855	88.885**	4.9
15	Duration of the crop	15.283	60.646**	4.512
16	Harvest index	4.298	89.634**	33.287
17	Leaf stem ratio	0.003	0.083**	0.008
18	Fiber content	1.185	3.940**	0.61
19	Test weight	1.01	0.494**	0.011
20	Yield kg/plot	0.006	0.260**	0.008

* Significant at 5%, **significant at 1%

Genetic advance as percentage of mean was observed high for Number of branches plant-1 (85.91%), fresh weight of plant (70.23 %), dry matter % (55.72 %), root weight (54.39 %), petiole length (50.23 %), leaf stem ratio (48.23 %), dry weight of plant (46.73 %), leaf width (46.55 %), yield kg per plot (37.04 %), test weight (29.52 %), plant height (27.54 %), leaf length (25.75 %), root length (23.66 %), duration of the crop (21.73 %). Stem girth (19.32 %), fiber content (18.07 %), internodal length (17.85 %), days to 50 % flowering (16.90 %), and number of leaves per plant (15.57 %) and harvest index (14.87) showed moderate genetic advance as percentage of mean.

The estimate of heritability alone is not very much useful on predicting resultant effect for selecting the best individual because it includes the effect of both additive gene as well as non-additive gene.

Table 2: Genetic parameter of variability for leaf yield and its component character in Chench

S. No.	Characters	Mean	Range		Coefficient of variation %		Heritability	GA	GA as percent of mean
			Min^{m}	Max^{m}	GCV	PCV	(h^{2}%)		
1	Plant height (cm)	32.1	21.23	42.82	14.06	14.79	90.42	8.88	27.54
2	Number of leaves plant^{-1}	15.6	10.67	18.03	10.14	13.61	55.54	2.43	15.57
3	Leaf length (cm)	5.53	3.65	8.39	15.36	18.88	66.19	1.42	25.75
4	Leaf width (cm)	2.39	1.38	5.47	25.42	28.59	79.05	1.13	46.55
5	Petiole length (cm)	2.45	1.33	5.7	26.22	28.2	86.48	1.23	50.23
6	Stem girth (cm)	1.83	1.5	2.65	13.09	18.26	51.34	0.35	19.32
7	Number of branches plant^{-1}	8.46	2.57	14.9	42.87	44.06	94.65	7.27	85.91
8	Root weight (g)	1.09	0.41	1.53	28.74	31.29	84.39	0.6	54.39
9	Root length (cm)	12.32	9.68	18.68	14.11	17.34	66.23	2.92	23.66
10	Fresh weight of plant (g)	6.5	1.96	12.37	36.86	39.84	85.57	4.57	70.23
11	Dry weight of plant (g)	1.14	1.08	1.65	30.28	40.43	56.11	0.53	46.73
12	Internodal length (cm)	1.38	1.08	1.65	10.06	11.68	74.16	0.25	17.85
13	Dry matter %	17.74	0.33	2.04	29.4	31.95	84.67	9.89	55.72
14	Days to 50% flowering	59.51	44	66.67	8.89	9.64	85.11	10.06	16.9
15	Duration of the crop	36.81	27.33	2.22	11.75	13.09	80.57	8	21.73
16	Harvest index	36.06	28.17	48.53	12.02	20.01	36.07	5.36	14.87
17	Leaf stem ratio	0.58	0.37	1.31	27.08	31.32	74.75	0.28	48.23
18	Fiber content	9.65	7.18	12.01	10.92	13.59	64.54	1.74	18.07
19	Test weight	2.71	1.63	3.35	14.81	15.3	93.67	0.8	29.52
20	Yield kg per plot	1.54	1.08	46	18.77	19.59	91.76	0.57	37.04

High genetic advance only occurs due to additive gene action (Panse and Shukhatme 1967) [11]. So heritability coupled with genetic advance would be more useful than heritability alone.

Heritability estimates along with genetic advance are more useful than the heritability value alone for selecting the best individual. High heritability coupled with high genetic advance was observed for number branches per plant, test weight, yield kg per plot, plant height, petiole length, fresh weight of plant, days to 50 % flowering, dry matter %, root weight, duration of the crop, leaf width, leaf stem ratio, and internodal length indicating that most likely the heritability is due to additive gene effects and selection may be effective. Therefore, selection based on phenotypic performance of these traits would be effective to select desirable plant type. Similar results were also reported Varalakshmi and Reddy (1994) [22], Rani and Veeragavathathan (2003) [13], Shukla et al. (2005) [16, 18], Anuja and Mohideen (2007a) [1] and Pan *et al*. (2008) [10]. Rest of the traits showed moderate to low heritability estimates coupled with moderate to low genetic advance as percentage mean indicated the role of non additive genetic variance in their expression.

Using the variability parameters we can identify the characters having high response to selection whether it has any economic importance or not. Plant breeders are mainly interested in characters having economic importance. If these characters have less variability, improvement through direct selection is difficult. These characters can be improved by indirect selection. For indirect selection, identification of component character is essential. The genotypic and phenotypic correlation coefficients are helpful in identification of such characters.

Conclusion

From the present study, it can conclude that, there is adequate genetic variability present in the material studied. The analysis of variance showed that considerable variability existed among the genotypes for most of the traits showing possibilities of further genetic improvement, in chench. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for traits *viz*., Number of branches plant^{-1} and fresh weight of plant indicating that these characters could be used as selection for crop improvement. Higher heritability estimates coupled with high genetic advance as percent of mean were observed for branches per plant, test weight, yield kg per plot, petiole length, plant height, fresh weight of leaves, days to 50 % flowering, dry matter %, root weight, leaf width, duration of the crop, leaf stem ratio, and internodal length. Therefore, the results suggest that the Number of branches plant^{-1}, number of leaves per plant and the internodal length are important yield contributing traits and selection based on these traits would be most effective.

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Reference

1. Anuja S, Mohideen MK. a. Variability, heritability and genetic advance studies in amaranthus (Amaranthus spp.). The Asian Journal of Horticulture. 2007; 2(1):63.
2. Anuja S, Mohideen MK. b. Genetic diversity for green yield characteristics in vegetable amaranthus (Amaranthus spp.), The Asian Journal of Horticulture. 2007; 2(1):158-160.
3. Burton GW. Quantitative inheritance in grases. Proc. 6th Int. Grassland Cong. 1952; 1:227-283.
4. Burton GW, De Vane EH. Estimating heritability in tall fesue (*Festuca arundinacea*) from replicated clonal material. Agron. J. 1953; 45:418-481.

5. Gopalan. C, Rama Sastri BV, Balasubramanian SC. Nutritive Value of Indian Foods, National Institute of Nutrition, ICMR, Hyderabad, 2004.
6. Johanson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of soybean. Agron. J. 1955; 47:314-318.
7. Kurrey VK, Sharma PK, Dixit A, Ramteke V. Estimation of genetic divergence among chench (*Corchorus acutangulus* L am.) genotypes. International quarterly journal of environmental sciences. 2015; 5:319-323.
8. Mobina P, Jagatpati T. Genetic variability of Amaranthus hybridus in tropical plains of west Bengal. Int. J Pure App. Biosci. 2015; 3(2):389-395.
9. Navangburuka CC, Denton OA. Heritability character association and genetic advance in six agronomic and yield related characters in leaf Corchorus olitorius, International journal of agricultural research. 2012; 7(7):367-375
10. Pan RS, Singh AK, Kumar S, Rai M. Genetic variation and character association in vegetable amaranth (*Amaranthus tricolor* L.). Veg. Sci. 2008; 35(1):81-83.
11. Panse VG, Shukhatme PV. Statistical Methods for agricultural workers. 2nd Edn. ICAR, New Delhi, 1967, 152-157.
12. Patel R. Evaluation of antibacterial activity of methanol extracts of leaves and arial parts of *Corchorus asanas* Linn., International research journal of pharmacy. 2011; 2(5):228-230.
13. Rani AR, Veeraragavathatham D. Genetic variability for green yield in amaranthus. South Indian Hort. 2003; 51(1-6):173-175.
14. Revanappa, Madalgeri BB. Genetic variability studies regarding quantitative and qualitative trait in amaranthus. Karnataka J Agri. Sci. 1998; 11(1):139-142.
15. Robinson HF. Quantitative genetics in relation to breeding on central of mendalism. Ind. J Genet. 1966; 26A:171-187.
16. Shukla S, Bhargava A, Chatterjee A, Srivastava A, Singh SP. a. Genotypic variability in vegetable amaranth (*Amaranthus tricolor* L.) for foliage yield and its contributing traits over successive cuttings and years. Euphytica. 2005; 151:103-110.
17. Shukla S, Bhargava A, Chatterjee A, Srivastava A, Singh SP. Genotypic variability in vegetable amaranth (*Amaranthus tricolor* L.) for foliage yield and its contributing traits over successive cuttings and years. Euphytica. 2006; 151:103-110.
18. Shukla S, Bhargava A, Chatterjee A, Srivastava A, Singh SP. b. Estimates of genetic variability in vegetable amaranth (A. tricolor) over different cuttings, Hort. Sci. (Prague). 2005; 32(2):60-67.
19. Singh AK, Ahmed N, Narayan R, Narayan S, Mufti S. Performance and genetic variability studies of spinach genotypes under Kashmir conditions. Haryana Journal of Horticultural Sciences. 2008; 37(1/2):119-120.
20. Sivasubramanian J, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agric. J. 1973; 12:15-16.
21. Steyn NP, Olivier J, Winter P, Burger S, Nesamvuni S. A survey of wild, green, leafy vegetables and their potential in combating micronutrient deficiencies in rural populations. S Afr J Sci. 2001; 97:276-279.
22. Varalakshmi B, Pratap Reddy VV. Variability, heritability and correlation studies in vegetable amaranth. South Indian Hort. 1994; 42(6):361-364.
23. Venkatesh L, Murthy N, Nehru SD Manjappa. b. Genetic variability, heritability and genetic advance in grain amaranth (Amaranthus spp.), Asian Journal of Bio Science. 2014; 9(1):67-70.