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Genetic analysis of root traits in response to phosphorous uptake under deficient and sufficient conditions in *Vigna* and *Phaseolus* species

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Abstract
Fourteen morphological traits were used to identify superior genotypes among eight *Vigna* and one *Phaseolus* species based on normal and deficient Phosphorous conditions on vermiculite with 2 replications. The species included nine blackgram and mungbean genotypes each, three wild relatives of blackgram and one mungbean, three genotypes of ricebean and five genotypes of cowpea and one genotype of frenchbean. In the present study, the analysis of variance for different traits indicated that sufficient variation was present among the genotypes as revealed from significant estimates of mean squares for different characters. In general, the value of genotypic coefficient of variation (GCV) was higher than the phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV). Root dry weight at 45DAS (126.96%), exhibited highest phenotypic coefficient of variation, followed by root dry weight at maturity (126.81%) and Total P uptake at maturity (68.79%), Root dry weight at 45 DAS (126.64%) also showed highest genotypic coefficient of variation, Similarly, the highest environmental coefficient of variation 46.50% was observed for root volume (for 100% P). Highest phenotypic coefficient of variation was recorded for Total P uptake at maturity (78.50%). Shoot dry weight at 45 DAS (76.70%) exhibited highest genotypic coefficient of variation and shoot P uptake exhibited highest environmental coefficient of variation for 50% P. Root dry weight at 45 DAS (99%), root dry weight at maturity (99%), seed yield per plant (99%) and total P uptake at maturity (99%) exhibited high heritability for 100% and plant height, shoot dry weight at 45 DAS exhibited 100% heritability for 50% phosphorous conditions.

Keywords: *Vigna*, *Phaseolus*, phosphorous, vermiculite, coefficient of variation, heritability

Introduction
Phosphorus is present in seed and fruit in large quantities and is essential for the seed formation. It is known to stimulate root growth and is associated with early maturity of crops. Phosphorus (P) is needed in virtually all metabolic processes such as energy transfer, signal transduction, macro-molecular biosynthesis, photosynthesis and respiration. Blackgram or urdbean (*Vigna mungo* (L.) Hepper) and Mungbean (*Vigna radiata* (L.) Wilczek) are widely cultivated in different seasons in India i.e. in *kharif* (rainy season) as a mixture with cereals, pigeonpea etc. in *rabi* and *zaid* (spring and summer) as a pure culture. Blackgram was originated from Indian subcontinent (Decandolle 1884, Vavilov 1926) [9, 22]. It is believed to have been domesticated from its wild progenitor, *Vigna. mungo* var. *silvestris*. The centre of origin of mungbean lies in India (Chandel and Lester 1991) [8]. *Vigna radiata* var *sublobata* is considered to be the putative progenitor of mungbean. The ricebean (*Vigna umbellata* (Thunb) is native to South-Eastern Asia. Ricebean is used both as cover crop or green manure, food and fodder. In India, it is sown in June-July and harvested in October-November as a *kharif* crop. Frenchbean (*Phaseolus vulgaris* (L.)) is an important legume crop and cultivated in French bean is grown during winter in plains, while it can be grown round the year except winter in hilly regions. The dry seed type varieties of frenchbean are called as "Rajmash" in India. The common bean originated in the new world, principally Central and South America (Kaplan 1981) [12]. Cowpea (*Vigna unguiculata* (L.) Walp) also called as southerpea and blakeyed pea, is well adapted to the tropics. In India it is known as *lobiya*, meaning a pod. Cowpea originated in Africa. Ethiopia, Central Africa, Central and South Africa and West Africa all have been considered as probable centers of domestication as reviewed by Ng and Marechal (1985) [16]. Cowpea (*Vigna unguiculata*) is considered as being more tolerant to phosphorus deficiency than soybean and common bean (Alkama *et al.* 2008) [3]. Phosphorus is an essential component of cell structures, mainly as nucleic acids and phospholipids. It is especially critical in establishing the enzymatic machinery in energy storage and transfer, which in many cases involves membrane processes. Not surprisingly, P deficiency results in a loss in cell integrity.

New crop varieties with improved root traits, able to unlock and absorb P from bound soil P resources may be of additional value for increasing the efficiency of fertilization (Abelson 1999) [1].

The extent of genetic variability and its exploitation, for selection of desirable types is the prime objective of any crop improvement breeding programme. To improve the effectiveness of selection, total variability has to be partitioned into heritable and non-heritable components. Genotypic and phenotypic and environment coefficient of variation, estimates of heritability and expected genetic advance are the genetic parameters which help to predict genetic gain besides indicating the type of gene action. The selection practiced for one character may simultaneously bring change in the other related character. Presence of sufficient genetic diversity is necessary to be present in the base population from which potential parents are to be selected as diverse parent for hybridization. The present study was conducted with the objective to investigate the inheritance of traits related to root system and P absorption at different doses in blackgram, mungbean, ricebean, frenchbean and cowpea, through the evaluation of various genetic parameters of variability.

Materials and Methods

Two experiments were conducted at the N. E. Borlaug Crop Research Centre (G. B. Pant University of Agriculture and Technology, Pantnagar), with two replications. Each experiment was composed of thirty one genotypes of eight *Vigna* and one *Phaseolus* species. The seeds were provided from the N. E. Borlaug Crop Research Centre Pantnagar and Pantnagar Centre of Plant Genetic Resources (PCPGR). The first and second experiment comprised of 620 plants each and conducted entirely into the greenhouse in the pots. The substrate in the pot was nutrient less vermiculite. In the first experiment to facilitate the isolation of roots, vermiculite received 100 per cent P of Hoagland's nutrient solution, while in the second experiment half of i.e. 50 per cent P of Hoagland's nutrient solution was applied. Plants were harvested at the stage of pod setting at 45 days after emergence and at time of maturity. Shoots and roots were separately ground, and P concentration in plant samples was determined by vanadomolybdate yellow colour method as outlined by Jackson (1973) [10]. The intensity of the yellow colour was measured using a spectrophotometer (UIV) at 470 nm. Concentration of P was worked out by referring to standard curve of 0.5, 1, 2, 3, 5, 7, 10, 12, 15, 18 and 20 ppm. The per cent phosphorous was calculated by following formula:

$$\% P = \frac{\text{Graph (ppm)}}{10^3 \times 10^3} \times \frac{\text{Volume of digested sample}}{\text{Weight of sample}} \times \text{Volume made} \times 100$$

Fourteen yield, yield contributing and root morphological characters viz. plant height (cm), root length (cm), lengthiest lateral root length (LLRL) (cm), root volume (mm^3), root collar diameter (mm), root dry weight at 45 DAS (mg), shoot dry weight at 45 DAS (mg), total P uptake at 45 DAS (mg per plant), root dry weight at maturity (mg), shoot dry weight at maturity (mg), seed yield per plant (gm), harvest index, shoot P uptake (mg per plant) and total P uptake (mg per plant) were calculated for each plant.

Mean data of the genotypes were used for estimation of components of variance, heritability in broad sense, genetic advance and genetic advance as per cent of mean. Genotypic coefficient of variance (GCV) and Phenotypic coefficient of variance (PCV) was worked out as per Burton and Devane (1952). Heritability in broad sense (H_b) was estimated as the ratio of genotypic variance to phenotypic variance (Allard 1960) [4]. Genetic advance expressed as per cent of population mean was calculated from the method:

$$\text{Genetic advance of mean (\%)} = \frac{\textit{Genetic advance}}{\textit{General mean population}(Gm)} \times 100$$

The coefficient of variation, heritability in percentage and genetic advance as per cent of mean were categorized as proposed by Sivasubramanian and Menon (1973) [21], Robinson *et al.* (1949) [17] and Johnson *et al.* (1955) [11] respectively.

Results and Discussion

Coefficient of variation

For experiment I (100% P) root dry weight at 45 DAS (126.96%), exhibited highest phenotypic coefficient of variation (Fig 1) followed by root dry weight at maturity (126.81%) , Total P uptake at maturity (68.79%), seed yield per plant (67.00%), total P uptake at 45 DAS (64.90%), shoot P uptake (61.67), root volume (46.50%), shoot dry weight at 45 DAS (44.47), shoot dry weight at maturity (37.93), Lengthiest Lateral Root Length (31.87%), root collar diameter (28.57%), plant height (25.68%) and harvest index (23.26%).

Whereas, root length (10.28%), exhibited moderate phenotypic coefficient of variation. None of the character possesses lowest i.e. between 0 to 10% of phenotypic coefficient of variation.

In relation to genotypic coefficient of variation root dry weight at 45 DAS (126.64%) exhibited highest genotypic coefficient of variation followed by root dry weight at maturity (126.09%) and total P uptake at maturity (68.34%). Root volume exhibited lowest genotypic coefficient of variation (0.71%), followed by root length (9.02%). None of the character possesses moderate i.e. between 10 to 20% of genotypic coefficient of variation.

Similarly, the highest environmental coefficient of variation was observed for root volume (46.50%), followed by shoot P uptake (35.96%) and total P uptake at 45 DAS (24.20%). Moderate environmental coefficient of variation was exhibited by root dry weight at maturity (13.42%) followed by shoot dry weight at maturity (12.91%) and shoot dry weight at 45 DAS.

However lowest environmental coefficient of variation was observed for harvest index (4.41%), followed by root length (4.94%) and seed yield per plant (5.91%) (Table 1).

For experiment II (50% P) highest phenotypic coefficient of variation (Table 2) was recorded for total P uptake at 45 DAS (78.50) followed by total P uptake at maturity (74.82%) and root dry weight at 45 DAS (71.43%).Root length (15.48%) exhibited moderate phenotypic coefficient of variation. Whereas none of the character exhibited lowest i.e. between 0 to 10% of phenotypic coefficient of variation. Highest genotypic coefficient of variation was observed for shoot dry weight at 45 DAS (76.70%) followed by total P uptake at 45 DAS (75.50%) and total P uptake at maturity (74.09%). While it was moderate only in case of root length (15.03%). None of the character possesses lowest i.e. between 0 to 10% of phenotypic coefficient of variation.

Similarly, root to shoot P uptake (25.25%), exhibited highest environmental coefficient of variation followed by shoot dry weight at maturity (21.82%) and total P uptake at 45 DAS

(21.47%). Total P uptake at maturity (10.44%) exhibited moderate environmental coefficient of variation followed root dry weight at maturity (11.59%). While lowest environmental coefficient of variation was observed for plant height (0.76%) followed by lengthiest lateral root length (3.30%) and root length (3.67).

Heritability and genetic advance as percentage of mean value

Estimates of heritability and genetic advance are important to find out the heritable portion of variability and genetic gain likely can be achieved in the next generation. The magnitude of heritability (in broad sense) and genetic advance for different traits varied considerably. For experiment I (100% P) high heritability estimates were observed for root dry weight at 45 DAS (99%), root dry weight at maturity (99%), seed yield per plant (99%) and total P uptake at maturity (99%) followed by lengthiest lateral root length (96%), harvest index (96%) and shoot dry weight at 45 DAS (93%).While, lowest heritability estimates were observed for root volume (00.00%). None of the character showed moderate heritability.

High estimates of genetic advancement as 5% value was recorded for shoot dry weight at maturity (969.1%), followed by shoot dry weight at 45 DAS (496.57%) and root dry weight at maturity (422.27%). Moderate genetic advancement as 5% value was observed in case of plant height (13.13%), whereas root volume (0.00%) showed lowest estimates of genetic advancement as 5% value followed by total P uptake at 45 DAS (0.07%) and harvest index (0.29%).

Genetic advancement as 1% was highest for shoot dry weight at maturity (1242.06%), followed by shoot dry weight at 45 DAS (636.39%) and root dry weight at maturity (541.117%), moderate genetic advancement as 1% was exhibited by plant height (16.83%), while root volume (0.00%) exhibited lowest genetic advancement as 1% followed by total P uptake at 45 DAS (0.09%) and harvest index (0.37%).

However genetic advancement as 5% of mean 5% was maximum for root dry weight at 45 DAS (260.22%), followed by root dry weight at maturity (258.30%) and total P uptake at 45 DAS (115.11%).

Moderate genetic advancement as 1% was exhibited by by root length (16.30%) and root volume (-0.02%) showed minimum genetic advancement as 5% of mean 5% followed by total P uptake at maturity (139.84%).

Root dry weight at 45 DAS (333.49%) exhibited highest genetic advancement as 1% of mean 1% followed by root dry weight at maturity (331.02%) and total P uptake at maturity (179.21%). While root volume (-0.03%) exhibited lowest genetic advancement as 1% of mean 1%. Whereas none of the character exhibited moderate i.e. between 10 to 20% of genetic advancement as 1% of mean 1%.

Expected mean next generation was highest for shoot dry weight at maturity (2372.17%) followed by shoot dry weight at 45 DAS (1077.40%) and root dry weight at maturity (585.76%). Whereas none of the character exhibited moderate expected mean next generation, while total P uptake at 45 DAS (0.14%) exhibited lowest expected mean next generation followed by root volume (0.38%) and shoot P uptake (0.81%) (Table 1).

For experiment II (50% P) high heritability was observed for plant height, shoot dry weight at 45 DAS i.e. 100% followed by lengthiest lateral root length (99%), root volume (99%), root dry weight at 45 DAS (98%), seed yield per plant (98%), total P uptake at maturity (98%), Whereas none of the character exhibited moderate i.e. 30 to 60% and lowest i.e. 0 to 30% heritability.

Shoot dry weight at maturity (990.02%) exhibited maximum value for genetic advancement as 5% followed by shoot dry weight at 45 DAS (502.20%) and root dry weight at maturity (109.41%). Moderate genetic advancement as 5% was recorded for plant height (14.32%). Total P uptake at maturity (0.03%), shoot P uptake (0.18%) and root volume (0.31%), showed lowest estimates of genetic advancement as 5% of mean 5% value.

However genetic advancement as 1% reported maximum in case of shoot dry weight at maturity (1268.76%) followed by soot dry weight at 45 DAS (643.60%) and root dry weight at maturity (140.21%). Moderate genetic advancement as 1% recorded for plant height (18.36%). Total P uptake at maturity (0.04%) showed minimum genetic advancement as 1% followed by shoot P uptake (0.23%) and root volume (0.40%).

Genetic advancement as 5% of mean 5% was recorded highest for shoot dry weight at 45 DAS (157.77%), followed by total P uptake at maturity (151.13%) and total P uptake at 45 DAS (149.60%). Whereas none of the character exhibited moderate i.e. 10 to 20% and lowest i.e. 0 to 10% genetic advancement as 5% of mean 5%.

Genetic advancement as 1% of mean 1% was also highest for shoot dry weight at 45 DAS (202.18%) followed by total P uptake at maturity (193.68%) and total P uptake at 45 DAS (191.72%). while none of the character exhibited moderate i.e. 10 to 20% and lowest i.e. 0 to 10% genetic advancement as 5% of mean 5%.

Shoot dry weight at maturity (1767.07%), Shoot dry weight at 45 DAS (820.52%) and root dry weight at maturity (190.55%) exhibited highest expected mean next generation while lowest recorded in total P uptake at 45 DAS (0.05%) followed by shoot P uptake (0.33%) and root volume (0.56%), While root length (10.02%) exhibited moderate expected mean next generation followed lengthiest lateral root length (12.18%) (Table 2).

Estimation of coefficient of variation at genotypic and phenotypic levels in a population is decisive factor for scope and efficiency of selection of individuals for future breeding programme in crop species. In general, the value of genotypic coefficient of variation (GCV) was higher than the phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV). Katna and Verma (2001) [13] in blackgram also recorded that GCV was generally higher than the corresponding phenotypic coefficient of variation for number of days to 50% flowering, plant height, number of days to maturity, number of pod-bearing branches, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, grain yield and protein content. In contrary to this Azizi *et al.* (2001) [6] in common bean recorded that the phenotypic coefficients of variability were greater than the genotypic ones for seed yield, number of pods per lateral branches and main stem, length of lateral branches and main stem, number of nodes per lateral branches and main stem, 100-seed weight and the number of lateral branches.

The presence of considerable genetic variability in the base material causes better chance of evolving desirable plant types (Sabharwal *et al.* 1995) [18]. Sahu *et al.* (2007) [19] also recorded high GCV and PCV estimates for yield in ricebean as in the present investigation i.e. high GCV (68.00%) and PCV (68.66%) estimates for seed yield per plant. Existence of sufficient variability in a crop is an inevitable requirement for an effective crop improvement. Natarajan and Rathinasamy (1999) [15] also observed high PCV and GCV for seed yield and plant height. This indicated that selection for these

characters in segregating generation for development of elite lines may be directed in desired direction. The variation for these characters can be utilized by breeder in future breeding programes. Arshad *et al.* (2009) [5] also observed a relatively higher heritability and genetic advance estimates in mungbean for plant height and yield per plant confirmed that these traits are governed by additive gene effects to a greater extent.

Sarkar *et al.* (2006) [20] in blackgram also noted high heritability for plant height. Ahamed and Salimath (2002) [2] in blackgram also revealed harvest index and seed yield per plant showed high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) with high heritability indicating their usefulness in the selection programmes and contrary to present results high genetic advance for harvest index and seed yield per plant. Jakkeral *et al.* (2009) in blackgram also reported that root traits like root length, root volume and number of lateral roots contributed to the total P uptake at 45 days after sowing. The results also indicated presence of variability in most of the root morphological traits and few genotypes sustained leaf area at both low and high P availability and an increase in root volume was noticed in low P level. The physiological and genetic analysis of P deficiency highlights the ability of plant to adapt and thrive under phosphate limiting conditions. The difference for lower levels of P was not evident at early growth stages but became prominent as the age of the plant increased. P content was significantly superior at all P levels in the early growth stages. Katna and Verma (2003) [14] also reported that 100-seed weight might be useful in breeding for improved cultivars to be used in intercropping systems.

Table 1: Estimates of genetic parameters for yield, yield contributing traits and root morphological traits for 100% phosphorous

Sl. No.	Character	PCV (%)	GCV (%)	ECV (%)	Heritability (h2) (%)	Genetic advancement 5%	Genetic advancement 1%	Genetic advancement As 5% of mean 5%	Genetic advancement As 1% of mean 1%	Expected mean next generation
	Plant height (cm)	25.68	24.34	8.20	90	13.13	16.83	47.51	60.89	40.70
	Root length (cm)	10.28	9.02	4.94	77	1.45	1.86	16.30	20.89	10.38
	Lengthiest Lateral Root Length (LLRL)	31.87	31.17	6.64	96	4.96	6.36	62.81	80.49	12.87
	Root volume (mm3)	46.50	0.71	46.50	00	0.00	0.00	-0.02	-0.03	0.38
	Root collar diameter (mm)	28.57	26.71	10.15	87	1.16	1.49	51.42	65.90	3.42
	Root dry weight (gm) at 45 DAS	126.96	126.64	9.00	99	170.94	219.07	260.22	333.49	236.63
	Shoot dry weight (gm) at 45 DAS	44.47	42.96	11.48	93	496.57	636.39	85.49	109.57	1077.40
	Total p uptake (mg/plant) at 45 DAS	64.90	60.22	24.20	86	0.07	0.09	115.11	147.52	0.14
	Root dry weight (gm) at maturity	126.81	126.09	13.42	99	422.27	541.117	258.30	331.02	585.76
	Shoot dry weight (gm) at maturity	37.93	35.66	12.91	88	969.18	1242.06	69.08	88.53	2372.17
	Seed Yield per plant	67.00	66.74	5.91	99	4.16	5.33	136.95	175.51	7.20
	Harvest index	23.26	22.84	4.41	96	0.29	0.37	46.20	59.21	0.92
	Shoot P uptake	61.67	51.48	35.96	70	0.38	0.49	88.51	113.43	0.81
	Total p uptake (mg/plant) at maturity	68.79	68.34	7.91	99	3.60	4.62	139.84	179.21	6.186

Table 2: Estimates of genetic parameters for yield, yield contributing traits and root morphological traits for 50% phosphorous

Sl. No.	Character	PCV (%)	GCV (%)	ECV (%)	Heritability (h2) (%)	Genetic advancement 5%	Genetic advancement 1%	Genetic advancement As 5% of mean 5%	Genetic advancement As 1% of mean 1%	Expected mean next generation
1.	Plant height (cm)	26.59	26.58	0.76	100	14.32	18.36	54.73	70.14	40.49
2.	Root length (cm)	15.48	15.03	3.67	94	2.32	2.97	30.09	38.56	10.02
3.	Lengthiest Lateral Root Length (LLRL)	32.93	32.76	3.30	99	4.89	6.27	67.15	86.05	12.18
4.	Root volume (mm3)	61.88	61.70	4.68	99	0.31	0.40	126.75	162.43	0.56
5.	Root collar diameter (mm)	30.75	29.74	7.85	93	1.23	1.57	59.23	75.90	3.30
6.	Root dry weight (gm) at 45	71.43	70.83	9.28	98	46.06	59.03	144.07	185.40	77.90
7.	Shoot dry weight (gm) at 45 DAS	46.82	76.70	4.24	100	502.20	643.60	157.77	202.18	820.52
8.	Total p uptake (mg/plant) at 45 DAS	78.50	75.50	21.47	93	0.03	0.04	149.60	191.72	0.05
9.	Root dry weight (gm) at maturity	67.45	66.44	11.59	97	109.41	140.21	134.84	172.80	190.55
10.	Shoot dry weight (gm) at maturity	68.77	65.22	21.82	90	990.02	1268.76	127.41	163.28	1767.07
11.	Seed Yield per plant	68.66	68.00	9.48	98	2.27	2.91	138.74	177.80	3.90
12.	Harvest index	25.57	24.98	5.44	95	0.33	0.43	50.28	64.44	1.00

13.	Shoot P uptake	63.78	58.57	25.25	84	0.18	0.23	110.80	142.00	0.33
14.	Total p uptake (mg/plant) at maturity	74.82	74.09	10.44	98	0.64	2.10	151.13	193.68	2.73

References

1. Abelson PH. A potential phosphate crisis. Science. 1999; 283(5410):2015.
2. Ahamed ML, Salimath PM. Correlation and path analysis of morpho-physiological traits in blackgram. New Botanist. 2002; 29:103-8.
3. Alkama NE, Bolou BB, Vailh H, Roger L, Ounane JM, Drevon JJ. Genotypic variability in P use efficiency for symbiotic nitrogen fixation is associated with variation in proton efflux in cowpea rhizosphere. Soil Biology and Biochemistry. 2008; 41:1823-24.
4. Allard RW. Principles of Plant Breeding. John Wiley and Sons. Inc. New York, 1960.
5. Arshad M, Aslam M, Irshad M. Genetic variability and character association among morphological traits of mungbean, (*Vigna radiata* (L.) Wilczek) genotypes. Journal of Agricultural Research Lahore. 2009; 47:121-6.
6. Azizi F, Rezai A, Maybodi SM. Genetic and phenotypic variability and factor analysis for morphological traits in genotypes of common bean (*Phaseolus vulgaris* L.). Journal of Science and Technology of Agriculture and Natural Resources. 2001; 5:127-41.
7. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuca cirunclinaceae*) from replicated clonal material. Agronomy Journal. 1953; 45:478-81.
8. Chandel KPS, Lester RN. Origin and evolution of Asiatic *Vigna* species. Golden Jubilee Celebrations Symp. Grain Legumes Proseedings, Feb. 9-11, IARI, New Delhi, Indian Society of Genetics and Plant Breeding, IARI, New Delhi, 1991, 25-45.
9. deCandolle A. Origin of Cultivated Plants, Haffner, New York, 1884, 346.
10. Jackson ML. Soil Chemical Analysis. Prentice Hall of India Private Limited New Delhi, 1973, 38-82.
11. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Journal of Agronomy. 1955; 47:14-318.
12. Kaplan L. What is the origin of common bean. Economic Botany. 1981; 35:240-54.
13. Kanta G, Verma S. Selection criteria for breeding blackgram varieties for hilly conditions of Himachal Pradesh. Himachal Journal of Agricultural Research. 2001; 27:1-6.
14. Katna G, Verma S. Genetic studies in blackgram under intercrop cropping system. National Journal of Plant Improvement. 2003; 5:38-42.
15. Natarajan C, Rathinasamy R. Genetic variability, correlation and path analysis in blackgram. Madras Agricultural Journal. 1999; 86:228-31.
16. Ng NO, Marechal R. Cowpea taxonomy, origin and germplasm, In S.R. Singh and K.O. Rachie (eds.), Cowpea: Reseach, Production and Utilization. John Wiley & Sons. 1985, 11-21.
17. Robinson HF, Comstock RE, Harvey VH. Estimates of heritability and degree of dominance in corn. Agronomy Journal. 1949; 41:353-59.
18. Sabharwal PS, Pahyaja SK, Lodhi GP. Germplasm evaluation for different fodder traits in forage sorghum (*Sorghum bicolour* (L.) Moench). H.A.U. Journal of Agricultural Research. 1995; 26:207-10.
19. Sahu PK, Mishra TK, Singh GS, Mishra CHP, Mishra RC. Genetic diversity, character association and path-coefficient study in rice bean. Environment and Ecology. 2007; 25S(3A):808-12.
20. Sarkar G, Panda S, Senapati BK. Genetic variability and character association in blackgram (*Vigna mungo* (L.) Hepper). Journal of Arid Legumes. 2006; 3:44-46.
21. Shivasubramanain S, Menon M. Heterosis and inbreeding depression in rice. Madras Agricultural Journal. 1973; 60:1139.
22. Vavilov NI. Studies on the origin of cultivated plants. Bulletin of Applied Botany. Leningrad, USSR. 1926, 26.