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Soumya Satpathy
Department of Genetics and Plant Breeding, Institute of Agriculture, Visva-Bharati, Sriniketan, Birbhum, West Bengal, India

Sandip Debnath
Department of Genetics and Plant Breeding, Institute of Agriculture, Visva-Bharati, Sriniketan, Birbhum, West Bengal, India

Corresponding Author:
Soumya Satpathy
Department of Genetics and Plant Breeding, Institute of Agriculture, Visva-Bharati, Sriniketan, Birbhum, West Bengal, India

Genetic analysis of yield and its attributing traits in lentil

Soumya Satpathy and Sandip Debnath

Abstract
Lentil is a potential pulse crop for rice fallows of dry regions of south Asian countries. Yield is a complex character which is believed to be the cumulative effect of several other characters. The field experiment was conducted at Agriculture farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati during two *rabi* seasons of year 2017-18 and 2018-19 with an objective to asses yield and its attributing traits in fifty different lentil genotypes. The genotypes of lentil were tested in randomized block design with three replications. The analysis of variance was carried out for sixteen different traits which exhibited highly significant differences among genotypes for each character under study. Statistical analysis was employed to find out the genetic parameters *viz.* Components of variance i.e. genotypic and phenotypic variance and their coefficient, heritability in broad sense and genetic advance. Grain yield recorded moderate heritability accompanied by low genetic advance. The performance of varieties *viz.* IC-04-07, BLC-173, ILL-10461, LEN-13-13 and BM-1 of lentil were found significantly superior over rest of the varieties with respect to yield as the major criterion.

Keywords: Lentil, GCV, PCV, heritability, genetic advance, yield attributes

Introduction
Lentil (*Lens culinaris* Medik.) is a cool season legume grown widely from Mediterranean region to Middle East in semi-arid climate and marginal environment as a low maintenance crop by virtue of its ability to fix nitrogen biologically through symbiotic association with *Rhizobium* bacteria and water use efficiency. *Rhizobium leguminosarum* bv. viciae is the symbiont of all *Lens* species. Its cultivation is extensive across the dry areas of the world, from Bangladesh in the east to Morocco in the west, and from Russia in the north to Ethiopia in the south. The Lentil is able to utilize residual soil moisture. Accordingly, it plays an important role as a rotation crop, enhances soil fertility and thereby, favors the production system (Materne, 2003) [16]. It can also be used as a green manure crop and fodder. Being a member plant of family Fabaceae it contributes organic nitrogen in the soil for subsequent cereal crops (Herridge and Bergersen, 1988; Zapata, 1990) [10, 26].

Seeds of lentil are rich in dietary proteins (22-25%), minerals (P, K, Zn, and Fe), vitamins, carbohydrates and essential amino acids lysine and tryptophan (Bhatty, 1988; Savage, 1988) [3, 21]. Therefore, this food legume is aptly having enormous potential to confront the problems of nutritional security, poverty and sustainable food systems in changing climate by being a part of cereal based cropping system. Besides providing nutritional security, it plays an important role among low-income Asian households, because of its capacity to address the challenges of hidden hunger. Once contemplated as the food for the poor, its virtues are now globally appreciated as it is a crop very much adapted to the farming systems of marginal lands. If lentils have been maintained by farmers since ages, it is most likely because of their better sustenance in poor soils, rough climates and harsh conditions.

In comparison to other field crops, legume show lower yield and harvest index. Their low productivity is a consequence of their peculiar capability of biological nitrogen fixation as photosynthesis produced by the plant is partly used for its own growth and partly utilized by the symbiont bacteria. Yield of a legume crop is tremendously influenced by several extrinsic and intrinsic factors including plant genotype, native *Rhizobium* population and quality of inoculants as well as the environmental and ecological growing conditions. Yield continues to be the prime target in crop improvement programme and is the outcome of cumulative effect of many contributing traits, collectively known as yield attributing traits. Genetics, being the science of heredity and variation helps to understand how yield attributing traits are being inherited from parents to offspring and influence of variation on those traits. Assessment of yield attributes at genotypic level assists in identification of desirable genotypes for further improvement strategies.

Materials and Methods

Profile of experimental area

The experiment was conducted in the farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, West Bengal. Agriculture farm was situated in geographical coordinates of 23.67°N 87.69°E latitude and longitude, respectively. It was on average elevation of 58 metres (190ft) above mean sea level. Red and lateritic soil stretched across the district of Birbhum, West Bengal. The soil of experimental site was sandy loam in texture with 68.6% sand, 19.9% silt and 11.2% clay. Land was well drained with low level of organic carbon, available Nitrogen (N) and Potash (K_2O) content and medium in phosphorous (P_2O_5). The soil was slightly acidic in reaction with a pH value of 5.9. Table I represents soil properties.

Table I: Composition of Experimental Soil

Particulars	Values
Mechanical analysis (0-15cm depth)	
Sand (%)	68.6
Silt (%)	19.9
Clay (%)	11.2
Chemical analysis	
pH	5.9
Organic carbon (%)	0.3
N (kg/ha)	137
P (kg/ha)	21.12
K (kg/ha)	102.24

Experimental materials

The experimental materials for investigation comprised of fifty genotypes. Their names have been indicated in Table II. Studies on genotypic and phenotypic variability, heritability and genetic advance were made on these genotypes.

Table II: Genotypes under Study

1.	L-46-05	26.	LIF-03-03
2.	LL-147	27.	WBL-77-108
3.	L-14-16-01	28.	BLC-103
4.	BLL-66	29.	BLC-16
5.	BLC-139	30.	LIF-03-11-07
6.	E-28	31.	BLC-180
7.	BLC-97	32.	F-23
8.	BLC-127	33.	BLC-01
9.	IC-05-03	34.	BLC-25
10.	L-94-03	35.	BLC-90
11.	IC-04-07	36.	BLC-58
12.	BLC-18	37.	MOITREE
13.	BLC-138	38.	SUBRATA
14.	BLC-60	39.	ASHA
15.	BLC-32	40.	RANJAN
16.	BLC-98	41.	PUSA AGETI
17.	BLC-88	42.	BM-6
18.	BLC-173	43.	BM-5
19.	BLC-08	44.	ILL-10461
20.	LEN-13-13	45.	BM-7
21.	NDL-01	46.	ILL-8108
22.	LIEN-07-E-32	47.	BM-1
23.	BLC-126	48.	ILL-10-971
24.	LIF-03	49.	BM-4
25.	LIEN-07-E-11	50.	ILL-10893

Details of experiment

The experiment was laid out in randomized complete block design (RCBD) with three replications. The crop was sown during two years in the winter (*Rabi*) seasons of 2017 and 2018 in the month of November in rows with a spacing of 30cm and 10cm between and within the rows, respectively. Seed treatment was done with *Rhizobium* culture before sowing and a basal dose of recommended nutrients were applied at the time of sowing. Other recommended packages of practices were adopted for optimum crop growth. Five competitive plants were selected randomly from each plot for each genotype across all replications and were tagged. The data for sixteen quantitative characters *viz.* days to 50% flowering, days to pod initiation, days to 50% pod maturity, plant height (cm), primary branches per plant, secondary branches per plant, total branches per plant, root length (cm), nodules per plant, pods per plant, seeds per pod, seeds per plant, biomass (g), 100 seed weight (g), harvest index (%) and grain yield/plant (g) were observed and recorded in the two seasons. The mean observations for the five selected plants of different genotypes were taken in each season to get the final data for analysis. The data thus obtained during two growing seasons was pooled and was subjected to statistical analysis using the software Windostat Version 9.2, licensed to Department of Genetics and Plant Breeding, Visva-Bharati.

Results

The result of pooled analysis of variance (ANOVA) of 50 genotypes over two seasons for the 16 characters under study *viz.* days to 50% flowering, days to pod initiation, days to 50% pod maturity, plant height (cm), primary branches/plant, secondary branches/plant, total branches/plant, root length (cm), nodules/plant, pods/plant, seeds/pod, seeds/plant, biomass (g), 100 seed weight (g), harvest index (%) and grain yield/plant (g) have been given in Table III. ANOVA is that statistical tool using which; the total variance was separated into various components. It was observed from the results that estimated variances due to various genotypes for all yield contributing traits were highly significant at probability (P) of 0.01. Also, it was noted that the variances due to season (year) for all concerned characters were highly significant. The error component and replication component of total variance indicated no significant effects through different characters under study.

Range

Variation due to days to 50% flowering ranged from 52.5 to 71.66. Genotype F-23 was earliest to have 50% flowering with mean 52.5, whereas LL-147 was the last to have 50% flowering. The character days to pod initiation varied from 56.25 to 79.66. BLC-126 was the genotype in which pod initiation was earliest and it was late in LL-147. Days to 50% pod maturity recorded a minimum value of 83.25 and a maximum value of 106.66. In BLC-126 50% pod maturity was earliest and it was last to be recorded in LL-147. Plant height (cm) had shown a range from 20.39 to 31.35. BM-4 was the shortest genotype and BLC-173 was the tallest. Primary branches/plant ranged from 1.76 to 2.43. F-23 had least number of primary branches/plant and highest numbers of primary branches/plant were recorded for the genotype LEN-13-13. In secondary branches/plant, variation ranged from 1.42 to 9.80. BLC-58 had least number of secondary branches/plant and highest numbers of secondary branches/plant were recorded for genotype ILL-10461. Total branches/plant ranged from 4.21 to 14.95. BLC-58 has least number of total branches/plant and ILL-10461 had highest number of total branches. Root length was recorded shortest for BM-7 (5.70cm) and longest root was recorded for ILL-10893 (11.15cm). The values for nodules/plant fluctuated

between 2.32 to 8.16. LIEN-07-E-11 had minimum number of nodules/plant where as, BLC-25 shown maximum nodulation/plant. The character pods/plant shown a range from 5.89 to with 43.70. F-23 had minimum pods/plant where as, ILL-10461 had maximum number of pods/plant. The number of seeds/pod had a minimum value of 1.22 whereas, maximum value for this character was recorded to be 1.49. BLC-16 recorded least number of seeds/pod and LIEN-07-E-11 recorded highest number of seeds/pod. Variation due seeds/plant was 8.88 to 47.86. BLC-58 had least number of seeds/plant and highest number of seeds/plant was found in ILL-10461. Biomass per plant (g) ranged from 0.95 to 1.72. F-23 had lowest biomass and biomass was highest for LEN-13-13. 100 seed weight (g) had a range of 1.29 to 1.67. BM-6 had lowest value for this character and NDL-01 had highest value. Harvest index (%) varied from 28.67 to 47.14. BLC-97 had lowest harvest index (HI) and BLC-180 had highest HI. Grain yield/plant (g) had a minimum value of 0.81 and a maximum value of 1.19. Genotype F-23 had lowest grain yield and highest yield was recorded for genotype IC-04-07.

Estimation of genetic parameters

Various genetic parameters as heritability (in broad sense), genetic advance and genetic advance as % mean (at 5% selection intensity) were worked out for each concerned trait under study. Values of grand mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated, that have been presented in Table IV. Grand mean is the mean of means, otherwise known as pooled mean. It gives coefficient of variation when divided with respective standard deviation i.e. square root of variance.

In the present study, the estimates of phenotypic variance for different traits ranged from a lowest value of 0.012 for number of seeds/pod to the highest of 225.088 for number of seeds/plant. Phenotypic coefficient of variation (in percent) was recorded highest for number of secondary branches/plant (69.726) while it was lowest for (6.189) days to 50% pod maturity. PCV was recorded as low less than 10% (<10%) for days to 50% flowering, days to pod initiation, days to 50% pod maturity, seeds/pod and 100 seed weight (g). It had a moderate value (10-20%) for characters, plant height (cm), primary branches, biomass (g), harvest index (%) and grain yield (g). It indicated high magnitude more than 20% (>20%) for secondary branches/plant, total branches/plant, root length (cm), nodules/plant, pods/plant and seeds/plant.

Values of genotypic variance ranged from 0.003 for number of seeds/pod to 70.515 for seeds/plant. Genotypic coefficient of variation (in percent) was highest for number of secondary branches/plant (48.92) and lowest for number of seeds/pod (4.005). A lower magnitude of GCV (<10%) was recorded for days to 50% flowering, days to pod initiation, days to 50% pod maturity, plant height (cm), primary branches, seeds/pod, 100 seed weight (g), harvest index (%) and grain yield (g). A moderate value of GCV between 10 to 20% was observed for characters as root length (cm) and biomass (g). It had a high magnitude i.e. more than 20% (>20%) for secondary branches/plant, total branches/plant, nodules/plant, pods/plant and seeds/plant.

Heritability and genetic advance

In present investigation heritability was recorded highest for days to 50% flowering (91.2%) followed by days to 50% pod maturity (63%), days to pod initiation (62.9%),secondary branches/plant (49.2%), total branches/plant (40.3%), biomass (39.3%),plant height (38.6%), 100 seed weight and harvest index (37.8% each), nodules/plant (36.7%), root length (35.9%), pods/plant (35%), seeds/plant (31.3%), grain yield (30.7%), seeds/pod (25.6%) and primary branches (22.2%).

The magnitude of genetic advance ranged from 4.174 for number of seeds/pod to 70.703 for secondary branches/plant as percentage of mean at 5% selection intensity. Value of genetic advance was low (<10%) for traits as days to 50% pod maturity, primary branches, seeds/pod, 100 seed weight and grain yield. Moderate genetic advance (10-20%) was observed for days to 50% flowering, days to pod initiation, plant height (cm), root length (cm), biomass (g) and harvest index. High genetic advance (above 20%) was recorded for secondary branches, total branches/plant, nodules/plant, pods/plant and seeds/plant.

Table III: Pooled Analysis of Variance (ANOVA) For Sixteen Quantitative Characters

Characters	Source of Variations	Degrees of Freedom	Sum of Squares	Mean Sum Squares	F -Ratio	Probability
Days to 50% Flowering	Genotypes	49	6545.720000	133.586122	63.1534	<0.01***
	Seasons (year)	1	152.653300	152.653300	107.2507	<0.01***
Days to Pod Initiation	Genotypes	49	7467.791921	152.403917	11.1621	<0.01***
	Seasons (year)	1	311.447200	311.447200	16.5112	<0.01***
Days to 50% Pod Maturity	Genotypes	49	7419.490635	151.418176	11.2121	<0.01***
	Seasons (year)	1	325.875100	325.875100	15.6315	<0.01***
Plant Height (cm)	Genotypes	49	1766.332292	36.047598	4.7736	<0.01***
	Seasons (year)	1	388.308400	388.308400	54.0423	<0.01***
Primary Branches/Plant	Genotypes	49	7.161347	0.146150	2.7101	<0.01***
	Seasons (year)	1	0.716385	0.716385	105.0983	<0.01***
Secondary Branches/Plant	Genotypes	49	1013.148537	20.676501	6.8165	<0.01***
	Seasons (year)	1	391.386300	391.386300	579.5502	<0.01***
Total Branches/Plant	Genotypes	49	1371.346080	27.986655	5.0469	<0.01***
	Seasons (year)	1	277.690900	277.690900	351.9373	<0.01***
Root Length (cm)	Genotypes	49	359.721781	7.341261	4.3668	<0.01***
	Seasons (year)	1	26.349960	26.349960	72.3038	<0.01***
Nodules/Plant	Genotypes	49	426.345403	8.700927	4.4740	<0.01***
	Seasons (year)	1	366.042400	366.042400	530.8896	<0.01***
Pods/Plant	Genotypes	49	18247.831049	372.404715	4.2339	<0.01***
	Seasons (year)	1	5491.840000	5491.840000	297.8601	<0.01***
Seeds/Pod	Genotypes	49	1.305670	0.026646	3.0638	<0.01***
	Seasons (year)	1	0.930747	0.930747	188.3720	<0.01***
Seeds/Plant	Genotypes	49	28305.370881	577.660630	3.7371	<0.01***

	Seasons (year)	1	2436.522000	2436.522000	169.4892	<0.01***
Biomass (g)	Genotypes	49	8.679108	0.177125	4.8792	<0.01***
	Seasons (year)	1	2.460696	2.460696	859.6779	<0.01***
100 Seed Weight(g)	Genotypes	49	1.712690	0.034953	4.6509	<0.01***
	Seasons (year)	1	4.902407	4.902407	14886.4300	<0.01***
Harvest Index (%)	Genotypes	49	3436.445137	70.131533	4.6465	<0.01***
	Seasons (year)	1	587.020500	587.020500	104.1663	<0.01***
Grain Yield/ Plant(g)	Genotypes	49	2.253400	0.045988	3.6544	<0.01***
	Seasons (year)	1	0.350892	0.350892	1763.3490	<0.01***

*** The values are significant at P=0.01

Table IV: Grand Mean, Components of Variance, Heritability and Genetic Advance for Sixteen Quantitative Characters

Characters	Grand Mean	Range (Lowest)	Range (Highest)	Genotypic Variance	GCV (%)	Phonotypic Variance	PCV (%)	(%) Heritability (Broad Sense)	Genetic Advance (5%)	Genetic Advance (as % mean)
Days to 50% Flowering	62.926	52.5	71.6667	21.912	7.439	24.027	7.79	91.2	9.209	14.634
Days to Pod Initiation	70.621	56.25	79.6667	23.125	6.809	36.779	8.587	62.9	7.855	11.123
Days to 50% POD Maturity	97.597	83.25	106.6667	22.986	4.912	36.49	6.189	63	7.838	8.031
Plant Height (cm)	25.592	20.39	31.3583	4.749	8.515	12.301	13.704	38.6	2.79	10.9
Primary Branches/Plant	2.070	1.7617	2.4383	0.015	5.988	0.069	12.714	22.2	0.12	5.809
Secondary branches/Plant	3.505	1.4267	9.8067	2.941	48.92	5.974	69.726	49.2	2.478	70.703
Total Branches/Plant	7.328	4.2133	14.9583	3.74	26.392	9.286	41.584	40.3	2.528	34.505
Root Length (cm)	7.828	5.7067	11.1583	0.943	12.406	2.624	20.693	35.9	1.2	15.322
Nodules/Plant	4.0621	2.325	8.1667	1.126	26.123	3.071	43.139	36.7	1.324	32.586
Pods/Plant	17.582	5.8983	43.7083	47.408	39.16	135.365	66.172	35	8.394	47.74
Seeds/Pod	1.365	1.225	1.4933	0.003	4.005	0.012	7.916	25.6	0.057	4.174
Seeds/Plant	23.726	8.885	47.86	70.515	35.393	225.088	63.234	31.3	9.682	40.808
Biomass(g)	1.309	0.9567	1.7233	0.023	11.696	0.06	18.665	39.3	0.198	15.098
100 Seed Weight (g)	1.473	1.2917	1.6733	0.005	4.591	0.012	7.464	37.8	0.086	5.817
Harvest Index (%)	37.489	28.6733	47.1483	9.173	8.079	24.266	13.14	37.8	3.836	10.232
Grain Yield (g)	0.977	0.8167	1.1983	0.006	7.634	0.018	13.785	30.7	0.085	8.71

Discussion

The estimated variances due to various genotypes for all yield contributing traits were highly significant was an indicator of the existence of considerable variability for all concerned characters under study among them. This ensured the fact that genetic variability existed among the experimental materials. Phenotypic variation is the summation of genotypic variation and environmental variation. The variances due to season (year) for all concerned characters were highly significant. This stipulated the role of environment in expression of the characters. This implied that if the concerned fifty genotypes would be examined for same sixteen traits in an environment other than the experimental site, then there may be variation in their performance.

The widely varying ranges of sixteen different characters revealed the presence of extensive variation for those traits under study and implied that, sufficient variability was present among experimental material to be utilized in future improvement programmes. These results were supported by the findings of Chakherchaman *et al.* (2009) [5], Singh *et al.* (2009) [23], Al-Ghzawi *et al.* (2011) [2], Hojjat and Galstayan, (2011) [11], Gupta *et al.* (2012) [9], Mondal *et al.*, (2013) [17] and Idrissi *et al.* (2017) [12].

For each character, GCV was found to be lower than PCV. This suggested that the apparent variation is not only due to the genotypes but also due to the influence of environment. This coincided with findings of Tyagi and Khan (2010) [25], Abdipur *et al.* (2011) [1] and Singh and Srivastava (2013) [24]. Characters that exhibited low magnitude of GCV (<10%) as days to 50% flowering, days to pod initiation, days to 50% pod maturity, plant height (cm), primary branches, seeds/pod, 100 seed weight (g), harvest index (%) and grain yield (g), indicated requirement of selection for several successive generations for their improvement. These findings are in agreement with results obtained by Reddy *et al.* (2016) [20] and Abdipur *et al.* (2011) [1]. The moderate values (10-20%) of GCV for two traits as root length (cm) and biomass (g) and a high magnitude (>20%) for secondary branches/plant, total branches/plant, nodules/plant, pods/plant and seeds/plant was an indicator of less amenability of these traits to environmental fluctuations. Hence, greater emphasis should be given to these characters, while breeding cultivars from the present material. Similar result were earlier observed by Crippa *et al.* (2009) [6], Tyagi and Khan (2010) [25], Abdipur *et al.* (2011) [1], Singh *et al.* (2012) [22], Singh and Srivastava (2013) [24], Gautam *et al.* (2014) [8], Kumar & Solanki (2014) [15] Pandey *et al.* (2015) [18], Kumar and Singh (2017) [14].

Low PCV (<10%) for days to 50% flowering, days to pod initiation, days to 50% pod maturity, seeds/pod and 100 seed weight (g) was previously enumerated by Abdipur *et al.* (2011) [1] and Fikiru *et al.* (2011) [7]. The characters with high PCV indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection program because the environmental variations are unpredictable in nature and may mislead the results. These findings were in agreement with results found by Crippa *et al.* (2009) [6] and Fikiru *et al.* (2011) [7].

Heritability is an indicator of magnitude of transmission of characters from one generation to next and influence of environment on it. It is defined as the ratio of genotypic variance to that of phenotypic variance or total variance. High (more than 80%) to moderately high (more than 60%) heritability for traits like days to 50% flowering, days to 50% pod maturity and days to pod initiation was documented earlier by Biçer and Şakar (2008) [4], Gupta *et al.* (2012) [9], Gautam *et al.* (2014) [8] and Reddy *et al.* (2016) [20]. High broad sense heritability for these characters indicated that they were least influenced by the effects of environment. Selection

of these traits for yield improvement may be rewarding. Moderate heritability for characters (30-60%) as secondary branches/plant, total branches/plant, biomass, plant height, 100 seed weight, harvest index, nodules/plant, root length, pods/plant, seeds/plant and grain yield were supported by the findings of Biçer and Şakar (2008) [4] and Singh *et al.* (2009) [23]. It was an attestation of the dependency of phenotypic expression which reflects the genotypic ability of cultivars to transmit the genes to their off-springs. Characters as primary branches and seeds/pod were documented for low heritability (<30%) and this result was in accord with the findings of Singh *et al*. (2012) [22] and Gautam *et al.* (2014) [8]. It revealed that influence of environment on expression of these traits was high and thus, genetic improvement through selection of these traits would be difficult.

Low genetic advance (<10%) was observed for traits as days to 50% pod maturity, primary branches, seeds/pod, 100 seed weight and grain yield. This result was supported by experiments of Pandey *et al*. (2015) [18] and Ranjithkumar, G. (2018) [19]. High estimates of genetic advance displayed that characters are governed by additive genes. Therefore, selection would be rewarding for improvement of such traits. Such results closely agreed with the findings of Kumar *et al.* (2009) [13], Singh *et al.* (2009) [23], Singh *et al*. (2012) [22], Singh and Srivastava (2013) [24], Gautam *et al.* (2014) [8] and Kumar & Solanki (2014) [15].

Heritability in conjunction with genetic advance provides better information for selecting the best individuals than heritability alone because though high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals.

Low heritability coupled with low genetic advance for two traits i.e. primary branches/plant and seeds/pod indicated that environment had its strong grip on these characters and therefore, selection would be ineffective for them. Characters like plant height, biomass, root length and harvest index exhibited moderate heritability with moderate genetic advance. Whereas, 100 seed weight and grain yield displayed moderate heritability coupled with low genetic advance. Days to 50% flowering shown high heritability with low genetic advance implied that selection for these traits for ultimate yield improvement may not be rewarding. High heritability coupled with moderate genetic advance was observed for days to 50% flowering and days to pod initiation. It indicated that most likely the heritability was due to additive gene effect and selection may be effective for these traits. Similar conclusion can be drawn for traits showing moderate heritability coupled with high genetic advance i.e. secondary branches/plant, total branches/plant, nodules/plant, pods/plant and seeds/plant. These findings were in close agreement with findings of Kumar e*t al.* (2009) [13], Singh *et al.* (2009) [23] and Reddy *et al* (2016) [20].

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