

Full Length Research Paper

Evaluation of genetic variability, heritability, genetic advance and correlation for agronomic and yield components in common bean landraces from South western Kenya

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The present study was conducted to estimate the genetic variability, heritability, genetic advance and association among selected agronomic traits of common bean landraces from South western Kenya. The field experiment was conducted using 52 common bean landraces at the Kenya Agricultural and Livestock Research Organization (KALRO), Kisii Research Center during 2015 and 2016 main cropping seasons. The experimental design was randomized complete block (RCBD) with three replications. Analysis of variance revealed significant differences indicating the existence of genetic variability among the 52 landraces for 14 quantitative traits studied. The genotypic coefficient of variation ranged from 1.00% for biological yield to 84.69% for pod width, while the phenotypic coefficient of variation ranged from 2.34% for biological yield to 84.40% for number of branches. The estimated broad sense heritability ranged from 60.20% for seeds per plant to 87.57% for days to emergence. Estimates of genetic advance as percent of mean ranged from 10.15% for biological yield to 97.45% for number of branches. Positive and highly significant association of plant height, days from planting to 50% flowering, number of pods per plant and biological yield was observed with seed yield per plant, hence these traits may be directly attributed for the improvement of seed yield. High heritability and genetic advance was obtained for plant height, 100 seed weight, pod width and number of branches, indicating additive gene effects in controlling the traits and these traits could be used as suitable criteria for selection and improvement of common bean in breeding programs.

Key words: *Phaseolus vulgaris*, phenotypic variability, genotypic variability, quantitative traits, heritability, genetic advance, breeding.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important grain legume, second to maize as a staple food

crop in Kenya. Africa produces 17% of the world total production, of which 70% is from Eastern Africa. Kenya

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produces 400-1200 kg/ha, mainly from intercropping with maize by small-scale farmers. Common bean is an important source of protein and minerals especially iron and zinc. It is a dual-purpose crop producing grains as well as fodder for livestock. Consumption of beans confers humans with various health benefits including reduction of cholesterol level, reduction of coronary heart diseases and decreases diabetes and obesity (Broughton et al., 2003; Pereira et al., 2015). Common beans also play a very important role in sustaining soil fertility by adding atmospheric nitrogen and organic matter to the soil. As a cover crop it is efficient in suppressing weeds and prevents soil erosion (Geil and Anderson, 2014).

Production of common bean in South western Kenya is constrained by various abiotic and biotic stresses. Diseases caused by fungi, bacteria and viruses are considered to be the second biggest constraint to bean production after low soil fertility, causing over 90% or total crop loss (IBPGR, 1982). Insect pests especially pod borers and weevils may also cause yield loss of up to 80%. In many bean producing areas of Kenya, there is lack of clean seed planting materials and varieties grown are often low yielding (Bennick, 2005). There is also a problem of lack of cultivars with market qualities and consumer quality attributes such as fast cooking. These factors have reduced the germplasm sources used in hybridization and have limited the genetic variability available for breeding programs. Development of high yielding cultivars with resistance to major bean diseases is an important breeding priority to reduce impact of diseases and increase common bean production in South-western Kenya. Characterization of plant germplasm using agronomic traits has been used for various purposes including identification of duplicates, correlation with characteristics of agronomic importance and identification of genotypes resistant to pests and diseases (Smartt, 1988a, b).

The selection of desirable genotypes is usually based on the genetic variation of agronomic or quantitative traits such as yield and its components. It is therefore necessary to study the relationship between genotype variability and yield components for efficient utilization of common bean genetic resources in improvement programs. Heritability is the degree of genetic control associated with certain heritable important traits (Addissu, 2011). It indicates how much of the genetic variability has a genetic origin and gives necessary information for the selection process (Falconer, 1981). The selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited (Scarano et al., 2014). Therefore, adequate information on the magnitude and type of genetic variability and their corresponding heritability is important in the improvement of grain yield potential of crops in breeding programs.

Yield improvement is an important breeding objective of most crop improvement programs (More and Borkar).

Similar to other crops, yield in common bean is a complex trait comprising of many morphological, physiological and agronomic traits. Seed yield is affected by genotype and environmental factors because of its quantitative properties. Effectiveness of selection is dependent upon the availability of large genetic variability present in the breeding material for the target character and the extent to which it is heritable (Atta et al., 2008). It also depends on the direction and magnitude of association between the traits to be improved (More and Borkar, 2016). However, limited attention has been given to studies on genetic variability, heritability and genetic advance of yield and associated traits in common bean landraces to improve the seed yield in south Western Kenya. Therefore, the present study was carried out to assess the extent of genetic variability, heritability and genetic advance among common bean landraces for yield and related traits and examine their correlation with seed yield for efficient design of common bean breeding schemes.

MATERIALS AND METHODS

Plant materials

A total of 52 common bean landraces were used in this study. Seeds of 26 common bean landraces were collected from farmers' fields in different agro-climatic zones and market centers of Kisii County, South western Kenya. The accessions were collected according to the procedure of Plant Genetic Resources International Institute (IBPGR, 1991). Seeds of 26 accessions were obtained from the National Genebank of Kenya, Muguga, Kiambu. The germplasm from the Genebank were collected from farmers' fields in South western Kenya in 1980 and preserved (Table 1).

Description of the study site

Fifty two common bean landraces were planted at the Kenya Agricultural and Livestock Organization (KALRO), Kisii County, South western Kenya (situated at about 0.68° South latitude, 34.77° East longitude, at an elevation of between 1450-2210 m above sea level). The site falls in the Lower Highlands one and two (LH1 and LH2), Upper Midland one (UM1), Lower Midland one and two (LM1 and LM2) Agro-Ecological Zones (AEZs). The soil type was deep, fertile, well-drained red volcanic (nitosols). The county has climatic conditions of average rainfall ranging from 1,400 - 2,600 mm per annum and mean annual temperature ranging from 15-28°C (FAO, 2015).

Experimental design and establishment of plants in the field

The genotypes were evaluated in two consecutive planting seasons namely between March and July, 2015 and repeated in the same period in 2016. The experiment consisted of a randomized complete block design (RCBD) with three plot replications for each landrace. The cultivars were grown in plots measuring 3 m × 4 m with distance between rows of 50 cm. Seeds were sown on raised beds with 40 cm row to row spacing and 15 cm plant to plant spacing at a depth of 5 cm. One teaspoonful of Diammonium phosphate (DAP) was added to each hole at planting. Normal crop.

Table 1. Origin, codes and local names of germplasm.

Entry	Genotype Code	Local name	Source of genotype
S1	LRC 006	Esaitoti	Daraja mbili mkt
S2	LRC 008	Cinchae	Kisii mnp mkt
S3	LRC 018	Richore	Marani
S4	GK030171	NNP	Gene bank
S5	GK030217	NNP	Gene bank
S6	GK030178	NNP	Gene bank
S7	GK030185	NNP	Gene bank
S8	GK036526	NNP	Gene bank
S9	GK030261	NNP	Gene bank
S10	GK030200	NNP	Gene bank
S11	GK030204	NNP	Gene bank
S12	GK030210	NNP	Gene bank
S13	GK030246	NNP	Gene bank
S14	GK036524	NNP	Gene bank
S15	GK030211	NNP	Gene bank
S16	GK030249	NNP	Gene bank
S17	LRC 001	Ekenagwa	Kisii Mn Mkt
S18	LRC005	Egirini	Kisii Mn Mkt
S19	LRC010	Bunda entambe	Daraja mbili mkt
S20	LRC016	Manoa emwamu	Kisii Mn Mkt
S21	LRC015	Ekoko enyenge	Suneka
S22	LRC026	Nyaibu/Bunda enetu	Daraja mbili mkt
S23	LRC011	Ekebure	Daraja mbili mkt
S24	LRC012	Enyamatobu	Kisii Mn Mkt
S25	LRC021	Morogi	Nyacheki
S26	LRC024	Ekoko entambe	Keumbu
S27	LRC019	Manoa endabu	Kisii Mn Mkt
S28	LRC022	Enyamwamu	Daraja mbili mkt
S29	GK030194	NNP	Gene bank
S30	GK030227	NNP	Gene bank
S31	GK030239	NNP	Gene bank
S32	GK036530	NNP	Gene bank
S33	LRC 023	Eosama	Nyamarambe
S34	LRC 009	Eroyoo	Kenyenya
S35	LRC025	Amaika inse	Kisii Mn Mkt
S36	LRC020	Ritinge	Daraja mbili mkt
S37	LRC 007	Eamini	Nyamache
S38	LRC 014	Esaire	Daraja mbili mkt
S39	LRC 017	MASAKU	Marani
S40	GK 030244	NNP	Gene bank
S41	GK 036527	NNP	Gene bank
S42	LRC 004	Emwetemania	Masimba
S43	LRC 013	Onyoro	Daraja mbili mkt
S44	GK036523	NNP	Gene bank
S45	GK030257	NNP	Gene bank
S46	GK036522	NNP	Gene bank
S47	GK030260	NNP	Gene bank
S48	GK030198	NNP	Gene bank
S49	GK030259	NNP	Gene bank
S50	GK030167	NNP	Gene bank
S51	LRC003	Enchano	Daraja mbili mkt
S52	LRC002	Egiero	Kisii Mn Mkt

management practices were carried out as recommended including weeding, pest/disease checks and top dressing

Agronomic data collection

Fourteen descriptors were surveyed for each common bean landrace at appropriate growth stage. The descriptors developed for *Phaseolus spp.* were used with some modifications (IBPGR, 2013). Data were recorded on a plot basis using ten individual plants selected randomly from the two central rows of each plot. Measurement unit and measurement procedure of each trait are given in Table 2.

Statistical analysis

Analysis of variance

The data collected on all the agronomic traits studied were subjected to analysis of variance (ANOVA) for the randomized complete block design (RCBD). The treatment means were clustered by Scott-Knott test at 5% probability levels for significance

Phenotypic and genotypic coefficient of variation

The estimates of phenotypic and genotypic coefficient of variation were calculated as described by Singh and Chaudhary (1979):

$$PCV (\%) = \frac{\sqrt{V_p}}{\text{Mean}} \times 100$$

$$GCV(\%) = \frac{\sqrt{V_g}}{\text{mean}} \times 100$$

$$GCV(\%) = \frac{\sqrt{V_g}}{\text{mean}} \times d$$

where PCV is phenotypic coefficient of variance, VP is phenotypic variance, GCV is genotypic coefficient of variance, and Vg is genotypic variance. GCV and PCV values were categorized as low (0-10%), moderate (10-20%), and high (20% and above) as indicated by Subramanian and Menon (1973) and Cherian (2000).

Heritability

It was estimated as the ratio of total genotypic variance to the phenotypic variance according to Falconer (1981):

$$H^2 = \frac{V_g}{v_P} \times 100$$

where H^2 = % Broad sense heritability. The heritability percentage was categorized as low (0- 30%), moderate (30 – 60%), and high \geq 60% as described by Johnson et al. (1955).

Genetic advance

The extent of genetic advance expected through selection for the character was calculated as described by Addissu (2011):

$$\text{Genetic Advance (GA): } H \times P \times K$$

where H is heritability, P is phenotypic standard deviation, and K is selection differential (2.06 at 5%).

Genetic Gain (%) = GA \times 100; it is categorized as low (0-10%), moderate (10-20%) and high (20% and above) as described by Johnson et al. (1955).

The genetic advance as a % of the mean (GAM) was calculated as:

$$GAM(\%) = \frac{GA}{X} \times 100$$

where GA = Genetic advance and X = Grand mean of a trait.

Clustering and principal component analysis (PCA)

Clustering and PCA were carried out to assess the relationships among the common bean landraces based on data from agronomic traits using NTSYS-pc software (version 2.1) (Rohlf, 1997). Data were analyzed based on Euclidian distance method and dissimilarity coefficient. Unweighted pair-group method of the arithmetic (UPGMA) mean and SAHN clustering were used to determine the genetic relationships among the common bean landraces. Principal component analysis (PCA) was calculated using EIGEN module of NTSYS-pc software.

RESULTS

Agronomic performance of the common bean landraces

There was significant variation ($P < 0.05$) for all the studied traits which also revealed possible amount of variability among the landraces (Table 3). Yield component traits including number of pods per plant, number of seeds per pod, number of seeds per plant, 100 seed weight and grain yield were significantly varied ranging from 12 to 52 NPPP, 4 to 9 NSPPO, 65 to 320 NSPP, 20 to 113 g WHSPP and 26 to 132 for GY, respectively, excluding the outlier (Table 3). The other traits indirectly contributing to agronomic performance varied significantly ($P < 0.001$); the number of branches varied from 1 to 17, plant length ranged from 8 to 16 cm and biological yield varied from 101 to 2296 g.

The plant height (PH) was highest in genotype LRC008 (185 cm) while the lowest was for GK030198 (40.4 cm). The number of branches (NOB) ranged from 3 (GK030167, GK030246 and LRC004) to 15 (LRC008), while the number of days to emergence (DTE) varied from 5 for cultivar LRC010 to 10 days for cultivars GK030244, GK030204 and GK0302194. The number of days from emergence (DESTF) varied from 95.5 (LRC008) to 34 (LRC019), whereas the length of time to maturity (DSM) ranged from 150 days for genotype LRC008 to 57 for genotype LRC015 (Table 3). The table shows that the highest number of pods per plant (NPPP) was obtained from accession LRC008 (238) and the lowest from LRC007 (15), but the average number of seeds per pod (NOSPP) in these genotypes ranged

Table 2. Fourteen observed common bean quantitative characters, codes, measurement units and procedures

Character	Code	Measurement unit/sampling procedure
Days from planting to emergence	DTE	Number of days from sowing to the time the plant emergence was 50% within the centre rows
Days from emergence to 50% flowering	DFSTF	Number of days from the date of emergence to the date on which 50% of the plants on a plot opened a flower
Days from sowing to 95% maturity	DSM	Number of days from sowing to the stage when 90% of the plants in a plot changed the colour of their pods from green to yellowish orange and texture hardened
Number of pods per plant	NPPP	Average number of pods counted at harvest, for 10 plants within plot centre
Number of seeds per pod	NSPPO	Determined from the average number of seeds per 10 pods per 10 sampled plants
Weight of 100 seeds per plant (gm)	WHSPP	Determined from the average 100-seeds mass at physiological maturity (12 - 14%) moisture content of the seed and expressed in grams
Number of seeds per plant	NSPPL	Determined from the average number of seeds from 10 pods per 10 sampled plants at physiological maturity
Number of branches per plant	NOB	Number of shoots arising from the main stem counted and recorded at physiological maturity.
Pod length	PL	Exterior distance of fully matured pod from the pod apex to the peduncle measured in centimeters at physiological maturity from an average of 10 plant within plot centre
Pod width	PW	Average width of 10 pods for each genotype from one end at its widest point of the central pod to the other at physiological maturity, in millimeters
Plant height	PH	The height of the plant from the ground surface to the tip of the main stem recorded in centimeters at physiological maturity
Biological yield (weight of roots, stalk and leaves)	BY	An average from 10 plants uprooted, cleaned and weighted to get the biological yield per plant in grams
Grain yield/weight of seeds per plant	GY/WSP	Dried grain yield in grams, obtained from 10 plants within central rows of each plot were harvested, threshed separately and seeds weighted
Harvest index (%)	HI	$HI = (GY/BY) \times 100$

Table 3. Mean performance of 52 common bean landraces evaluated for 14 agronomic traits at KALRO-Kisii Research Center field during the 2015 and 2016 cropping seasons.

Code of landrace	PH (cm)	NOB	DTE	DESTF	DSM	NPPP	NSPPO	WHSPP (gm)	NSPPL	PL (cm)	PW (cm)	GY (gm)	BY	HI
LRC001	95.20	4.00	7.70	43.60	68.40	16.60	5.50	67.50	80.10	12.00	1.40	53.60	219.00	0.25
LRC002	130.00	4.00	7.40	42.00	65.80	21.70	7.00	68.50	147.00	12.00	1.20	99.96	252.10	0.39
LRC003	50.50	5.00	8.70	34.50	55.60	17.30	6.00	46.60	102.80	13.00	1.50	47.38	217.50	0.22
LRC004	102.70	3.00	8.50	40.00	62.00	23.00	6.00	43.00	138.60	12.00	1.50	58.91	223.00	0.26
LRC005	93.40	4.00	7.00	36.60	58.00	21.00	4.20	42.00	84.40	10.00	1.50	35.28	235.50	0.15
LRC006	45.00	6.00	8.00	35.00	60.90	19.50	4.70	73.70	76.20	10.00	1.50	56.24	234.00	0.24
LRC007	37.00	15.00	7.90	35.70	60.00	15.00	6.00	69.00	90.00	13.50	1.60	62.10	218.00	0.28
LRC008	185.00	7.00	6.00	95.50	150.00	238.00	5.00	46.90	690.00	12.00	1.50	324.30	2300.00	0.10
LRC009	79.80	6.00	6.30	37.00	62.70	16.00	7.60	27.80	112.00	8.00	1.00	31.36	220.20	0.14
LRC010	66.00	5.00	5.00	48.40	72.00	32.00	7.00	36.70	224.00	11.00	1.30	82.88	251.40	0.33

Table 3. Contd.

LRC011	50.30	5.00	8.40	45.00	74.80	35.10	9.40	28.50	315.50	11.00	1.30	88.20	230.00	0.38
LRC012	43.00	5.00	7.00	35.00	60.00	21.20	5.70	72.40	147.00	15.00	1.80	105.84	240.00	0.44
LRC013	148.00	4.00	6.70	40.50	63.00	15.00	7.80	29.50	105.40	13.00	1.40	30.74	220.00	0.14
LRC014	95.50	6.00	6.00	40.60	65.50	38.30	6.00	21.00	228.00	11.00	1.30	47.88	253.70	0.19
LRC015	74.70	4.00	5.30	38.00	57.00	22.80	5.50	56.80	110.00	10.50	1.50	62.70	234.40	0.27
LRC016	118.00	6.00	9.40	35.00	59.90	23.00	4.00	107.00	92.80	14.00	2.50	99.51	300.00	0.33
LRC017	81.10	5.00	6.70	35.00	61.80	17.00	4.00	66.00	68.40	11.00	1.40	44.88	230.00	0.19
LRC018	50.00	6.00	7.00	43.80	69.00	24.00	4.80	62.40	96.00	12.50	1.50	59.52	235.80	0.25
LRC019	120.00	7.00	6.00	34.00	61.00	25.00	3.60	103.00	75.00	13.00	2.50	77.25	334.20	0.23
LRC020	64.60	4.00	5.80	36.30	62.00	24.00	6.00	64.80	144.00	14.00	1.50	93.60	218.30	0.43
LRC021	56.90	6.00	5.70	42.90	73.60	33.00	6.00	31.50	198.60	10.00	1.40	63.36	219.00	0.29
LRC022	100.00	6.00	5.50	40.00	70.00	36.00	7.00	27.00	252.00	11.50	1.40	68.04	194.00	0.35
LRC023	91.80	5.00	9.00	36.00	68.70	38.00	6.80	32.00	246.00	10.00	1.30	78.72	196.70	0.40
LRC024	56.50	7.00	8.00	40.00	70.10	19.00	4.00	57.70	76.60	12.00	1.50	44.08	240.00	0.18
LRC025	84.80	4.00	7.10	42.50	70.00	17.10	6.00	62.00	102.40	12.00	2.00	63.24	270.00	0.23
LRC026	52.00	5.00	8.00	37.70	63.00	21.70	6.00	64.00	126.00	13.50	1.50	80.64	260.00	0.30
GK036527	97.30	6.00	9.30	43.80	68.40	28.00	6.30	57.80	168.60	14.00	1.50	97.00	198.40	0.49
GK036528	86.40	6.00	6.70	41.40	65.00	25.60	6.70	48.00	150.50	12.40	1.20	72.00	297.00	0.24
GK036530	75.20	7.00	6.40	40.30	63.90	36.00	6.80	42.00	216.60	10.00	1.30	91.00	291.00	0.31
GK036524	121.10	6.00	7.00	38.90	62.30	37.80	8.70	43.70	296.00	9.40	1.00	130.00	295.00	0.44
GK030260	60.50	4.00	9.00	36.00	60.20	36.50	4.00	46.50	144.00	10.00	1.50	67.00	231.00	0.29
GK030261	123.00	5.00	7.40	41.90	68.80	33.00	7.80	44.40	231.00	11.00	1.40	102.00	278.60	0.36
GK036522	119.00	6.00	8.00	40.20	72.00	33.00	6.60	58.50	198.20	14.00	1.50	117.00	290.40	0.40
GK030211	98.3.00	7.00	7.00	40.80	71.70	40.40	8.00	41.00	320.20	11.00	1.50	131.00	271.00	0.48
GK030227	65.00	5.00	8.50	44.70	73.80	30.60	6.00	58.60	180.40	12.50	1.50	106.00	269.50	0.39
GK030239	40.40	7.00	9.00	38.00	65.60	15.40	5.00	42.10	75.00	11.50	1.40	32.00	216.00	0.15
GK030244	67.40	6.00	10.00	37.60	66.10	27.50	5.60	46.00	135.00	10.50	1.50	62.00	263.00	0.23
GK030180	78.00	6.00	5.60	36.500	65.00	32.00	6.70	52.00	192.70	14.00	1.50	100.00	248.40	0.40
GK030194	65.30	4.00	10.00	43.00	71.00	32.00	5.00	53.00	160.00	10.50	1.50	84.00	251.00	0.33
GK030198	40.20	4.00	9.40	37.00	63.20	17.70	6.00	42.00	102.20	12.50	1.50	43.00	233.90	0.18
GK030200	61.00	5.00	9.00	40.60	70.20	35.50	4.00	48.50	140.70	10.40	1.40	67.00	260.00	0.26
GK030204	82.50	7.00	10.00	41.70	73.30	34.70	6.00	65.00	204.00	15.00	1.50	132.00	238.00	0.55
GK030210	58.60	4.00	7.30	35.00	60.00	16.30	5.80	38.70	80.60	10.50	1.50	31.00	263.00	0.12
GK030167	110.00	3.00	7.80	40.00	68.30	33.00	7.00	43.00	231.80	11.00	1.30	98.00	282.00	0.35
GK030171	46.20	5.00	6.20	38.00	68.40	23.30	7.00	54.00	161.90	10.00	1.30	87.00	216.00	0.40
GK030178	116.00	5.00	6.0	42.80	73.00	34.00	7.70	42.00	238.60	10.50	1.30	100.00	236.50	0.42
GK036523	78.80	6.00	7.60	36.0	67.80	24.00	6.70	38.50	144.00	11.00	1.50	56.00	239.80	0.23
GK036526	64.20	7.00	9.70	35.40	63.00	52.00	5.40	41.00	260.00	14.50	1.80	106.00	305.00	0.35
GK030246	126.	3.00	8.00	40.70	73.00	22.6.00	8.00	43.00	176.00	11.50	1.40	76.00	273.70	0.28

Table 3. Contd.

GK030249	121	08	8.3	40.50	70.70	35.00	6.60	37.00	210.00	10.00	1.20	78.00	255.00	0.30
GK030257	98.1	05	7.4	36.00	68.40	25.00	6.00	42.00	150.50	10.00	1.40	63.00	267.20	0.23
GK030259	58	05	7.4	37.00	63.00	37.10	5.00	48.00	185.10	10.50	1.40	89.00	236.30	0.38
Mean	83.26	5.50	7.55	40.23	63.00	31.31	6.08	50.45	170.82	11.65	1.47	80.33	247.76	0.30
CV (%)	37.88	32.71	17.71	21.04	20.04	97.09	21.16	33.41	57.82	13.70	18.04	54.18	12.18	35.00
LSD (0.05)	0.11	0.10	0.05	0.06	0.06	0.30	0.06	0.10	0.16	0.04	0.05	0.15	0.03	0.10

LRC - Landrace; DTE - Days from planting to emergency; DFSTF - Days from sowing to 50% flowering; DSM - Days from sowing to maturity; NOPPP - Number of pods per plant; NOSPP - Number of seeds per pod; WOSPP - Weight of seeds per pod; NSPP - Number of seeds per plant; PWPP - Pod weight per plant; SSZ - Seed size; GH - Growth habit; PH - Plant height; NOB - Number of branches per plant; PL - Pod length; PW - Pod width; PS - Plant size; BY - Biological yield; HI - harvest index (%); GY/WSPP - Grain yield/weight of seeds per plant; NA - Not available; GK - Genebank of Kenya.

from 4.2 in LRC 005 to 9.7 for LRC011. Accessions LRC016 and LRC 019 recorded the highest weight of hundred seeds per plant (WHSP) (107 and 103 gm, respectively), compared to genotype LRC 014 which recorded the lowest (21). There was wide variation in the number of seeds per plant (NSPPL) ranging from 320 (GK320211) to 68 (LRC017) not considering the outlier (LRC 008). Pod length (PL) and pod width (PW) varied from 8.0 cm and 1.2 cm for cultivars LRC009 and GK030249 and GK 036528 as lowest values; while highest values were recorded for landraces LRC016 (14 for PL and 2.5 for PW). The highest biological yield (BY) and grain yield (GY) was 334 and 132 for accessions LRC 019 and GK 030204 respectively, disregarding the outlier. The harvest index ranged from 0.48 to 0.10 of which landraces GK036527 and LRC008 recorded the highest and lowest, respectively (Table 3).

Variation in agronomic characteristics of the common bean landraces

The analysis of variance in the present study showed that there were highly significant ($P \leq 0.001$) differences among the common bean

landraces for all the 14 agronomic traits (Table 4). The coefficients of variation were generally low except for biological yield (60.66). The range and mean values for the 14 traits are presented in Table 4.

Phenotypic and genotypic variability and estimation of genotypic and phenotypic coefficient of variation

The extent of variability in respect of phenotypic and genotypic variances and phenotypic and genotypic coefficients of variance (PCV and GCV) for the yield determining quantitative characters studied is represented in Table 5. In the present study, the highest genotypic variance were observed for days to maturity (59.44) and number of seeds per plant (31.13) while the lowest genotypic variance was found for pod length (2.57), pods per plant (2.14) and pod width (1.55). The highest phenotypic variances were for days to maturity (76.34) followed by seeds per plant (51.73) while the lowest were for pod length (3.17) and pod width (2.02). The genotypic coefficients of variation (GCV) ranged from 1.00% for biological yield to 84.69% for pod width, while phenotypic coefficients of variation (PCV) ranged

from 2.34% for biological yield to 96.68 for pod width. Moreover, moderate GCV and PCV were observed (>10%) in the traits for yield. Moderate (29.46) and high (75) GCV were also recorded for number of seeds per pod and number of branches respectively, while PCV values were 35.12 and 84.40 for number of seeds per pod and number of branches respectively. The lowest GCV was recorded for biological yield (1.00) and grain yield (2.21) while PCV values were 2.34 and 2.72 for the same variables respectively (Table 5).

Heritability and genetic advance

Broad sense heritability and genetic advance values are presented in Table 4. Heritability in broad sense estimates of the 13 quantitative traits ranged from 60.20% for number of seeds per plant to 87.57 for days to emergency. Genetic advance varied from 1.78 for number of seeds per pod to 92.71 for number of seeds per plant. All the traits showed a relatively high heritability values (>60%). However, almost all variables recorded moderate to low genetic advance (<60%) except values for plant height (78.13) and number of seeds per plant (92.71), (Table 5).

Table 4. Mean values, coefficients of variation, ranges and mean squares from a combined analysis of variance for 14 agronomic traits of 52 common bean landraces.

Trait	Mean square	Error	Range		Mean	CV (%)
			Minimum	Maximum		
PH (cm)	2983.23**	1441.3	36	186	83.26	4.51
NOB	9.71**	414.04	3	17	5.5	36.63
DTE	5.35**	121.65	4.6	13.1	7.55	14.48
DFETF	215.63**	851.84	32	102	40.23	7.17
DSM	478.41**	2018.51	50	154	63	6.57
NPPP	2772.44**	793.64	12	244	31.31	8.91
NSPPO	4.95**	287.72	0.8	11	6.08	27.64
WHSP	852.66**	893.72	20	113	50.45	5.86
NSPPL	29264.55**	3755.96	65	698	170.82	3.55
PL	7.63**	150.18	8	16	11.65	10.42
PW	0.21**	1.85	0.8	2.7	1.47	9.15
GY	5683.92**	1645.86	26	329	80.33	5
BY	109105.3**	2822475	101	2296	274.76	60.66
HI	0.03**	0.36	0.1	0.586	0.3	19.82

** Highly significant at ($P \leq 0.001$); PH - Plant height; NOB - number of branches per plant; PL - Pod length; PW - Pod width; PS - Plant size; BY - biological yield; GY Grain yield; HI - Harvest index; NSPPL - Number of seeds per plant; WHSP - Weight of 100 seeds per plant; NSPPO - Number of seeds per pod; DFETF - Days from emergence to flowering; DSM - Number of days from sowing to maturity; NPPP - Number of pods per plant.

Association among the agronomic trait components

The genotypic or phenotypic correlation coefficients were significant (Table 6). The highest positive correlation (highly significant $P \leq 0.01$) was between number of pods per plant ($r = 0.97$) and days from emergency to flowering, closely followed by biological yield ($r = 0.96$) and days from emergency to flowering. Seed yield per plant showed significant ($P \leq 0.01$) positive correlation with plant height ($r = 0.68$), days from planting to 50% flowering ($r = 0.68$), number of pods per plant ($r = 0.67$), and biological yield ($r = 0.68$). Plant height was observed to have a highly significant ($P \leq 0.01$) and positive correlations with days from sowing to flowering ($r = 0.68$), number of pods per plant ($r = 0.67$), grain/seed yield ($r = 0.68$) and biological yield ($r = 0.68$) but low and non-significant correlation with days to emergence ($r = 0.22$), weight of hundred seeds per plant ($r = 0.34$), pod length ($r = 0.35$) and pod width ($r = 0.36$) as estimated from the pooled analysis. Number of branches per plant revealed a fairly low to medium correlation with all traits ranging from $r = 0.31$ for number of seeds per pod to $r = 0.47$ for pod length. Harvest index expressed significant ($P \leq 0.01$) and positive correlation with number of seeds per pod ($r = 0.61$) but had low and non-significant correlation with days from emergency to flowering ($r = 0.26$) and biological yield ($r = 0.18$).

Cluster analysis

Cluster analysis based on the 14 agronomic traits

grouped the 52 common bean landraces into four distinct clusters (Figure 1 and Table 6). Cluster I was the largest constituting 36.5% of the total landraces. This cluster consists of landraces with the smallest number of branches and had the minimum number of days to emergence, flowering and maturity. The landraces in cluster I were also characterized by fewer numbers of pods and seeds per plant which resulted in low grain yield compared to other clusters. Clusters II and III constituted 34.6 and 15.38% of the landraces, respectively. The landraces in clusters II and III were characterized by intermediate number of pods per plant and a relatively large number of seeds per pod. However, landraces in cluster II had a higher biological yield and produced more seeds per plant than cluster III (Table 7). Landraces with the large seeds, seed weight, pod length and width but a low number of pods per plant were grouped in cluster IV which constituted 11.5% of the total number (Table 7). Landrace LRC008 was clustered as an out group and was characterized with tall and large plants which recorded a higher number of pods per plant and medium seed size but a lower number of seeds per pod. The landrace had the longest period from planting to maturity as well as the largest biomass, although the harvest index (HI) was low (Table 7).

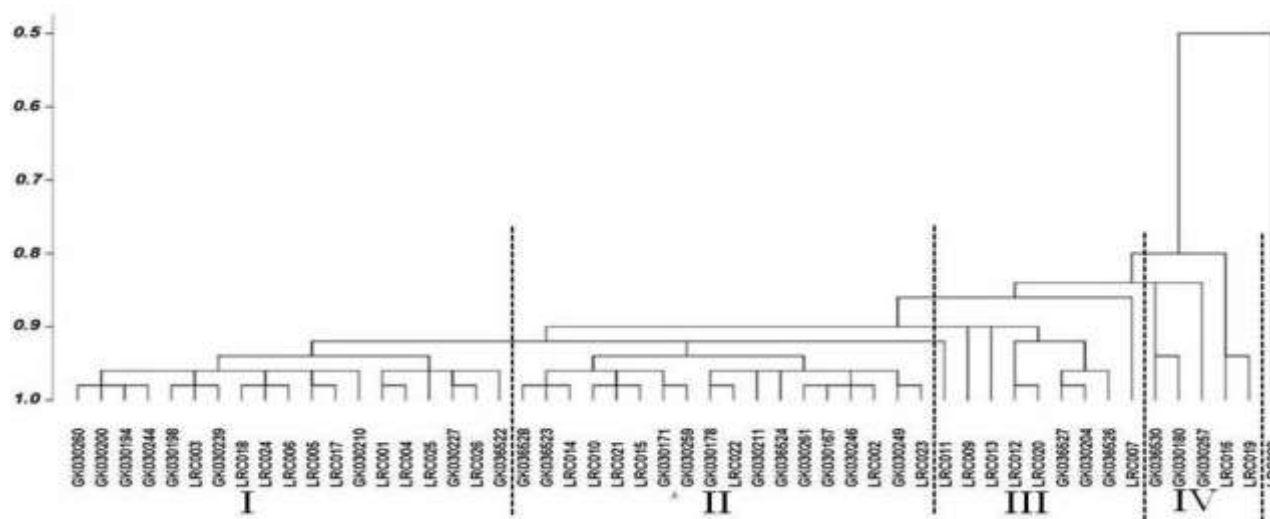
Principal component analysis (PCA)

Principal component analysis (PCA) of the quantitative data was performed to determine the importance of different traits in explaining the variations among the

Table 5. Estimation of genetic variables of the 14 agronomic traits of 52 common bean landraces evaluated.

Trait	GM	GV	PV	GCV (%)	PCV (%)	H ² (%)	GA	GAM
PH	83.25	20.34	24.56	5.41	59.52	81.97	78.13	93.84
NOB	5.5	17.02	21.55	75	84.4	78.97	5.36	97.45
DTE	7.54	16.43	18.76	53.75	57.44	87.57	6.78	89.92
DETF	40.27	12.46	16	8.76	10	77.87	5.94	14.75
DTM	67.71	59.44	76.34	11.38	13	77.86	13.84	20.44
NPPP	31.31	2.14	3.21	4.67	5.72	66.66	16.02	51.16
NSPPO	6.1	3.23	4.59	29.46	35.12	70.37	1.78	29.2
WHSP	50.45	5.44	6.31	4.62	5	86.21	39.16	77.62
NSPPL	170.81	31.13	51.73	3.26	4.21	60.2	92.71	54.27
PL	11.64	2.57	3.17	14	15.29	81.07	2.51	21.56
PW	1.47	1.55	2.02	84.69	96.68	84.43	1.22	83
GY	80.33	3.18	4.79	2.21	2.72	66.38	25.37	31.6
BY	274.22	7.43	9.45	1	2.34	78.62	27.84	10.15

GM – Mean of traits; GV – Genotypic variance; PV – Phenotypic variance; GCV – Genotypic coefficient of variation (%); PCV – Phenotypic coefficient of variation (%); H² – Heritability (%); GA – Genetic advance; GAM – Genetic advance as percentage of mean; PH – Plant height; NOB – Number of branches per plant; PL – Pod length; PW – pod width; PS – Plant size; BY – Biological yield; GY – grain yield; HI – Harvest index; NSPPL – Number of seeds per plant; WHSP – Weight of 100 seeds per plant; NSPPO – Number of seeds per pod; DFETF – Days from emergence to flowering; DSM – Number of days from sowing to maturity; NPPP – Number of pods per plant.

**Figure 1.** Dendrogram showing relationship among 52 common bean landraces based on 14 agronomic traits using UPGMA method.

landraces (Figures 2 and 3). In the principal components analyses of the 52 common bean landraces performed using 14 agronomic traits, the first principal component (F1) and the second principal component (F2) accounted for 29.33 and 19.27%, respectively of the total variation (48.60%). Trait eigenvectors indicated that F1 was mainly a positive indicator of biological yield, grain yield, number of pods per plant, and of characteristics contributing to high to medium-term biological yield and high seed yield (Figure 2) F2 was mainly a positive indicator of earlier days to emergency and maturity and characteristics with

low harvest index. Accordingly, the first two principal components revealed that the landraces were scattered in all the quarters (Figure 3), which showed the high level of genetic diversity in the evaluated genotypes.

DISCUSSION

Breeding programs aimed at crop improvement requires heritable variation in important agronomic traits of the crop. The efficacy of selection depends upon the

Table 6. Summary of the main characteristics of the genotypes clusters of common been evaluated.

Cluster number	Number of landraces (percentage)	Landraces	Unique agronomic traits of the landraces
I	19 (36.5%)	LCR003, LCR018, LCR024, LRC006, LCR005, LCR017, LCR001, LRC004, LRC025, LCR 026, GK030260, GK030200, GK030194, GK030244, GK030198, GK030239, GK030210, GK030227, and GK036522	Fewer number of branches, pods, seeds; earlier emergence, flowering and maturity; low yield
II	18 (34.6%)	LCR014, LCR010, LCR021, LCR015, LCR022, LCR002, LCR023, LCR011, GK036528, GK030171, GK030259, GK030178, GK030211, GK036524, GK030261, GK030167, GK030246 and GK030249	Intermediate number of pods per plant; a relatively large number of seeds per pod; high biological yield; a higher number of seeds per plant
III	8 (15.38%)	LCR011, LCR009, LCR013, LRC012, LRC020, GK036527, GK030204 and GK036526	Medium number of pods per plant and a large number of seeds per pod
IV	6 (11.5%)	LRC007, LRC016, LRC019, GK036530, GK030180 and GK030257	Large sized seeds, seed weight, pod length and width but low number of pods per plant
Outgroup		LRC 008	Long period from planting to maturity, large biomass, high yield, many pods and branches.

Table 7. Cluster means for fourteen different agronomic traits in 52 common bean landraces

Traits		Means of clusters			
		I	II	III	IV
Plant height	PH	67.82	94.43	78.71	87.71
Number of branches	NOB	4.63	5.23	5.5	7.66
Days to emergence	DTE	8.25	6.85	7.9	7.11
Days from sowing to 50% flowering	DESTF	38.98	40.32	39.33	36.25
Days from sowing to maturity	DSM	65.31	68.03	65.9	65.63
Number of pods per plant	NOPPP	23.19	31.53	28.25	26
Number of seeds per pod	NOSPP	5.22	6.91	6.77	5.52
100 seed weight	WHSPP	53.62	42	48.35	69.16
Seeds per plant	NSPPL	114.08	208.37	182.06	136.26
Pod length	PL	11.6	10.79	13.06	21.41
Pod width	PW	1.5	1.32	1.47	1.8
Grain yield	GY	60.67	84.58	85.59	82.14
Biological yield	BY	244.34	249.01	233.73	276.46
Harvest index	HI	0.24	0.34	0.36	0.29

magnitude of genetic variability for yield and yield contributing traits in the breeding material. The knowledge of heritability and genetic advance guides the breeder to select superior parents to initiate an effective and successful crossing program (Johnson et al., 1955). Therefore, the available genetic variation, heritability and expected genetic gain in important agronomic characters are useful to design better and effective breeding strategies in common bean landraces. In the present study, all the fourteen agronomic traits showed highly

significant ($P < 0.05$) variations indicating the presence of sufficient amount of genetic variability among the landraces for all the studied traits. In common bean genotypes, significant variations have been previously reported for various agronomic traits (Amanulla et al., 2016; Salehi et al., 2008a, b; Nechifor et al., 2015; Fivano and Msolla, 2011).

Knowledge about the variability using parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of paramount importance

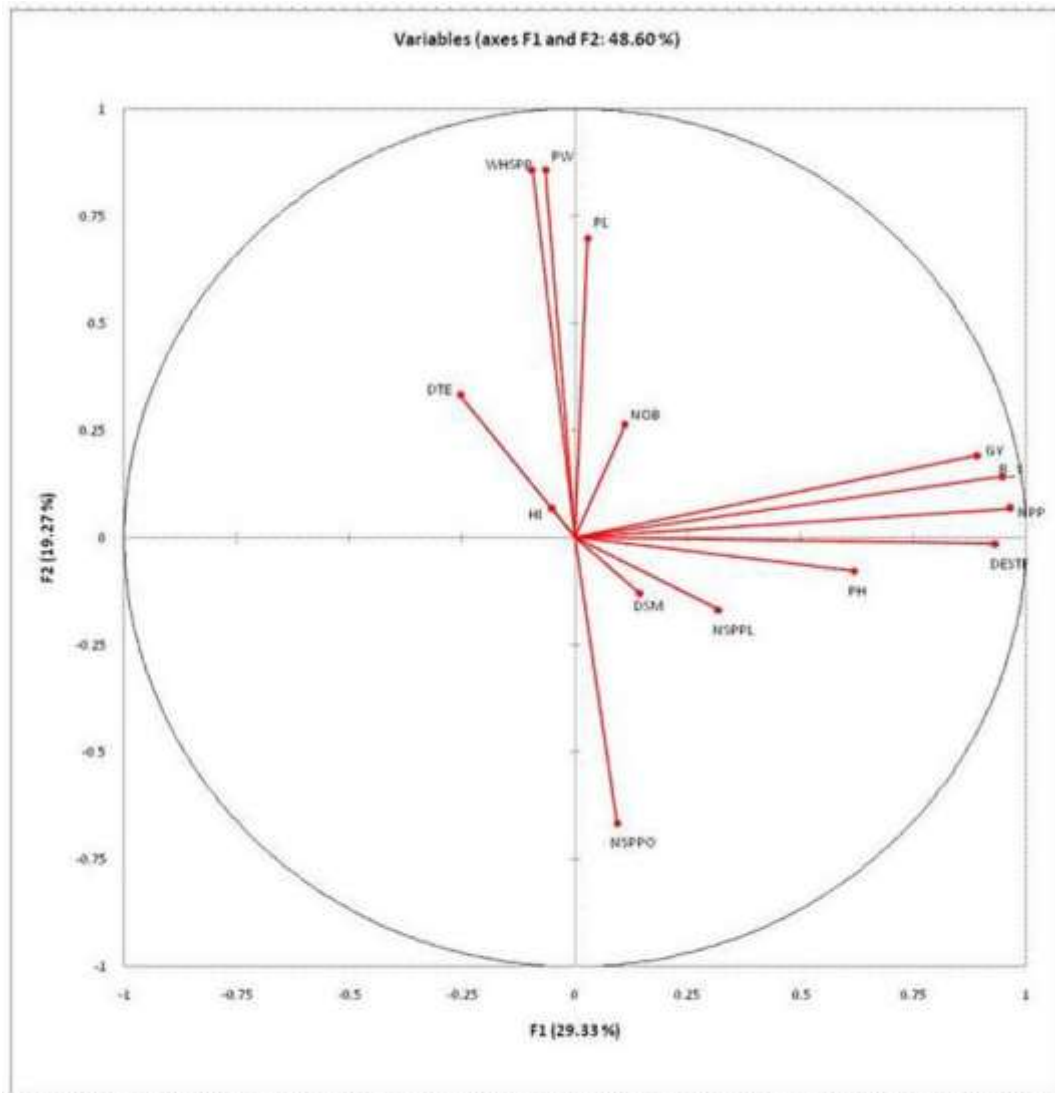


Figure 2. Two dimensional ordination of 14 agronomic traits in common bean landraces on principal component analysis. PH - plant height; NOB - number of branches per plant; PL - pod length; PW - pod width; PS - plant size; BY - biological yield; GY - grain yield; HI - harvest index; NSPPL - number of seeds per plant; WHSPP - weight of 100 seeds per plant; NSPPO - number of seeds per pod; DFETF - days from emergence to flowering; DSM - number of days from sowing to maturity; NPPP - number of pods per plant. F1 and F2 = Principal component 1 and 2, respectively.

for an effective breeding program in crops like common bean. According to Miklas et al. (2006), genotypic and phenotypic coefficients of variation values are categorized as low (<10%), moderate (10-20%), and high (>20%). In this study, based on the classification, high and close values of PCV and GCV were recorded for pods per plant, seeds per pod, 100 seed weight, seeds per plant, grain yield and biomass yield, which suggest the potential variability available in the landraces for these traits for effective selection and improvement as there was minimal influence of environment. Similar results were also reported by Stoilova et al. (2004) for clusters per plant, seed yield per plant, and biological

yield per plant. Aghamdi (2015) also reported high GCV and PCV for plant height, primary number of branches per plant, days to maturity indicating the predominance of additive gene action. Nechifor et al. (2015) also reported high genetic variability for numbers of pod per plant and weight of pods per plant in common beans. Stoilova et al. (2015) performed a field trial of 42 germplasm of exotic beans at the valley of Kashmir in order to obtain superior genotype of beans under temperate condition and the findings from their study showed medium genetic variability for days of flowering and days of harvesting and low genetic variability for early flowering and early maturity.

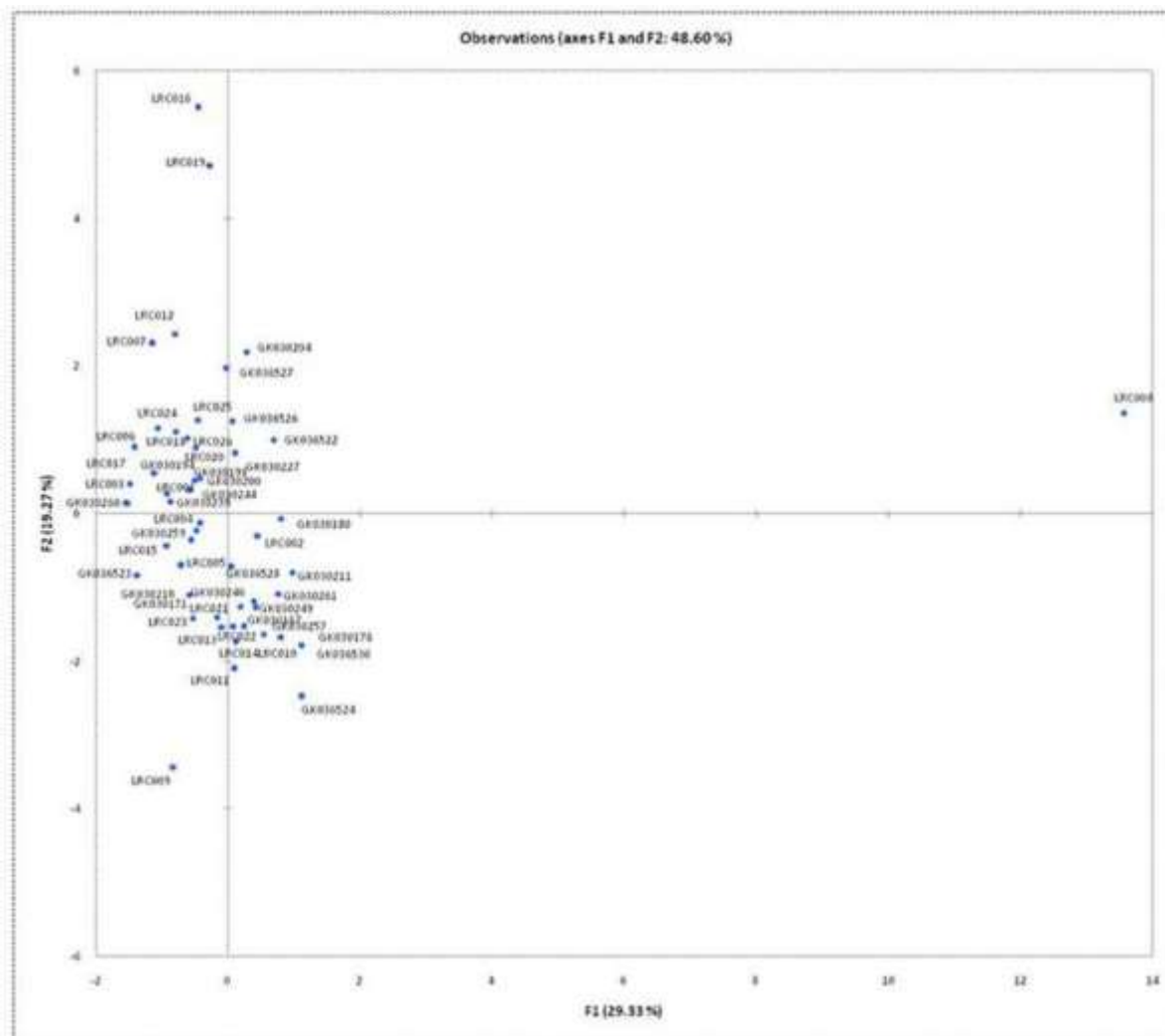


Figure 3. Biplot of first and second principal components in common bean landraces.

In the present study, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. This would be due to the fact the variation at the phenotypic level was due to the effect of genotypes and influence of environment as reported by Singh (1999). Moderate values of GCV and PCV were observed in the present study for some traits including plant height and number of branches. Low GCV and PCV were observed for days to 50% flowering, days to maturity. Phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits except days to emergence and 100 seed weight. However, the differences between PCV and GCV were small. The narrow differences between PCV and GCV for most of the traits indicate low effect of environmental influence on the expression of these traits. These findings are in agreement with Salehi et al. (2008) who reported narrow differences between PCV and GCV on the study of interrelationship between different traits

in common bean.

The heritability estimates help the breeders in selection based on the basis of phenotypic performance. According to Robinson et al. (1949), heritability can be classified as low (0-30%), moderate (30-60%) and high (>60%). Most traits showed a high heritability values (>60%) except number of pods per plant and biological yield which were moderate. Similar findings were also reported by Singh et al. (2015) in pea crop. Salehi et al. (2008) and Duarte and Adams (1972) also reported similar results for yield component traits which included number of pods per plant, 100-seed weight and number of seeds per pod in common bean.

However, when heritability is coupled with genetic advance (GA) together with GCV provides the best prediction of expected gain through phenotypic selection than heritability alone. Estimates of all these parameters help to understand the type of gene action involved in the expression of traits especially for polygenic traits.

Johnson et al. (1955) suggested genetic advance as percent mean can be categorized as 0-10% for low, 10-20% for moderate and >20% for high. In the present study, the genetic advance as percent of mean ranged from 10.15% for biological yield to 97.45% for number of branches. High heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean were recorded by plant height followed by number of branches and days to emergence which indicates that the traits were simply inherited in nature and possessed additive gene effects. These traits can be considered as favorable for common bean improvement through effective phenotypic selection of these traits and high expected genetic gain from selection for these characters can be achieved. Similar results were reported by Dursun (2007) who tested the variability, heritability and co-relation studies of 40 common bean genotypes. However, high heritability and GA (%) along with low GCV for days to flowering and maturity indicates that expression of these traits is under the involvement of non-additive gene action and phenotypic selection of these traits might not be effective. Grain yield is a complex character which is as a result of many yield contributing traits, which are in turn influenced by the environment and genotype. Consequently, the direct evaluation and improvement of grain yield itself may be misleading due to involvement of environmental component. Therefore, to assess the magnitude of correlations for various traits with yield would be immense help in the indirect selection for the improvement of yield. The correlation coefficients of yield and its components determined in the present study indicated that most of the traits studied were positively and significantly correlated with yield. Significant and positive correlation of seed yield/plant was found with plant height, days from sowing to 50% flowering, number of pods/plant and biological yield. These findings are in agreement with previous study in common beans by Dursun (2007) who reported positive and significant correlation of seed yield/plant with number of pods/plant. Valenciano et al. (2006) also reported significant positive correlation of pod weight with seed yield and length of pods, number of pods with seed weight/plant, number of pods/plant with number of pod bearing nodes. This study also showed that plant height at maturity was positively and significantly correlated with days from sowing to flowering, number of seeds/plant, seed yield and biological yield. This is in agreement with the findings of Pereira et al. (2015) who reported significant positive correlation of plant height with seeds/plant. However, our results contradict reports by Stoilova et al. (2015) and Singh et al. (1979) who found negative correlation of plant height with seed yield. This deviation may be attributed to the differences in genotypes and effect of the experimental conditions (Pereira et al., 2005).

Cluster analysis based on fourteen agronomic traits grouped 52 common bean landraces into four different

clusters indicating that the landraces exhibited notable genetic divergence in terms of agronomic traits. Formation of different clusters using agronomic characters in diverse common bean genotypes has also been reported (Nechifor et al., 2015). The maximum inter-cluster distance was recorded between cluster I and the out-group (LCR 008) followed by cluster II and the out-group, suggesting wide diversity among these groups. On the other hand, the minimum distance between cluster IV and the out-group and cluster I and II indicates their close relationship. Essentially, crossing of genotypes belonging to the same cluster is not expected to generate superior hybrids or segregants, because genotypes grouped in the same cluster diverge little from one another. However, the larger the divergence between the genotypes, the higher will be the amount of heterosis in F1 progeny and subsequent generations. It may be useful to produce crosses between genotypes belonging to the clusters separated by large estimated genetic distances (Negri and Tosti, 2002). Success might therefore be expected through making crosses between the genotypes from cluster II and cluster III, followed by the one between cluster IV and the outgroup. Genotypes from these clusters can be selected for hybridization program that can evolve high heterotic crosses, which might prove potential in isolating superior hybrids. The PCA grouped the accessions into groups over the four quadrants based on the quantitative traits. The accessions remained scattered in all four quadrants, showing large genetic variability for the traits studied.

Conclusion

The present study revealed significant levels of genetic variability among the 52 common bean landraces for all the agronomic traits. High values of genotypic coefficient of variation, broad sense heritability and genetic advance were recorded for pod width, plant height, number of branches and days to emergence and therefore these traits are favorable attributes for common bean improvement through simple selection and high expected genetic gain can be achieved for these characters. Cluster analysis using the fourteen different traits classified the common bean landraces into four separate clusters, exhibiting that hybridization of landraces across clusters could lead to an increase in heterosis in progenies.

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CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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