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Genetic Variability, Heritability and Genetic Advance of Common Bean (*Phaseolus vulgaris* L.) Genotypes at Mountain Environment of Nepal

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Abstract

Bean (Phaseolus vulgaris, L) is the major cash generating and protein rich crop in hill and mountain of Nepal. Assessment of variability is crucial to identify the most important traits in common bean improvement program. An experiment was conducted at Agricultural Research Station (ARS), Vijayanagar, Jumla Nepal consisting twelve genotypes of bean during 2015 in RCB design replicated thrice to observe genetic variability, correlation, heritability, and genetic advance using eight quantitative traits and selection and advancement of early maturing, high yielding, disease resistant, genotypes for high mountain environment of Nepal. Analysis of variance showed all characters were highly significant differences indicating presence of inherent genetic variability for the studied traits among the genotypes. The observed range of the traits were (DFF) days to fifty percent flowering (38.3-62.3), (DM) days to maturity (82-104.3), (Pht) plant height (46.6-123.3 cm), (NPPP) number of pods per plant (12.3-31), (NSPP) number of seeds per pod (3.63-6.16), (PL) pod length (8.43-12.53 cm), (HSW) hundred seed weight (25.23-47.37 gm) and (Yld) grain yield (1333-3221 kg/ha). High broad sense heritability coupled with high expected genetic advance as percent of mean were observed in NPPP (93 and 67.52%), Yld (84 and 55.24%), HGW (99 and 49.31%), NSPP (96 and 35.75%) and PL (98 and 24.28%) indicating these parameters are governed by additive gene action and direct selection can be applied in varietal development. All parameters obtained high phenotypic coefficient of variance than genotypic coefficient of variance indicating role of environmental for expression of the traits. Parameters NPPP (0.918**), PL (0.879**), NSPP (0.725**), DM (0.43**), HGW (0.371*) and Pht (0,374*) correlated with grain yield indicating indirect selection of these traits can be applied for yield increment. Total four clusters were obtained in eighty percent euclidean similarity clusturing indicating genetic closeness/distances among the genotypes. Clusture 1 carries the superior two genotypes including PB-0001 and KBL-3.

Keywords: Correlation, Genetic Advance, Heritability, Phaseolus, Variability

Introduction

Mid western mountain is cool, remote, and food deficit area of Nepal and it comprises five districts namely; Jumla, Humla, Mugu, Dolpa and Kalikot. Jumla is one of the high hill and food deficit districts of Karnali zone in mid western region of Nepal. Major crops grown in Jumla are rice, wheat, barley, bean, maize and millet. Small area covered by buck wheat, prosomillet, foxtail millet, amaranths and naked barley as minor crops. Pulses are grown in marginal lands under low fertility and soil moisture stress condition. Bean (*Phaseolus vulgaris* L) is a highly diversified and indigenous crop of Jumla and whole Karnali zone. Earlier it was usually cultivated in virgin, marginal land, and all type of upland but after realizing the nutritive value, market price and availability of high yielding genotypes, farmer have started to grow bean after wheat crop in low land too. The possible centre of origin/diversity of bean is southern Mexico and Central America (Reddy, 2004). Bean is an important cash crop in Jumla and adjoining high hill districts and Mustang. The bean locally is called "Jumlee simi" and consumed as dual purpose dal and vegetable. Bean is one of the important high value and cash crop among "apple, bean, potato, and walnut" of Jumla and is an exportable commodity. Farmers consider beans as a cash-generating crop and grow a number of landraces with varying morphology (Neupane and Vaidya, 2002). It is taken as gift and souvenir of Jumla. It receives up to NRs 150/kg a good source of income as cash crop.

The area of bean has not been included in statistical data of country; however District Development Committee (DDC) of Jumla reported that the cultivated area was 467.01 ha (DDC Jumla, 2010). But District Agricultural Development Office (DADO Jumla, 2013) reported total cultivated area of bean in Jumla was 2250 ha. Average yield of bean under irrigated condition is 1100 kg/ha (DADO Jumla, 2012). According to (Neupane et al., 2007), PB-0001 and PB-0048 were the varieties recommendable for Jumla condition. One genotype of bean PB-0001 has been registered for general cultivation from terai to high hill named PDR-14 in 2018.

Agriculture Research Station (ARS) Vijayanagar, Jumla has been conducting varietal development trials on bean since last few years. ARS, Vijayanagar, Jumla collected local germplasm, characterize and identified certain promising types. The local germplasm of bean have high variation in color, shape, size of seed and trailing habit of plant. The local collection have given name as KBL (Karnali bean line) and maintained as KBL-1 to KBL-8. Among them KBL-3, has superior performance (Bhujel et al., 2012).

Common bean (Phaseolus vulgaris L.) is the world's most important food legume. Mainly it is grown in the tropics and subtropics (Darkwa et al., 2016). It is a key source of dietary protein, rich in iron, fibers, and polysaccharide carbohydrates (Beebe et al., 2013). Most of crop improvement programs follow major breeding objective for yield improvement (Hallauer, 1981; Wilson, 1981). In common beans, yield is improved by direct and indirect selection for plant ideotype traits affecting yield. Adams (1982), has defined a common bean ideotype based mostly

on morphological traits, while (Wallace and Masaya, 1988), have favored a combined phenological and physiological ideotype. The collective term for these traits was used "yield system" traits (Wallace and Massaya, 1988). Numerous studies have estimated the heritabilities and correlations of the morphological traits included in the bean ideotype, but few have foccused on the phenological and physiological traits.

Varietals improvement in crops is slow due to lack of efficiency in utilizing genetic variation for various quantitative traits, which provides genetic basis for choosing parents for the breeding program. Identifying suitable genotypes from existing accessions for biotic and abiotic stress resistance is one of the current thrust areas of plant breeding in Nepal. Genetic variability is the basis for the enhancement of any plant breeding and varietal improvement activities. The breeder should identify the variation of desired character and select with his skill towards desired improvement of the crop. Genetic improvement is a major tool to develop high yielding drought tolerance varieties (Farshadfar et al., 2013).

The process of establishing a relationship or connection between two or more traits is correlation. The knowledge on genetic constituents and correlation between the parameters can be utilized to develop effective breeding methods by breeder. Similarly, heritability is a statistic used in the fields of breeding and genetics that estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population (Wray and Visscher, 2008).

Genetic variability, heritability, correlation, expected genetic advance and clusturing of the genotypes with similarity are key important for crop improvement programs. In general heritability is the ratio of genetic variance to the total phenotypic variance of a trait in the population. It is the good index of transmission of character from parent to their offsrings. Improvement in the mean genetic value of selected plants over the parental population is genetic advance. It is measure of gain under selection. Relationship between yield and yield associated traits are prime important for direct and indirect selection of traits to which contributes to yield. Therefore, this study was carried out to estimate genetic variability, heritability, correlation, genetic advance as percent of mean and clusturing of genotypes in relation to yield and yield associated traits and selection and advancement of cold tolerance,

early maturing, high yielding, disease resistant, and drought tolerance bean genotypes for high mountain environment of Nepal.

Materials and Methods

Experimental Location, Experimental Design, and Planting Materials

Twelve genotypes of bean which comprises local collections and introduced genotypes from neighbour country were evaluated at Agricultural Research Station (ARS), Vijayanagar, Jumla during regular bean growing season of high hill (First week of July to mid of October 2015). Geographically ARS is situated at altitude of 2290m amsl and 29^o 17' north latitude and 28^o 10' east longitudes of mid west Nepal (ARS, 2014). This station is located at high hill region and thus is characterized by cool temperate to alpine

eco belts with low rainfall. Soil of this station as developed on recent to old river, moderately deep to very deep and moderately to poor drained. The topography is gently sloppy to rolling lying in the high mountain region. Surface soil and sub-surface soils are dominantly coarse textured (Sandy loam) and are acidic to moderately alkaline in reaction .The nitrogen content of the soil is generally very low to medium while available phosphorous is high to very high and available potassium is medium to high. The organic carbon content of farm soil is low to high. The average maximum and minimum temperature is about 25°C in June and 2^oC in February. Total rainfall during bean growing period of 2015 was satisfactory 292.6 mm with an average of 73.15 mm. (Meteology office, Jumla, 2016). Detail of weather data is given in Annex 1. List of genotypes and recorded parameters and their abbreviation are given in Table 1.

Year		Average Te	emperature	Relative	Total Rainfall (mm)	
Month		Maximum (⁰ C)	Minimum (⁰ C)	Humidity %		
January		14.8	-4.4	NA	42	
	February	15.1	-2.5	NA	13.2	
2015	March	18.7	0.2	NA	57.6	
	April	22.6	0.4	NA	15.9	
	May	25.1	7.1	NA	43.7	
	June	28.2	13.1	NA	24.5	
	July	24.01	15.08	75.29	111	
	August	24.67	15.56	78.32	117.7	
	September	27.18	11.98	67.59	29.6	
	October	23.07	4.64	62.95	34.3	
	November	20.18	-0.2	55.91	6.8	
	December	16.25	-4.23	-4.23	0	

Annex 1: Weather data of research place Jumla 2015.

Table 1. List of genotypes and quantitative traits of bean used in the study

En	Genotypes	En	Genotypes	Traits	Abbreviation
1	PB-0001	9	KBL-6	Days to 50% flowering	DFF
2	PB-0002	10	KBL-7	Days to 90% maturity	DM
3	PB-0048	11	KBL-8	Plant height (CM)	Pht
4	KBL-1	12	KBL-9	Number of pods per plant	NPPP
5	KBL-2		KBL (Karnali Bean Line)	Pod length (CM)	PL
6	KBL-3			Number of seed per pod	NSPP
7	KBL-4			Hundred seed weight (g)	HSW
8	KBL-5			Grain yield kg per hac	YLD

Experiment was laid out in RCBD (Randomized Complete Block Design) in three replications in 6 m2 plot size for each entry spacing maintained as 50 x 10 cm row to row and plant to plant. Fertilizer applied at the rate 100:60:40 kg N: P_2O_5 :K₂O, the full dose phosphorus and potas with half dose of nitrogen was applied as basal dose and remaining half dose of nitrogen applied as top dress. Irrigation and intercultural operation was carried out as per need of crop and recommendation. Planting of crop was done on 5th July 2015.

Data Collection

Two boarder rows were excluded while recoding parameters days to heading, days to maturity, grain yield on plot basis, while plant height, number of pods per plant, number of seed per pod, and pod length was recorded from randomly selected five plants from inner lines of the plot. Thousands grain weight and grain yield was adjusted in 14% moisture content.

Statistical analysis

Analysis of variance done by using Genstat 18^{th} edition, correlation was computed by using statistical software SPSS at significance level of (0.05), mean separation among the lines was done with statistical software ADEL-R and clusuring of the genotypes was done with statistical software MINITAB. The phenotypic and genotypic variances were derived according to Falconer (1964), and broad sense heritability was calculated according to Allard (1960). Broad sence heritability values are characterized as low <30%, moderate 30-60% and high >60% Johnson et al., (1955). Estimation and categorization of genetic advance was done according to Johnson et al., (1955).

Methods proposed by (Sivasubramanian and Madhavamenon, 1973), was used to categorize genotypic cofficient variation (GCV) and phenotypic cofficient variation (PCV).

Results and Discussion

Analysis of variance

Analysis of variance among 12 genotypes of bean for eight ancillary characters revealed highly significance differences (<0.001) for all the traits under study: days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seed per pod, panicle length, hundred seed weight and grain yield indicating presence of inherent genetic variation among the genotypes for the concerned traits (Table 2). The result showed presence of variation in genetic constituent Breeder can utilize the variability for selection and may use in hybridization for trait improvement, gene transfer to the other genotypes. Mammo et al., (2019), reported similar findings that all parameters 50%DF, DM, PH, POPL (pods per plant), SEPO (seed per pod), HGW, BYIE, HI, BRPL, YLD were highly significant among the tested genotypes of common bean for genotypic effect. Like wise Ncbimbi and Mduruma (2007), supported our findings that highly significance differences were obtained for days to flowering, days to maturity, number of seeds per pod and seed yield in common bean lines. Seed yield, hundred seed weight, number of seed per pod, and plant height all possessed significant differences (<0.01) in dry bean genotypes reported by Esho (2018), supports our result.

As to the present experiment, the existence of genotypic variation for grain yield and yield components has been reported in previous studies in common bean (Atuahene-Amankwa and Mechaels, 1997; Fageria et al., 2010; Balcha, 2010, 2014). This suggests the possibility of selection to improve grain yield in the materials studied. Variation in plant height of phaciolus bean differ with genotypes (Neupane et al., 2007). Similar results were also reported by other researchers. Alghamdi (2007), reported that faba bean genotypes significantly differed in flowering date and plant height. Grain yield resembled highest variability (12.52) followed by number of pods per plant (9.4) and followed by plant height (7.28). Lowest variability was observed by panicle length, then thousands grain weight and plant height (Table 2).

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SN	Traits	Rep	Treat	Error	Fcal	CV	P value
1	DFF	15.53	138.23	6.77	20.42	4.97	**
2	DM	32.44	155.18	8.60	18.05	3.02	**
3	Pht	47.41	300.51	38.85	77.23	7.28	**
4	NPPP	0.78	128.82	3.20	40.23	9.40	**
5	NSPP	0.03	1.95	0.03	77.62	3.50	**
6	PL	0.04	4.79	0.04	121.00	1.89	**
7	HGW	1.21	186.09	0.47	398.02	2.09	**
8	Yld	189166.33	1120060.09	64754.15	17.30	12.52	**

Table 2. Analysis of variance for the eight ancillary character of bean genotypes

Note; DH: Days to 50% flowering, DM: Days to maturity, NPPP: Number of pods per plant, Pht: Plant height (cm), PL: Pod length (cm), NSPP: Number of seeds per pod, HSW: Hundred seed wt (gm) and Yld: Grain yield (kg/ha) Mean separation and range.

Mean separation and range of 12 bean genotypes for eight yield and yield attributing character is presented in Table 3 and Table 4. Earlier maturing genotypes was KBL-8 (82 days) while late maturing genotype was KBL-4 (104 days) and mean was 97 days. Maximum NPPP was produced by PB-0001 (31) and minimum was recorded in KBL-5, KBL-6 and KBL-8 (12) and mean was 19. Genotype KBL-4 was tallest (123.3 cm) but it was statistically at par with KBL-9 and KBL-4 and KBL-5 was dwarfest (46.7 cm) and statistically at par with KBL-6, KBL-8 and PB-0001 and mean was 85.6 cm. The obtained range for pod length was (8.43 to 12.43cm) minimum recorded in KBL-6 and highest in KBL-3 which is statistically at par with PB-0001 (12.2cm) with mean value 10.5 cm. Lowest number of seed per pod obtained in KBL-6

(3.6) and highest KBL-3 (6.2) and mean 4.5. Highest HSW (47.37 gm) recorded in PB-0048 and lowest was obtained by KBL-4 (25.23 gm) and mean was 32.7 gm. The grain yield varied from highest 3221 kg/ha (KBL-3) this is statistically at par with PB-0001 (3022 kg/ha) and lowest 1333 kg/ha (KBL-6) and mean 2032.5 kg/ha. From the variation breeder can select genotypes having high number of pods per plant, more pod length, high number of seeds per pod, high hundred seed weight and having high yield for further improvement, hybridization gene transfer for betterment of breeding program. Similar result higher no. of pods per plant, larger grain size and longer maturity period results higher yield obtained by (Bhujel et al., 2012).

EN	Genotypes	DFF	DM	Pht	NPPP	NSPP	PL	HSW	Yld
1	PB0001	52 ^{bcd}	100 ^{ab}	54.0 ^d	31 ^a	4.8 °	12.2 ^a	43.8 ^b	3022 ^a
2	PB0002	49 ^{cd}	100^{ab}	109.1 ^b	25 ^b	5.3 ^b	10.7 ^{cd}	36.5 ^d	2128 bc
3	PB0048	55 abc	92 ^{bc}	73.3 °	25 ^b	4.5 ^d	11.4 ^b	47.4 ^a	2556 ^b
4	KBL-1	48 ^{cd}	103 ^a	123.0 ^a	16 ^d	4.2 ^e	10.2 ^d	25.8 ^g	1900 cde
5	KBL-2	58^{ab}	98 ^{ab}	69.6 ^ª	16 ^d	4.2 ^e	11.3 ^{bc}	25.5 ^g	2011 ^{cd}
6	KBL-3	49 ^{cd}	103 ^a	120.3 ^a	28 ^b	6.2 ^a	12.5 ^a	28.5 ^{ef}	3221 ^a
7	KBL-4	38 ^e	104 ^a	123.3 ^a	14 ^{de}	3.8 ^f	9.5 ^e	25.2 ^g	1583 def
8	KBL-5	59 ^{ab}	85 ^{cd}	46.7 ^d	12 ^e	3.7 ^f	9.0 ^{ef}	29.7 ^e	1417 ^f
9	KBL-6	59 ^{ab}	96 ^{ab}	51.0 ^d	12 ^e	3.6 ^f	8.4 ^f	26.8 ^{fg}	1333 ^f
10	KBL-7	54 ^{bcd}	98 ^{ab}	77.3 ^a	16 ^d	5.2 ^b	10.5 ^d	35.5 ^d	1747 cdef
11	KBL-8	62 ^a	82 ^d	56.7 ^d	12 ^e	3.7 ^f	9.5 ^e	41.2 °	1528 ^{ef}
12	KBL-9	46 ^{de}	102 ^a	123.0 ^a	20 °	5.2 ^b	11.2 bc	27.0 ^{fg}	1944 ^{cde}
	Grand mean	52	97	85.6	19	4.5	10.5	32.7	2032.5
	SEM	2.602	2.93	6.233	1.7894	0.1584	0.199	0.6838	254.47
	LSD (0.05%)	4.406	4.96	10.554	3.03	0.2683	0.337	1.1579	430.89

Table 3. Mean performance and LSD vale of the quantities traits of bean at high hill of Nepal in 2015

Note; DH: Days to 50% flowering, DM: Days to maturity, NPPP: Number of pods per plant, Pht: Plant height (cm), PL: Pod length (cm), NSPP: Number of seeds per pod, HSW: Hundred seed wt (gm) and Yld: Grain yield (kg/ha) Genetic variability, heritability and genetic advance

Heritability, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and genetic advance at 5% selection intensity as percent of mean for quantitative traits of bean genotypes is presented in Table 4. The success of genetic advance under selection depends upon three factors (Allard, 1960). Genetic variability : greater the amount of genetic variability in base populations higher the genetic advance, Heritability : the G.A. is high with characters having high heritability and Selection intensity : the proportion of individuals selected for the study is called selection intensity high selection intensity gives better results. Heritability is a measure of the value of selection for particular characters and an index of their transmissibility (Ali et al., 2006). Our result showed PCV is higher than GCV for all traits. Higher the difference between PCV and GCV indicates higher influence of environment for the expression of traits. Smaller the difference little effect of environment and selection will be effective in this condition. High broad sence heritability obtained for the trait HSW (0.99), followed by pod length (0.98), number of seeds per pod (0.96), NPPP (0.93), DFF (0.87), DM (0.85), yld (0.84), and pht (0.69). Similar result was obtained by (Scully et al., 1991) reported high broad sence heritability as seed yield (0.90), biomass (0.93), harvest index (0.92), days to maturity (0.96), days to flower (0.98), days of pod fill (0.94), biomass growth rate (biomass/days to maturity) (0.87), seed growth rate (seed yield/ days of pod fill) (0.87) in common bean. Similarly, (Wondwosen and Abebe, 2017), obtained high heritability >60% for the traits grain yield, hgw, DM, DF, NSPP, NPPP in support of our result. Raffi and Nath (2004), reported high heritability >60% for DF, DM, Yld, seed weight, pod length, plant height that supports our findings. Result obtained by (Langat et al., 2019), is in favour of our findings; he reported high heritability (> 60%) for DF, DM, NPPP, HSW, NGPP, Yld in stressed condition. Aklade et al., (2018), obtained high heritability for the traits days to 50% flowering, pod length, days to maturity, hundred seed weight, number of seed per pod in french bean genotypes which supports our finding. Esho (2018), reported high heritability for plant height, pod length,

number of seed per pod, HSW, and seed yield. Alghamdi (2007) observed that the highest estimates of heritability were recorded for number of pods and number of seeds per plant. High heritability was recorded by days to maturity in common bean.

High estimates of heritability indicated that selection based on mean would be successful in improving these traits. Higher the broad sence heritability character are least influenced by environment and selection for improvement of such characters may be useful. Lower the broad sence heritability genetic improvement through selection will be difficult.

Our result showed higher GA as percent of mean by traits number of number of pods per plant (67.52%), grain yield (55.24%), hundred seed weight (49.31%), number of seeds per pod (35.75%), pod length (24.28%), days to fifty percent flowering (24.23%) and medium by traits days to maturity (13.69%) and plant height (18.69). If the value of genetic advance high the character is governed by additive genes and selection will be beneficial for such traits. If genetic advance is low the character is governed by non additive genes and heterosis breeding may be useful. Genetic advance as percent mean ranged from 13.69% for days to maturity to 67.52% for number of pods per plant indicating that selecting the top 5% of the genotypes could result in an improvement range of 13.69% for days to maturity to 67.52% for number of pods per plants and 55.24% for grain yield. Esho (2018), reported high genetic advance as percent of mean for plant height, hundred seed wt and grain yield in support of our result. Langat et al., (2019), reported high GA as percent of mean in traits; Yld, NSPP and NPPP in favour of our finding.

High heritability coupled with high genetic advance were recorded for grain yield, number of pods per plant, hundred seed weight, pod length, number of seeds per pod. These characters are governed by additive gene effects and direct selection for these traits would be more effective for desired genetic improvement.

SN	Traits	Range	Std	Vg	Vp	Н	GCV	PCV	% mean GA
1	DFF	38.33-62.33	6.79	43.82	50.59	0.87	12.64	13.58	24.23
2	DM	82-104.33	7.19	48.86	57.46	0.85	7.21	7.82	13.69
3	Pht	46.66-123.33	31.63	87.22	126.07	0.69	10.91	13.12	18.69
4	NPPP	12.33-31	6.55	41.87	45.07	0.93	34.01	35.28	67.52
5	NSPP	3.63-6.16	0.81	0.64	0.67	0.96	17.69	18.03	35.75
6	PL	8.43-12.53	1.26	1.58	1.62	0.98	11.93	12.08	24.28
7	HGW	25.23-47.37	7.88	61.88	62.34	0.99	24.03	24.12	49.31
8	Yld	1333-3221	611.03	351768.65	416522.80	0.84	29.18	31.75	55.24

Table 4. Range, standard deviation, variance, broad sence heritability, PCV, GCV and percent mean genetic advance for quantitative traits of bean genotypes

Note; DH: Days to 50% flowering, DM: Days to maturity, NPPP: Number of pods per plant, Pht: Plant height (cm), PL: Pod length (cm), NSPP: Number of seeds per pod, HSW: Hundred seed wt (gm) and Yld: Grain yield (kg/ha) Clusturing

Dendrogram generated based on UPGMA clustering method and Euclidean similarity coefficient among twelve bean genotypes is given in table 5 and figure 1. Clusturing was done with UPGMA clustering method with 80% eucdian similarity coefficient and four clusture were generated. Clusture 1 contains 2 genotypes named (PB-0001 and KBL-3). This clusture carries higher value for grain yield, hundred seed weight, pod length, number of seeds per pod, number of pods per plant than total average. Both genotypes in the clusture are superior and can be selected for variety release and registration. PB-0001 has already registered for general cultivation and KBL-3 is pipe line genotype. Similarly, clusture 2 carries four genotypes 33.3% of total. This clusture is inferior than clusture one values of quantitative traits yld, HSW are below the total average but pod length, NSPP, pht and DM is higher than grand centroid. Clusture 3 contains single genotype PB-0048 having highest hundred grain weight and more yield than centroid. Clusture 4 carries four genotypes lowest yielder and lower other values than grand centroid. Earliness may be desired trait from this clusture.

Table 5. The average of traits for each cluster obtained from UPGMA cluster analysis

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Grand centroid
DFF	50.5	51	55	54.5	52.42
DM	101.5	100.2	92	91.75	96.92
Pht	87.15	100.4	73.3	69.43	85.61
NPPP	29.5	18.6	25	12.5	18.92
NSPP	5.5	4.82	4.5	3.7	4.53
PL	12.35	10.78	11.4	9.1	10.53
HSW	36.15	30.06	47.4	30.73	32.74
Yld	3121.5	1946	2556	1465.25	2032.5

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Fig 1. Unwaited pair group method with arithmetic mean (UPGMA) clusturing of cold tolerance bean genotypes Correlation

Correlation is very important tool in plant breeding because we can use indirect selection to improve another targeted parameter. There are positive and negative effect in correlation which results in simultaneous changes in related character. Phenotypic correlation between eight parameters of 12 genotypes of bean is illustrated in table 6. Result showed all parameters significantly correlated each other number of pods per plant and plant height, plant height and pod length, plant height and grain yield, number of seed per pod and hundred seed weight, and hundred seed weight and pod length. Hundred seed weight showed significant negative correlation with days to fifty percent flowering and plant height indicating lower HSW in longer and late flowering genotypes.

Parameters HSW (0.371*), NSPP (0.725**), NPPP (0.918**), PL (0.897**) and DFF and DM cotribute for higher grain yield. We can select plants having high number pods per plant, more hundred grain weight, more number of seed per pod, longer pod etc

for higher grain yield. Esho (2018), reported highly significant correlation between HGW and grain yield in favour of our result. Mesele (1997), indicated the relationship between seed yield and number of pods per plant was highly significant at phenotypic and genotypic level. He also reported that yield per plant was highly and significantly correlated with number of seeds per plant both at phenotypic and genotypic levels which in favour with our result. According to Kassaye (2006), days to flowering and maturity had positive direct effect on seed yield. In contrast, these phenological traits contributed their negative indirect effects through 100- seed weight partial support with our findings. Shah et al., (1990), observed between pod yield and pod length. Singh et al., (2000), Shinde and Dumare, (2001), Rai et al., (2001), and Atilla (2007), observed between pod yield, plant height, pod length, pod width, pod weight and number of seeds/pod at both genotypic and phenotypic level this supports our findings.

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	FFD	DM	Pht	NPPP	NSPP	PL	HSW
MD	0.902**						
Pht	0.82**	0.734**					
NPPP	0.381*	0.42*	0.237				
NSPP	0.471**	0.516**	0.509**	0.745**			
PL	0.357*	0.43**	0.313	0.857**	0.79**		
HGW	-0.385*	0.389*	-0.413*	0.482**	0.111	0.292	
Yld	0.374*	0.43**	0.249	0.918**	0.725**	0.897**	0.371*

Table 6: Phenotypic correlation coefficient between eight parameters of bean

Note; DH: Days to 50% flowering, DM: Days to maturity, NPPP: Number of pods per plant, Pht: Plant height (cm), PL: Pod length (cm), NSPP: Number of seeds per pod, HSW: Hundred seed wt (gm) and Yld: Grain yield (kg/ha)

Conclusion

Obtained results indicates presence of sufficient genetic variability for the studied traits and genotypes are suitable for breeding purpose. High heritability coupled with high genetic advance were recorded for grain yield, number of pods per plant, hundred seed weight, pod length, number of seeds per pod. These characters are governed by additive gene effects and direct selection for these traits would be more effective for desired genetic improvement. Mean separation and clusturing showed genotypes PB-0001and KBL-3 are superior and can be selected for variety release and registration. PB-0001 has already registered for general cultivation and KBL-3 is pipe line genotype. Parameters HSW, NSPP, NPPP, PL and DFF and DM contribute for higher grain yield. We can select plants having high number pods per plant, more hundred grain weight, more number of seed per pod, longer pod etc for higher grain yield.

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Conflict of Interest

The authors declare that there is no conflicts of interest regarding publication of this manuscript.

Authors contribution

N.H. Ghimire: Designed and performed experiment, analyzed data and wrote the paper.

H.N. Mandal: Performed experiment, data recorded.

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