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Variability, correlation and association studies for seed yield and component traits in common bean genotypes under North Western Himalayas

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Abstract
One sixty nine land races of common bean were used in variability, correlation and path analysis studies. Significant variation was observed for all traits under study with higher magnitude of phenotypic coefficient of variation as compared to genotypic coefficient of variation. High variability for all the traits indicates the scope of selection and improvement of these traits. High heritability coupled with high genetic advance was observed for traits like 100-seed weight, seed yield per plant and biological yield per plant. Significant positive correlation of seed yield with all the traits studied except days to flowering clearly indicated that selection for higher seed yield per plant through these traits would be effective. Path analysis revealed positive and high direct effects on seed yield per plant by biological yield per plant followed by harvest index. Highest indirect effects were observed on seed yield per plant through biological yield per plant followed by plant height and harvest index. Significant influence of biological yield per plant directly and indirectly on seed yield per plant suggested the role of high biomass in enhancing the grain production in common bean, hence preference should be given for selecting plants with higher biomass to develop high yielding genotypes.

Keywords: Common bean, correlation coefficient, heritability, genetic advance, path analysis, variability

Introduction
Common bean (*Phaseolus vulgaris* L.), locally known as rajmash, belongs to family *Leguminoseae* and subfamily *Papilionaceae.* This new world crop is originated in the South Mexico and Central American Center of origin and its secondary centre of origin is western China (Vavilov, 1951; Singh, 2015). It is one of the premier grain legumes and provides 15% of the protein and 30% of the caloric requirement to the world's population representing 50% of the grain legume consumed worldwide (McConnell, 2010) [14].

Rajmash is a major commercial crop in the north-western Himalayan region of India comprising hilly states of Himachal Pradesh, Jammu & Kashmir, Uttar Pradesh and Uttarakhand. In Himachal Pradesh, its cultivation is mainly confined to high and mid hills, and is popularly grown as intercrop with maize as well as monocrop. There exists a vast diversity in plant, grain morphology and in agro-ecological adaption of landraces cultivated in north-western Himalayan region which may be due to the reason that this region is close to the secondary centre of origin (western China) of common beans (Pathania *et al*., 2006). The statistics with respect to this crop is very deficient owing to the small area of production and short duration. However, as per as the FAO [8] estimates, beans are grown in the world in an area of about 36 m ha with annual production of 31 m t with productivity of 861 Kg/ha (FAO, 2017) [8]. In India the area under different beans including is about 15 m ha with annual production of 6.39 m t and productivity 414 kg/ha (FAO, 2017) [8].

The success of any crop improvement programme will largely depend upon the nature and magnitude of genetic variability present in that crop germplasm (Mohapatra *et al*., 2007; Meena and Bahadur, 2014) [16, 15]. It serves as raw material for any plant breeder to initiate any crop improvement programme. The genetic variability in relation to total variability can be exploited to predict the genetic gain during selection. Larger variability increases the chances of developing superior varieties. The estimates of heritability provide important information about the inheritance of the quantitative traits. During selection process to develop superior varieties it is important to focus on the traits having high heritability to make selection effective. It is difficult to select the traits with low heritability, so it is important to study the relationship between different traits to perform indirect selection for traits with low heritability. Majority of the traits of breeder's interest are complex and resulted from interactions among different components.

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So understanding the relationship among these different components is important to exploit these relationships in during selection. However total relationship studies do not provide the information about direct and indirect influences of component traits. A trait may have high and positive relationship with yield but may have low direct impact on yield and vice versa. Therefore, it is very important to know the direct and indirect effects of various component traits on yield as well as total relationship between yield and component traits (Kulaz and Ciftçi, 2012) [12].

So a critical assessment of nature and magnitude of genetic variability and characters association is one of the important pre-requisites in formulating efficient breeding methods. Therefore, the present investigation was undertaken to study the components of variation, heritability, genetic advance, the correlation among different characters and their direct and indirect effects on yield.

Materials and methods
The present investigation was carried out at the Experimental Farm CSK HPKV, Mountain Agricultural Research and Extension Centre (MAREC), Sangla, Distt. Kinnaur during summer season 2015. The experimental material comprising one sixty nine landraces of common bean including three checks were evaluated in Simple Lattice Design with two replications. The crop was raised following standard package of practices and data was recorded pertaining to various quantitative traits *viz.*, Days to flowering, Days to maturity, Plant height, Branches per plant, Number of pods per plant, Pod length, Number of seeds per pod, 100-seed weight, Biological yield per plant, Seed yield per plant and Harvest Index. Phenotypic and genotypic coefficients of correlation were worked out following the procedure of Al-Jibouri *et al.* (1958) [3] and Dewey and Lu (1959) [6]. The path analysis of important yield component traits with grain yield was done following Dewey and Lu (1959) [6]. The genotypic and phenotypic coefficients of variation were estimated following Burton and De Vane (1953) [4]. Heritability in broad sense (h^2_{bs}) was calculated as per the following formula given by Burton and De Vane (1953) [4] and Johnson *et al.* (1955) [11]. The expected genetic advance (GA) resulting from the selection of 5 per cent superior individuals was calculated as per Burton and De Vane (1953) [4] and Johnson *et al.* (1955) [11].

Results and discussion
The analysis of variance revealed that mean sum of squares due to genotypes were significant for all the traits studied, suggested the presence of wide range of genetic variability and scope of selection for these traits.

The estimates of phenotypic coefficient of variation (PCV) were higher than corresponding genotypic coefficient of variation (GCV) for all the traits studied indicated that the apparent variation is not only due to genotypic differences but also due to the influence of environment (Table 1). Therefore, caution has to be exercised in making selection for these traits on the basis of phenotype alone due to unpredictable nature of environmental variation. More variability was observed for plant height, 100-seed weight, seed yield per plant and biological yield per plant, moderate for number of pods per plant and low for days to flowering, days to maturity, branches per plant, pod length, seeds per pod and harvest index. The coefficient of variation alone cannot be used to partition the heritable components of variation (Burton, 1952) [18]. Therefore, GCV together with heritability estimates

would give the best picture of gain to be expected from selection. The present study revealed that h^2_{bs} was very high for days to flowering, days to maturity, plant height and 100-seed weight, high for seed yield per plant and biological yield per plant. Moderate heritability (50-70%) was observed for number of pods per plant, pod length and harvest index plant whereas, it was low (<50%) for number of seeds per pod and branches per plant. The traits which exhibited high heritability revealed lesser influence of the environment and greater role of genetic component of variation. Therefore, selection for these traits on the basis of phenotypic expression would be more effective and can be relied upon. However, the improvement through selection will depend not only on the heritability of traits under consideration but also on the phenotypic variation as well as the selection intensity. Therefore, the selection based on heritability estimates only might not help in identifying traits needed in further selection. Further, Johnson *et al.* (1955) [11] had suggested that heritability estimates along with genetic advance are more reliable in predicting the performance from selection as compared to heritability alone. The information about the magnitude of inheritance of traits is obtained by studying heritability whereas genetic advance assist in designing suitable selection strategy. Genetic advance expressed as percentage of mean was observed to be high (>50%) for plant height, 100-seed weight, seed yield per plant and biological yield per plant. The present study revealed that phenotypic selection would be effective for the traits viz. 100-seed weight followed by seed yield per plant, biological yield per plant and plant height as these traits showed high GCV, high heritability coupled with high genetic advance. The traits showed high heritability along with high genetic advance might be controlled by additive genes. Similarly, Jhanavi *et al.* (2018) [10] reported high heritability coupled with high genetic advance for plant height, pod width, number of pods per plant, yield per plant and other traits studied. High heritability coupled with high genetic advance was also reported by Panchbhaiya *et al.* (2017) for plant height, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant and for other yield related traits studied. Wondimu and Bogale (2017) reported similar results for number of pods per plant, 100-seed weight and grain yield. However, Alemayehu (2010) [1] and Nichifor *et al.* (2011) reported moderate heritability coupled with moderate genetic advance for seed number per pod. Similarly Ejara *et al.* (2016) [7] reported moderate heritability coupled with moderate genetic advance for plant height and number of seeds per pod and low heritability coupled with low genetic advance for seed yield which are in contrary to the results of present investigation. Similarly, Sofi *et al.* (2011) observed high genetic advance for especially plant height and seed yield. However, Mudasir *et al.* (2012) [17] reported high genetic advance (>30%) for days to maturity, number of pods per plant, 100-seed weight and seed yield plant. Traits showing low heritability coupled with high genetic advance are difficult to select due to high influence of non-genetic variations.

In the present study, the estimates of phenotypic and genotypic correlation coefficients were also computed for different traits and have been presented in Table 2. The improvement for target traits for example seed yield can be achieved by indirect selection for other traits that are highly heritable and easier to select. For this understanding of interrelationship among traits and with target trait is required. The estimation of genotypic and phenotypic correlations

among traits provided this information which facilitates the indirect selection for the target traits. The magnitude of genotypic correlations was higher than phenotypic coefficient for most of the correlations suggesting more influence of genetic factors than environmental factors. Correlations whether positive or negative are either due to pleiotropy or genetic linkage among genes. Gonçalves et al. (2017) [9] also reported similar results while evaluated common bean germplasm. Similar results were reported by Lad et al. (2017) [13] in french bean and Choyal et al. (2018) [5] in cluster bean. Seed yield per plant showed significant and positive correlation with all the traits studied except days to flowering. These results clearly indicated that simultaneous selection for these traits might bring improvement in seed yield per plant. Biological yield per plant was positively correlated with plant height, branches per plant, number of pods per plant, days to maturity, 100-seed weight and seed yield per plant where as it was negatively correlated with number of seed per pod and harvest index. It shows the late maturing genotypes with more height, more branches and number of pods per plant possess more seed weight and grain yield probably due to more accumulation of photosynthate in the seeds. Alemu et al. (2017) [2] found significant positive genotypic correlations between green pod yield and number of pods per plant, pod length and significant negative genotypic correlations between green pod yield and days to 50% flowering and days to first picking while evaluated snap bean genotypes. Lad et al. (2017) [13] also reported significant positive correlation of seed yield per plant with all yield related traits studied in French bean. Kulaz and Ciftçi (2012) [12] reported significant and positive relationship among seed yield and biological yield per plant, number of branches per plant, number of pods per plant. Ahmad and Kamaluddin (2013) found that seed yield was positively correlated with days to 50% flowering, plant height, number of pods per plant, pod length and number of seeds per pod. Onder et al. (2013) reported positive and significant correlation between seed yield and biological yield, harvest index where as significantly negative correlation between seed yield and flowering day, plant height and pod number per plant. Choyal et al. (2018) [5] observed non significant but positive correlation of seed yield per plant with fruit cluster per plant, pod per cluster and 100-seed weight in cluster bean. Singh et al. (2018) reported positive and significant correlation of pod yield per plant (q/ha) with number of pods per plant, number of clusters per plant, green pod yield per plant (g) and plant height was observed.

As we know that the correlation studies among yield and component traits were not sufficient for effective selection, the path analysis was done to find out the direct and indirect relationship among variables. Path analysis helps in identification of components influencing correlation and can be exploited in planning effective selection strategy. The values of path analysis at the phenotypic and genotypic levels are presented in Table 3. Although all the characters except days to flowering showed highly positive correlation with seed yield per plant but when direct and indirect contributions of the correlation was estimated, the direct effect were found to be positive and high for biological yield per plant followed by harvest index. Highest indirect effects on seed yield per plant were through biological yield per plant followed by branches per plant, plant height and harvest index. However, Alemu et al. (2017) [2] reported positive direct effect of pod number per plant on green pod yield followed by single green pod weight whereas plant height exerted maximum negative direct effect. Onder et al. (2013) observed positive direct effects of biological yield, harvest index, number of main branches per plant and days to flowering on seed yield. Gonçalves et al. (2017) [9] found that number of seeds per plant and grain weight showed larger estimates of direct effects on seed yield. Choyal et al. (2018) [5] reported positive direct effects of number of pods per plant on seed yield and however seeds per pod showed negative direct effect on seed yield. Ahmad and Kamaluddin (2013) found positive direct effects of 50% flowering, number of pods/plant, pod length and 100-seed weight on seed yield. Kulaz and Ciftçi (2012) [12] observed strong positive direct effects of biological yield, 1000-seed weight, plant height and number of seeds per plant on seed yield per plant. Singh et al. (2018) found high positive direct effects of green pod yield per plant followed by number of clusters per plant, seed length and pod width on green pod yield per plant. Low residual effect at phenotypic and genotypic level indicated that the traits used for path analysis were adequate and appropriate. Path coefficient analysis enable the breeders to concentrate on the traits which shows high direct effect on seed yield, finally can reduce the time by restricting selection to one or few important traits instead on focusing on large number of component traits (Dewey and Lu, 1959) [6]. In the present study biological yield per plant showed positive and direct effect on seed yield per plant followed by harvest index which clearly indicated that preference should be given to these traits in selection programme to isolate superior genotypes with higher genetic potential for seed yield.

Table 1: Estimates of parameters of variability for various traits in Rajmash genotypes

Traits	Mean ± S.E.(m)	Range	PCV (%)	GCV (%)	Heritability h²bs (%)	Genetic advance as (%) of mean
Days to flowering	75.87±0.35	61.50-21.50	5.99	5.84	94.80	11.66
Days to maturity	129.00±0.65	110.50-144.50	6.61	6.53	97.56	13.27
Plant height (cm)	64.77±1.42	27.00-117.50	29.04	28.02	93.11	55.41
Branches per plant	3.46±0.05	2.00-5.50	23.35	13.09	31.40	18.23
Number of pods per plant	12.42±0.27	6.00-29.00	31.54	25.00	62.79	40.84
Pod length (cm)	10.22±0.10	6.50-13.80	14.36	11.80	67.47	19.85
Number of seeds per pod	4.82±0.06	3.00-7.00	18.39	12.55	46.60	19.19
100-seed weight (g)	33.00±0.83	10.85-90.54	35.53	35.27	98.53	71.99
Biological yield per plant (g)	26.66±0.68	9.40-49.50	35.57	31.04	76.18	57.06
Seed yield per plant (g)	10.85±0.32	4.50-23.00	40.72	35.74	77.04	65.02
Harvest index (%)	41.17±0.47	21.69-61.76	17.24	12.38	51.57	18.45

Table 2: Estimates of correlation coefficients for various traits in rajmash

Traits		Plant height	Branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	Biological yield per plant	Harvest index	100 seed weight	Days to flowering	Days to maturity
Branches per plant	G	0.109*									
	P	0.083									
Number of pods per plant	G	0.472**	0.557**								
	P	0.349**	0.223**								
Pod length	G	-0.034	0.208**	-0.09							
	P	-0.017	0.164**	-0.045							
Number of seeds per pod	G	0.114*	0.058	0.445**	0.097						
	P	0.083	0.114*	0.270**	0.165**						
Biological yield per plant	G	0.488**	0.483**	0.303**	0.207**	-0.035					
	P	0.411**	0.232**	0.234**	0.177**	0.069					
Harvest index	G	-0.236**	0.200**	0.385**	0.185**	0.385**	0.038				
	P	-0.144**	0.210**	0.213**	0.110*	0.166**	-0.111*				
100 seed weight	G	-0.098	-0.118*	-0.310**	0.449**	-0.391**	0.160**	0.016			
	P	-0.096	-0.063	-0.230**	0.383**	-0.250**	0.150**	-0.002			
Days to flowering	G	0.367**	-0.011	0.284**	-0.237**	0.022	0.039	-0.086	-0.267**		
	P	0.343**	-0.009	0.211**	-0.179**	0.038	0.012	-0.053	-0.258**		
Days to maturity	G	0.440**	0.095	0.114*	0.001	-0.177**	0.205**	-0.141**	0.016	0.240**	
	P	0.424**	0.066	0.084	0.002	-0.108*	0.166**	-0.091	0.015	0.255**	
Seed yield per plant	G	0.371**	0.493**	0.433**	0.274**	0.121*	0.995**	0.319**	0.167**	-0.006	0.136*
	P	0.331**	0.300**	0.295**	0.196**	0.112*	0.854**	0.338**	0.143**	-0.021	0.118*

*$P \leq 0.05$; and **$P \leq 0.01$

Table 3: Estimates of direct and indirect effects at genotypic and phenotypic level for different traits in rajmash

Traits		Plant height	Branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	Biological yield per plant	Harvest Index	100 seed weight	Days to flowering	Days to maturity	Correlation with yield
Plant height	G	-0.28437	-0.02676	0.14779	-0.00302	0.00154	0.55183	-0.02860	0.00164	-0.00724	0.01816	0.371**
	P	0.04565	0.00028	-0.00545	0.00025	-0.00170	0.36661	-0.06481	-0.00059	-0.00644	-0.00233	0.331**
Branches per plant	G	-0.03096	-0.24583	0.17420	0.01849	0.00078	0.54572	0.02431	0.00196	0.00021	0.00390	0.493**
	P	0.00377	0.00339	-0.00349	-0.00244	-0.00233	0.20743	0.09458	-0.00039	0.00017	-0.00036	0.300**
No. of pods per plant	G	-0.13434	-0.13688	0.31286	-0.00796	0.00600	0.34235	0.04663	0.00517	-0.00561	0.00469	0.433**
	P	0.01593	0.00076	-0.01562	0.00067	-0.00554	0.20867	0.09583	-0.00143	-0.00396	-0.00046	0.295**
Pod length	G	0.00966	-0.05119	-0.02806	0.08878	0.00131	0.23424	0.02239	-0.00750	0.00469	0.00005	0.274**
	P	-0.00078	0.00056	0.00071	-0.01489	-0.00338	0.15830	0.04947	0.00239	0.00336	-0.00001	0.196**
Number of seeds per pod	G	-0.03242	-0.01415	0.13926	0.00863	0.01348	-0.03899	0.04662	0.00653	-0.00044	-0.00732	0.121*
	P	0.00378	0.00039	-0.00422	-0.00246	-0.02052	0.06143	0.07492	-0.00156	-0.00072	0.00059	0.112*
Biological yield per plant	G	-0.13886	-0.11872	0.09478	0.01840	-0.00046	1.13005	0.00459	-0.00267	-0.00076	0.00846	0.995**
	P	0.01875	0.00079	-0.00365	-0.00264	-0.00141	0.89248	-0.04988	0.00094	-0.00022	-0.00091	0.854**
Harvest Index	G	0.06708	-0.04929	0.12031	0.01640	0.00518	0.04278	0.12124	-0.00026	0.00169	-0.00580	0.319**
	P	-0.00657	0.00071	-0.00333	-0.00164	-0.00342	-0.09891	0.45002	-0.00001	0.00100	0.00050	0.338**
100 seed weight	G	0.02787	0.02890	-0.09687	0.03989	-0.00527	0.18088	0.00190	-0.01670	0.00527	0.00068	0.167**
	P	-0.00436	-0.00021	0.00360	-0.00571	0.00514	0.13413	-0.00093	0.00622	0.00484	-0.00008	0.143**
Days to flowering	G	-0.10431	0.00263	0.08888	-0.02108	0.00030	0.04371	-0.01039	0.00446	-0.01974	0.00990	-0.006
	P	0.01564	-0.00003	-0.00329	0.00266	-0.00078	0.01035	-0.02392	-0.00160	-0.01880	-0.00140	-0.021
Days to maturity	G	-0.12517	-0.02326	0.03553	0.00011	-0.00239	0.23157	-0.01704	-0.00027	-0.00474	0.04126	0.136*
	P	0.01938	0.00022	-0.00131	-0.00003	0.00221	0.14824	-0.04101	0.00009	-0.00479	-0.00549	0.118*

Residual effect = 0.07835 (P), -0.10060 (G)

*$P \leq 0.05$; and **$P \leq 0.01$

Conclusion

Sufficient genetic variability was observed for seed yield and its component traits suggesting the scope of selection and hence improvement for these traits. High heritability coupled with high genetic advance was observed for 100-seed weight, seed yield per plant and biological yield per plant. So selection based on phenotypic performance of genotypes for these traits could increase the mean performance of the selected progenies. In general, genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients indicating the inherent association among the various traits. Seed yield per plant showed significant and positive correlation with all the characters studied except days to flowering indicating that selection for higher seed yield per plant through these traits would be effective. Path analysis revealed positive and high direct effects on seed yield per plant by biological yield per plant followed by harvest index. Highest indirect effects were observed on seed yield per plant through biological yield per plant followed by branches per plant, plant height and harvest index. The path analysis suggested the importance of high biomass in improving the seed yield in common bean genotypes. In common bean breeding programme, preference should be given for high biomass to develop high yielding genotypes.

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