

Genetic variability, heritability and genetic advance in Lentil (*Lens culinaris* Medik.)

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ABSTRACT

The present study was carried out to study the variation, broad-sense heritability, and genetic advance, correlation among traits for growth, yield, and its attributing traits in lentil genotypes. Sixty lentil genotypes were evaluated in augmented design in 2020 at Khajura, Banke. The results indicated that the genotypes were significantly different for days to flowering, days to maturity, 500 seed weight and grain yield kg/ha. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variance (GCV) for all traits. The 500 seed weight showed the highest PCV (22%) and GCV (21%) whereas days to maturity showed the lowest PCV (5.5%) and GCV (3.2%). The highest value (90%) of heritability (broad sense) was in and lowest (3%) in pods per plant. Genetic Advance Mean 40% was the highest for seed weight but lowest at 1.2% in pods per plant. Grain yield showed a positive and significant correlation in genotypic level with days to maturity ($r = 0.7^{**}$), plant height ($r = 1.66^{*}$), pods per plant ($r = 1.15^{**}$) and seed weight ($r = 0.56^{*}$). Path analysis found that the seed weight had the most impact on grain yield followed by pod per plant. Thus, selection for yield in lentils through these characteristics would be effective in the varietal developmental program.

Keywords: Correlation, Heritability, Path analysis, Lentil

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INTRODUCTION

Lentil (*Lens culinaris* Medik. subsp. *culinaris*) is a major cool season grain legume of the Indian Sub-continent, the Middle East, North America, North Africa and West Asia including Bangladesh (Erskine *et al.*, 1996). It is one of the first domesticated pulse crops that originated from the Near East center of origin (Zohary, 1999) and subsequently spread to central Asia and the Mediterranean Basin (Cubero, 1981; Lev-Yadun, 2000). Lentil is grown in a total of 5.0 million hectares of land worldwide and the top 5 countries are Canada, India,

Australia, Türkiye and Nepal (FAO, 2020). In Nepal, lentil is the main pulse crop accounting for 62.64% of the area and 64.35% in the production of the total legume area and production. (Darai *et al.*, 2017).

The study on genotypic and phenotypic correlations is an essential tool in crop improvement. Genetic variation between and within populations of crop species is a major interest of plant breeders and geneticists for its improvement (Hayward and Breese, 1993). A breeder will be able to define to what extent the environment impacts on yield by determining genotypic and phenotypic yield and yield attributes of diverse crop genotypes (Ullah *et al.*, 2012). Lentil showed a wide range of significant morphological variations among different quantitative characteristics that have also been described for use in breeding and selection programs in lentil (Sarker & Erskine, 2001). Knowledge of the genetic variation and relationship between lentil genotypes is important for the efficient utilization of germplasm resources (Saini *et al.*, 2004). Therefore, the lentil breeders have a great opportunity to yield betterment by exploiting the genetic variations that exist in germplasm (Roy *et al.*, 2013). Usually, direct selection for seed yield is misleading because it is highly influenced by component characters and environment. Moreover, grain yield depends on a number of yield attributing characters (Nath *et al.*, 2014). Therefore, to improve yield, it is necessary to estimate the correlation between the contributing features and seed yield (Das & Sarma 2015). The degree of variability present in the germplasm can be determined using genetic factors like the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Idris 2012). Therefore, the goal of the present study was to assess the genetic variability and relationship between morphological traits and yield by identifying the attribute that contributed most to variation in lentil yield that might be improved by breeding programs.

MATERIALS AND METHODS

Site selection for research

The present experiment was conducted at Grain Legume Research Program, Khajura Banke in (Longitude 81° 59" E and Latitude 28° 11" N) Terai region of Lumbini province. The trial was evaluated in 2020. The physical and chemical composition of soil in this location is clay (34.68%) and Sand (18.88%). The pH value is slightly acidic at 6.52. The soil has 2.16% organic matter. Available major plant nutrients were; Total nitrogen 0.11%, available phosphorus 159.43 kg/ha and potassium 39.24 kg/ha. The annual temperature ranged from 7.6°C to 36°C with 27-63% Relative Humidity (RH). The highest precipitation (17 mm) and humidity (63%) were measured in the July.

Selection of genotypes

Sixty Lentil genotypes including two released variety Khajura Masuro 3 and Sagun were used for research.

Experimental design and cultural practices

Sixty genotypes were evaluated in Augmented Block Design in 10 blocks. The individual plot had 6 rows of 4-meter length, with spacing 25 cm row to row and continuous seeding. Farm yard manure@ 4 t/ha and 20:20:20 kg NPK/ha was applied through Urea, DAP and Murate of potash during field preparation. To manage weed 5 mL Penda methylene (weedicide)/litter water was sprayed just after sowing and one-hand weeding was performed 30 days after sowing.

Data collection and observations

The quantitative characters viz., days to flowering, days to maturity, plant height, number of pods per plant, 500 seed weight and seed yield per hectare were recorded. The plant height and number of pod data were collected from ten single competitive plants of each genotype over three replications.

Data observation and analysis

The phenotypic and genotypic coefficients of (Singh and Chaudhary, 1985), Heritability (in the broad sense) (Johnson *et al.*, 1955), genetic advance (Burton, 1952), and genetic advance as a percentage of the mean (Johnson *et al.*, 1955) were all calculated. The GCV, PCV, Heritability, Genetic advance, and Genetic Advance percentage of the Mean (GAM) were calculated using the following formulas;

$$\text{GCV}(\%) = \frac{\sqrt{\delta^2 g}}{x}$$

$$\text{PCV}(\%) = \frac{\sqrt{\delta^2 p}}{x}$$

where: $\delta^2 g$ = genotypic variance, $\delta^2 p$ = phenotypic variance and x = sample mean.

$$\text{Heritability (h}^2\text{)} = \frac{\delta^2 g}{\delta^2 p}$$

Genetic Advance (GA) = (K) ($\delta^2 p$) (h^2)

Where, GA = expected genetic advance, K = selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes, δp = phenotypic standard deviation and h^2 = heritability (in broad sense).

Expected genetic advance percentage of mean (GAM) was calculated according to (Shukla *et al.*, 2006) as;

$$\text{GAM} = \frac{GA}{x} \times 100$$

where x = Grand mean The Pearson correlation coefficient of growth, yield and its attributing traits was worked out according to the procedure outlined (Eq. 7)

$$r = \frac{\sum i(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i(x_i - \bar{x})^2} \sqrt{\sum_i(y_i - \bar{y})^2}}$$

Where, r = Pearson correlation coefficient

x_i = x variable, y_i = y variable

\bar{x} = Mean of x variable

\bar{y} = Mean of y variable

Statistical analysis

MS Excel 2007 was used to process the experimental data and R-stat 3.5. was used to analyze it.

RESULTS AND DISCUSSION

RESULTS

A trial was conducted to explore the genetic variability and correlations in agromorphological traits in lentil genotypes. The results were evaluated and discussed, with evidence from former research to back them up.

Genetic variability

Recorded all the yield attributing parameters were showed PCV value higher than the GCV value was influencing the expression of traits in given environments. High genotypic and phenotypic coefficient of variation was estimated in 500 seed weight 21 and 22. Similarly, low GCV and PCV (3.2 and 5.5) were estimated in days to maturity in Table 2. The number of pods per plant, plant height, and days to flowering showed a higher difference between genotypic and phenotypic variance, indicating that these traits were heavily influenced by the environment.

Heritability and genetic advance

Heritability is a vital parameter for analyzing quantitative characters. In present study, days to flowering, days to maturity, seed weight and grain yield showed high heritability in Table 1. The highest heritability (90%) was found in 500 seed weight, followed by (40 %) in days to maturity. Traits showed high heritability indicating their importance for getting priority for the improvement of seed yield lentil through the selection of different traits. However, low heritability (3%) observed in number of pods per plant and (8%) in plant height.

The genetic advance serves as an appropriate indicator of the improvement that may be predicted as a result of applying selection to the relevant genotypes. In this study seed weight showed the highest GAM in (40%) and moderate in days to flowering (11%) and grain Yield (19%) however days to maturity (4%), plant height (2%) and number of pods per plant (1.2%) estimated lower GAM.

Table 1: Estimation of genetic parameters for quantitative traits in lentil genotypes

Parameters	Range	General Mean	Variance		CV%		Heritability %	Genetic Advance	Genetic Advance (1%) in mean
			G	P	G	P			
DTF	47-85	63	37	132	9.6	18	20	6.64	11
DTM	121-154	144	22	62	3.2	5.5	40	5.79	4
PH	27-51	39	1.8	22	3.4	12	8	0.78	2.0
NPP	74-158	106	12	388	3.3	18	3	1.27	1.2
SW	8-16	9.9	4.2	4.6	21	22	90	40	40
YLD	982-2161	1537	1708	5995	8.5	16	20	90	19

DTF=Days to flowering, DTM=Days to maturity, PH=Plant height (cm), NPP=Number of pods per plant, SW=500 seed weight (g), YLD=Grain yield (kg/ha), CV= Coefficient of Variation, G=Genotypic, P=Phenotypic

Genotypic and phenotypic correlation coefficient

Values of the genotypic and phenotypic correlation for traits are shown in presented Table 2. Positive and significant correlation indicates that additive gene is less affected by the influence of environment and grain yield (kg/ha) can be directly improved by selecting those characters. In present investigation positive and significant phenotypic correlation was found in seed weight (0.2*) and number of pods per plant (0.09*) with grain yield. Where, days to

flowering and maturity has positive but non-significant correlation with yield (0.03, 0.03 and 0.09), respectively.

Table 2: Phenotypic (P) and Genotypic (G) correlation coefficients among agronomic characters in lentil

Characters		DTF	DTM	PH	NPP	YLD
DTF	G	1.19**	0.4	0.1	-0.6**	0.4
	P	0.4*	-0.2	-0.2	-0.3*	0.03
DTM	G		0.4	0.04	-0.6*	0.7**
	P		-0.2	0.04	-0.2	0.03
PH	G			-0.8**	-0.1	1.66*
	P			0.2	-0.2	-0.1
NPP	G				0.7**	1.15**
	P				0.02	0.09*
SW	G					0.56*
	P					0.2*

DTF=Days to flowering, DTM=Days to maturity, PH=Plant height (cm), NPP=Number of pods per plant, SW=500 seed weight (g), YLD=Grain yield (kg/ha)

Path coefficient analysis

The correlation coefficients between grain yield/ha and the other parameters under evaluation were calculated. Through the use of yield/ha as a dependent variable, the path coefficients were divided into direct and indirect effects. Path coefficient analysis (Table 3) showed that the parameters days to flowering, plant height, pods per plant and seed weight were showed positive direct effect on grain yield. This showed that using direct selection based on these factors will raise grain yield. Path analysis found that the seed weight had the most impact on grain yield followed by pod per plant. However, days to maturity showed negative effects on yield.

Table 3: Phenotypic (P) and Genotypic (G) path coefficient analysis showing direct (bold) and indirect effects of different characters in lentil

Characters		DTF	DTM	PH	NPP	SW	YLD
DTF	G	5.29	-10.44	2.68	0.94	1.98	0.4
	P	0.12	-0.04	-0.03	-0.02	0.12	0.03
DTM	G	6.30	-8.77	1.92	-0.23	1.49	0.7**
	P	0.04	-0.11	-0.02	0.00	0.12	0.03
PH	G	2.59	-3.08	5.46	-3.89	0.58	1.66**
	P	-0.03	0.02	0.11	0.02	0.01	-0.1
NPP	G	1.01	0.41	-4.32	4.92	-0.87	1.15**
	P	-0.02	0.00	0.02	0.13	-0.02	0.09*
SW	G	-4.69	5.82	-1.42	1.91	2.24	0.56*
	P	-0.05	0.05	0.00	0.01	0.27	0.2*

DTF=Days to flowering, DTM=Days to maturity, PH=Plant height (cm), NPP=Number of pods per plant, SW=500 seed weight (g), YLD=Grain yield (kg/ha)

DISCUSSION

Available of significant degree of genetic diversity is indicated by GCV, however, the amount of heritable variation can only be analyzed using heritability estimates and genetic gain (Rao & Rao, 2015). PCV value was higher than GCV value in all parameters. PCV value higher than the GCV value was influencing the expression of traits in given environments (Mishra *et al.*, 2015; Pandey *et al.*, 2015). The high value of PCV and GCV was reported in seed weight. The high magnitude of GCV indicates the presence of wide

variation in the character to allow further improvement by selection of the individual traits. So, there is plenty of scope for varietal development through selection based on these traits (Biçer & Sakar, 2008; Haddad *et al.*, 1982).

The highest heritability was found in 500 seed weight. Similar high heritability result has been reported by (Magar *et al.*, 2021) in maize and (Bhagasara *et al.*, 2017) in Sorghum. Positive and significant phenotypic correlation was found in seed weight and number of pods per plant with grain yield. Similar results also observed by (Abo-Hegazy *et al.*, 2012; Mekonnen *et al.*, 2014; Tadele *et al.*, 2014) who stated positive and significant correlation in number of pods per plant and seed weight with grain yield.

CONCLUSION

The phenotypic variations in the characteristics studied were higher than the genotypic variances, indicating that these traits are more affected by environmental factors. The correlation analysis revealed that grain yield per hectare was significantly and positively correlated to seed weight and number of pods per plant. The yield may be increased by improving these traits. A yield path analysis revealed that seed yield and pod per plant had the highest direct effect. These characteristics significantly influenced yield and therefore escalation the success of breeding research of lentil in the Lumbini region of Nepal.

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Authors' contributions

P.P. Poudel and R. Darai designed the research plan. R. Sah and K. Subedi implement the trial and recorded data. P.P. Poudel analyzed data and prepared the manuscript. L. Aryal, R. Darai, B. Acharya and J. Shrestha provided comments and feedback and revise to finalize this manuscript. Final form of manuscript was approved by all authors.

Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

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