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Exploring Genetic Parameters and Yield-Related Traits in Indigenous Lentil Germplasm

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Abstract

An experiment encompassing seventy genotypes of Lentil (*Lens culinaris* Medik.) was conducted at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiya (U.P.) during the *Rabi* season of 2021-22. The genotypes exhibited significant variability across traits such as days to 50% flowering, days to maturity, plant height, number of pods per plant, number of primary branches, number of secondary branches, number of seeds per plant, hundred-seed weight, and seed yield per plant. Genetic variability studies revealed substantial variation among the twenty genotypes, with the highest phenotypic and genotypic coefficients of variation recorded for the traits of number of pods per plant, number of primary branches, and 100-seed weight. Genotypic coefficients of variation ranged from 4.72 (days to 50% flowering) to 25.75 (seed yield per plant). Traits like days to maturity, days to 50% flowering, seed yield per plant, number of primary branches, number of pods per plant, and number of seeds per pod exhibited high heritability, coupled with moderate to high genetic gain and genotypic coefficients of variation. Significant positive correlations were observed at the phenotypic level, with seed yield per plant showing highly significant positive correlation coefficients with the number of pods per plant (0.643), number of secondary branches (0.456), number of primary branches (0.215), and plant height (0.387).

Key words: *Lentil, Lens culinaris, genetic variability, GCV, PCV, heritability, genetic advance, correlation*

Introduction

Lentil *(Lens culinaris* Medik.) stands out as an edible diploid, autogamous species and is regarded as one of the oldest cultivated crops globally. Renowned for their nutritional richness, lentil is a source of protein, micronutrients, minerals, vitamins, and both soluble and insoluble dietary fibres. It holds significance as a vital dietary component and serves as an effective complement to cereals like wheat, maize, and rice, creating a nourishing meal that balances a spectrum of essential amino acids. It is attributable to important dietary sources and effective complementary foods with cereals like wheat, maize and rice, making a nourishing meal by balancing most essential amino acids (Mekonnen et al. 2014). Because of having better carbon sequestration, lentil is very important for improving soil health (Kumar *et al*. 2013). Yield is one of the major complex traits that is an outcome of the interaction of plant traits. It is highly influenced by environmental fluctuation (Tadesse *et al.* 2014). The direct selection based on the seed yield of plants without considering other traits of interest may be ambiguous. In the examination of yield and yield contributing traits, conducting association analysis is a more effective method (Mahajan *et al*. 2011).

Path analysis is a structural technique to assess the relationships between a dependent variable and two or more independent traits or variables. However, the correlation of traits and path coefficient analysis must be considered to understand the impact of genotype and environment towards the final yield before selection (Kumar *et al*. 2013; Hussan *et al*. 2018). Therefore, considering the importance of generating information on genetic variability, heritability, genetic advance, and association of traits that could be made in introduced lentil genotypes as pre-requisite for improving the crop, and the importance of information on the association of protein content and agro-morphological traits in lentil breeding programs. The primary objectives of this study were to assess the genetic variability, heritability, and genetic advance in lentil genotypes for morpho-agronomic traits. Furthermore, the study intended to estimate the association of traits and determine the direct and indirect effect on seed yield and yield-attributing traits of lentil genotypes.

Materials and Methods

Lentil *(Lens culinaris* Medik.) stands out as an edible diploid, autogamous species and is regarded as one of the oldest cultivated crops globally. Renowned for their nutritional richness, lentil is a source of protein, micronutrients, minerals, vitamins, and both soluble and insoluble dietary fibres. It holds significance as a vital dietary component and serves as an effective complement to cereals like wheat, maize, and rice, creating a nourishing meal that balances a spectrum of essential amino acids. It is attributable to important dietary sources and effective complementary foods with cereals like wheat, maize and rice, making a nourishing meal by balancing most essential amino acids (Mekonnen et al. 2014). Because of having better carbon sequestration, lentil is very important for improving soil health (Kumar *et al*. 2013). Yield is one of the major complex traits that are an outcome of the interaction of plant traits. It is highly influenced by environmental fluctuation (Tadesse *et al.* 2014). The direct selection based on the seed yield of plants without considering other traits of interest may be ambiguous. In the examination of yield and yield contributing traits, conducting association analysis is a more effective method (Mahajan *et al*. 2011). Therefore, considering the importance of generating information on genetic variability, heritability, genetic advance, and association of traits that could be made in introduced lentil genotypes as a pre-requisite for improving the crop, and the importance of information on the association of protein content and agro-morphological traits in lentil breeding programs.

Results and Discussion

The statistical analysis utilized the mean values of quantitative traits derived from five randomly selected plants within each genotype. These average data for the nine characters underwent analysis of variance to evaluate the experimental design. Table 1 displays the mean sum of squares for various morphological traits. The analysis of variance revealed notable differences among the germplasm lines for all characters. This designates that the manifestation of a sufficient degree of variability in the tested genotypes will improve the possibility of getting better lentil genotypes through selection. Various scholars formerly explained the highly significant morpho-agronomic trait differences among lentil genotypes (Pandey *et al*., 2015; Hussan *et al*., 2018; Sakthivel *et al*., 2019). The estimated range and mean for all studied traits also indicated wide ranges of variation, which revealed a possible amount of variability among the genotypes in Table 2.

Table 1: Analysis of variance for nine characters of lentil genotypes.

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of secondary branches /plant	No. of pods /plant	No. of seeds/ pod	100-seed weight (g)	Seed yield/ plant (g)
Replications	2	68.51	119.05	268.31	1.37	94.24	442.43	0.09	5.01	47.54
Treatments	69	78.57**	15.83**	52.26**	1.53**	19.48*	9890.62**	0.06**	0.77**	15.86**
Error	138	10.02	15.83	22.51	0.55	12.63	3615.73	0.02	0.31	5.22

** and * = Significant at 1% and 5% probability levels, respectively.

Table 2: Estimates of range mean and genetic variability components of lentil genotypes.

Trait	Range		Mean	GCV (%)	PCV (%)	H^2 (BS)	GA	GA (%)
	Min.	Max.						
Days to 50% flowering	85.57	109.2	101.4	4.72	5.66	69.50	10.51	10.37
Days to Maturity	108.46	137.0	127.4	4.95	5.85	71.44	14.04	11.04
Plant Height (cm)	24.58	52.85	45.64	6.90	12.47	30.58	4.59	10.07
No. of primary branches/plant	3.95	7.63	5.33	10.74	17.78	37.27	0.92	17.29
No. of secondary branches/plant	22.93	36.27	31.03	4.87	12.45	15.30	1.56	5.03
Number of pods/plant	155.8	403.3	270.2	16.92	27.96	36.65	73.09	27.05
Number of seeds/pods	1.35	1.98	1.68	7.00	11.60	36.40	0.18	11.15
100-seed weight (g)	2.33	4.67	3.66	10.63	18.74	32.20	0.58	15.93
Seed yield/plant(g)	2.23	13.17	7.31	25.75	40.51	40.41	3.16	43.22

H^2 (BS) = Heritability (h^2) Broad sense (%), GA = Genetic advance, GA (%) = Genetic advance as % of mean

The amount of genotypic and phenotypic variability that exists in a species is essential and a prerequisite for developing better varieties and initiating a breeding program. The estimation of variance components, genotypic and phenotypic coefficient variations are explained in Table 2. Genotypic and phenotypic coefficient of variation were categorized as high > 20%, medium 10%—20%, and low < 10% according to Deshmukh *et al.* (1986). Based on this explanation, a high phenotypic coefficient of variation (PCV) estimate was observed for seed yield/plant (40.51%) and number of pods per plant (27.96%), while a high Genotypic coefficient of variation (GCV) was observed only for seed yield/plant (25.75%). Medium estimates were observed for both the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) in traits such as the number of primary branches/plant (PCV: 10.74%, GCV: 17.78%) and 100-seed weight (PCV: 10.63%, GCV: 18.74%). Similarly, traits like plant height (PCV: 12.47%), number of secondary branches per plant (PCV: 12.45%), and number of seeds per pod (PCV: 11.60%) exhibited only moderate PCV, while the number of pods per plant (16.92%) showed only moderate GCV. In contrast, low estimates of both PCV and GCV were recorded for days to 50% flowering (PCV: 4.72%, GCV: 5.66%) and days to maturity (PCV: 4.95%, GCV: 5.85%). These findings align with those of Paliya *et al.* (2015), who similarly reported medium PCV for traits such as harvest index, days to 50% flowering, and plant height. Hussan *et al.* (2018) and Sakthivel *et al*. (2019) noticed high GCV for the number of seeds/pod and seed yield.

The disparity between PCV and GCV was notably lower for traits such as days to 50% flowering and days to maturity compared to other traits considered. This minimal difference suggests that a larger portion of the phenotypic variation can be attributed to genetic factors, indicating a reduced influence of the environment. Comparable findings were reported by Lego and Nath (2016) and Gautam *et al*. (2014). The differences between PCV and GCV were recorded for days to 50% flowering and days to maturity, which were relatively less than the other considered traits. This minimum difference between PCV and GCV expressed that more of the phenotypic expression came from genotypic influences and as well as it also indicated that the environmental influence was less. Similar results were observed by Lego and Nath (2016) and Gautam et al. (2014).

Heritability estimates in a broad sense ranged from 15.30% for the number of secondary branches per plant to 71.44% for days to maturity (Table 2). Citing the categorization by Robinson *et al*. (1949), heritability values were classified as high (> 60%), moderate (40–60%), and low (< 40%). In accordance with this classification, the heritability estimates were high for days to 50% flowering (71.44%) and days to maturity (69.50%). Such high values suggest a lesser influence of environmental conditions on these traits, indicating that the observed phenotypes closely reflect their genotypes. Consequently, mass selection based on phenotypic performance would be reliable for lentil improvement, facilitating the increased frequency of favourable alleles through hybridization. Moderate heritability was observed for seed yield/plant (g), while low heritability was noted for the number of primary branches/plant (37.27%), number of pods/plant (36.65%), number of seeds/pod (36.40%), 100-seed weight (32.20%), plant height (30.58%), and number of secondary branches/plant (15.30%). These findings suggest a higher environmental influence on these traits, indicating that their phenotypic expression is more susceptible to environmental factors.

Table 4: Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficient of nine traits for sixty genotypes lentil.

TRAITS	DF	DM	PH	NPBP	NSBP	NPPP	NSPP	HSW	SYPP
DF	**1.000**	0.972**	0.251**	0.025	0.067	0.071	-0.049	0.060	0.112
DM	0.963**	**1.000**	0.223**	0.055	0.056	0.068	-0.069	0.071	0.107
PH	0.493**	0.411**	**1.000**	0.071	0.368**	0.334**	0.003	0.009	0.387**
NPBP	0.018	0.090	0.287**	**1.000**	0.291**	0.257**	-0.151*	-0.141*	0.215**
NSBP	0.265**	0.215**	1.166**	0.995**	**1.000**	0.549**	-0.091	-0.045	0.456**
NPPP	0.150*	0.141*	0.742**	0.644**	1.016**	**1.000**	0.107	-0.229**	0.643**
NSPP	-0.164*	-0.191**	0.275**	-0.123	-0.264**	0.210**	**1.000**	0.096	-0.001
HSW	0.026	0.050	-0.300**	-0.230**	-0.294**	-0.630**	0.080	**1.000**	-0.106
SYPP	0.194**	0.175*	0.935**	0.624**	0.968**	0.898**	-0.081	-0.519**	**1.000**

** and * = Significant at 1% and 5% probability levels, respectively.

DF=Days to 50% flowering, DM=Days to maturity, PH= Plant height (cm), NPBP= No. of primary branches/plant, NSBP= No. of secondary branches/plant, NPPP=No. of Pods/plant, NSPP= No. of seeds/pod, HSW=100-seed weight(g), SYPP= Seed yield/plant (g)

Genetic advance as a percentage of the mean is commonly categorized as low, moderate, and high, corresponding to ranges of < 10%, 10–20%, and > 20%, respectively (Johnson et al., 1955). In line with this classification, seed yield per plant (43.22) and number of pods per plant (27.05) exhibited high genetic advance. The number of primary branches/plant (17.29), 100-seed weight (15.93), number of seeds per pod (11.15), number of pods/plant (36.65%), days to maturity (11.04), days to 50% flowering (10.37), and plant height (10.07) showed moderate genetic advance. Conversely, the genetic advance was low for the number of secondary branches per plant (5.03). The majority of traits exhibited moderate heritability and moderate to high genetic advance, suggesting an equal influence of additive and non-additive gene action in their manifestation. These findings are consistent with studies by Pandey *et al*. (2015), Raturi *et al*. (2015) and Chowdhury *et al*. (2019).

Seed yield is a complex trait influenced by various interconnected factors. Several of these traits are intricately linked both among themselves and with seed yield. Analyzing the relationships among these traits and their associations with seed yield is crucial for establishing effective selection criteria (Singh and Ceccerelli, 1996). Table 4 presents the estimates of phenotypic and genotypic correlation coefficients between each pair of traits. Seed yield/plant exhibited a significant positive phenotypic correlation ($P \leq 0.01$) with the number of pods/plant (0.643), followed by the number of secondary branches/plant (0.456), plant height (0.387), and number of primary branches/plant (0.215). The strong positive correlation between seed yield and these yield-related traits suggests that these traits could be targeted for indirect selection to enhance seed yield in the tested genotypes. Similar findings of positive and significant correlations between different traits and yield at the phenotypic level have been observed by Hamdi *et al*. (2012), Sharma et al. (2014), and Ghimire and Mandal (2019). Such positive correlations between desirable traits are crucial for plant breeders as they facilitate the simultaneous improvement of both traits (Bhima *et al*., 2016).

Seed yield per plant exhibited a highly significant positive correlation at the probability level of ($P \leq 0.01$) with the number of secondary branches per plant (0.968), plant height (0.935), number of pods per plant (0.898), number of primary branches per plant (0.624), and days to 50% flowering (0.194). Additionally, significant associations were observed at the probability level of ($P \leq 0.05$) with days to maturity (0.175). These findings suggest that an increase in the number of branches per plant, the number of pods per plant, and other contributing factors positively influences seed yield per plant. However, a highly significant negative correlation was noted between seed yield per plant and 100-seed weight (-0.519). Similar results indicating a significant and positive genotypic association of seed yield per plant with various traits have been reported by Ali *et al*. (2011), Mekonnen *et al*. (2014), Kumar *et al*. (2017), and Pandey *et al*. (2017).

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