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Inter-Relationship between Seed Yield and Some Morphological and Biochemical Traits in Lentil (*Lens culinaris* L.)

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ABSTRACT

Correlation Study with Path analysis was performed on 29 Lentil Genotypes to determine direct and indirect effect of some morphological as well as Biochemical parameters on Yield. Following traits were studied: Root Nodule number, Nodule weight, Primary Root Length, Secondary root numbers, Root Fresh and Dry weight, Plant Height, Pods per plant, Days to 50% Flowering, 100 seed weight, Leaf chlorophyll content, Seed Carbohydrate with Starch content, Seed Protein content and Yield. Considering both genetic Advance and GCV, it was observed that selection for the following characters viz. Plant Height, Pods per plant, Days to 50% flowering, 100 seed weight, Seed Protein content & Yield will be rewarding. Seed Yield per plant showed significantly Positive correlation with the following traits: 100 Seed weight, Pod number per plant, Plant height and seed starch. Negative association with yield was found for Days to 50% flowering. Path coefficient study revealed that there was a strong positive direct effect of 100 seed weight and Pod no. per plant along with Leaf Chlorophyll content on Yield. Hence, direct selection only for Pods number and 100 seed weight will be rewarding as these characters also gave higher heritability % along with high Genetic advance. Plant height gave strong negative direct effect on yield, but it gave a positive correlation due to high indirect effect in association with pod number. It may be due to short winter span of West Bengal which results into forced maturity of the crops. So short plants with higher pod numbers will be desirable for higher yield in short winter span condition.

Keywords: *Seed Protein, Yield, Seed Starch, Genetic*

INTRODUCTION

Lentil (*Lens culinaris*) (2n=2X=14) is an edible pulse. It is a self pollinating diploid with a genomic size of 4gbp. It is a bushy annual plant of the legume family, grown for its lens-shaped seeds. It is about 40 cm tall and the seeds grow in pods, usually with two seeds in each.

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Lentils have been part of the human diet since the aceramic (before pottery) Neolithic times, being one of the first crops domesticated in the Near East. Lentils with about 30% of their calories from protein, have the third-highest level of protein (25%), by weight, of any legume or nut, after soybeans (42%) and hemp (31%). Proteins include the essential amino acids isoleucine and lysine, and lentils are an essential source of inexpensive protein in many parts of the world, especially in West Asia and the Indian subcontinent, which have large vegetarian populations. Under current situation the principal aim of lentil production is to obtain high yield. Therefore, we must use the available lentil species towards this aim. Genotype and environmental conditions are dominant factors influencing the amount of harvested yield. Even though environmental conditions are partially controllable, genotype of the plant can only be changed by breeding. Information on genetic variability and heritability is useful to formulate selection criteria for improvement of seed yield. As we know, yield stability is a major objective in any breeding program. This could be achieved through a better understanding of the components contributing to final yield. However, these components vary from year to year and from location to location, even for the same lentil genotype (Muehlbauer et al., 1985 from). Negative correlations are often found between morphological components of yield in crop plants. They probably arise primarily from developmentally-induced relationships. Path analysis is used to determine the amount of direct and indirect effects of the causal components on the complex component (Güler et al., 2001).

With the view of above mentioned preface my current research objective has been aimed to study the genetic variability among the yield attributing and biochemical characters of lentil genotypes and to understand both the direct and indirect relationships between yield and the other plant characters in order to select the lentil genotypes with high yield potential.

MATERIALS AND METHODS

The experiment was conducted at District seed farm A-B Block, Kalyani, Nadia under Bidhan Chandra Krishi Viswavidyalaya. Material consisted of 29 Lentil Genotypes availed from the ICARDA and AICRP on Lentil, BCKV, West Bengal. The seeds were sown in Randomised Block Design with 10cm x 25cm spacing. The recommended dose of fertilizer was N: P: K @ 20:40:20 kg/ha. Data were recorded from three randomly taken plants from each plot in each replication excluding the border lines on Plant Height (cm), Root nodule numbers, Weight of total nodules/plant, Length of primary root (cm), Number of Secondary Roots, Root Fresh Weight (g), Root Dry weight (g), Days to 50% Flowering, 100 Seed Weight, Pod number per plant, Leaf Chlorophyll content at 45 DAS and 65 DAS (g/mg), Seed Total Carbohydrate (g/100g) [Anthrone Method], Seed Starch content (g/100g) [Anthrone Method], Seed Protein content. (g/100g) [Bradford protein assay] and Seed Yield per plant (g), The average data were subjected to standard statistical techniques for analysis of variance to test the significance level of variation among the genotypes for different characters according to Burton & De vane. (1953). The genetic advance was calculated as per formula given by Johnson et al. Genetic parameters, correlation coefficients were computed according to the method suggested by Singh & Chaudhry (1979). The significance of genotypic correlation coefficients was tested with the help of standard errors as suggested by Reeve & Rao (1981). Path co-efficient analysis splits the correlation co-efficients into direct and indirect effects. It measures the direct and indirect contribution of independent variables on dependent variable. Path co-efficient analysis was suggested by Wright (1934) and elaborated by Dewey and Lu (1959).

RESULT AND DISCUSSION

The analysis of variance for the Randomized Block Design, accommodating 29 lentil genotypes was done for 15 characters. The mean squares due to Replication, treatments and error for all the characters are presented in **Table 1.** The estimates of phenotypic and genotypic coefficient of variability for 15 characters are reported in **Table 2**. In general, magnitude of phenotypic coefficient of variability (PCV) was Higher than genotypic coefficient of variability (GCV) for all the morphological as well bio chemical traits. Plant height, Days to 50 % flowering, Seed Protein and Starch content showed medium magnitude, whereas Leaf Chlorophyll content gave low estimates (less than 10%) of PCV and GCV. The high magnitude (more than 20%) of PCV along with GCV was observed for Nodule Number, Weight of Nodules, Primary Root Length, Secondary Root number, Root Fresh weight, Root Dry weight, 100 seed weight, Pods per Plant and Yield. Heritability (broad sense) estimates were high (>80%) for Plant Height, Root Fresh and Dry weight, 100 seed weight, Pods/Plant, Yield [Balyan and Singh**,** 1986 also reported significant genetic variability for plant height (cm), pods per plant, 100-seed weight (g), days to maturity, peduncles per plant and seed yield per plant (g).] and Leaf Chlorophyll content and for Seed Protein Content. Moderate Heritability was observed for. Characters showed moderate heritability estimates are Seed total Carbohydrate and Starch Content. Primary root length showed comparatively low heritability. Genetic advance as per cent of mean for different characters ranged from 12.12 % to 71.91% and were high for almost all the characters except seed carbohydrate and starch content. The tallest plant was recorded 52.1 cm with the shortest as 32.5 cm. Heritability was High (97.9%) with high genetic advance (39.16%). This revealed plant height was governed by additive gene action and selection for this character will be effective. Similarly Nodule weight & number, Secondary root numbers, Root weight, Days to 50% flowering and Seed Protein content showed higher Heritability with high genetic advance and indicate that selection will be awarding. In case of Seed Carbohydrate and Starch content lower GCV value (7.78 and 11.8 respectively) along with Medium Heritability (57.2 and 55 respectively) and medium Genetic advance value (12.12-13.50) indicating influenced by environmental effects which limits improvement through selection. Wide variation in number of pods per plant was observed with a maximum value of 107 and minimum value of 37. Heritability was found to be moderate (70.8%) indicating environmental influence. But considering both genetic Advance and GCV, selection for plant hight would be effective due to preponderance of additive genes as revealed by their high values. Similarly for 100 seed weight and Yield selection will be rewarding.

Association of seed yield per plant with all the other parameters, presented in **Table 3,** was positive and significant with 100 Seed weight (rg = 0.533, rp = 0.415), Pod number per plant (rg= 0.701, rp=0.635), Plant height (rg = 0.992. rp =0.571) and seed starch content (rg= 0.607, rp = 0.334). Negative association with yield was found for Days to 50% Flowering (rg = -0.349, rp = -0.249) [**Shrivastava** (1993) also reveled negative association of 50% flowering date with 100 seed weight and plant height]. Pod numbers per plant showed strong negative correlation with Days to 50% Flowering but it showed positive significant association with Plant height. It illustrate higher yield was obtained with short duration genotypes particularly in short winter span of West Bengal.

Correlation coefficients are the indication of simple association between variables. In a biological system, however, the relationships may exist in a very complex form. It is therefore, essential to study the relationships among the variables in a comprehensive way. Path coefficient analysis is a powerful tool which enable partioning of the given relationship in its further components. In other words, it taken into account not only the relationship of a component characters with a dependent character (seed yield in present case) but simultaneously takes care of its relationship with other components also. Thus it helps in understanding causes of a given effect. The main effects of all the three traits mentioned above except for leaf chlorophyll content were significantly positive. The direct and indirect effects of different characters on seed yield per plant estimated under genotypic and phenotypic path coefficient analysis using simple correlations are given in **Table4.** Path analysis showed that only Pod Number per plant , 100 seed weight and leaf chlorophyll content had strong positive direct effects (1.823, 0.568 and 0.537 respectively), in that order on the seed yield while other traits had strongly negative or negligible direct effects. Days to 50% flowering exerted negative direct effect towards yield (-0.266). Most importantly though Plant height had high positive correlation with yield but it gave a negative direct effect (-1.141) on yield. It may be due to environmental effect as Sowing was late (last week of November) which may exerted a significant adverse effect on plant growth and development as the crops were subjected for forced maturity. Though the direct of plant height was negative but it had a high positive correlation with yield due to higher positive indirect effect with Pod numbers.

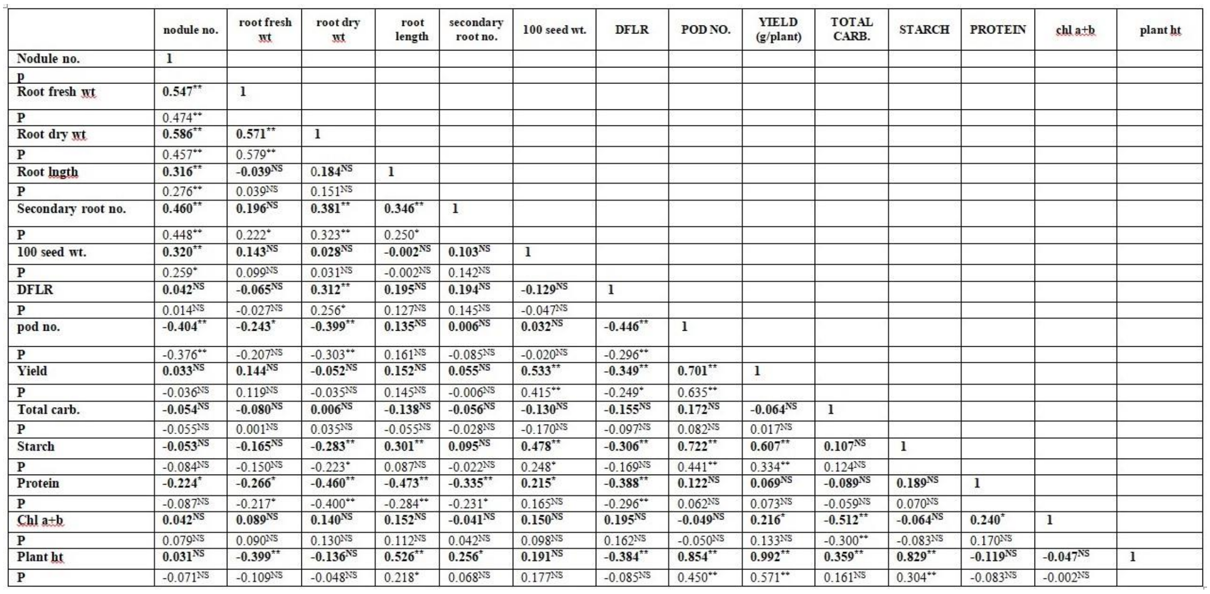
Table 1: Analysis of Variance

Character		REPLICATION	TREATMENT	ERROR
	df	2	28	56
Plant Height	MEAN SUM OF SQUARES	156.90	84.20	55.16
Nodule No.		11.77	61.81	8.62
Wt. of Nodule		0.00015	0.00064	$5.6X10^{-5}$
Primary root Length		0.27	11.47	3.21
Secondary root No.		0.56	41.63	4.83
Root fresh wt.		0.0050	0.039	0.0018
Root Dry wt.		0.00022	0.0027	0.00014
Days to 50% Flowering		0.21	334.68	20.57
100 seed wt.		2.72	312.85	20.08
Pods/Plant		149.70	1137.70	137.46
Yield		0.35	0.52	0.58
Leaf Chlorophyll		0.44	2.00	0.17
Seed Total Carbohydrate		10.56	81.22	16.21
Seed Starch Content		38.30	56.43	12.43
Seed Protein		5.24	39.29	2.48

Table 2: Components of variability, Heritability and Genetic Advance of all the 15 characters

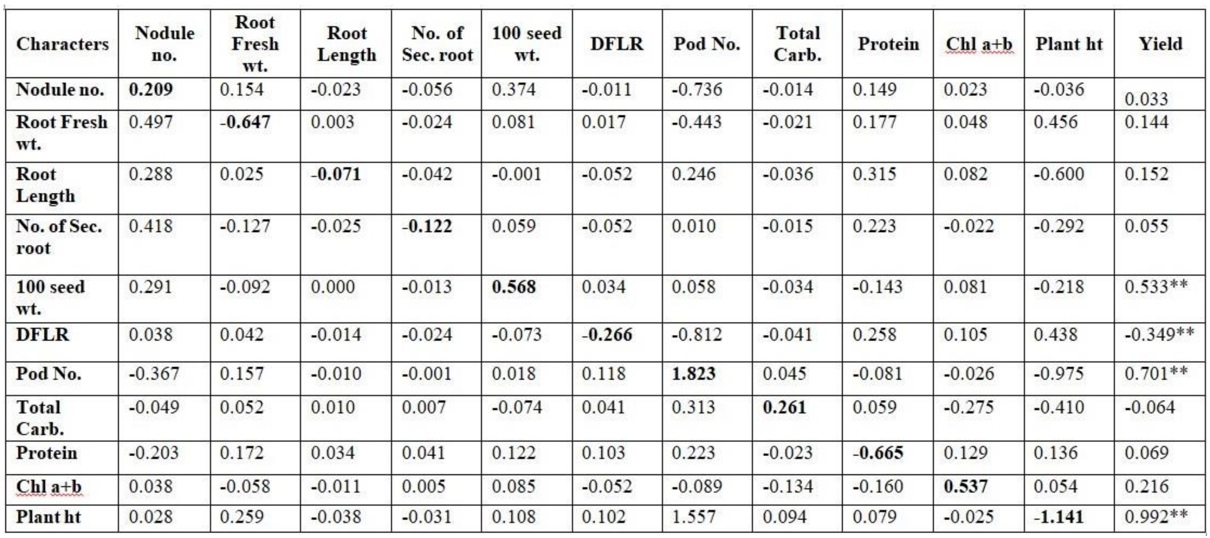
NO.	Characters	Range	GCV	PCV	HERITABILITY(%)	GA % Mean
1	Plant Height	32.3-52.1 cm	19.21	19.41	97.9	39.16
2	Nodule No.	9-27	27.24	33.21	67.3	46.01
3	Wt. of Nodule	0.014-0.068 g	39.59	44.91	77.7	71.91
4	Primary root Length	3.2-11.6 cm	23.82	35.07	46.1	33.33
5	Secondary root No.	5-22	31.71	37.44	71.7	55.31
6	Root fresh wt.	0.19-0.83 g	35.04	37.48	87.4	67.48
7	Root Dry wt.	0.077-0.183 g	24.61	26.53	86.0	47.04
8	Days to 50% Flowering	54-85	14.98	16.39	83.6	28.21
9	100 seed wt.	1.32-4.52 g	28.59	33.82	71.5	49.78
10	Pods/Plant	37-107	28.52	33.89	70.8	49.44
11	Yield	0.93-2.93 g/P	27.4	32.16	72.7	48.21
12	Leaf Chlorophyll	6.42-9.63 g/mg	9.57	10.79	78.6	
13	Seed Total Carbohydrate	40.63-70.44 g/100g	7.78	10.29	57.2	12.12
14	Seed Starch Content	31.72-57.65 g/100g	14.66	27.09	55.08	16.34
15	Seed Protein	19.48-35.07 g/100g	14.18	15.55	83.2	26.64

Table 3: Genotypic and Phenotypic correleation matrix (* = 5% level significance ** = 1% level significance)



	nodule no.	root fresh wt	root dry wt	root length	secondary root no.	100 seed wt.	DFLR	POD NO.	YIELD (g/plant)	TOTAL CARB.	STARCH	PROTEIN	chl a+b	plant ht
Nodule no.	1													
P														
Root fresh wt	0.547**	1												
P	0.474**													
Root dry wt	0.586**	0.571**	1											
P	0.457**	0.579**												
Root lngth	0.316**	-0.039^{NS}	0.184^{NS}	1										
P	0.276**	0.039^{NS}	0.151^{NS}											
Secondary root no.	0.460**	0.196^{NS}	0.381**	0.346**	1									
P	0.448**	0.222*	0.323**	0.250*										
100 seed wt.	0.320**	0.143^{NS}	0.028^{NS}	-0.002^{NS}	0.103^{NS}	1								
P	0.259*	0.099^{NS}	0.031^{NS}	-0.002^{NS}	0.142^{NS}									
DFLR	0.042^{NS}	-0.065^{NS}	0.312**	0.195^{NS}	0.194^{NS}	-0.129^{NS}	1							
P	0.014^{NS}	-0.027^{NS}	0.256*	0.127^{NS}	0.145^{NS}	-0.047^{NS}								
pod no.	-0.404**	-0.243*	-0.399**	0.135^{NS}	0.006^{NS}	0.032^{NS}	-0.446**	1						
P	-0.376**	-0.207^{NS}	-0.303**	0.161^{NS}	-0.085^{NS}	-0.020^{NS}	-0.296**							
Yield	0.033^{NS}	0.144^{NS}	-0.052^{NS}	0.152^{NS}	0.055^{NS}	0.533**	-0.349**	0.701**	1					
P	-0.036^{NS}	0.119^{NS}	-0.035^{NS}	0.145^{NS}	-0.006^{NS}	0.415**	-0.249*	0.635**						
Total carb.	-0.054^{NS}	-0.080^{NS}	0.006^{NS}	-0.138^{NS}	-0.056^{NS}	-0.130^{NS}	-0.155^{NS}	0.172^{NS}	-0.064^{NS}	1				
P	-0.055^{NS}	0.001^{NS}	0.035^{NS}	-0.055^{NS}	-0.028^{NS}	-0.170^{NS}	-0.097^{NS}	0.082^{NS}	0.017^{NS}					
Starch	-0.053^{NS}	-0.165^{NS}	-0.283**	0.301**	0.095^{NS}	0.478**	-0.306**	0.722**	0.607**	0.107^{NS}	1			
P	-0.084^{NS}	-0.150^{NS}	-0.223*	0.087^{NS}	-0.022^{NS}	0.248*	-0.169^{NS}	0.441**	0.334**	0.124^{NS}				
Protein	-0.224*	-0.266*	-0.460**	-0.473**	-0.335**	0.215*	-0.388**	0.122^{NS}	0.069^{NS}	-0.089^{NS}	0.189^{NS}	1		
P	-0.087^{NS}	-0.217*	-0.400**	-0.284**	-0.231*	0.165^{NS}	-0.296**	0.062^{NS}	0.073^{NS}	-0.059^{NS}	0.070^{NS}			
Chl a+b	0.042^{NS}	0.089^{NS}	0.140^{NS}	0.152^{NS}	-0.041^{NS}	0.150^{NS}	0.195^{NS}	-0.049^{NS}	0.216*	-0.512**	-0.064^{NS}	0.240*	1	
P	0.079^{NS}	0.090^{NS}	0.130^{NS}	0.112^{NS}	0.042^{NS}	0.098^{NS}	0.162^{NS}	-0.050^{NS}	0.133^{NS}	-0.300**	-0.083^{NS}	0.170^{NS}		
Plant ht	0.031^{NS}	-0.399**	-0.136^{NS}	0.526**	0.256*	0.191^{NS}	-0.384**	0.854**	0.992**	0.359**	0.829**	-0.119^{NS}	-0.047^{NS}	1
P	-0.071^{NS}	-0.109^{NS}	-0.048^{NS}	0.218*	0.068^{NS}	0.177^{NS}	-0.085^{NS}	0.450**	0.571**	0.161^{NS}	0.304**	-0.083^{NS}	-0.002^{NS}	

Table 4: Path coefficient analysis showing direct and indirect effect of yield component traits in Lentil Residual = 0.301



Characters	Nodule no.	Root Fresh wt.	Root Length	No. of Sec. root	100 seed wt.	DFLR	Pod No.	Total Carb.	Protein	Chl a+b	Plant ht	Yield
Nodule no.	**0.209**	0.154	-0.023	-0.056	0.374	-0.011	-0.736	-0.014	0.149	0.023	-0.036	0.033
Root Fresh wt.	0.497	**-0.647**	0.003	-0.024	0.081	0.017	-0.443	-0.021	0.177	0.048	0.456	0.144
Root Length	0.288	0.025	**-0.071**	-0.042	-0.001	-0.052	0.246	-0.036	0.315	0.082	-0.600	0.152
No. of Sec. root	0.418	-0.127	-0.025	**-0.122**	0.059	-0.052	0.010	-0.015	0.223	-0.022	-0.292	0.055
100 seed wt.	0.291	-0.092	0.000	-0.013	**0.568**	0.034	0.058	-0.034	-0.143	0.081	-0.218	0.533**
DFLR	0.038	0.042	-0.014	-0.024	-0.073	**-0.266**	-0.812	-0.041	0.258	0.105	0.438	-0.349**
Pod No.	-0.367	0.157	-0.010	-0.001	0.018	0.118	**1.823**	0.045	-0.081	-0.026	-0.975	0.701**
Total Carb.	-0.049	0.052	0.010	0.007	-0.074	0.041	0.313	**0.261**	0.059	-0.275	-0.410	-0.064
Protein	-0.203	0.172	0.034	0.041	0.122	0.103	0.223	-0.023	**-0.665**	0.129	0.136	0.069
Chl a+b	0.038	-0.058	-0.011	0.005	0.085	-0.052	-0.089	-0.134	-0.160	**0.537**	0.054	0.216
Plant ht	0.028	0.259	-0.038	-0.031	0.108	0.102	1.557	0.094	0.079	-0.025	**-1.141**	0.992**

CONCLUSION

The analysis of variance revealed that the mean sum of square due to genotypes were significant for all the characters. This indicates that sufficient amount of variability is present among genotypes. Higher value for GCV, PCV, Heritability and Genetic Advance % over mean was recorded for Plant height, Nodule numbers and weight, Root weight along with secondary root numbers, Number of Pods per Plant, 100 seed weight and Yield. This reflects that the traits are governed by additive gene action and as a result selection for these characters will be effective during further breeding programme. 100 seed weight, Pods number, Plant Height and Seed Starch content showed positive significant correlation with yield. Improvement of any of these characters will simultaneously improve the seed yield, specially the first three characters mentioned above. Days to 50 % flowering gave negative correlation coefficient towards yield which reveals Higher yield was obtained with short duration genotypes particularly in short winter span of West Bengal. According to Path analysis Number of Pods per plant showed the highest positive effect towards yield followed by 100 seed weight. Plant height was giving a huge negative direct effect on yield but the effect was hugely minimized due to indirect effect of pods number which reveals that selection of short statured plant with higher pod numbers will be effective.

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