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Research Article

Study on character association in *Lens culinaris* medik.

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Abstract

A field trial with fifty genotypes of lentil was undertaken in Agriculture Farm of the Institute of Agriculture, Visva –Bharati University during two consecutive winters of the year 2017-18 and 2018-19, with an intention to find out the nature of the association between thirteen different plant characters with each other and with yield. A randomized block design was used with three replications. Traits' correlation along with path analysis was studied by focusing on yield as the key output. The study revealed that seed/plant was strong and positively associated with grain yield at the genotypic level. It was also true at the phenotypic level. Direct and indirect effects in path coefficient at genotypic and phenotypic level revealed the effects of various traits on yield either directly or *via* component traits. In the present experimental study, fourteen character combinations of lentil explained that total variance up to 82.74 per cent at the phenotypic level and 82.23 per cent at the genotypic level.

Key words

Phenotypic correlation, Genotypic correlation, Path analysis, Direct effect, Indirect effect

INTRODUCTION

Lentil (*Lens culinaris* Medik.) is a crop having enormous potential to confront the problems of nutritional security, poverty and sustainability in a changing climate. Cultivated lentil is an annual, herbaceous diploid plant with seven pairs of chromosomes (2n=2x=14). It is autogamous and is having a lens-shaped grains. The plant is typically 20–45 cm tall, which produces many small purse shaped pods containing one to two seeds each. Its estimated genome size is 4063Mbp/C (Arumuganathan and Earle, 1991). It is believed to be originated from the Near East center of origin (Zohary, 1999) and grown widely in Mediterranean and semi-arid climates during the cool season. Its grains are rich in 24-26 per cent dietary proteins, vitamins and minerals, carbohydrates and amino acids like lysine and tryptophan (Bhatty, 1988; Savage, 1988). Farmers take this mostly as a rainfed crop during winter. For the improvement of lentil on both the genetic and agronomic front, it is imperative to evaluate the crop systematically. Yield remains to be the prime objective for any breeding programme. However, it is a complex character and resulted due to the interaction of various genes governing diverse traits among themselves as well as with the environment. A successful selection depends upon the information on the association of morpho-agronomic traits with seed yield (Kumar *et al.,* 2013). The correlation coefficient measures the degree and direction of the association between characters. The association among yield contributing traits helps to select the superior genotypes from the divergent population. The estimates of correlation coefficients alone may be often misleading due to the mutual cancellation of component characters. So, the study of correlation coupled with a path analysis is a more effective tool in the study of yield contributing characters (Mahajan *et al.,* 2011). Path analysis is a form of multiple regression statistical analysis used to evaluate causal models by examining the relationships between a dependent variable and two or more independent variables. An attempt was made to identify major yield components and the association of these traits was studied in our present experiment.

MATERIALS AND METHODS

The present field trial was carried out with fifty lentil germplasm at Agriculture Farm of Institute of Agriculture, Visva-Bharati University, West Bengal, India during the winters of the year 2017-18 and 2018-19 under the rice fallow condition. The experiment was laid on Randomized Block Design (RBD) with three replications. A considerable amount of genetic variability was found to exist among the experimental materials *viz.* L-46-05, LL-147, L-14-16-01, L-94-03, LEN-13-13, LIEN-07-E-32, LIEN-07-E-11, E-28, F-23,LIF-03, LIF-03-03, LIF-03-11-07, ILL-10461, ILL-10-971, ILL-10893, ILL-8108, IC-05-03, IC-04-07, WBL-77-108, NDL-01, BLL-66, BLC-18, BLC-60, BLC-138, BLC-97, BLC-139,BLC-127, BLC-103, BLC-16, BLC-180, BLC-08, BLC-98, BLC-58, BLC-32, BLC-88, BLC-173, BLC-126, BLC-01, BLC-25, BLC-90, Moitree, Pusa Ageti, Asha, Ranjan, Subrata, BM-6, BM-4, BM-1, BM-7 and BM-5. The genotypes were randomly allotted in plots to each block. Each plot had inter and intra row spacing of 30 and 10 cm, respectively. Five healthy and competitive plants were randomly selected on the basis of appearance from each plot and data on 14 distinct characters was recorded. Traits were, days to 50% flowering; plant height (cm), primary branches/plant, secondary branches/plant, total branches/plant, root length (cm), nodules/plant, pods/plant, seeds/pod, seeds/plant, biomass (g), 100 seed weight (g), harvest index (%) and grain yield/ plant (g) were subjected statistical analysis using software Windostat Version 9.2. The Calculation of the correlation coefficient at the genotypic and phenotypic level was carried out by using the formula suggested by Johnson *et al.* (1955) and Al-Jibouri *et al.* (1958). The estimates of a direct and indirect contribution of various characteristics under study to seed yield were calculated through path coefficient analysis as suggested by Dewey and Lu (1959).

Table 1. Phenotypic Correlation Analysis for Fourteen Character Combinations

CHARACTERS	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	r_p (X_{14})
X_1.Days to 50% flowering	**1**	0.043	0.161**	0.242 **	0.246 **	0.035	-0.005	0.100	0.043	0.101	0.182 **	-0.105	-0.127*	**0.095**
X_2.Plant Height		**1**	0.279**	0.209**	0.263**	0.332**	0.164**	0.456**	0.074	0.475**	0.431**	0.054	0.157**	**0.468****
X_3.Primary Branches/Plant			**1**	0.369 **	0.657**	0.342**	0.275**	0.480**	0.074	0.473**	0.519**	-0.080	0.014	**0.449****
X_4.Secondary Branches				**1**	0.939**	0.140 *	0.301**	0.650**	0.030	0.575**	0.642**	-0.101	-0.062	**0.546****
X_5.Total Branches/Plant					**1**	0.226**	0.348**	0.698**	0.053	0.635**	0.700**	-0.113	-0.045	**0.599****
X_6.Root Length						**1**	0.202**	0.277**	0.048	0.310**	0.297**	0.119*	0.052	**0.305****
X_7.Nodules/Plant							**1**	0.440**	-0.003	0.376**	0.261**	-0.301**	-0.040	**0.234****
X_8.Pods/Plant								**1**	-0.012	0.921**	0.808**	-0.045	0.194**	**0.835****
X_9.Seeds/Pod									**1**	0.297**	0.104	0.060	0.120*	**0.141***
X_{10}.Seeds/Plant										**1**	0.802**	0.010	0.257**	**0.868****
X_{11}.Biomass											**1**	0.156**	0.009	**0.903****
X_{12}.100 Seed Weight												**1**	0.256**	**0.239****
X_{13}.Harvest Index													**1**	**0.375****

Signifiicance Levels: *(5%) and ** (1%); r_p is phenotypic correlation with grain yield/plant

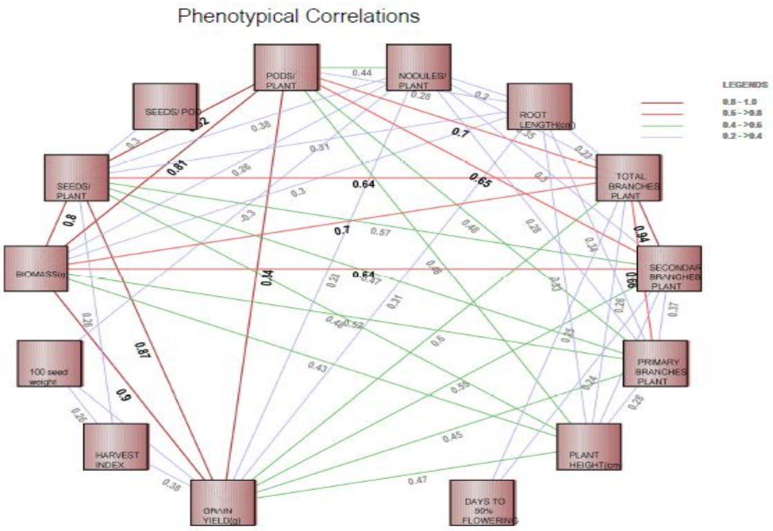

Fig. 1. Phenotypic Correlation Diagram

RESULTS AND DISCUSSION

A simple correlation coefficient was calculated at both genotypic and phenotypic levels. At the phenotypic level, grain yield/plant manifested highly significant and positive correlation with biomass followed by seed/plant, pods/plant, total branches/plant, secondary branches/plant, plant height, primary branches, harvest index, root length, 100 seed weight, and nodules/plant. It had a positive and significant correlation with the number of seeds/pod whereas, insignificant correlation with days to 50% flowering. **Table 1**. represents the direction and magnitude of the phenotypic correlation between characters under study. **Fig. 1.** depicts the phenotypic correlation between traits under study. This kind of result was earlier found by Sarwar *et al.* (2010). Grain yield indicated a positive and highly significant genotypic correlation with all characters under study except for seeds/pod. The highest genotypic correlation of grain yield was recorded with seeds/plant followed by pods/plant, biomass, total branches/plant, secondary branches/plant, primary branches/plant, plant height, nodules/plant, 100 seed weight, root length, days to 50% flowering and harvest index. The values of genotypic correlation have been represented in **Table 2. Fig. 2** depicts the genotypic correlation between traits under study. From the results of genotypic correlation it can be inferred that grain yield was very strongly r > 0.65) and positively associated with traits such as seeds/plant, pods/plant, biomass and total branches/plant.

Table 2. Genotypic Correlation Analysis for Fourteen Character Combinations

CHARACTERS	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	r_g (X_{14})
X_1.Days to 50% flowering	1	0.117*	0.392**	0.406**	0.457**	0.080	0.039	0.199**	0.126*	0.222**	0.329**	-0.193**	-0.209**	**0.209****
X_2.Plant Height		1	0.133*	0.092	0.114*	0.172**	0.168**	0.328**	0.216**	0.370**	0.331**	0.158**	0.014	**0.383****
X_3.Primary Branches/Plant			1	0.283**	0.520**	0.238**	0.222**	0.500**	-0.040	0.396**	0.566**	-0.281	-0.221	**0.403****
X_4.Secondary Branches				1	0.966**	0.052	0.256**	0.667**	0.117*	0.636**	0.708**	0.001	-0.208**	**0.621****
X_5.Total Branches/Plant					1	0.088	0.296**	0.738**	0.079	0.676**	0.782**	-0.092	-0.245**	**0.662****
X_6.Root Length						1	0.181**	0.178**	-0.129**	0.169**	0.227**	0.243**	0.031	**0.214****
X_7.Nodules/Plant							1	0.562**	-0.125**	0.548**	0.270**	-0.311**	0.022	**0.344****
X_8.Pods/Plant								1	-0.084	0.955**	0.802**	-0.083	0.067	**0.882****
X_9.Seeds/Pod									1	0.173**	-0.025	-0.100	0.147*	**0.055**
X_{10}.Seeds/Plant										1	0.762**	-0.089	0.168**	**0.908****
X_{11}.Biomass											1	0.167**	-0.314**	**0.872****
X_{12}.100 Seed Weight												1	0.258**	**0.282****
X_{13}.Harvest Index													1	**0.158****

Significance Levels: *(5%) and ** (1%) ; r_g is genotypic correlation with grain yield/plant

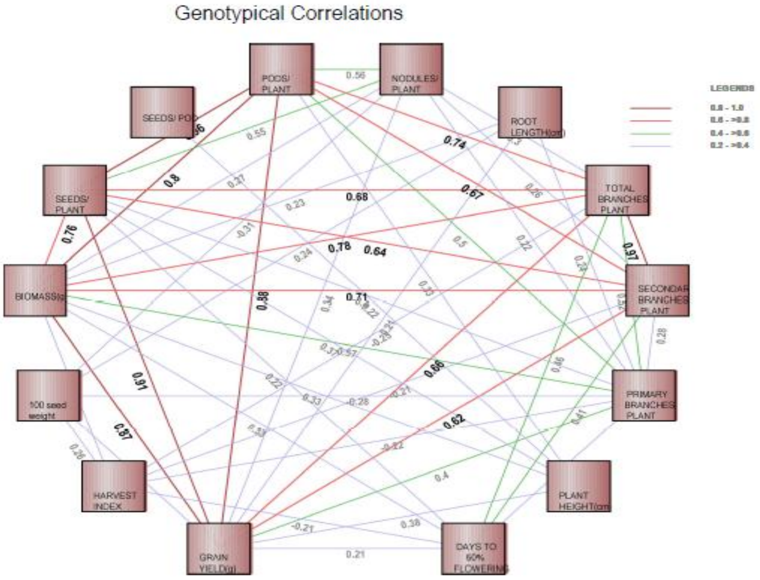

Fig. 2. Genotypic Correlation Diagram

It had a moderately strong association ($0.50 < r < 0.64$) with secondary branches/plant whereas, moderately weak association ($0.30 < r < 0.49$) with primary branches/plant, plant height and nodules/plant. Grain yield has a very weak ($r < 0.30$) association with 100 seed weight, root length, days to 50% flowering and harvest index. This scale was followed as given in Singh and Narayan (1993). It implied that grain yield tends to increase as a consequence of the increase in any of above mentioned characters. Findings by Chakherchaman *et al.* (2009), Kumar *et al.* (2009), Tyagi and Khan (2010), Al-Ghzawi et *al.* (2011), Gupta *et al.* (2012), Alom and Chowdhury (2014), Goghari *et al.* (2014), Kumar and Solanki (2014), Sharma *et al.* (2014), Pandey *et al.* (2015), Yadav *et al.* (2015), and Kumar *et al.* (2017) were in close agreement with such results. By comparing genotypic and phenotypic correlations for traits under examination it can be concluded that genotypic correlation was greater than the phenotypic correlation for seeds/plant, pods/plant, total branches/plant, secondary branches/plant, nodules/plant,100 seed weight and days to 50% flowering. Thus, it can be interpreted that there was a strong association between these characters and yield genetically but the phenotypic value is lessened by environmental interaction. Characters as seeds/pod, biomass, primary branches/plant, plant height, root length and harvest index (HI) had shown a greater phenotypic correlation with grain yield than respective genotypic correlation. This indicated that the apparent association between these characters and yield is not only due to genes, but also favorable influence of the environment. In the present study, considering yield as an effect of thirteen characters as causes that were studied for correlation analysis, phenotypic and genotypic path analyses have been presented in **Table 3** and **Table 4**, respectively. **Fig. 3** and **4** show the phenotypic and genotypic path diagram for grain yield (g).

Table 3. Phenotypic Path Analysis for Fourteen Characters under Study

CHARACTERS	**X_1**	**X_2**	**X_3**	**X_4**	**X_5**	**X_6**	**X_7**	**X_8**	**X_9**	**X_{10}**	**X_{11}**	**X_{12}**	**X_{13}**	**r_p**
X_1.Days to 50% flowering	**-0.010**	-0.005	-0.001	-0.002	-0.002	-0.004	0.001	-0.001	-0.005	-0.001	-0.002	0.001	0.001	0.095
X_2.Plant Height(cm)	0.001	**0.002**	0.007	0.005	0.006	0.008	0.004	0.001	0.002	0.001	0.001	0.001	0.004	0.468**
X_3.Primary Branches/Plant	-0.009	-0.016	**-0.058**	-0.021	-0.038	-0.020	-0.016	-0.028	-0.004	-0.027	-0.030	0.004	-0.008	0.449**
X_4.Secondary Branches	-0.014	-0.012	-0.022	**-0.059**	-0.056	-0.008	-0.018	-0.038	-0.001	-0.034	-0.038	0.006	0.003	0.546**
X_5.Total Branches/Plant	0.013	0.014	0.035	0.050	**0.053**	0.012	0.018	0.037	0.002	0.034	0.037	-0.006	-0.002	0.599**
X_6.Root Length(cm)	0.002	0.002	0.002	0.009	0.001	**0.006**	0.001	0.001	0.003	0.002	0.002	0.008	0.004	0.305**
X_7.Nodules/Plant	0	-0.002	-0.003	-0.003	-0.004	-0.002	**-0.001**	-0.005	0	-0.004	-0.003	0.003	0	0.234**
X_8.Pods/Plant	-0.016	-0.076	-0.080	-0.109	-0.117	-0.046	-0.074	**-0.168**	0.002	-0.154	-0.135	0.007	-0.032	0.835**
X_9.Seeds/Pod	-0.003	-0.006	-0.006	-0.002	-0.004	-0.004	0.003	0.001	**-0.088**	-0.026	-0.009	-0.005	-0.010	0.141*
X_{10}.Seeds/Plant	0.037	0.177	0.177	0.214	0.237	0.115	0.140	0.344	0.111	**0.373**	0.299	0.004	0.096	0.868**
X_{11}.Biomass (g)	0.141	0.334	0.402	0.498	0.542	0.230	0.202	0.626	0.081	0.621	**0.775**	0.121	0.007	0.903**
X_{12}.100 Seed Weight (g)	-0.002	0.001	-0.002	-0.002	-0.002	0.002	-0.007	-0.001	0.001	0.003	0.003	**0.024**	0.006	0.239**
X_{13}.Harvest Index (%)	-0.039	0.049	0.004	-0.019	-0.014	0.016	-0.012	0.060	0.037	0.080	0.003	0.080	**0.312**	0.375**

Residual effect: 0.1726; r_p is phenotypic correlation with grain yield, Bold diagonal values are direct effects

Table 4. Genotypic Path Analysis for Fourteen Characters under Study

CHARACTERS	**X_1**	**X_2**	**X_3**	**X_4**	**X_5**	**X_6**	**X_7**	**X_8**	**X_9**	**X_{10}**	**X_{11}**	**X_{12}**	**X_{13}**	**r_g**
X_1.Days to 50% flowering	**0.201**	0.023	0.079	0.082	0.092	0.016	0.008	0.040	0.025	0.044	0.066	-0.039	-0.042	0.209**
X_2.Plant Height (cm)	-0.012	**-0.104**	-0.013	-0.009	-0.011	-0.017	-0.017	-0.034	-0.022	-0.038	-0.034	-0.016	-0.001	0.383**
X_3.Primary Branches/Plant	-0.773	-0.264	**-1.971**	-0.558	-1.025	-0.470	-0.437	-0.987	0.079	-0.782	-1.116	0.555	0.430	0.403**
X_4.Secondary Branches/Plant	-2.059	-0.467	-1.437	**-5.071**	-4.901	-0.267	-1.298	-3.386	-0.595	-3.226	-3.591	-0.007	1.059	0.621**
X_5.Total Branches/Plant	2.391	0.597	2.720	5.055	**5.230**	0.463	1.552	3.861	0.413	3.537	4.092	-0.484	-1.284	0.662**
X_6.Root Length	0.015	0.033	0.046	0.010	0.017	**0.193**	0.035	0.034	-0.025	0.032	0.044	0.047	0.006	0.214**
X_7.Nodules/Plant	0.005	0.022	0.029	0.034	0.039	0.024	**0.134**	0.075	-0.016	0.073	0.036	-0.041	0.003	0.344**
X_8.Pods/Plant	0.388	0.639	0.973	1.298	1.435	0.346	1.093	**1.944**	-0.163	1.857	1.561	-0.162	0.131	0.882**
$X_{9.}$Seeds/Pod	0.082	0.141	-0.026	0.076	0.051	-0.084	-0.081	-0.05	**0.653**	0.113	-0.016	-0.065	0.096	0.055
X_{10}.Seeds/Plant	-0.468	-0.780	-0.83	-1.338	-1.423	-0.355	-1.154	-2.010	-0.364	**-2.104**	-1.605	0.187	-0.353	0.908**
X_{11}.Biomass	0.550	0.554	0.946	1.183	1.307	0.380	0.451	1.341	-0.042	1.274	**1.671**	0.279	-0.525	0.872**
X_{12}.100 Seed Weight	0.027	-0.022	0.040	-0.002	0.013	-0.034	0.044	0.011	0.014	0.012	-0.023	**-0.143**	-0.037	0.282**
X_{13}.Harvest Index	-0.140	0.009	-0.148	-0.139	-0.164	0.021	0.015	0.045	0.099	0.112	-0.210	0.173	**0.669**	0.158**

Residual Effect: 0.1777

r_g is the genotypic correlation with yield, Bold diagonal values are direct effects.

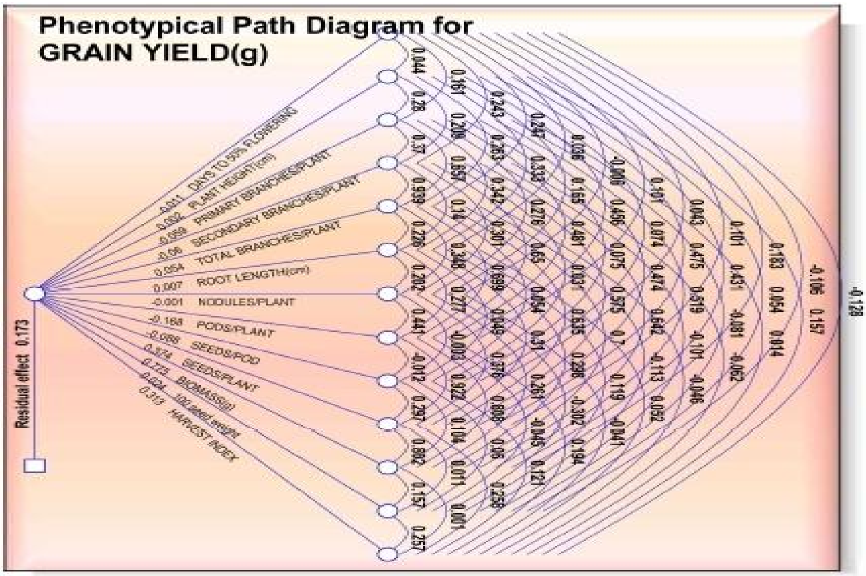

Fig. 3. Phenotypic Path Diagram for Grain yield

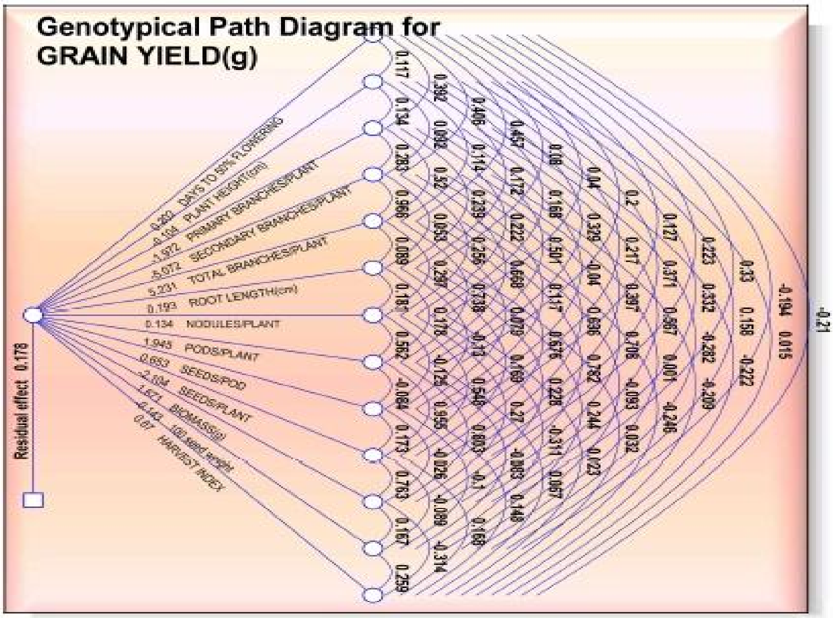

Fig. 4. Genotypic path diagram for grain yield

Biomass had the highest positive direct effect on yield followed by, seeds/plant, harvest index, total branches/plant, 100 seed weight, and root length and plant height. The large gap between direct effects and correlation of traits as biomass, seeds/plant, total branches/plant, root length, plant height and 100 seed weight indicates that the correlation was mainly due to indirect effects of characters via another component trait. Thus, the indirect selection of the above mentioned traits would be rewarding. However, the closeness of phenotypic correlation and phenotypic path coefficient for harvest index revealed a true relation between HI and yield. Thus, direct selection for this trait is rewarding in yield improvement. According to the scale provided by Lenka and Mishra (1973), direct effects of biomass followed by seeds/plant and harvest index were high on grain yield. Negative direct effects were rendered by nodules/plant followed by days to 50% flowering primary branches/plant, secondary branches/plant, seeds/pod and pods/plant. For these traits, the correlation was positive, thus indirect effects seem to be the cause of correlation. In such a situation indirect causal factors are to be considered simultaneously for selection.

Days to 50% flowering exerted positive indirect effects on yield only via nodules/plant, 100 seed weight and harvest index. Plant height, root length, seed/plant and biomass had a positive indirect effect through all characters on yield. Primary branches imparted a positive indirect effect on yield by 100 seed weight. Secondary branches show similar trends with 100 seed weight and harvest index. Total branches had a negative effect through 100 seed weight and harvest index. Nodules/plant had positive indirect effects by 50% flowering, seeds/pod, 100 seed weight and harvest index. Pods/plant had a positive indirect effect via seeds/pod and 100 seed weight. Seeds/pod had a positive indirect effect via pods/plant and nodules/plant. 100 seed weight imparted positive indirect effect via plant height, root length, seeds/pod, seeds/plant, and biomass while. Harvest index had a positive indirect effect via plant height, primary branches, root length, pods/plant, seeds/pod, seeds/plant, biomass and 100 seed weight. This result was supported by Palshetkar *et al.* (2019). The residual effect was calculated to be 0.1726. It implied that the independent variables included in this study explained 82.74 per cent of the total variation in the dependent variable i.e. grain yield. A similar trend of results was observed by Singh *et al*. (2009) for days to 50% flowering, Karadavut and Kavurmaci (2013) for pods/plant, Singh and Srivastava (2013) for branches/plant, Pandey *et al.* (2015) for seeds/plant, Tyagi and Khan (2010) for biomass.

Its estimates had the highest positive direct effect on yield via total branches/plant. According to the scale provided by Lenka and Mishra (1973), the direct effect was very high via total branches/plant followed by pods/plant and biomass on grain yield. The direct effect was negative by the characters plant height, 100 seed weight, primary branches/plant, seeds/plant and secondary branches/plant. For these traits, as the direct effect was negative but the corresponding genotypic correlation was positive, it was evident that indirect effects seemed to be the cause of correlation and indirect causal factor to be considered for selection.

Days to 50% flowering exerted negative indirect effects on yield for 100 seed weight and harvest index. Plant height had a negative indirect effect via all characters. Seeds/plant had shown a similar trend except for 100 seed weight. Primary branches show a positive indirect effect for seeds/pod, 100 seed weight and harvest index. Secondary branches have a positive indirect effect of harvest index only. Total branches had a negative indirect effect through 100 seed weight and harvest index. Root length imparted a positive indirect effect via all characters except for seeds/pod. Nodules/plant exerted a negative indirect effect via seeds/pod and 100 seed weight. Pods/plant had shown a positive indirect effect via all characters except for seeds/pod and 100 seed weight. Seeds/pod manifested negative indirect effect via primary branches, root length, nodules/plant, pods/plant, biomass and 100 seed weight while it was positive via other characters. Biomass had a positive indirect effect using all characters except for seeds/pod and harvest index. 100 seed weight exerted positive indirect effect via days to 50% flowering, primary branches, total branches/plant, nodules/plant, pods/plant, seeds/pod and seeds/plant. It was negative via the remaining characters. Harvest index exerted negative indirect effect by means of days to 50% flowering, biomass, primary branches, secondary branches and total branches/plant. The difference between direct effects and genotypic correlation of traits indicated that the correlation was mainly due to the indirect effect of characters via other component traits. Thus, the indirect selection of above mentioned trait tends to be rewarding. Therefore, simultaneous selection for indirect causal factors is needed for the improvement programme. The residual effect was 0.177. It indicated that the independent variables included in this study explained only 82.23 per cent of the total variation in the dependent variable *i.e*. grain yield. Similar results were obtained by Azizi *et al*. (2009) for pods/plant, Singh and Srivastava (2013) for branches/plant, Kumar *et al.* (2017) for biological yield and harvest index. Gangele, (2005) and Oljira, T. (2018) also presented results in accordance with above findings.

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