Genetic Relationship and Selection Indices of Nine Irradiated Quantitative Traits of F1 Materials in lentils (Lens Culinaris Medic.)

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ABSTRACT

F1 materials of half-diallel crosses for nine characters in lentils were studied for correlation, path-coefficient, and selection index. The phenotypic component of variation ($\sigma 2p$) was higher than the genotypic component of variation ($\sigma 2g$). The highest $\sigma 2g$ and $\sigma 2p$ were obtained for CAMF. Investigation showed that genotypic correlations (rg) were higher than the respective phenotypic correlations (rp) for most of the characters. SWPP showed a highly significant and positive correlation coefficient with other characters except for the NPBFF at the genotypic level and except NPBFF and DF at the phenotypic level. The highest significant and positive genotypic correlation coefficient was recorded for NSBFF with PdWPP at the genotypic level and PdWPP with SWPP at the phenotypic level. PdWPP had the highest positive direct effect on SWPP at both genotypic and phenotypic levels. The maximum expected genetic gain of 4603.196% was found when NPBFF and RW were included in the index. These two characters a had high correlation coefficient with most of the characters studied as well as a direct effect at the genotypic level may be considered as primary yield components.

Keywords: Correlation, direct and indirect effects, selection index, lentil.

INTRODUCTION

Lentil (*Lens culinaris* Medic.) is an important crop in Bangladesh. It is the second most important pulse crop in terms of both area and production and rates the highest consumer preference in Bangladesh (BBS, 2002). Lentil is an important cool season food legume crop that is cultivated predominantly in the Indian subcontinent, the Middle East, Northern America, Southern Europe, and Eastern and Northern Africa for food (Gupta *et al*., 2011). It is a short stature, annual, self-pollinate high value crop which has great significance in cereal-based cropping systems (Meena *et al.,* 2020). Lentil crop is extremely good in nitrogen fixation from the atmosphere (Kushwaha & Singh, 2020). It is a good source of protein and some other nutrients. So, by adding lentils to their daily diets, suffering people from malnutrition can be relieved to some extent. It is used in soups, stews, casseroles, and salad

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dishes. However, besides a high level of proteins, lentils also contain a rich supply of copper and selenium and are a good source of iron, vitamin B_6, folate, and zinc (Bender & Bender, 2005). Health magazine has selected lentils as one of the five healthiest foods (Raymond, 2006). The contribution of lentils to heart health lies not just in their fiber, but in the significant amounts of folate and magnesium, they supply. Lentils' magnesium is a calcium channel blocker and helps to relax the heart muscles.

The global production of lentils was 6.3 million tonnes, led by Canada with 33% and India with 25% of the world total (FAO, 2019) but in Bangladesh, this important crop faced tough competition in the recent past from cereals, particularly wheat and boro (winter) rice, due to the expansion of irrigation facilities and the availability of high-yielding varieties. A tremendous diversion of land from winter pulses to these cereals is seen. Therefore, there is a need to increase the productivity of lentils. Lentil is responsive to both chemical and physical mutagens. Mutagenesis has also been used to improve existing cultivars for specific traits. Among various mutagens, gamma rays are highly preferred to induce variability in lentils (Singh *et al.,* 2011). It was successfully employed for the improvement of qualitative and quantitative traits such as high yield, earliness in flowering and maturity, and resistance to various diseases (Rajput *et al.*, 2001, Sadiq *et al.*, 2008). It was, therefore, essential to study the correlation and path coefficient analysis for both the dependent and independent traits along with the selection index. Knowledge of the correlation among different traits and further partitioning of the correlation values into direct and indirect effects on yield through path coefficient analysis is one of the approaches to understanding the nature and extent of the relationship among characters (Mekonnen *et at*., 2014). Dewey and Lu (1959) demonstrated the validity of path analysis in effective plant selection that results in the selection of desirable genotypes. Path analysis and correlation is used in the selection of elite cultivar. Selection will be more effective when the simultaneous improvement of the component characters occurs. The characters that show a high

positive genotypic correlation with yield may serve as the basis for selection (Punia *et al*., 1982). Therefore, the present study was planned with characters association, path-coefficient, and construction of a suitable selection index using several yields and yield contributing characters from 15 crossing materials in lentils.

Materials and Methods

To conduct the present investigation, 12 lines of lentils viz. ILL 4404, ILL 4605, SEL 5888, ILL 6002, ILL 6024, ILL 7543, ILL 7979, SELL 8006, ILL 8008, SEL 8009, ILL 8010, and L-4147 were collected from International Centre for Agricultural Research in the Dry Areas (ICARDA), Syria and 4 lines viz. Bari Masur-1, Bari Masur-2, Bari Masur-3, and Bari Masur-4 were from the Regional Agricultural Research Station (RARS) of Bangladesh Agricultural Research Institute (BARI). To create a variation, radiation of different doses of Kradgamma-rays (Kr) i.e., 20 Kr, 25 Kr, and 30 Kr were put to the lines from the Co^{60} source in the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, Bangladesh. Screening of the mutant lines was maintained based on survivability and maturity for flowering and the crossing was done in half diallel fashion for getting F_1 materials amongBari Masur-4 as parent 1 (P_1), Bari Masur-3 (20 Kr) as parent 2 (P_2), Bari Masur-2 (20 Kr) as parent 3 (P_3), Bari Masur-4 (30 Kr) as parent 4 (P_4), Bari Masur-4 (20 Kr) as parent 5 (P_5) and ILL 6002 (20 Kr) as parent 6 (P_6).

The experiment was laid down in a randomized complete block design with two replications having 42 plots. The plot size was about 50cm × 30cm with two rows and each row had three hills. On each hill, one plant was maintained. The gap between plants in the row was 25cm, between rows was 30 cm, between plots was 40 cm and between replication was 100cm. In this experiment, single-plant randomization was done. For the healthy experimental plants, all necessary cultural practices were done. In these practices, weeding, watering, and applying of fungicides and insecticides were done.

Collection and techniques of the analyses of data

Nine yield and yield contributing characters of F_1 plants viz., days to flower (DF), plant height at the first flower (PHFF), number of primary branches at the first flower (NPBFF), number of secondary branches at the first flower (NSBFF), canopy area at the maximum flower (CAMF), pod weight per plant (PdWPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) were recorded.

Collected data were analyzed following the biometrical techniques of analysis as developed by Mather (1949) based on the mathematical models of Fisher $et\ al.$, (1932). Based on purpose, data were analyzed in the following sub-heads:

I. *Components of variation and covariation*

For the correlation coefficient, the analysis of both variance and covariance is required (Miller $et\ al.$, 1958). Therefore, variances and covariances at the phenotypic and genotypic levels were calculated. These were measured as follows:

The plant-to-plant variation of crosses was calculated according to the following formula:

Variance $(S^2) = [\sum x_i^2 - (\sum x_i)^2 / n] / (n-1)$

Where, x_i = the individual reading recorded on each of the plants, n = the total number of observations, $\sum$ = Summation, $(n-1)$ = degrees of freedom and i = 1,2,3,..............n.

Covariances were calculated between all possible pairs of characters using the following formula:

$$\text{Covariance} = \sum_{i=1}^{n} x_i y_i - \left(\sum_{i=1}^{n} x_i\right) \times \left(\sum_{i=1}^{n} y_i\right) / n$$

Where,

$\sum_{1=1}^{n} x_i y_i$ = Sum of x and y,

$\sum_{1=1}^{n} x_i$ = Grand total of x,

$\sum_{1=1}^{n} y_i$ = total of y, n = the total number of observations,

$\sum$ = Summation, n-1 = degrees of freedom and i = 1,2,3, ..., n.

II. *Character association*

The correlation coefficient at phenotypic (r_p) and genotypic (r_g) levels were estimated according to Kwon and Torrie (1964) as follows:

$r_p = \sigma^2 P_{12} / [\sigma^2 P_{11} \times \sigma^2 P_{22}]^{1/2}$ and $r_g = \sigma^2 G_{12}/[\sigma^2 G_{11} \times \sigma^2 G_{22}]^{1/2}$

Where, $\sigma^2 P_{12}$ and $\sigma^2 G_{12}$ represent phenotypic and genotypic covariance of characters 1 and 2, $\sigma^2 P_{11}$ and $\sigma^2 G_{11}$ represent phenotypic and genotypic variances of characters 1 and $\sigma^2 P_{22}$ and $\sigma^2 G_{22}$ represent phenotypic and genotypic variances of character 2.

III. *Path-coefficient*

The path-coefficient analysis was carried out using Wright's (1921 & 1923) formula as illustrated by Dewey and Lu (1959). This analysis was done both at phenotypic and genotypic levels by solving the simultaneous equation using matrix algebra as:

$r_{xy} = p_{xy} + r_{x2} p_{2y} + r_{x3} p_{3y} + ...r_{xn}p_{ny}$

Where, r_{xy} = correlation between one component's character and yield, p_{xy} = path-coefficient between the same character and yield, and $r_{x2}, r_{x3}........r_{xn}$ = represent correlation coefficient between that character and each of the other yield components in turn. Path-coefficient analysis that measures the direct, as well as the indirect effects of one variable through another on the end product, was worked out for eight quantitative characters at both genotypic and phenotypic levels. The direct and indirect effects of the component characters on seed weight per plant (SWPP) were estimated separately for each of the contributing characters.

IV. Selection index

The phenotypic and genotypic variances and covariances as obtained were used for constructing the selection index using different character combinations according to the method developed by Smith (1936). Yield/plant was also included as one of the independent characters as suggested by Robinson *et al.*, 1951.

The expected genetic advance from straight selection [GA(S)]and from discriminant function [GA(D)] was calculated as follows:

$$GA(S) = \frac{Z}{P}\left(\frac{g_{yy}}{\sqrt{t_{yy}}}\right) and$$

$$GA(D) = \frac{Z}{P}\sqrt{\left(b_1 g_{1y} + b_2 g_{2y} + ... + b_n g_{ny}\right)}$$

Where, Z/P = the selection differential in standard units, for the present study it was 2.06 at a 5% level of selection (Lush, 1949), g_{yy} and t_{yy}= the genotypic and phenotypic variances of character, $b_1, b_2, ...b_n$ = the relative weights for character and $g_{1y}, g_{2y}, ...g_{ny}$ = the genotypic covariances of independent character with 'y'.

The expected gain from the discriminant function over straight selection was calculated for all the functions as, expected gain (%) = [GA(D) / GA(S)] × 100.

Results
Components of variation

Results of the estimates of phenotypic ($\sigma^2{}_P$), genotypic ($\sigma^2{}_G$), and error ($\sigma^2{}_E$) components of variation for all the characters are presented in table 1. For all the characters, the phenotypic component of variation was higher than the genotypic and error component of variation. The phenotypic component of variation was the joint product of $\sigma^2{}_G$ and $\sigma^2{}_E$. The highest values of $\sigma^2{}_P$ and $\sigma^2{}_G$ and $\sigma^2{}_E$were recorded for CAMF and the lowest value of $\sigma^2{}_P$ and $\sigma^2{}_G$ and $\sigma^2{}_E$ were recorded for RW.

Components of covariation

The component of covariance for all possible pairs of characters, genotypic ($\sigma^2{}_{G12}$) and phenotypic ($\sigma^2{}_{P12}$) components of covariation were calculated and shown in Table 2.

These components of a total of thirty-six pairs of characters were measured. The pairs of any character with NSBFF except PHFF and with CAMF except NPBFF showed the maximum genotypic and phenotypic components of covariation. Among the thirty-six pairs of characters, PHFF × CAMF showed the highest genotypic and phenotypic covariation. Combinations of CAMF × PdWPP, CAMF × IPlW, CAMF × RW, and CAMF × SWPP also showed noticeable genotypic and phenotypic covariation.

Correlation coefficient (r)

The correlation coefficient (r) between pairs of characters at genotypic (r_g) and phenotypic (r_p) levels was analyzed separately and shown in Table 3.

Genotypic correlation coefficient (r_g)

The highest significant and positive genotypic correlation coefficient was recorded for NSBFF with PdWPP. DF with the association of RW exhibited the lowest but most significant genotypic correlation coefficient. Other pairs of characters showed significant genotypic correlation coefficients except for PHFF × NSBFF, PHFF × RW and NPBFF × RW, and NPBFF × SWPP. The highest negative significant correlation coefficient value was obtained by the DF × PHFF combination (-1.35331).

Phenotypic correlation coefficient (r_p)

The highest positive and significant phenotypic correlation coefficient value was obtained by the combination of PdWPP × SWPP (0.984186) followed by PdWPP × RW, RW × SWPP, PHFF × CAMF, and CAMF × SWPP. The highest negative value was obtained by DF × IPlW. All pairs with SWPP at this level showed a significant phenotypic correlation coefficient except with DF and NPBFF.

Path-coefficient at the genotypic level

Results of the path-coefficient analysis at the genotypic level are presented in Table 4. It was observed that PdWPP had the highest positive direct effect of 0.687275 on SWPP followed by RW (0.2574), PHFF (0.166225), and NPBFF (0.125647). DF, NSBFF, CAMF,

and IPlW had direct negative effects on SWPP. The highest negative direct effect was obtained by DF on SWPP. The character DF via NPBFF, CAMF and IPlW showed positive indirect effects while through rest of the characters, it showed negative indirect effects on SWPP.PHFF had a positive direct effect of 0.166225. This character via DF, NSBFF, PdWPP, and RW showed positive indirect effects, and the rest of the characters showed negative indirect effects on SWPP. The character NPBFF had a positive direct effect on SWPP. The indirect effects of this character via CAMF, PdWPP an,d IPlW were found to be positive while negative indirect effects were found via the rest of the characters. NSBFF had a negative direct effect on SWPP. It exhibited a positive indirect effect through NPBFF, PdWPP and RW. NSBFF through the rest of the characters showed a negative indirect effect. The character CAMF showed a negative direct effect. The indirect effect of this character via D

F, PHFF, PdWPP and RW was found to be positive. The total effect of this character was 1.203651. The highest positive direct effect was observed for the character PdWPP. This character via DF, PHFF, NPBFF, and RW expressed positive indirect effects. Via the rest of the characters, this trait showed negative indirect effects on SWPP. IPlW had a negative direct effect on SWPP. It showed positive indirect effects via DF, PHFF, PdWPP and, RW. Via the rest of the characters, this trait showed negative indirect effects on SWPP.RW had a positive direct effect on SWPP. This character via DF, PHFF, and PdWPP showed positive indirect effects on SWPP. At this level, the residual effect is 0.132461 (Table 4).

Path-coefficient the at phenotypic level

Results of the path-coefficient analysis at the phenotypic level are presented in Table 5. It was observed that PdWPP had the highest positive direct effect of 1.05769 on SWPP at the phenotypic level followed by PHFF, CAMF, and NPBFF.DF had a negative direct effect on SWPP. It showed negative indirect effects via PHFF, NSBFF, CAMF, and RW on SWPP. This character through the test of the traits exhibited positive indirect effects. PHFF showed a positive direct effect on SWPP.

It had positive indirect effects through DF, NPBFF, CAMF and PdWPP. Negative indirect effects were present via the rest of all characters for this character. NPBFF had a positive direct effect. It showed positive indirect effects through the characters viz., PHFF, CAMF, and PdWPP. Negative indirect effects were shown through the rest of the characters by NPBFF.NSBFF had a negative direct effect on SWPP. It showed positive indirect effects through PHFF, NPBFF, CAMF and, PdWPP. Negative indirect effects were shown by this trait via the rest of the characters. The character CAMF showed a positive direct effect. This character via DF, PHFF, NPBFF, and PdWPP showed positive indirect effects. It showed indirect negative effects through the rest of the characters on SWPP. PdWPP had the highest positive direct effect on SWPP. It showed indirect positive effects through PHFF, NPBFF and CAMF. Negative indirect effects were shown by the character via the rest of the characters. IPlW had a negative direct effect. It showed positive indirect effects on SWPP through DF, PHFF, NPBFF, CAMF, and PdWPP. Negative indirect effects were shown by the character via NSBFF and RW.RW had a negative direct effect. It showed positive indirect effects on SWPP through PHFF, NPBFF, CAMF, and PdWPP. Negative indirect effects were shown via the rest of the characters by RW. The residual effect at this level is 0.136646 (Table 5).

Selection indices

Results obtained for different indices contributing seed weight per plant and its components with expected gain in percent over straight selection are presented in Table 6. The maximum expected genetic gain of 4603.196% was found when NPBFF and RW were included in the discriminant function. It was followed by 4556.836% when RW and SWPP were included in the discriminant function. Table 6 revealed that any character associated with RW (8) and SWPP (9) gave positive high values.

In the discriminant function analysis of the present study, when the individual character was considered separately, RW (8) showed the highest expected gain of 1272.823% followed by SWPP (9) of 1054.986% and

IPlW (7) of 618.7894%. Considering the two characters association in discriminant function, NPBFF (3) and RW (8) showed the highest expected genetic gain of 4603.196%. On the other hand, DF (1) in association with RW (8) gave the maximum expected genetic gain of 298.9399% in this series. PHFF (2) associated with RW (8) gave the maximum expected genetic gain of 502.2892% in this series. NSBFF (4) in association with RW (8) gave the maximum expected genetic gain of 427.3018% in this series. IPlW (7) associated with RW (8) gave the maximum expected genetic gain of 1923.761% and RW (8) in association with SWPP (9) gave the maximum expected genetic gain of 4556.836%. In the present study, when three characters were associated in different combinations, NPBFF (3), RW (8), and SWPP (9) showed the highest expected genetic gain of 3083.323%. It was found that DF (1) in association with RW (8) and SWPP (9) gave 373.5102%; PHFF (2) in association with RW (8) and SWPP (9) gave 705.441%; NSBFF (4) in association with RW (8) and SWPP (9) gave 494.8328%; PdWPP (6) in association with RW (8) and SWPP (9) gave 2020.246% and IPlW (7) in association with RW (8) and SWPP (9) gave 1820.893%.

Considering the four characters association in discriminant function, the maximum genetic gain was recorded as 1522.762% for the combination of NPBFF (3), IPlW (7), RW (8), and SWPP (9). DF (1) in association with NPBFF (3), RW (8), and SWPP (9) gave a maximum value of 354.7259% in this series. PHFF (2) in association with NPBFF (3), RW (8), and SWPP (9) gave 640.8198%; NPBFF (3) in association with IPlW (7), RW (8) and SWPP (9) gave 1522.762%. NSBFF (4) in association with IPlW (7), RW (8), and SWPP (9) gave 426.5144% and PdWPP (6) in association with IPlW (7), RW (8) and SWPP (9) gave 1035.431%. All were the highest values for the respective characters when associated with the other characters in four-character combinations. Considering five characters association in discriminant function, the maximum genetic gain was recorded as 884.1068% for the combination of NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), IPlW (7), RW (8), and SWPP (9) gave the highest value of 314.3404%; PHFF

(2) in association with NPBFF (3), IPlW (7), RW (8) and SWPP (9) gave the maximum value of this series of 513.1741% and NSBFF (4) in association with PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the highest value of 307.0693% of this series. In the present study, when six characters were associated in different combinations, the maximum genetic gain was recorded of 291.4154% for NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the maximum value of 210.4544% in this series and PHFF (2) in association with NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the highest value of 267.5051% in this series. Considering seven characters association in discriminant function, the maximum genetic gain was recorded of 164.2183% for the combination of PHFF (2), NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8), and SWPP (9) gave the maximum value of 140.0703% in this series. Considering eight characters association in discriminant function, the maximum genetic gain was recorded of 88.21749% for the combination of DF (1), PHFF (2), NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9).

Discussion

Components of variation varied differently for different characters. The phenotypic component of variation (σ^2_P) was higher than the genotypic (σ^2_G) and error (σ^2_E) components of variation. Similar results were obtained by Younis *et al*., (2008) and Al-Aysh (2014) in lentils. In the present study, the highest phenotypic, genotypic, and variations were obtained for CAMF. The high genotypic values caused high phenotypic values. Larger genotypic values for any character are always helpful for effective selection. Sakthivel *et al*., (2019) recorded the highest phenotypic and genotypic components of variation for the number of pods per plant, the number of seeds per plant, biological yield per plant, and seed yield per plant. Kumar (2020) observed the high genotypic component of variation for 100-seed weight, plant height and seed yield in lentils. Again, Meena *et al*.,

(2020) noted high genotypic components of variation for biological yield per plant, number of peduncles per plant, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, and seed yield per plant in lentil. A combination of PHFF × CAMF showed the highest genotypic and phenotypic covariation. Except that, the decided amount of genotypic and phenotypic covariation was found in the combination of CAMF × PdWPP, CAMF × IPlW, CAMF × RW, and CAMF × SWPP which indicates the wide scope of selection for these pair of characters for improvement of yield.

It was observed from the correlation analysis that genotypic correlations were higher than the respective phenotypic correlations for most of the characters. This result is in agreement with the findings of Crippa *et al.,* (2009). Genotypic correlation revealed that the number of pods per plant had a positive and highly significant association with seed yield, whereas hundred seed weight, days to maturity, number of seeds per plant, and plant height had a positive but non-significant association with seed yield per plot (Tadesse *et al.,* 2014). The non-significant correlation coefficients between the investigated features were also found by Cokkizgin *et al.,* (2021). The high genotypic correlation indicating the strong inherent associations between characters does not reflect the nature and magnitude of phenotypic variation. Most of the character combinations had a highly significant correlation coefficients. SWPP showed a highly significant correlation with other characters except for NPBFF at the genotypic level and NPBFF and DF at the phenotypic level. These results indicate that characters were genetically related to seed weight per plant. These findings were supported by Younis *et al.,* (2008), Singh *et al.,* (2012), and Mekonnen *et al.,* (2014) as they observed that most of the yield contributing characters were positively and significantly correlated both at phenotypic and genotypic levels in lentil. Gill *et al.,* (2010) also found that grain yield had a highly significant and positive correlation with plant height. Chowdhury *et al.,* (2019) found that seed yield per plant was significantly and positively correlated with the number of primary

branches plant per plant, pods per plant, seeds per plant per plant, and 100-seed weight in lentils. At the phenotypic level, yield per plot exhibited a highest positive correlation with 100-seed weight followed by a number of seeds per pod, number of pods per plant, number of secondary branches per plant and number of primary branches per plant (Meenakshi *et al.,* 2019). The present investigation was supported by their result as SWPP showed a significant correlation with plant height at the genotypic level. Singh and Singh (2006) observed seed yield per plant had a significant and positive association with plant height in pea. Samad *et al.,* (2010) found seed yield had a highly significant and positive correlation with branch number in lentils which was supported by the present investigation as a number of secondary branches at the first flower has a positive correlation with seed weight per plant. That, various lentil researchers viz., Sarwar *et al.,* (1984), Tyagi and Khan (2011), Aghili *et al.,* (2012), Dalbeer *et al.,* (2015), Adhikari *et al.,* (2018), Tabti *et al.,* (2018) and Meena *et al.,* (2020) found a significant correlation between yield and yield contributing traits in lentil.

Traits PHFF, NPBFF, PdWPP, and RW showed a positive direct effect on SWPP at the genotypic level and the rest of the characters obtained a negative direct effect. Tadesse *et al.,* (2014) also observed that number of pods per plant and seeds per pod had a very high and positive direct effect on seed yield, whereas days to maturity and plant height had a negative direct effect on seed yield in lentils at this level. Kushwaha and Singh (2020) noticed that secondary branches showed the highest positive direct effect on grain yield followed by test weight and a number of pods per plant at the genotypic level in lentils. The negative direct effect of important characters at the genotypic level was also found by Azizi-Chakherchaman *et al.,* (2009) in lentils. Characters PHFF, NPBFF, CAMF and PdWPP showed a positive direct effects on SWPP at the phenotypic level. At this level, different yield components showed a positive direct effect on seed yield as noted by Chowdhury *et al.,* (2019), Meenakshi *et al.,* (2019), and Kushwaha and Singh (2020). In lentils, the positive direct effect of the number of primary branches

on seed yield was reported by Rasheed *et al.*, in 2008 and Tyagi and Khan in 2011. Deb *et al.*, (2009) marked from the path-coefficient analysis that NPdPP and NSPP had the highest direct effect on SWPP both at genotypic and phenotypic levels. The path analysis indicated that total biological yield, number of clusters, and pods per plant had a very high positive direct effect on seed yield (Bicer& Sakar, 2008). Days to flower, plant height, number of primary branches, biological yield, harvest index, and hundred seed weight had a positive direct effect on seed yield was reported by Younis *et al.*, (2008) in lentils. Cokkizgin *et al.*, (2021) noted the highest positive direct effect of pod number per plant on seed yield. In this study, the highest positive direct effect was showed by PdWPP on SWPP both at genotypic and phenotypic levels suggesting that through the improvement of this character, SWPP can be improved in lentils. Through the path analysis Sakthivel *et al.*, (2019) showed that biological yield per plant, number of branches per plant, and harvest index were the three important characterstics of yield improvement. On the other hand, Hassan *et al.*, (2021) illustrated that 100 seed weight and the number of pods plant per plant were the two important traits for seed yield improvement in lentils.

Direct selection of yield may be misleading as yield is a complex character that depends on the number of yields contributing traits. So, to ensure high yield, the multiple selection criteria based on the selection index of most of the yield contributing characters to yield would be most effective. For this purpose, estimation of the relative efficiency of the character and character combinations through discriminant function selection is necessary. In this study, when RW and SWPP were included most of the characters showed a high value of genetic gain. Thus, the inclusion of any character noted above, was one of the important components for higher yield. The highest value of expected genetic gain was obtained as 4603.196%for the association of NPBFF and RW. Nandan and Pandya (1980) obtained the highest genetic gain as 22% in lentils in a combination of the number of grains/pods, a number of branches/plants, and number of pods/plants along with grain yield. Yadav et al., (2008) observed that the

discriminant functions based on a single character were less efficient while on the basis of combination it was in general more efficient in opium poppy. In chickpeas, Deb and Khaleque (2007) obtained the highest genetic gain in five characters combination whereas Hasan and Deb (2014) found the highest genetic gain in two characters combination. As the two traits, NPBFF and RW had the fourth and second highest direct positive values in path-coefficient analysis at the genotypic level, respectively and as RW had a significant association with most of the characters at the genotypic level, therefore these two characters were considered as primary yield components and hence the improvement of these two characters, the yield of lentil crops can be improved.

Conclusions:

With SWPP both at phenotypic and genotypic levels traits PHFF, NSBFF, CAMF, PdWPP, IPlW, and RW has shown a positive and significant correlation. Therefore, these traits are useful in direct selection for the improvement of lentils. Path analysis revealed that three traits viz, PHFF, NPBFF, and PdWPP had high positive direct effects both at phenotypic and genotypic levels. Thus, these traits could be used as effective selection for gaining high yields in lentils through the appropriate breeding methods. Except that, NPBFF and RW are the important yield component as they showed the highest amount of genetic gain among the combinations of selection indices and also exhibited significant genetic correlation with SWPP, therefore the selection of these traits could be used in future lentil breeding programs for the improvement of seed yield.

Table 1: Values of phenotypic (σ2P), genotypic (σ2G) and error (σ2E) components of variation for nine characters in lentils.

Characters	Components		
	σ^2_P	σ^2_G	σ^2_E
Days to flower (DF)	11.60683	3.694652	7.912178
Plant height at first flower (PHFF)	4.814858	1.004899	3.809959
Number of primary branches at first flower (NPBFF)	1.572455	0.061948	1.510507
Number of secondary branches at first flower (NSBFF)	10.81044	2.986855	7.823583
Canopy area at maximum flower (CAMF)	22393.77	8391.63	14002.14
Pod weight per plant (PdWPP)	2.536825	0.082482	2.454343
Individual plant weight (IPlW)	1.532839	0.190957	1.341882
Root weight (RW)	1.202013	0.002021	1.199992
Seed weight per plant (SWPP)	1.438964	0.097082	1.341882

Table 2: Values of phenotypic (σ2P12), genotypic (σ2G12) and within error (σ2W12) components of covariation of all possible pairs for nine characters in lentil.

Combinations	Components			Combinations	Components		
	σ^2_{P12}	σ^2_{G12}	σ^2_{W12}		σ^2_{P12}	σ^2_{G12}	σ^2_{W12}
DF × PHFF	-2.60762	-0.24958	2.35804	DF × NPBFF	0.538625	1.889921	1.351296
DF × NSBFF	1.7375	5.033433	3.295933	DF × CAMF	-155.222	-48.0444	107.1774
DF × PdWPP	-0.40975	1.089017	1.498766	DF × IPlW	-0.74038	-0.83383	-0.09345
DF × RW	-0.00035	0.07748	0.077831	DF × SWPP	-0.45886	0.852121	1.310979
PHFF × NPBFF	-0.6888	0.538062	1.226858	PHFF × NSBFF	-0.2986	2.203047	2.501647
PHFF × CAMF	100.4104	249.1724	148.762	PHFF × PdWPP	0.364716	1.12765	0.762934
PHFF × IPlW	0.653079	1.220898	0.567819	PHFF × RW	0.00902	0.054698	0.045678
PHFF × SWPP	0.293677	1.021904	0.728227	NPBFF × NSBFF	0.203492	2.001943	1.79845
NPBFF × CAMF	-24.1556	14.05964	38.21523	NPBFF × PdWPP	0.053574	0.181847	0.128273
NPBFF × IPlW	-0.11164	0.290509	0.402153	NPBFF × RW	-0.00095	0.017353	0.018307
NPBFF × SWPP	-0.00043	0.149539	0.149974	NSBFF × CAMF	64.48301	134.4806	69.99764

NSBFF × PdWPP	1.121326	1.868239	0.746912	NSBFF × IPlW	0.547115	0.288914	-0.2582
NSBFF × RW	0.057006	0.082633	0.025627	NSBFF × SWPP	0.734607	1.473221	0.738613
CAMF × PdWPP	39.01017	169.44	130.4299	CAMF × IPlW	42.97545	128.3616	85.38613
CAMF × RW	1.996459	6.57083	4.574372	CAMF × SWPP	34.36349	132.9074	98.54391
PdWPP × IPlW	0.20633	1.220217	1.013886	PdWPP × RW	0.01958	0.104005	0.084426
PdWPP × SWPP	0.09343	1.880388	1.786957	IPlW × RW	0.01549	0.054332	0.038841
IPlW × SWPP	0.193493	0.861371	0.667878	RW × SWPP	0.01559	0.07557	0.05998

Table 3: Values of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for nine characters in lentils.

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPlW	RW	SWPP
DF	1	-1.35331**	1.125864**	0.523035**	-0.88154**	-0.74225**	-0.88145**	-0.00405**	-0.76617**
PHFF	-0.03339 NS	1	-2.76069**	-0.17235NS	1.093438**	1.266817**	1.49086**	0.200153 NS	0.940241**
NPBFF	0.442382**	0.195547 NS	1	0.473071**	-1.05945**	0.749481**	-1.02645**	-0.0849 NS	-0.00554 NS
NSBFF	0.449351**	0.305359 NS	0.485558**	1	0.407301**	2.259151**	0.724442**	0.73372**	1.364202**
CAMF	-0.09424 NS	0.75883**	0.074924 NS	0.273322 NS	1	1.482774**	1.073568**	0.48479**	1.20394**
PdWPP	0.200693 NS	0.322654*	0.091048 NS	0.356751*	0.710898**	1	1.64405**	1.516526**	1.044089**
IPlW	-0.20752 NS	0.471772**	0.196433 NS	0.074506 NS	0.727304**	0.649585**	1	0.788498**	1.421111**
RW	0.289481 NS	0.317298*	0.176146 NS	0.319903*	0.558912**	0.831182**	0.586391**	1	1.112996**
SWPP	0.208506 NS	0.388234*	0.099412 NS	0.373526*	0.74039**	0.984186**	0.608849**	0.801884**	1

Table 4: Values of direct (bold diagonal) and indirect (off-diagonal) effects of yield components on yield (SWPP) at the genotypic level.

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPlW	RW	Total effect
DF	**-0.37429**	-0.22495	0.141462	-0.04476	0.213029	-0.51013	0.03472	-0.00104	-0.76597
PHFF	0.50653	**0.166225**	-0.34687	0.014751	-0.26424	0.870652	-0.05872	0.051519	0.939844
NPBFF	-0.4214	-0.4589	**0.125647**	-0.04049	0.256022	0.5151	0.040431	-0.02185	-0.00544

NSBFF	-0.19577	-0.02865	0.05944	**-0.08559**	-0.09843	1.552657	-0.02854	0.18886	1.363994
CAMF	0.329953	0.181757	-0.13312	-0.03486	**-0.24166**	1.019073	-0.04229	0.124785	1.203651
PdWPP	0.277819	0.210577	0.09417	-0.19335	-0.35832	**0.687275**	-0.06476	0.390354	1.043768
IPlW	0.32992	0.247819	-0.12897	-0.062	-0.25943	1.129914	**-0.03939**	0.20296	1.420818
RW	0.001516	0.033271	-0.01067	-0.0628	-0.11715	1.04227	-0.03106	**0.2574**	1.112783
The residual effect is 0.132461								

Table 5: Values of direct (bold diagonal) and indirect (off-diagonal) effects of yield components on yield (SWPP) at the phenotypic level.

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPlW	RW	Total effect
DF	**-0.01506**	-0.00298	0.017827	-0.01516	-0.005	0.212271	0.02941	-0.0128	0.208501
PHFF	0.000503	**0.089391**	0.00788	-0.0103	0.040253	0.341268	-0.06686	-0.01403	0.388104
NPBFF	-0.00666	0.01748	**0.040297**	-0.01639	0.003974	0.096301	-0.02784	-0.00779	0.099378
NSBFF	-0.00677	0.027296	0.019567	**-0.03375**	0.014499	0.377332	-0.01056	-0.01414	0.373479
CAMF	0.00142	0.067833	0.003019	-0.00922	**0.053047**	0.75191	-0.10307	-0.02471	0.740222
PdWPP	-0.00302	0.028842	0.003669	-0.01204	0.037711	**1.05769**	-0.09206	-0.03674	0.984047
IPlW	0.003126	0.042172	0.007916	-0.00251	0.038581	0.68706	**-0.14172**	-0.02592	0.608697
RW	-0.00436	0.028364	0.007098	-0.0108	0.029648	0.879133	-0.0831	**-0.04421**	0.801777
Residual effect is 0.136646								

Table 6: Expected genetic gain in percent of seed weight per plant over a straight selection from the use of various selection indices in lentils. Index showing values over 88% are shown only.

Selection Indices	Expected Gain in%	Selection Indices	Expected Gain in%	Selection Indices	Expected Gain in%	Selection Indices	Expected Gain in%
DF (1)	146.4253	2+4+8	223.4569	2+3+4+8	212.4498	1+4+6+7+9	93.96757
PHFF (2)	-536.038	2+4+9	208.9656	2+3+4+9	198.8433	1+4+6+8+9	155.5127
NPBFF (3)	103.5193	2+7+8	400.2911	2+3+7+8	364.9551	1+4+7+8+9	198.4229
NSBFF (4)	277.9674	2+7+9	354.6596	2+3+7+9	324.9316	2+3+4+7+8	194.0595
CAMF (5)	-97.2855	2+8+9	705.441	2+3+8+9	640.8198	2+3+4+7+9	182.478
PdWPP (6)	-7164.36	3+4+7	231.0947	2+4+7+8	203.3384	2+3+4+8+9	274.3434
IPlW (7)	618.7894	3+4+8	400.9213	2+4+7+9	191.0826	2+3+6+8+9	306.0184
RW (8)	1272.823	3+4+9	371.5586	2+4+8+9	286.8375	2+3+7+8+9	513.1741
SWPP (9)	1054.986	3+7+8	1502.55	2+6+7+8	146.3465	2+4+6+7+8	85.13121
1+3	135.8556	3+7+9	1187.162	2+6+8+9	338.255	2+4+6+7+9	76.12294
1+4	118.325	3+8+9	3083.323	2+7+8+9	554.7213	2+4+6+8+9	186.5148

1+7	141.8594	4+6+8	234.5534	3+4+6+8	218.7383	2+4+7+8+9	258.8172
1+8	298.9399	4+6+9	212.7148	3+4+6+9	198.6913	2+6+7+8+9	290.6178
1+9	277.3222	4+7+8	367.0771	3+4+7+8	347.0194	3+4+6+7+8	199.2414
2+4	104.4199	4+7+9	342.3004	3+4+7+9	324.1848	3+4+6+7+9	182.9172
2+8	502.2892	4+8+9	494.8328	3+4+8+9	467.3062	3+4+6+8+9	330.4197
2+9	431.6049	6+7+8	325.1406	3+6+7+8	254.1386	3+4+7+8+9	405.3722
3+4	258.6269	6+7+9	195.1805	3+6+7+9	154.4775	3+6+7+8+9	884.1068
3+7	561.7619	6+8+9	2020.246	3+6+8+9	1517.018	4+6+7+8+9	307.0693
3+8	4603.196	7+8+9	1820.893	3+7+8+9	1522.762	1+2+3+4+7+8	101.6341
3+9	2580.477	1+2+3+8	144.4776	4+6+7+8	211.9972	1+2+3+4+7+9	96.63309
4+7	246.2488	1+2+3+9	134.2852	4+6+7+9	194.4161	1+2+3+4+8+9	141.4593
4+8	427.3018	1+2+4+8	111.4285	4+6+8+9	350.2515	1+2+3+6+8+9	117.1806
4+9	395.0003	1+2+4+9	105.7605	4+7+8+9	426.5144	1+2+3+7+8+9	193.3225
7+8	1923.761	1+2+7+8	142.3095	6+7+8+9	1035.431	1+2+4+6+8+9	96.27506
7+9	1448.455	1+2+7+9	132.9403	1+2+3+4+7	54.41699	1+2+4+7+8+9	137.0548
8+9	4556.836	1+2+8+9	219.8593	1+2+3+4+8	107.3318	1+2+6+7+8+9	117.2993
1+2+8	152.0978	1+3+4+7	107.3391	1+2+3+4+9	101.8601	1+3+4+6+7+8	95.88723
1+2+9	141.3354	1+3+4+8	171.0296	1+2+3+7+8	135.6503	1+3+4+6+7+9	89.91595
1+3+4	113.1008	1+3+4+9	162.8047	1+2+3+7+9	126.7342	1+3+4+6+8+9	149.8188
1+3+7	132.7679	1+3+6+8	106.253	1+2+3+8+9	210.6124	1+3+4+7+8+9	192.0757
1+3+8	282.0425	1+3+6+9	92.79279	1+2+4+7+8	105.374	1+3+6+7+8+9	210.4544
1+3+9	262.0726	1+3+7+8	251.4564	1+2+4+7+9	100.2045	1+4+6+7+8+9	145.1587
1+4+7	112.0412	1+3+7+9	235.1685	1+2+4+8+9	146.0919	2+3+4+6+8+9	177.5972
1+4+8	177.6178	1+3+8+9	354.7259	1+2+6+7+8	14.88096	2+3+4+7+8+9	248.3445
1+4+9	169.0213	1+4+6+8	105.0423	1+3+4+6+8	100.3201	2+3+6+7+8+9	267.5051
1+6+8	114.8477	1+4+6+9	98.16097	1+3+4+6+9	93.7153	2+4+6+7+8+9	171.8913
1+6+9	100.4474	1+4+7+8	164.8441	1+3+4+7+8	159.0161	3+4+6+7+8+9	291.4154
1+7+8	265.0194	1+4+7+9	157.2189	1+3+4+7+9	151.6967	1+2+3+4+6+8+9	92.6652
1+7+9	247.5607	1+4+8+9	214.4968	1+3+4+8+9	207.3027	1+2+3+4+7+8+9	132.8536
1+8+9	373.5102	1+6+7+8	116.0065	1+3+6+7+8	108.3648	1+2+3+6+7+8+9	111.7506
2+3+4	97.41482	1+6+7+9	103.7822	1+3+6+7+9	96.86077	1+2+4+6+7+8+9	91.5384
2+3+8	446.8005	1+6+8+9	245.3727	1+3+6+8+9	232.2612	1+3+4+6+7+8+9	140.0703
2+3+9	387.264	1+7+8+9	329.4043	1+3+7+8+9	314.3404	2+3+4+6+7+8+9	164.2183
2+4+7	104.2823	2+3+4+7	97.98835	1+4+6+7+8	100.1715	1+2+3+4+6+7+8+9	88.21749

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