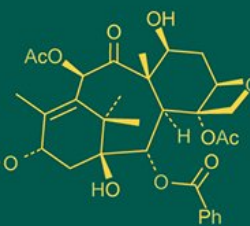
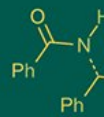


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Genetic variability and trait association analysis for yield and quality attributes in parents, F_1 and F_2 generations of lentil (*Lens Culinaris* Medik)

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Abstract

The present investigation was undertaken to assess genetic variability and trait association for yield and quality attributes in Parents, F_1 and F_2 generations of lentil (*Lens culinaris* Medik.). The experimental material comprised lentil populations evaluated for agronomic, yield-contributing and quality traits. Analysis of variance revealed significant differences among the evaluated populations for all the traits studied, indicating the presence of substantial genetic variability. Genetic variability parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, and genetic advance as percentage of mean (GA%) were estimated in both generations. In general, PCV was slightly higher than GCV for most traits, indicating the influence of environmental factors on trait expression. High heritability coupled with appreciable genetic advance was observed for plant height, primary and secondary branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, 100-seed weight, biological yield per plant and seed yield per plant, suggesting the predominance of heritable genetic effects and good prospects for selection. Number of pods per cluster recorded the highest GA% in both F_1 (37.94%) and F_2 (40.08%), indicating considerable scope for improvement through selection. Seed yield per plant exhibited high heritability with moderate-to-high genetic advance in both generations, demonstrating its potential as an important selection criterion. Days to 50% flowering and days to maturity showed relatively low GCV, PCV and GA% despite high heritability, suggesting limited scope for improvement through direct selection. Seeds per pod showed a marked decline in heritability from 73.97% in F_1 to 31.57% in F_2 , indicating increased environmental influence in the segregating generation. Protein content exhibited exceptionally high heritability in both generations, whereas methionine content showed a substantial increase in heritability and genetic advance in F_2 . Trait association analysis further revealed important relationships among yield and its component traits, particularly between biological yield and seed yield and among major yield-contributing attributes.

Keywords: Lentil, genetic variability, heritability, genetic advance, GCV, PCV, correlation

1. Introduction

Lentil (*Lens culinaris* Medik.) is an important cool-season pulse crop valued for its nutritional quality, adaptability and contribution to sustainable agriculture. Its seeds are rich in protein, dietary fibre, minerals and other essential nutrients, making lentil an important component of food and nutritional security (Kaale *et al.*, 2023; Bueckert *et al.*, 2022) [8]. Improving both seed productivity and nutritional quality is therefore an important objective of lentil breeding programmes. Seed yield is a complex quantitative trait controlled by several component characters and strongly influenced by environmental conditions. The assessment of genetic variability is essential for identifying traits that can be effectively exploited through selection. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are important genetic parameters for understanding the magnitude and nature of variation and predicting the response to selection (Burton and DeVane 1953; Johnson *et al.*, 1955) [6, 7]. Previous studies have reported considerable genetic variability and high heritability for several yield and yield-related traits in lentil, indicating opportunities for genetic improvement (Alemu

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et al., 2022) [3]. Evaluation of F₁ and F₂ generations is particularly useful in breeding programmes because the F₂ generation undergoes substantial segregation and recombination, creating opportunities for selecting desirable genetic combinations. Comparative assessment of these generations can provide information on the magnitude of genetic variation and the potential effectiveness of selection for important agronomic and yield traits. In addition to yield, nutritional traits such as protein and methionine content are important targets for improving the nutritional value of lentil. Considerable genetic variation for protein and nutritional quality has been reported in lentil germplasm (Bueckert *et al.*, 2022). The association among yield and its component traits is also important for developing effective selection strategies. Correlation analysis helps determine the direction and magnitude of relationships among agronomic, yield and quality attributes and can identify traits that may serve as useful indirect selection criteria. Significant associations among yield and its component traits have been reported in lentil, demonstrating the usefulness of trait association analysis in breeding programmes (Alemu *et al.*, 2022) [3]. Therefore, the present study was undertaken to assess genetic variability, heritability, genetic advance and trait associations for yield and quality attributes in F₁ and F₂ generations of lentil (*Lens culinaris* Medik.). The study aimed to identify traits with substantial heritable variation and favourable associations with seed yield that could be effectively utilized in selection and genetic improvement programmes.

2. Materials and methods

2.1 Experimental material

The present investigation entitled Genetic Variability and Trait Association Analysis for Yield and Quality Attributes in F₁ and F₂ Generations of Lentil (*Lens culinaris* Medik.) was conducted to assess the magnitude of genetic variability and the association among agronomic, yield-related and quality traits in F₁ and F₂ generations of lentil. The experimental material consisted of 10 diverse parental genotypes of lentil, namely KLS 1457, KLS 1465, KLS 1467, KLS 1469, PL 357, IPL 220, PL 370, IPL 241, LL 1655 and LL 1694. These parental lines were selected on the basis of their morphological and agronomic variation. The parental material was used for developing F₁ and subsequent F₂ generations through a half-diallel mating programme. The original experimental material comprised 10 parents, 45 F₁ crosses and 45 F₂ populations.

2.2 Development of f₁ hybrids and f₂ populations

The parental genotypes were grown during the rabi season under field conditions. The selected parents were crossed in a half-diallel mating design to generate 45 F₁ crosses. The resultant hybrid seeds were harvested separately for each cross and maintained for evaluation. The F₂ generation was developed by selfing the F₁ plants, and the resulting F₂ seed was harvested separately for each cross. The procedure of growing the parental lines for crossing and harvesting the resultant F₁ seed followed the methodology described in the experimental material.

2.3 Experimental design and layout

The experiment was conducted during the rabi season at the Student Instructional Farm, College of Agriculture, C. S. Azad University of Agriculture and Technology, Kanpur,

Uttar Pradesh. A total of 100 genotypes/populations, comprising 10 parents, 45 F₁ crosses and 45 F₂ populations, were evaluated in a randomized block design (RBD) with three replications. Each parent and F₁ cross was grown in a single row, whereas the F₂ populations were grown in two rows. The experimental layout followed the design described for the final trial in the source material.

2.4 Observations recorded

Observations were recorded on individual plants selected from each treatment in each replication. A total of 15 agronomic, yield-related and quality traits were evaluated in both the F₁ and F₂ generations. The traits considered were days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of clusters per plant, number of pods per cluster, total number of pods per plant, seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant, harvest index, protein content and methionine content.

Days to 50% flowering was recorded as the number of days from sowing to the stage when approximately 50% of the plants in a population exhibited flowering. Days to maturity was recorded as the number of days from sowing to the stage when the plants attained physiological maturity. Plant height (cm) was measured at maturity from ground level to the tip of the main shoot and expressed in centimetres. Primary branches per plant were recorded by counting the total number of branches arising directly from the main stem, whereas secondary branches per plant were determined by counting the branches originating from the primary branches.

The number of clusters per plant was recorded by counting the total number of clusters borne by each selected plant at maturity. Number of pods per cluster was determined by counting the pods borne on individual clusters and calculating the average number of pods per cluster. Total number of pods per plant was recorded by counting all seed-bearing pods produced by each selected plant at maturity. Seeds per pod were determined by counting the seeds obtained from randomly selected mature pods and calculating the average number of seeds per pod.

For 100-seed weight (g), 100 randomly selected, well-dried seeds from each treatment were weighed using an electronic balance and the weight was expressed in grams. Biological yield per plant (g) was determined by harvesting the selected plants from the base after attaining complete maturity and drying, followed by weighing the total dry biomass of each plant. Seed yield per plant (g) was recorded after harvesting and thorough drying by weighing all the seeds obtained from each selected plant.

Harvest index (%) was calculated as the ratio of seed yield (economic yield) to biological yield per plant and expressed as percentage:

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant}}{\text{Biological yield per plant}} \times 100$$

Protein content (%) was estimated from representative seed samples of each treatment using the prescribed biochemical laboratory assay and expressed as percentage protein content. Methionine content (%) was similarly estimated from representative seed samples using the prescribed biochemical assay and expressed as percentage of the sample. The observations obtained for these traits were

subsequently used for the estimation of genetic variability parameters and trait association among the evaluated experimental materials.

2.5 Statistical analysis

Analysis of variance (ANOVA) was performed to assess differences among genotypes for each trait following the randomized block design described by Panse and Sukhatme (1967) [9]. The significance of genotype effects was tested using the F-test, and standard error, critical difference (CD), and coefficient of variation (CV) were estimated where appropriate. Genotypic variance (V_g) and phenotypic variance (V_p) were estimated for each trait in the F_1 and F_2 generations. Genotypic and phenotypic coefficients of variation were calculated according to Burton (1952) [4], as:

$$GCV (\%) = (\sqrt{V_g} / \bar{X}) \times 100$$

$$PCV (\%) = (\sqrt{V_p} / \bar{X}) \times 100$$

Broad-sense heritability was estimated as:

$$H^2 (\%) = (V_g / V_p) \times 100$$

Expected genetic advance (GA) at 5% selection intensity was estimated according to Robinson *et al.* (1949) [12]:

$$GA = k \times \sigma_p \times H^2$$

where $k = 2.06$ and σ_p is the phenotypic standard deviation. Genetic advance as percentage of mean (GA%) was calculated as:

$$GA\% = (GA / \bar{X}) \times 100$$

Correlation coefficients among the studied traits were estimated following Al-Jibouri *et al.* (1958) [2], and their significance was tested statistically. The combined estimates of GCV, PCV, heritability and GA% were used to assess the genetic variability and potential response to selection.

3. Results and Discussion

3.1 Analysis of variance

The combined analysis of variance revealed highly significant differences among the treatments for all the characters studied, indicating the presence of substantial genetic variability in the experimental material. The combined analysis of variance for the studied traits is presented in Table 2. The treatment mean squares were significant at the 1% level for days to 50% flowering (11.34), days to maturity (41.61), plant height (48.35), primary branches per plant (0.939), secondary branches per plant (19.77), number of clusters per plant (1.03), total number of pods per plant (259.96), seeds per pod (0.088), 100-seed weight (0.463), protein content (6.07), methionine content (0.215), biological yield per plant (1.95), harvest index (21.74) and seed yield per plant (0.339). The analysis also showed significant variation among parents and within both F_1 and F_2 generations for the majority of the traits, confirming the presence of sufficient variability for further genetic analysis and selection. The analysis of variance for the Parents, F_1 and F_2 generations is presented in Table 3, further confirming significant variation among the evaluated populations. The significant treatment effects observed in the present study indicate that the parental combinations generated considerable variation in the segregating populations.

3.2 Genetic variability for agronomic traits

The estimates of mean, range, genotypic and phenotypic variance, heritability, genetic advance, genetic advance as percentage of mean, GCV and PCV for the studied traits are presented in Table 1 and figure 1. For days to 50%

flowering, the mean was 48.79 days in F_1 and 49.79 days in F_2 , with ranges of 45.00-54.00 and 46.00-54.00 days, respectively. The genotypic coefficient of variation (GCV) was 4.09% in F_1 and 3.77% in F_2 , whereas the corresponding phenotypic coefficient of variation (PCV) was 4.36 and 4.13%, respectively. The relatively small differences between GCV and PCV indicated limited environmental influence on the expression of flowering time. Heritability was high in both generations (88.04% in F_1 and 83.60% in F_2), whereas genetic advance as percentage of mean (GA%) was comparatively low (7.91 and 7.11%). Thus, although flowering time showed high heritability, the relatively low expected genetic advance suggested limited scope for substantial improvement through direct selection. Days to maturity showed a similar pattern, with means of 116.58 and 117.66 days in F_1 and F_2 , respectively, GCV values of 3.35 and 3.20%, PCV values of 3.54 and 3.36%, and heritability estimates of 89.25 and 90.67%. The corresponding GA% values were only 6.52 and 6.28%. Similar low GCV and PCV for days to flowering and maturity have been reported in lentil, indicating comparatively limited genetic variability for these phenological traits (Rathi *et al.*, 2002) [11].

Plant height exhibited considerably greater genetic variability than the phenological traits. The mean plant height was 42.02 cm in F_1 and 40.50 cm in F_2 , with ranges of 32.78-51.11 and 33.67-49.93 cm, respectively. GCV and PCV were almost identical in both generations, being 9.91 and 9.94% in F_1 and 9.92 and 10.01% in F_2 , respectively. The trait recorded exceptionally high heritability of 99.48% in F_1 and 98.09% in F_2 , accompanied by GA% of 20.36 and 20.23%. Such a combination of high heritability and appreciable genetic advance indicated substantial exploitable genetic variation and favourable prospects for selection. Primary branches per plant recorded means of 3.43 and 3.32 in F_1 and F_2 , respectively, with GCV values of 16.73 and 16.72% and PCV values of 17.63 and 18.38%. Heritability was 90.05% in F_1 and 82.76% in F_2 , while GA% remained high at 32.71 and 31.33%. Secondary branches per plant also displayed high heritability (99.02% in F_1 and 98.82% in F_2), with GCV of 11.80 and 12.05%, PCV of 11.85 and 12.12%, and GA% of 24.18 and 24.68%, respectively. The high genetic variability and genetic advance observed for branching traits are consistent with earlier lentil studies, in which primary and secondary branches showed substantial variability and useful selection potential (Tiwari *et al.*, 2021) [13].

The number of clusters per plant showed a mean of 27.21 in F_1 and 26.20 in F_2 , with ranges of 18.00-34.73 and 18.00-33.60, respectively. GCV and PCV were 13.51 and 13.58% in F_1 and 13.31 and 13.39% in F_2 , while heritability was exceptionally high at 99.04 and 98.83%. The corresponding GA% values were 27.70 and 27.25%, indicating considerable scope for improvement through selection. Number of pods per cluster exhibited the highest genetic variability among the major yield-component traits, with GCV of 19.75% in F_1 and 21.12% in F_2 and PCV of 21.18 and 22.93%, respectively. Heritability was 86.95% in F_1 and 84.86% in F_2 , while GA% reached 37.94 and 40.08%, respectively, representing the highest genetic advance as percentage of mean among the traits studied. The combination of relatively high heritability and high genetic advance suggested substantial exploitable genetic variation and strong potential for selection for pods per cluster.

Comparable high heritability and genetic advance for important yield-contributing traits have also been reported in lentil germplasm evaluated under Indian conditions (Akkati *et al.*, 2024) ^[1].

Total number of pods per plant also showed substantial genetic variation. Its mean was 73.38 in F₁ and 70.61 in F₂, with ranges of 50.53-91.93 and 50.53-89.40, respectively. GCV and PCV were very close, at 13.35 and 13.41% in F₁ and 13.26 and 13.30% in F₂. Heritability was exceptionally high at 99.24% in F₁ and 99.39% in F₂, accompanied by GA% of 27.41 and 27.24%. These estimates indicated a strong genetic contribution to the observed variation and considerable potential for improvement through selection. Seeds per pod showed a contrasting pattern. In F₁, GCV was 9.05%, PCV was 10.52% and heritability was 73.97%, with GA% of 16.03%. In F₂, however, GCV was 10.05%, whereas PCV increased markedly to 17.89%, resulting in a substantial decline in heritability to 31.57% and GA% to 11.64%. The wider difference between GCV and PCV in F₂ indicated a relatively greater environmental contribution to the phenotypic expression of seeds per pod, thereby reducing the reliability of direct selection. Similar differences between PCV and GCV and variation in heritability among yield-related traits have been documented in lentil (Rana *et al.*, 2020) ^[10].

The 100-seed weight recorded means of 3.23 g in F₁ and 3.11 g in F₂, with GCV values of 12.96 and 12.12% and PCV values of 13.25 and 13.36%, respectively. Heritability was high in both generations, although it decreased from 95.71% in F₁ to 82.33% in F₂. Genetic advance as percentage of mean was 26.12% in F₁ and 22.66% in F₂, indicating good prospects for selection for seed size. Biological yield per plant showed means of 9.02 and 8.72 g in F₁ and F₂, respectively. GCV and PCV were 9.45 and 9.70% in F₁ and 9.11 and 9.46% in F₂, while heritability was 94.92 and 92.75%. GA% was 18.97% in F₁ and 18.08% in F₂, demonstrating a favourable combination of high heritability and appreciable genetic advance. Harvest index recorded means of 36.43 and 38.41% in F₁ and F₂, respectively. Heritability increased from 76.56% in F₁ to 87.24% in F₂, whereas GA% remained similar at 12.24 and 12.42%. These results indicated moderate prospects for improvement in harvest index through selection. High heritability and useful genetic advance for seed weight, biological yield and related yield traits have similarly been reported in lentil breeding populations (Alemu *et al.*, 2022) ^[3]. Seed yield per plant, the principal economic trait, had means of 3.28 g in F₁ and 3.14 g in F₂, with ranges of 2.28-4.00 and 2.19-3.85 g, respectively. GCV was 10.18% in F₁ and 10.41% in F₂, while PCV was slightly higher at 11.01 and 11.65%, respectively. Heritability was high in both generations (85.53% in F₁ and 79.83% in F₂), and GA% was 19.40 and 19.16%, respectively. The relatively close GCV and PCV values, together with high heritability and appreciable genetic advance, indicated substantial heritable variation for seed yield and suggested that selection for higher-yielding segregants could be effective. The favourable combination of heritability and genetic advance observed for seed yield agrees with previous lentil variability studies, where seed yield was identified as a trait with substantial genetic variation and selection potential (Akkati *et al.*, 2024) ^[1].

The quality traits showed distinct genetic behaviour. Protein content had means of 27.50% in F₁ and 27.37% in F₂, with

GCV values of 5.63 and 5.68% and PCV values of 5.71 and 5.69%, respectively. Heritability was exceptionally high, reaching 97.27% in F₁ and 99.74% in F₂, while GA% was 11.44 and 11.69%. Thus, protein content exhibited very high heritability but only moderate expected genetic advance, suggesting that although its variation was predominantly heritable, the magnitude of response to selection could be moderate. Methionine content showed a marked difference between generations. In F₁, its mean was 2.84%, with GCV of only 0.45%, PCV of 0.53%, heritability of 71.62% and GA% of 0.78%. In F₂, the mean was 2.77%, while GCV and PCV increased to 9.75 and 9.83%, respectively, with heritability of 98.38% and GA% of 19.91%. Therefore, methionine displayed very limited expected response to selection in F₁ but considerably greater genetic variability and selection potential in F₂. The high heritability observed for protein content is consistent with lentil studies demonstrating useful genetic variation for protein concentration and its potential integration into breeding programmes (Alemu *et al.*, 2022) ^[3].

4. Conclusion

The present study demonstrated substantial genetic variability among the lentil populations evaluated in the F₁ and F₂ generations for agronomic, yield-related and quality traits. Significant variability, coupled with high heritability and appreciable genetic advance, was particularly evident for plant height, primary and secondary branches, clusters per plant, pods per cluster, total pods per plant, 100-seed weight, biological yield and seed yield. Among these traits, number of pods per cluster exhibited the highest genetic advance as percentage of mean, indicating considerable potential for effective selection. Seed yield per plant also showed a favourable combination of heritability and genetic advance in both generations, suggesting that selection for superior yielding segregants could be effective. In contrast, days to 50% flowering and days to maturity exhibited relatively low genetic variability and genetic advance despite high heritability, indicating comparatively limited scope for improvement through direct selection. Seeds per pod showed a marked reduction in heritability in F₂, suggesting greater environmental influence and reduced selection efficiency for this trait at this generation. Protein content maintained exceptionally high heritability across generations, whereas methionine content showed greater selection potential in F₂ than in F₁. Overall, the combined assessment of GCV, PCV, heritability and genetic advance identified plant architecture, reproductive and yield-contributing traits as promising selection criteria for improving seed yield and associated attributes in lentil. These findings provide useful guidance for selecting superior segregants and advancing promising breeding material in subsequent generations.

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