

GENETIC VARIABILITY AND TRAIT CORRELATIONS IN BRASSICA GENOTYPES FOR YIELD OPTIMIZATION

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Abstract. This study explores the genetic variability and trait interrelationships among 15 *Brassica juncea* genotypes, focusing on six key traits: Leaf Area (LA), Stomatal Conductance (SC), Chlorophyll Content (CC), Length of Silique (LS), Number of Seeds per Silique (NS), and Total Yield per Plant (TY). Using a randomized complete block design (RCBD) with three replications were used in this experiment under field conditions. Highly significant differences ($p < 0.01$) were found for LA, CC, and LS, indicating these traits are strongly influenced by genetic factors. The results highlighted the superior performance of genotypes G12, G6, and G1. Genotypes G12 and G6 showed greater vegetative growth and photosynthetic efficiency, while G1 excelled in reproductive traits such as LS and NS. Genotypes G7 and G9 exhibited lower performance across most of the studied traits. Correlation analysis showed strong positive associations among LA with SC ($r = 0.98^{**}$) and CC ($r = 0.87^{**}$); SC with LS ($r = 0.94^{**}$) and NS ($r = 0.84^{**}$). While TY showed positive association with LS ($r = 0.93^{**}$), LA ($r = 0.84^{**}$), and NS ($r = 0.85^{**}$), indicating that improvement in one trait could enhance the others. The study underscores the importance of these interrelated traits in influencing overall yield and provides valuable insights for *Brassica juncea* breeding programs. These findings provide a foundation for selecting high-performing genotypes and targeting specific traits to improve Brassica crop productivity.

Keywords: *genetic, biomass, photosynthesis, yield, leaf, breeding*

Introduction

Brassica crops, including canola (*Brassica napus*), cabbage (*Brassica oleracea*), and mustard (*Brassica juncea*), are vital to global agriculture due to their nutritional value and resilience. They also contribute to the agricultural economy to a great extent, both in food supply to humans and as oilseeds, vegetables, and cover crops (Rehman et al.,

2019; Gadi et al., 2020). Because of their agricultural value, Brassica plants have received tremendous scientific attention. The need to enhance Brassica productivity and resilience amidst changing environmental conditions and rising global food demand underscores the importance of advanced breeding methodologies. Improvement of Brassica crops by breeding programs is founded on a deep understanding of intra- and interpopulation genetic diversity. This genetic diversity serves as the foundation for breeding and selecting genotypes with desirable traits. Besides knowing the genetic mechanisms of yield control in Brassica crops, the possibility to modify a trait through breeding has an additional value for sustainable agriculture (Meena et al., 2020; Moradpour et al., 2021).

The area of the leaf in a plant represents a basic factor that involves its photosynthetic activity. Increase in leaf area is highly associated with high photosynthesis, hence providing more accumulations of biomass and yield. Photosynthetically, it is a very important process in the growth and development of the plants; selection of the genotype with a higher leaf area should significantly contribute to the overall increase in crop productivity (Nandi et al., 2021; Ram et al., 2021). Stomatal conductance simply measures the rate of gas exchange-between plants and their surrounding atmosphere-of water vapor and carbon dioxide. High levels of stomatal conductance quite often occur with high water-use efficiency and with increasing photosynthesis. This trait is highly relevant under variable environmental conditions, given it affects the plant's capacity to control water loss while sustaining photosynthetic efficiency (Singh et al., 2017; Nandi et al., 2021; Verma et al., 2021).

It can be considered that chlorophyll concentration is one of the key indicators of photosynthetic capacity and overall plant vitality. The photosynthetic efficiency of chlorophyll increases with increasing amounts, contributing to increased biomass and yield. The chlorophyll content depends on genetic and environmental factors; therefore, it is useful to know this feature for understanding plant performance. Besides that, silique length represents another critical determinant of seed production (Kaur and Banga, 2015; Naznin et al., 2015; Neeru et al., 2016). In other words, a larger silique size indicates a greater number of seeds, and thus, is associated with higher productivity in Brassica crops. A selection for long silique can be made further to promote better seed production and productivity. Seed numbers in each silique are among the major factors that need consideration in respect to reproductive success. The greater the number of seeds in one silique, the better the production and yield would be. This trait has a very high correlation with seed development and plant fertility (Ali et al., 2016; Gupta et al., 2018; Ilyas et al., 2018). Larger siliques support a higher number of seeds, and this positively affects the yield of Brassica crops. Longer siliques may, therefore, be selected to gain higher seed production and productivity. The most important traits are a successful seed set and maximum yield number towards plant reproduction success. The number of seeds per silique, the more the number, the better the production of seed that yields a high total yield. This trait is associated with seed development and plant fertility (Shyam et al., 2021; Bijarania et al., 2022).

All such aspects of genetic variation within Brassica populations provide fertile ground for successful breeding. Therefore, modifications of traits of things like leaf area, stomatal conductance, and chlorophyll content can be well bred through the varieties that offer desirable improvement. It thus gives an empirical basis for the choice and following integration into advantageous traits in their breeding programs (Rehman et al., 2019; Gadi et al., 2020). Taken together, the application of molecular markers and genetic maps has

led to significant improvement in understanding the genetics behind the determination of agronomical traits in Brassica crops. These are among the most successful methods that permit breeders to identify and then select a plant possessing a more desirable combination of traits. In this context, MAS and QTL-seq have been applied to a wide range of crops including Brassica for accelerated crop improvement with enhanced performance (Jan et al., 2016; Verma et al., 2021; Ahmed et al., 2024; Khan et al., 2024).

Genetic diversity and correlations among key agronomic traits in Brassica crops have been discussed. For instance, certain characteristics, such as leaf area and stomatal conductance, are positively related to photosynthetic efficiency and yield. Chlorophyll content relates to better biomass production and general health of the plant. Of course, silique length and number of seeds per silique, as well as % oil in seed, though being important for seed production and yield, show a very large variability between genotypes (Pankaj et al., 2017; Khushboo et al., 2018; Li et al., 2024; Saeed et al., 2025; Zeng et al., 2024).

Breeding various Brassica species faces significant bottlenecks and challenges primarily due to limited genetic diversity, biotic and abiotic stress resistance, and the complexities of hybridization. The loss of biodiversity, exacerbated by climate change and selective breeding for specific traits, restricts the genetic resources available for breeding programs, which is critical for enhancing productivity and quality traits in crops like mustard (Subramanian et al., 2023). Traditional breeding methods have yielded modest gains, necessitating the integration of advanced genomic techniques such as marker-assisted selection and genome editing to improve yield and oil quality (Sunagar and Pandey, 2024). Additionally, the presence of both self-compatible and self-incompatible species complicates breeding strategies, as it affects the stability of genetic traits and the efficiency of hybrid seed production. Furthermore, regulatory concerns and technical hurdles associated with biotechnological approaches pose additional challenges to the successful implementation of innovative breeding strategies (Singh and Prakash, 2024).

The research underlines understanding in the case of co-association of the traits. Co-assessment is exemplified by, for instance, a high positive correlation between leaf area and chlorophyll content, which means that an increase in one of these traits raises the other, hence supportive to the enhancement in the performance of the plant. The trait silique length is associated with the number of seeds per silique, hence showing that yield improvement might require multiple-trait selection. Despite these insights, unresolved questions remain regarding the impact of genetic diversity and trait interactions on Brassica crop performance (Rehman et al., 2019; Nandi et al., 2021; Yadav et al., 2021). Seed production is a polygenic character, so it depends on several traits. It has both positive and negative effects on a particular trait. In that connection, more care should be given to the contribution of each one of these traits to seed yield, particularly emphasizing those contributing highly. This will involve studying those traits which will contribute to the photosynthetic efficiency, seed yield, and overall productivity to ascertain what characteristic contributes most to crop yield. Different genotypes will also be screened as to whether they have good or inferior performance with regards to the traits considered. This will help in bringing out the elite genotypes which may be utilized for breeding purposes (Afrin et al., 2016; Ilyas et al., 2018; Nandi et al., 2021).

The results obtained in this work could greatly help in understanding genetic variation and relationship in different traits in Brassica genotypes. In this work, a way was worked out to augment high-yielding varieties of *Brassica juncea* by detecting the

genotypes with the desired traits and establishing relationships among the basic agronomic traits. Evidence could be seen how the variation in yield and agronomic traits detected in this study could provide useful parents for Brassica breeding program.

Materials and methods

The study aimed to examine the interrelationships among six yield and yield related traits of 15 Brassica juncea genotypes to assess genetic diversity (*Table 1*). To ensure reliable and statistically valid results, a randomized complete block design (RCBD) with three replications implemented at the research field area of the Faculty of Agriculture and Environment, The Islamia University of Bahawalpur, Pakistan. This design effectively minimized environmental variability and provided dependable estimates of treatment effects. The 15 selected Brassica juncea genotypes chosen from known and potential sources of variation for economically significant agronomic traits. These genotypes included high-yielding and commercially relevant varieties, ensuring a comprehensive representation of genetic diversity within the species. The seeds sown manually in well-prepared plots, maintaining a plant-to-plant distance of 45 cm and a row-to-row distance of 60 cm to ensure adequate spacing for plant growth and accurate observation of traits. Each plot consisted of 5 meter long and three rows for each entry. Standard agronomic practices, including timely land preparation, irrigation, and pest management, followed to create optimal growing conditions for all genotypes. Fertilizer applied based on recommended rates for Brassica juncea, ensuring uniform nutrient availability across plots. Weed control managed manually throughout the growing season to reduce competition and ensure proper plant development.

Table 1. List of studied 15 Brassica juncea studied genotypes

Code	Genotype name	Code	Genotype name
G1	Super Canola	G9	KN-331
G2	AARI Canola	G10	ZCA-13
G3	Khanpur raya	G11	KJ-274
G4	ZBJ-08051	G12	Super Raya
G5	17CBJ007	G13	CHS-2
G6	RBN-13017	G14	RBN-13017
G7	RBJ-19003	G15	ZBJ-17017
G8	Chakwal Sarson		

Traits to be measured

At the maturity stage of the Brassica juncea genotypes, six yield and yield related traits carefully observed to assess their performance and genetic variability. The leaf area was determined using a leaf area meter (Model: Li-3100C, Manufacturer: LI-COR Biosciences, USA), ensuring precise and consistent measurements for each plant. This parameter was vital for evaluating the photosynthetic capacity and overall growth potential of the genotypes. Stomatal conductance was measured using a portable photosynthesis meter (Model: Li-6400, Manufacturer: LI-COR Biosciences, USA) at the flowering stage, a critical growth phase when the leaves were fully expanded. This timing ensured the capture of accurate data on the plant's ability to regulate gas

exchange and maintain water use efficiency under optimal physiological conditions. To evaluate the photosynthetic pigment content, the chlorophyll content was assessed using a chlorophyll meter (Model: SPAD-502, Manufacturer: Konica Minolta, Japan) on healthy, green leaves. This measurement provided insights into the plants' photosynthetic efficiency and health. The silique length, a critical trait related to seed development, was measured using a caliper (Model: 500-199-30, Manufacturer: Mitutoyo, Japan) from mature siliques harvested from the plants. Additionally, the number of seeds per silique counted from a set of randomly selected siliques to determine seed production efficiency. The total yield per plant calculated by harvesting all fully developed siliques from each genotype and weighing them to determine the total seed yield for each plant. This comprehensive assessment of the key agronomic traits allowed for a thorough evaluation of the genetic diversity and agronomic potential of the tested Brassica juncea genotypes (Saroj et al., 2021).

Biometrical analysis

Analysis of variance (ANOVA) performed to determine the significance of differences in each trait among genotypes from the recorded data. The analysis was performed using Statistix 8.1, with a significance threshold set at $p < 0.05$ (Steel and Torrie, 1960). In the present investigation, descriptive statistics calculated for each trait in respect of mean, variance, standard deviation, and coefficient of variation. Such calculation summarizes the data and provides an estimation of variability between the genotypes. Values for the correlation coefficients among the six traits are presented (Falconer and Mackay, 1983). This analysis explains inter-relationship and its implication in the breeding program. Ranking of genotypes with respect to performance of each of the studied traits identified those genotypes expressing the highest and lowest values of each particular characteristic.

Results and discussion

Analysis of variance (ANOVA) performed on 15 Brassica genotypes for six yield and yield related traits showed significant differences between genotypes in studied traits, highlighting the significant variation in examined germplasm of Brassica (*Table 2*). Specifically, genotypes showed highly significant variation ($p < 0.01$) in leaf area with a mean square value of 171.098. This finding implies significant differences in leaf area between genotypes, which may benefit breeding strategies. Furthermore, there was a significant variation present in stomatal conductance among genotypes ($p < 0.05$) with a mean square value of 52.734. This indicates that genotypes exhibit different stomatal regulation, possibly related to changes in water use efficiency (Ali et al., 2011; Mahmud et al., 2011; Santhosha et al., 2011). The very highly significant difference in the chlorophyll content of genotypes under analysis is evidenced with a mean square value of 70.5582 at $p < 0.01$. This property assumes very important importance in optimizing photosynthetic efficiency and may bring about serious consequence variations in overall biomass production of a genotype. Length of silique also showed highly significant differences among the genotypes under study with a mean square value of 157.394 out at $p < 0.01$. This result therefore indicates the possibility and potential for diversity in silique development among genotypes, a factor important for proportional production of seeds. One-way ANOVA results showed that there was significant variation, $p < 0.05$, among the genotypes for the number of seeds per silique, with a mean square value of 838.521.

This character is directly related to the reproductive success and potential yield of the genotype. Finally, the total yield per plant showed significant differences between genotypes ($p < 0.05$) with a mean square value of 48.9134. This indicates that genotypes have different yield potential, which is crucial for the selection of high-yielding varieties (Afrin et al., 2012; Jahan et al., 2013; Khan et al., 2013).

Table 2. ANOVA for the studied traits in 15 Brassica genotypes

Sources of variation	DF	LA	SC	CC	LS	NS	TY
Replications	2	1.862	5.6821	6.7395	8.974	9.847	3.4263
Genotypes	14	171.098**	52.734*	70.5582**	157.394**	838.521*	48.9134*
Error	28	2.174	1.1293	3.6418	8.632	7.258	1.6432
Total	44						

Leaf area (LA), Stomatal conductance (SC), Chlorophyll Contents (CC), Length of silique (LS), No of seeds per silique (NS), Total yield per plant (TY)

The considerable variation detected ANOVA analysis of the traits studied indicated presence a fair enough genetic diversity within population in each one. Significance levels were more heightened for traits such as leaf area, chlorophyll content and silique length which have utmost genetic contribution to expression of the trait implying that selection would lead to superior performance (Nasim et al., 2013; Halder et al., 2014). Variation in stomatal conductance between genotypes suggests divergence in their management of water loss and photosynthetic capacity under changing environmental conditions. This characteristic is very much important in the development of Brassica cultivars that can survive under unfavorable conditions. Also, there is an enormous difference in the content of chlorophyll, and it widely may be a reason to change efficiency photosynthetic properties. Genotypes accumulating more chlorophyll can be potentially beneficial for biomass production and total grain yield due to possible competitive advantage. The length of the siliques and ensuing number of seeds per silique are also key contributors to overall yield (Singh et al., 2014; Kaur and Banga, 2015; Jan et al., 2016). In fact, dramatic changes detected in those traits have suggested that the selection for siliques and seed number is applicable to the direct improvement of yield potential. Furthermore, the significant detected total yield per plant among accessions suggests that these traits are very important in determining the overall productivity of Brassica genotypes. Thus, the genetic variability reported in this study is a considerable asset for breeding programs with an objective to improve yield along with other agronomically important traits in Brassica crops (Naznin et al., 2015; Neeru et al., 2016; Singh et al., 2017; Ilyas et al., 2018).

The descriptive statistics for the 6 traits of 15 Brassica genotypes are summarized in Table 3. These data give some idea of the range and proportionate frequency of characteristics within a population having certain genotypic differences. Leaf area (from 10.13 to 24.13; mean = 16.44) had a higher CV than vegetative biomasses and was intermediate relative to most reproductive traits except for capsule armature dimensions at some sites. Variance and standard deviation in leaf area Variance 16.71 standard deviation 4.09 (Table 3). Its coefficient of variation (CV) was calculated at 24.86%, representing the amount it varied to its mean value. The evaluation of 15 Brassica juncea genotypes for six key agronomic traits revealed significant differences among genotypes, with the LSD test identifying distinct groups for each trait (Table 4). The

genotypes were categorized into 7 distinct groups (A-G), indicating a wide variation in leaf area across the genotypes. This diversity highlights the potential for selecting genotypes with superior photosynthetic capacity. Genotype G12 exhibited the highest mean leaf area (24.13 cm²), significantly outperforming most genotypes, suggesting its superior photosynthetic capacity. G6 and G1 also showed high values (23.17 and 22.15 cm², respectively), whereas G7 had the smallest leaf area (10.13 cm²), indicating potential limitations in growth and productivity.

Table 3. Summary statistics of studied traits in 15 Brassica genotypes

Parameters	LA	SC	CC	LS	NS	TY
Minimum	10.13	9.35	11.33	3.99	13.34	9.29
Maximum	24.13	23.90	27.52	7.13	32.32	21.72
Mean	16.44	15.65	17.61	4.96	21.6	15.94
Variance	16.71	18.28	23.13	1.63	33.97	13.82
Std	4.09	4.28	4.81	1.28	5.83	3.72
CV	24.86	27.32	27.31	25.74	26.98	23.32

Leaf area (LA), Stomatal conductance (SC), Chlorophyll Contents (CC), Length of silique (LS), No of seeds per silique (NS), Total yield per plant (TY), Standard Deviation (Std), Coefficient of Variation (CV)

Table 4. Mean values of studied traits and their significance using LSD comparison test in 15 Brassica juncea varieties

LA	SC	CC	LS	NS	TY
G12 (24.13) A	G12 (23.90) A	G12 (27.52) A	G1 (7.13) A	G1 (32.32) A	G1 (21.72) A
G6 (23.17) A	G6 (22.84) AB	G6 (26.48) AB	G12 (6.94) A	G12 (31.77) A	G12 (21.35) A
G1 (22.15) A	G1 (21.33) B	G1 (24.65) B	G6 (6.60) AB	G6 (29.97) A	G6 (20.22) A
G10 (18.25) B	G11 (18.54) C	G11 (19.08) C	G13 (5.79) BC	G5 (23.75) B	G13 (19.45) AB
G11 (17.82) BC	G10 (17.52) CD	G10 (17.46) CD	G3 (5.64) CD	G4 (23.72) B	G4 (17.04) BC
G4 (16.30) BCD	G5 (15.95) DE	G5 (17.36) CD	G4 (5.49) CD	G10 (22.40) B	G5 (16.82) BCD
G14 (16.14) BCD	G13 (14.37) EF	G4 (17.20) CD	G5 (4.94) DE	G3 (20.55) BC	G10 (15.93) CDE
G5 (15.53) CDE	G3 (14.22) EF	G3 (16.12) DE	G10 (4.85) DEF	G14 (20.28) BC	G8 (15.56) CDE
G3 (15.32) DE	G14 (14.06) EF	G14 (15.97) DE	G14 (4.45) EFG	G11 (18.77) CD	G3 (14.76) CDEF
G13 (15.22) DE	G4 (13.33) FG	G15 (14.80) EF	G2 (4.12) FGH	G2 (18.73) CD	G11 (14.39) CDEF
G15 (14.15) DEF	G8 (12.70) FG	G2 (14.73) EF	G11 (4.03) GH	G13 (17.86) CD	G14 (13.81) DEF
G8 (13.16) EF	G15 (12.67) FG	G8 (14.51) EF	G8 (3.99) GH	G8 (17.40) CD	G2 (13.43) EF
G2 (13.12) EF	G2 (12.64) FG	G13 (14.16) EF	G15 (3.84) GHI	G15 (17.26) CD	G9 (13.10) EF
G9 (12.18) FG	G9 (11.42) GH	G9 (12.99) FG	G9 (3.57) HI	G9 (16.09) DE	G15 (12.38) FG
G7 (10.13) G	G7 (9.35) H	G7 (11.33) G	G7 (3.10) I	G7 (13.34) E	G7 (9.29) G

Leaf area (LA), Stomatal conductance (SC), Chlorophyll Contents (CC), Length of silique (LS), No of seeds per silique (NS), Total yield per plant (TY), The genotypes of Brassica juncea are labeled as G1 to G15 each corresponding to a specific genotype name as mentioned in Table 1. The mean values of each genotype provided in parentheses. The capital letters (A, B, C, etc.) represent different groups based on the mean comparison using the LSD test, with a significance level of 0.05. These groupings indicate the statistical differences among the genotypes for the respective traits

Stomatal conductance (SC) varies between 9.35 and 23.90, with an average of 15.65. This trait showed a moderate degree of variation (Table 3) and had an 18.28 variance

with a standard deviation of 4.28. A total of 8 groups (A-H) were identified, reflecting substantial variability in stomatal conductance. This trait is critical for understanding the water use efficiency and gas exchange capability of the genotypes. G12 recorded the highest stomatal conductance ($23.90 \text{ mmol m}^{-2} \text{ s}^{-1}$), followed by G6 ($22.84 \text{ mmol m}^{-2} \text{ s}^{-1}$). These values indicate efficient gas exchange in these genotypes. In contrast, G7 ($9.35 \text{ mmol m}^{-2} \text{ s}^{-1}$) showed the lowest conductance, reflecting its suboptimal physiological performance (*Table 4*). Similar findings reported by previously studied in brassica crop (Halder et al., 2014; Ali et al., 2016; Ram et al., 2021)

The chlorophyll content (CC) ranges from 11.33 to 27.52, with an average value of 17.61. This provided a calculated variance of 23.13 and the standard deviation measured was 4.81, which tells that there is large variation in between genotypes. The CV estimated to be 27.31%, which is almost near by the stomatal conductance, and therefore suggests that there exists high variability in between the genotypes. The genotypes were divided into 7 groups (A-G), showing noticeable differences in photosynthetic pigment levels. This variation emphasizes the genetic potential for improving photosynthetic efficiency in Brassica juncea (*Table 4*). G12 again ranked highest (27.52 SPAD units), highlighting its robust photosynthetic potential. G6 and G1 were also among the top performers (26.48 and 24.65 SPAD units, respectively). Conversely, G7 displayed the lowest chlorophyll content (11.33 SPAD units), indicating limited photosynthetic efficiency (*Table 4*).

In terms of silique length (SL), measurements ranged from 3.99 to 7.13, with a mean of 4.96. This trait had a variance of 1.63 and a standard deviation of 1.28, reflecting low variability compared to other traits. The CV for silique length was 25.74%, indicating moderate variability (*Table 3*). Nine groups (A-I) were observed for silique length, demonstrating considerable diversity in this trait, which directly impacts seed production and yield potential. G1 had the longest silique length (7.13 cm), closely followed by G12 (6.94 cm) and G6 (6.60 cm). This trait is directly related to seed production, and longer siliques suggest better reproductive capacity. G7 showed the shortest silique length (3.10 cm), which could limit its seed yield as displayed in *Table 4*.

The number of seed (NS) per silique ranged between 13.34 and 32.32 with an average of 21.60. This trait accounted for most of the variability with a variance of 33.97 and standard deviation value established at 5.83. The CV for this trait also showed a high degree of variation at 26.98% (*Table 3*). Five distinct groups (A-E) were identified, indicating moderate variability in the number of seeds per silique among the genotypes. This is a critical yield-determining trait. G1 had the longest silique length (7.13 cm), closely followed by G12 (6.94 cm) and G6 (6.60 cm). This trait is directly related to seed production, and longer siliques suggest better reproductive capacity. G7 showed the shortest silique length (3.10 cm), which could limit its seed yield (*Table 4*).

The total yield (TY) per plant ranged from 9.29 to 21.72, with a mean value of 15.94. The coefficient of variation for this trait was 13.82%, and the standard deviation was 3.72 (*Table 3*), indicating intermediate variability (Ahmad et al., 2009; Singh et al., 2017; Kumar et al., 2018). The genotypes were classified into 7 groups (A-G), reflecting significant differences in their overall productivity. G1 and G12 also excelled in total yield per plant, producing 21.72 g and 21.35 g, respectively. G6 (20.22 g) was another top performer, while G7 had the lowest yield (9.29 g), consistent with its poor performance in other traits (*Table 4*).

Variation among the Brassica genotypes in these traits is essential to select elite lines to incorporate breeding advantageous traits. The genotypes G12, G6 and G1 appeared consistently superior for most of the traits, which suggest their candidacy in Brassica breeding programs aimed at developing high yielding cultivars. G12 had a larger leaf area, and both replicates G6 indicate increased vegetative growth in many plants might help photosynthetic capacity to increase yield broadly. They also have higher stomatal conductance to support more efficient gas exchange which is an important strategy for maintaining the photosynthetic capacity over a full range of environmental conditions. Furthermore, the higher chlorophyll content observed in these genotypes is an important indicator of photosynthetic efficiency, meaning they are able to sustain higher photosynthetic levels, thereby promoting greater biomass accumulation. Our results supported by previously findings (Rashid et al., 2009; Gangapur et al., 2010; Jahan et al., 2013; Pankaj et al., 2017). Genotypes G12 and G6 with increased chlorophyll content have an added advantage in the environmental conditions where higher photosynthetic activity is required to get better yields. G1, G6 and G12 were unique in their siliques length as they had higher number of seeds per silique thereby having a high reproductive vigor. These traits are directly related to yield and, as the higher measured values found in these genotypes indicate they have a greater capacity for seed production (which is important when trying to increase yields).

Genotype G1, G6 and G12 were enriched for all traits simultaneously indicating these as three dominant genotypes with higher combined trait. Their superior performance in various traits emphasizes their potential utility as parental lines in breeding programs focusing on yield enhancement and other agronomically significant characteristics of Brassica species. Current findings supported by the study of these scientists (Sadia et al., 2009; Singh et al., 2010; Khan et al., 2013; Khushboo et al., 2018). In contrast, genotypes G7 and G9 consistently showed lower performance on most traits, indicating that they may not be suitable for environments requiring high yields. However, certain characteristics of such genotypes become very useful in specialized breeding situations, for example, variety development through which improvement in the stress tolerance or specialized market niche can be achieved. Variability observed among 15 Brassica genotypes assessed represents genetic diversity, which is crucially important for any breeding program. High-performance genotypes identified in this study represent a very important resource to advance yield and other key characteristics in Brassica crops (Kaur and Banga, 2015; Gadi et al., 2020; Nandi et al., 2021).

Correlation matrix of the tested properties between the 15 genotypes of Brassica: leaf area, stomatal conductance, chlorophyll content, length of silique, number of seeds per silique, total yield per plant. In this figure (*Fig. 1*), a correlation coefficient is given for every couple of features; statistically significant correlations are marked with asters (**). The scatter plots in the diagonals show the distribution of individual characteristics and off-diagonal scatter plots represent relationships of the measured characteristics (Naznin et al., 2015; Khushboo et al., 2018).

The correlation matrix among traits studied in 15 Brassica genotypes, as shown in *Figure 1*, revealed strong associations between several key traits. *Table 1* highlights significant positive correlations, suggesting that these traits are interrelated and relevant for selection in breeding programs. Leaf Area (LA) exhibited strong positive correlations with Stomatal Conductance (SC) ($r = 0.98^{**}$) and Chlorophyll Content (CC) ($r = 0.87^{**}$), indicating that genotypes with larger leaf areas also tend to have

higher stomatal conductance and chlorophyll content, both of which are critical for optimizing photosynthetic performance (Santhosha et al., 2011; Nasim et al., 2013; Khushboo et al., 2018). SC was similarly correlated with CC ($r = 0.97^{***}$), Silique Length (LS) ($r = 0.94^{**}$), and the Number of Seeds per Silique (NS) ($r = 0.84^{**}$), suggesting that higher stomatal conductance is associated with enhanced chlorophyll content, longer siliques, and increased seed numbers. Chlorophyll Content (CC) also showed positive correlations with LS ($r = 0.94^{**}$) and Total Yield (TY) ($r = 0.81^{**}$), indicating that genotypes with higher chlorophyll levels tend to produce longer siliques and greater overall yield. Furthermore, TY exhibited strong positive correlations with NS ($r = 0.85^{**}$), LS, and LA, with correlations of $r = 0.93^{**}$ and $r = 0.84^{**}$, respectively. This indicates that increased yield is linked to a greater number of seeds, longer siliques, and larger leaf area (Singh et al., 2014; Naznin et al., 2015).

Overall, the strong interrelationships observed between basic agronomic traits, such as LA, SC, and CC, highlight the potential for simultaneous improvements in photosynthetic efficiency and plant vigor through targeted selection (Jan et al., 2016; Neeru et al., 2016; Singh et al., 2017). The strong correlation between TY, NS, LS, and LA further underscores the importance of these traits in determining yield potential. This suggests that selecting for one of these traits may also improve others, which is a significant advantage for breeding programs. Additionally, the positive relationship between CC and LS implies that increased chlorophyll content may enhance silique formation, leading to more seeds and higher yield (Khushboo et al., 2018; Raza et al., 2021). These results emphasize the interconnectedness of traits in Brassica breeding and provide multiple avenues for improving crop performance through targeted selection strategies.

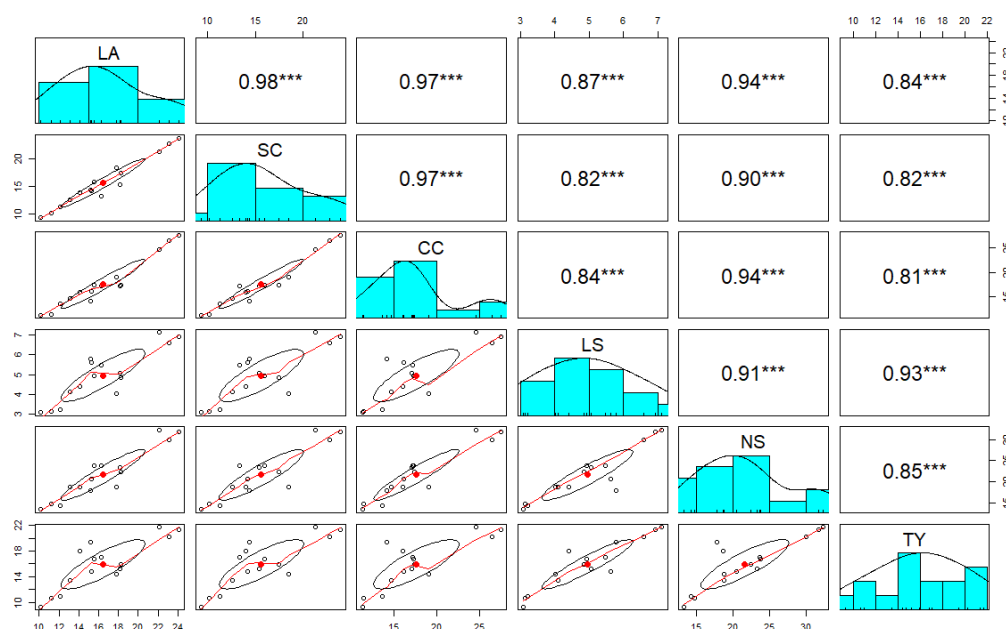


Figure 1. Scatter plot (correlation) for studied traits in 15 Brassica genotype

Conclusion

This study aimed to evaluate the genetic variability and interrelationships among key agronomic traits in *Brassica juncea* genotypes, with a focus on yield potential. The

purpose was to identify promising genotypes for breeding programs and to understand how traits such as LA, SC, CC, LS, NS and TY interrelate and contribute to overall productivity. The results revealed significant genetic diversity across the 15 genotypes. Correlation matrix analysis showed strong positive associations between key traits. Notably, LA was positively correlated with SC ($r = 0.98^{**}$) and CC ($r = 0.87^{**}$), indicating that genotypes with larger leaf areas also tend to have better photosynthetic capacity. Furthermore, SC was positively correlated with CC ($r = 0.97^{**}$), LS ($r = 0.94^{**}$), and the NS ($r = 0.84^{**}$), suggesting that improved SC enhances both photosynthesis and reproductive traits. Total yield per plant exhibited strong positive correlations with SL ($r = 0.93^{**}$), LA ($r = 0.84^{**}$), and the NS ($r = 0.85^{**}$), highlighting these traits' role in determining yield potential. The genotypes G1, G6, and G12 showed superior performance across multiple traits, marking them as promising candidates for future breeding as compared to the other studied genotypes. In contrast, G7 and G9 exhibited poor performance, indicating limited adaptability to high-yield environments. These findings emphasize the importance of studied traits in optimizing yield, and suggest that selection for these traits could lead to significant improvements in *Brassica juncea* productivity. Future breeding efforts should prioritize these traits and consider genetic diversity to enhance yield potential in *Brassica* cultivation.

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