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Evaluating the genetic parameters, heritability, and genetic diversity of datashak (*Amaranthus lividus*) under hot summer growing conditions

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Abstract: Datashak (*Amaranthus lividus*) are climate-smart, stress-resistant, C_4 leafy vegetables. Fourteen datashak genotypes were evaluated in three replicates during the summer growing season at Bangabandhu Shiekh Mujibur Rahman Agricultural University. The results revealed highly significant differences among the genotypes, indicating a wide range of variability. By considering the genetic parameters, selection was performed based on the total biomass per plant (TBPP), shoot weight (SW), stem weight (StW), and shoot length to improve the biological yield (BY) of the genotypes. The correlation results revealed that almost all the features showed a significant increase in the BY of datashak. The StW, root length, leaf weight, and SW demonstrated a strong direct and positive effect on and a noteworthy genotypic association with the BY, indicating that direct choice depending on these traits will be useful for enhancing the BY of datashak. The datashak accessions were divided into four clusters based on the Euclidean distance matrix using Ward's statistics method. Clusters II and III datashak might be selected for the next breeding programs based on the mean cluster values and distances within the clusters and between clusters since these two clusters had superior mean values for the majority of the characteristics. Redtower and Data (cross) could be selected as multitrait high-performance accessions based on the multitrait genotype-ideotype distance index (MGIDI), as these datashak displayed balanced traits related to the SW, StW, TBPP, and BY without assigning weights, and were free from multicollinearity. Lalgolapi, Lolita, and BARI lalshak-1 were more promising than the others due to their strong positive contributions; therefore, choosing these datashak accessions would be better in terms of the yield, according to the principal component analysis, heatmap, and cluster dendrogram. These datashak accessions could be considered high-yielding, promising varieties for future breeding activities.

Key words: Phenotypic variation, correlation, box plot, cluster, cluster mean, multitrait stability index

1. Introduction

Datashak is a member of the family *Amaranthaceae*. There are 70 species in this family, of which approximately 17 are grown for the edibility of the leaves and three are utilized as pseudocereals.[1] It is a year-round crop and the only vegetable crop available during the summer when other vegetable crops are grown only on a small scale in the field. These plants have a wide geographic distribution across Africa, America, Europe Australia, and Asia, and are climatically smart, stress-resistant, highly adapted, fast-growing C_4 plants. Amaranth is a promising new vegetable with a wide range of diversity (Rastogi and Shukla, 2013; Rastogi et al., 2015; Das (2016); Nguyen et al., 2019; Jahan et al., 2023). Datashak leaves and stems are alternate sources of nutrients because of their richness in minerals like magnesium, calcium,

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[1]Jansen PCM (2021). *Amaranthus hypochondriacus* L. [online]. Website https://prota.prota4u.org/protav8.asp?g=pe&p=Amaranthus+hypochondriacus+L [accessed 15 December 2023].

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potassium, iron, phosphorus, copper, zinc, etc., and vitamins (Chakrabarty, 2018; Sarker et al., 2018), protein with amino acids essential for human nutrition, vitamin C, carotenoids (Sarker et al., 2017; Sarker and Oba, 2019), digestible fiber, leaf pigments, like betacyanins, betaxanthins, betalains, and chlorophylls (Sarker and Oba, 2020), phenolic compounds, and flavonoids (Sarker et al., 2020) with strong antioxidants (Sarker and Oba, 2021; Sarker et al., 2022a, 2022b).

The biological yield (BY) of datashak has a complicated character that is determined by several yield-contributing factors. Morphologically, datashak has two types, red and green, respectively. Red datashak is a richer source of natural pigments compared to green datashak in terms of the, minerals, antioxidants, and phytochemicals. Both red and green datashak leaves are extensively used as a vegetable in Bangladesh as well as South America, Africa, and southeast Asia for their appealing color, taste, and nutritional value of leaves. In Bangladesh, red datashak is cultivated year-round even during the hot summer, a lag period for green leaves in terms of vegetables. It tolerates drought (Sarker and Oba, 2018) and salinity (Hossain et al., 2022; Sarker and Ercisli, 2022; Sarker et al., 2023).

Datashak accessions are used in numerous conventional medications, particularly for their antimicrobial (Moyer et al., 2019; Terzieva et al., 2019; De Vita, 2021), antiviral (Chang et al., 2020), anthelmintic (Baral et al., 2010), antiulcer (Hussain et al., 2009), antiinflammatory (Olajide et al., 2004; Lin et al., 2005), hepatoprotective (Zeashan et al., 2008, 2009, 2010; Aneja et al., 2013), anticancer (Allegra et al., 2007; Amornrit and Santiyanont, 2015; House et al., 2020), antihyperlipidemic (Clemente and Desai, 2011; Yang et al., 2021), and antidiabetic, snake antidote, and antimalarial activities (Hilou et al., 2006; Hsiao et al., 2021). The major groups of bioactive leaf pigments of red datashak leaves are implicated in the protection of many ailments together with cancer, atherosclerosis, arthritis, cardiovascular diseases, emphysema, cataracts, neurodegenerative, and inflammation, and possess antiaging properties (Sarker and Oba, 2018).

Various governmental and private organizations in Bangladesh have developed several high-yield potential datashak; however, their comparative studies are not yet accessible. The yield-contributing traits, character associations, and selection criteria for these high-yielding genotypes are still unexplored. Some traits may contribute greatly to the BY of datashak, aiding future breeding operations by enhancing datashak's yield potential. This research was planned with the following objectives: 1) to evaluate phenotypic variations, their association, and their contribution in response to the BY and its related traits in datashak, and 2) to establish suitable selection criteria for the further improvement of datashak.

2. Materials and methods

2.1. Location of the experimental site
The experimental site was located at Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh (90°08′E, 24°23′N), with a mean altitude of 8.4 m from sea level (Sarker and Oba, 2018).

2.2 Edaphic and climatic condition
The site is a typical Salna Series of the Madhupur Tract of Agroecological Zone (AEZ 28). The soil type of the research field is a shallow red-brown terrace, characterized by silty clay at a pH of 5.5. It has a subtropical climate with high rainfall from June to September and little precipitation in winter, with a steady drop in temperature at the beginning of September.

2.3 Experimental materials
The mature seeds of 14 red and green datashak were collected from different sources and cultivated in the study field (Table 1).

2.4. Experimental design and layout, and plant husbandry
The selected datashak genotypes were sown in a completely randomized block design with three repetitions. Plots of 2 m² were used for BY and yield-contributing characters. Weeding was performed allowing single plants to remain at 5-cm intervals with all the plants removed in between. Row-to-row and plant-to-plant distances were 20 cm and 5 cm, respectively (Sarker et al., 2014). The experimental plot had a higher water retention capacity and was located at a lower elevation. The ground of the experimental was plowed using a tractor-drawn disc plow and then harrowed. The soil was extensively prepared by cross-plowing and plow-laddering three to four times. The field was ultimately prepared by removing weeds and branches and adding the recommended dosage of fertilizers (Sarker and Oba, 2018). During the final land preparation, total biological and chemical fertilizers like gypsum, urea, triple superphosphate, and muriate of potash were applied at 30, 200, 100, and 150 kg/ha, respectively (Sarker and Oba, 2018). The seeds were sown in the experimental field on March 11th, 2022. The intercultural operation was maintained properly. Proper plant density was maintained by thinning between the rows. Hoeing and weeding were done seven days apart. Irrigation was applied every five to seven days. Certain interrow cultivation was applied to maintain the crust-free soil and low occurrence of weeds. During the whole season, wild species of datashak and goosefoots were regularly removed.

2.5. Data collection and statistical analysis
The amaranth was harvested at 55 days after sowing (DAS) when the crop reached edible size. Data were documented from randomly selected 10 plants from each replication. Plant samples were collected randomly from each row of the respective plots. To characterize the

Table 1. List of plant materials used in this study and their morphological features.

Serial number	Cultivar	Source	Origin	Leaf color	Stem color	Petiole color	Plant growth habit
1	Lolita	Lal Teer Seed Ltd.	Exotic	Mixed with red and green	Red	Red	Erect
2	Panna	Lal Teer Seed Ltd.	Bangladesh	Greenish red	Mixed with red and green	Greenish red	Erect
3	Lalgolapi	Hybrid Seed Co.	China	Red	Pinkish red	Red	Erect
4	Redtower	Lal Teer Seed Ltd.	Bangladesh	Green	Red	Red	Erect
5	Greentower	Lal Teer Seed Ltd.	Bangladesh	Green	Green	Green	Erect
6	Sabujshak	Krishan Seed	Bangladesh	Green	Green	Green	Erect
7	RM	Rafi Seed Co.	Bangladesh	Red	Red	Red	Erect
8	Lota	M. R. Hybrid Seed	Taiwan	Green	Green	Green	Erect
9	Data (cross)	Kusum Seed	Bhutan	Green	Greenish red	Green	Erect
10	Redforce	Mollica Seed	India	Red	Greenish red	Red	Erect
11	Payra	Daijan Seed Co.	Bhutan	Green	Green	Green	Erect
12	Golapirani	M. R. Hybrid Seed	Taiwan	Pinkish green	Pink	Pink	Erect
13	BARI lalshak-1	BARI	Bangladesh	Dark red	Bright red	Red	Erect
14	Altapati	Lal Teer Seed Ltd.	Exotic	Pink	Pink	Pink	Erect

BARI: Bangladesh Agricultural Research Institute.

material under study, observations were made of various morphological traits at specific phonological stages (Table 2). Data were recorded for each trait using amaranth descriptors, as recommended by the International Board for Plant Genetic Resources based on taxonomic keys. All values were the means of three replicate determinations. Replication-wise mean data of a trait were obtained by averaging the mean of the sample (Mamun et al., 2022; Hossain et al., 2023). The average data of various traits were analyzed statistically (Prodhan et al., 2022; Rahman et al., 2022) and biometrically (Azad et al., 2022; Fatema et al., 2023). All mean data obtained for each character were analyzed using Statistix 8 software (Azam et al., 2022a; Hasan et al., 2022). Data for all determinations were subjected to analysis of variance (ANOVA) using Tukey's method for mean separation using R-4.1.3 software (R Core Team, 2015). Narrative statistics for the boxplots and histograms of all the characters were prepared using Excel v.2020 (Microsoft Corp., Redmond, WA, USA). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using a method of reported previously (Sarker et al., 2015a; Hasan et al., 2020; Rashad and Sarker, 2020). The heritability (h²b) was calculated using a previously described method

(Sarker et al., 2016; Hasan-Ud-Daula et al., 2020; Faysal et al., 2022). The genetic advance (GA) was estimated using the method of previous researchers (Kulsum et al., 2022; Sarker et al., 2015b). The GA in percent of the mean (GAPM) was estimated using the method given by Jahan et al. (2023). The h²b was categorized with a value of 0%–10% as low, 10%–20% as moderate, and 20% and above as high, as reported by Burton and DeVane (1953). The GA was calculated using the equation by Singh and Chaundry (1985). Genotypic and phenotypic correlation coefficients were utilized to compute the direct and indirect contributions toward the net weight of the plants. The correlation matrix was created from replicated data using the variability package in R 4.1.3 software (R Core Team, 2015). Path analysis of the traits was performed following the method of Dewey and Lu (1959). Principal component analysis (PCA), eigenvalues, eigenvectors, and biplot analysis were conducted with FactoMineR, factoextra[2], Azam et al. (2023) and ggbiplot[3], respectively, using R 4.1.3 software (R Core Team, 2015). These PCAs were derived from the correlation matrix. Data were adjusted to determine the genetic distance matrix using the Euclidean method distance and then hierarchical clustering was performed using Ward's method (Murtagh

[2]Kassambara A, Mundt F (2016). Factoextra [online]. Website https://CRAN.R-project.org/package=factoextra [accessed 10 December 2023].

[3]Wickham H, Chang W, Henry L, Pedersen TL, Takahashi K et al. (2016). ggplot2 [online]. Website https://ggplot2.tidyverse.org [accessed 12 December 2023].

Table 2. List of the quantitative agromorphological traits used as well as their phenotype code, description, and phenotype scores.

Traits	Phenotypic code	Descriptions
Shoot length (cm)	SL	The lengths of 10 randomly selected shoots (cm) from each plot were measured on the harvesting date using a ruler. The sum of the SLs was divided by 10 to obtain the mean SL of the plant.
Root length (cm)	RL	The lengths of 10 randomly selected roots (cm) from each plot were measured using a ruler. Then, the sum of the RL was divided by 10 to determine the mean RL of the plant.
Ratio of the SL and RL (RSRL)	RSRL	The RSRL was measured as the ratio of the mean length of the roots to the mean length of the shoots.
Shoot weight (g)	SW	The fresh SWs (g) of 10 randomly selected plants from each plot were measured using an electric scale and the sum was averaged to calculate the mean SW.
Stem weight (g)	StW	The StWs of 10 randomly selected plants were measured separately on the harvesting date using an electric scale and the sum was averaged to calculate the mean StW.
Root weight (g)	RW	The RWs of 10 selected plants were measured separately on the harvesting date using an electric scale, and the sum was averaged to calculate the mean RW.
Ratio of shoot and root weight	RSRW	The RSRW was measured as the ratio of the mean weight of the roots to the mean weight of the shoots.
Leaf weight (g)	LW	The weight of all the leaves of 10 randomly selected plants in each plot was measured and averaged by dividing the sum by 10.
Number of leaves per plant	LPP	The number of leaves on 10 randomly selected plants in each plot was counted on the harvesting date and averaged by dividing the sum by 10.
Stem base diameter (cm)	SBD	The SBD was measured at the base using a caliper and recorded for 10 randomly selected plants on the harvesting date, and averaged by dividing the sum by 10.
Total biomass per plant (g)	TBPP	The weights of 10 randomly selected whole plants, including the roots, separately, were measured and the sum was averaged by dividing the value by 10.
Biological yield (ton/hectare)	BY	The BY was recorded on a whole plot basis. The BY of the amaranth per hectare was calculated by converting it to the total yield (kg) of the amaranth per plot.

and Legendre, 2011). For the cluster analysis, hierarchical clustering across the genotypes was detected using the Cluster statistical package[4] and factoextra[5]. The heatmap was produced using the Euclidean distance and average methods using the pheatmap (Olivoto and Lúcio, 2020) package in the R software functions. The statistical analysis for the multitrait genotype-ideotype distance index (MGIDI) was performed utilizing R Package metan v.1.16.0 (Olivoto and Lúcio, 2021).

3. Results

3.1. Mean performance and genetic variations
Significantly different performances were documented in the evaluated traits of the datashak (Table 3). The degree of variation between the datashak in terms of the 12 traits

was investigated. The overall mean value, standard error, coefficient of variation (CV), and the critical difference (at 1% significance level) for the datashak are presented in Table 3. The performance of the germplasm is explained below for each trait. The scree histogram was made to show the frequency distribution of the traits (Figure 1). All the attributes fit the normal distribution except for certain features that were skewed left and right (Figures 1 and 2). The box plots (Figure 2) also showed the outliers for several characteristics, including the BY. The datashak had highly noteworthy variations for the SL. The highly significant genotypic difference proved that there was a widespread difference in the SL among the datashak, which ranged from 38.60 to 97.23 cm, with an average of 73.04 cm (Table 3). The longest SL was observed in the Data (cross) (97.23

[4]Maechler M, Rousseeuw P, Struyf A, Hubert M, Hornik K et al. (2023). Cluster [online]. Website https://CRAN.R-project.org/package=cluster [accessed 16 November 2023].

[5]Kolde R (2019). Package 'pheatmap' [online]. Website https://cran.r-project.org/web/packages/pheatmap/index.html [accessed 15 December 2023].

Table 3. Performance for the BY and yield contributing to the agronomic traits of the 14 datashak.

Genotypes	SL	RL	RSRL	SW	StW	RW	RSRW	LW	LPP	SDB	TBPP	BY
Lolita	78.97d	8.70j	8.99b	104.58f	94.00d	9.79g	10.68g	10.58k	25.68e	17.80f	114.37f	83.93f
Panna	62.22i	15.99f	3.89j	80.63k	61.97j	9.23h	8.73i	18.66h	16.78h	14.20i	89.86i	64.83k
Lalgolapi	69.74g	9.92i	7.03c	80.69k	71.73i	3.70l	21.86a	8.96l	14.76i	15.50h	84.39j	64.87k
Redtower	88.74b	19.13c	4.64g	189.03a	167.15a	13.68d	13.82e	21.87g	27.71d	23.32b	202.71a	151.50a
Greentower	84.96c	16.02f	5.30f	116.22e	85.63f	17.57b	6.62k	30.59c	28.90c	13.73i	133.79d	93.23e
Sabujshak	38.60j	16.37e	2.36l	127.52c	115.71i	7.66j	16.64c	11.82i	22.72g	19.08e	135.19c	102.33c
RM	64.70h	6.63k	9.76a	34.65m	23.69m	1.86m	18.60b	10.96j	13.73j	10.37k	36.51l	34.97m
Lota	64.01h	15.71g	4.07i	100.49g	75.03h	8.63i	11.64f	25.47f	25.62e	20.72d	109.13g	80.73g
Data (cross)	97.23a	16.39e	5.93e	122.63d	93.33e	11.93f	10.28h	29.30e	31.70b	21.91c	134.56c	98.33d
Redforce	84.03c	18.24d	4.61gh	151.28b	121.27b	14.39c	10.51gh	30.00d	25.96e	20.72d	165.67b	121.43b
Payra	70.99f	19.79b	3.59k	96.22h	61.39j	12.50e	7.70j	34.81b	32.83a	25.12a	108.72g	77.27h
Golapirani	77.49e	21.60a	3.58k	90.9j	55.20k	28.62a	3.18l	35.71a	23.83f	16.56g	119.52e	73.07j
BARI Lashak-1	70.31fg	11.22h	6.27d	91.84i	79.75g	5.77k	15.90d	12.10i	16.67h	17.47f	97.62h	73.80i
Altapati	70.56fg	15.82fg	4.46h	48.36l	37.93l	5.72k	8.46i	10.43k	12.70k	11.59j	54.08k	48.73l
Mean ± SE	73.04 ± 1.39	15.12 ± 1.07	5.32 ± 2.05	102.50 ± 1.23	81.70 ± 2.21	10.79 ± 1.06	11.76 ± 2.09	20.81 ± 2.32	22.83 ± 3.01	17.71 ± 3.23	113.29 ± 3.21	8.35 ± 1.89
Significance	**	**	**	**	**	**	**	**	**	**	**	**
CV%	3.86	5.45	5.84	4.39	3.43	4.06	6.43	7.03	5.66	4.32	4.34	5.45

SE: standard error difference, CV: coefficient of variation, ** Significant at 1%, different letters indicate significant differences among traits in each genotype. SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).

cm) genotype, which was followed by Redtower (88.74 cm) and Greentower (84.96 cm). The shortest SL was recorded for Sabujshak (38.60 cm) followed by Panna (62.22 cm), Lota (64.01 cm), and RM (64.70 cm). The CV of the SL was 3.86%. The ANOVA results for the RL showed a highly noteworthy difference at 1% significance level, which indicated that there were extensive variability among the RLs. The RL of the 14 datashak ranged from 6.63 to 21.60 cm (Table 3). The longest RL was observed in Golapirani (21.60 cm) and RM (6.63 cm) displayed the lowest, with a grand mean performance of 15.12 cm. Ten datashak genotypes exhibited above-average performance, while four had below average. The CV of the RL was 0.86%. The ANOVA results showed extensive variability across the genotypes for the RSRL, which ranged from 2.36 to 9.76. The highest RSRL was recorded for RM (9.76) followed by Lolita (8.99), Lalgolapi (7.03), and BARI lalshak1 (6.27), respectively (Table 3). The average mean performance for the RSRL was 5.32 and five genotypes demonstrated above-average mean performance. The CV of the RSRL was 1.84%. The ANOVA of the 14 datashak illustrated a highly significant SW at 1% significance level. The mean SW of the 14 datashak ranged from 34.65 to 189.03 g, with a grand mean performance of 102.50 g (Table 3).

The highest SW was recorded for Redtower (189.03 g). Among the 14 datashak, six exhibited above-average mean performance. The lowest SW was recorded for RM (34.65 g). The CV of the SW was 2.39%. The ANOVA of the 14 datashak showed a highly significant mean sum of square for the StW. The mean StW of the 14 datashak ranged from 23.69 to 167.15 g, with a grand mean of 81.70 (Table 3). Redtower had the highest StW (167.15 g), while RM had the lowest (23.69 g). Among the 14 datashak, six exhibited above-average mean performance. The CV of the SW was 1.43%. The highest RW was recorded for Golapirani (28.62 g), followed by Greentower (17.57 g), Redforce (14.39 g), and Redtower (13.68 g). Among the 14 datashak, six demonstrated above-average mean performance. The mean RW of the 14 datashak ranged from 1.86 to 28.62 g (Table 3). The lowest RW was recorded for RM (1.86 g). The grand mean RW was 10.79. The CV of the RW was 1.06%. The ANOVA of the RSRW showed a highly significant MS across the genotypes. The average RSRW of the 14 datashak ranged from 3.18 to 21.86, with a grand mean performance of 11.79 (Table 3). The maximum RSRW was observed for Lalgolapi and the lowest for Golapirani genotype. Five of the 14 datashak exhibited above-average mean performance. The CV of the RSRW was 1.43 %.
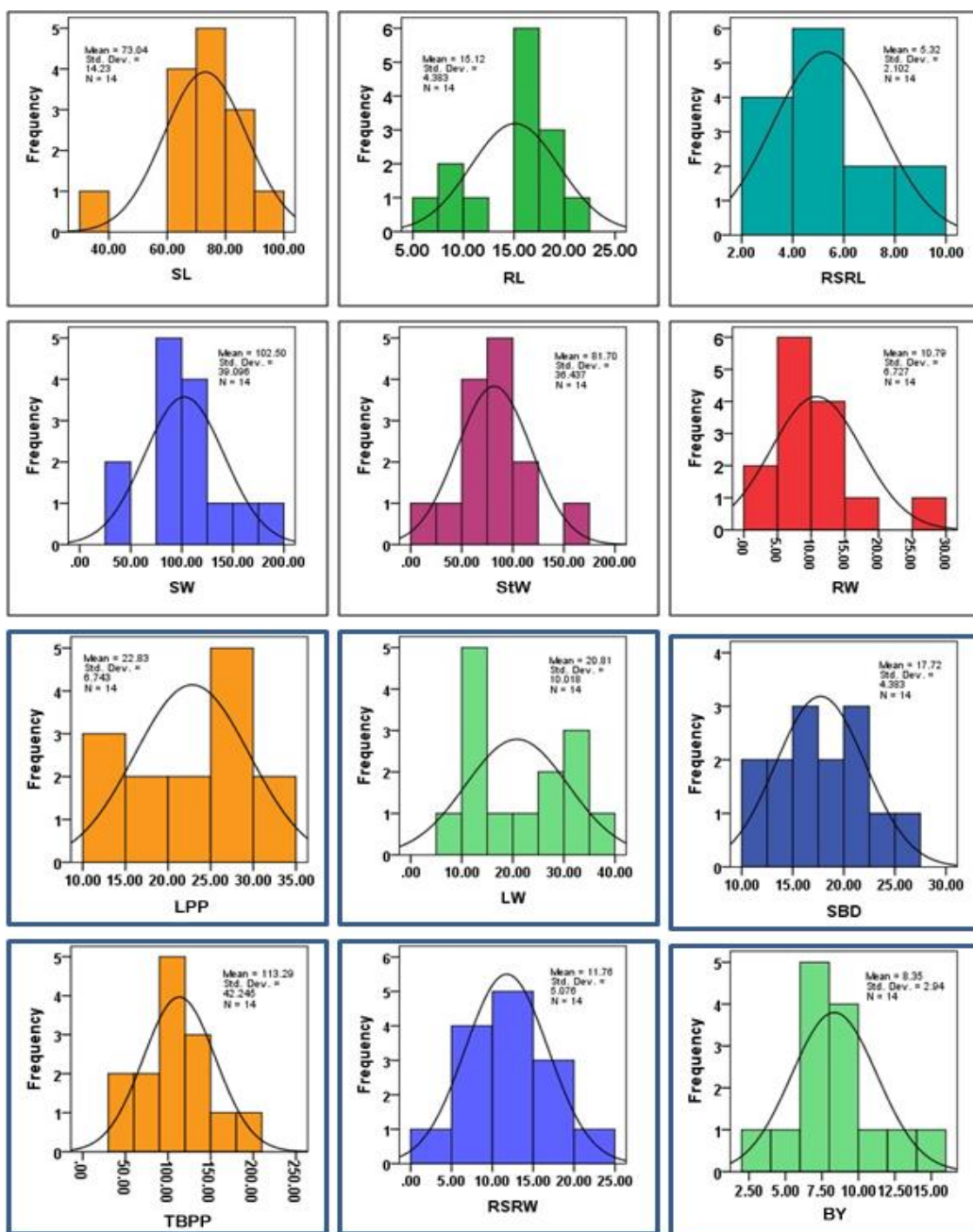
Figure 1. Histograms of the frequency distribution and normal curves of the datashak. The trait codes are SBD: stem base diameter, LPP: number of leaves per plant, SW: shoot weight, StW: stem weight, RW: root weight, BY: biological yield, RL: root length, RSRW: ratio of the shoot and root weight, SL: shoot length, RSRL: ratio of the shoot and root length, LW: leaf weight, and TBPP: total biomass per plant.

Among the 14 datashak, three displayed above-average mean performance. The mean LW of the 14 datashak ranged from 8.96 to 35.71 g, with a grand mean performance of 20.81 (Table 3). Golapirani had the highest LW (g), which was 35.71 g, and was statistically similar to that of Payra (34.81). The lowest LW (8.96 g) was observed for Lalgolapi. The grand mean LW was 20.81. The CV of the LW was 1.03%. Seven of the genotypes showed above-average performance and seven exhibited below-average. The LPP of the 14 datashak ranged from 12.70 to 32.83, with a grand mean of 22.83 (Table 3). The maximum LPP was recorded for Payra (32.83), followed by Data (cross) (31.50), Greentower (28.90), and Redtower (27.71), respectively. Among the 14 datashak, eight showed above-
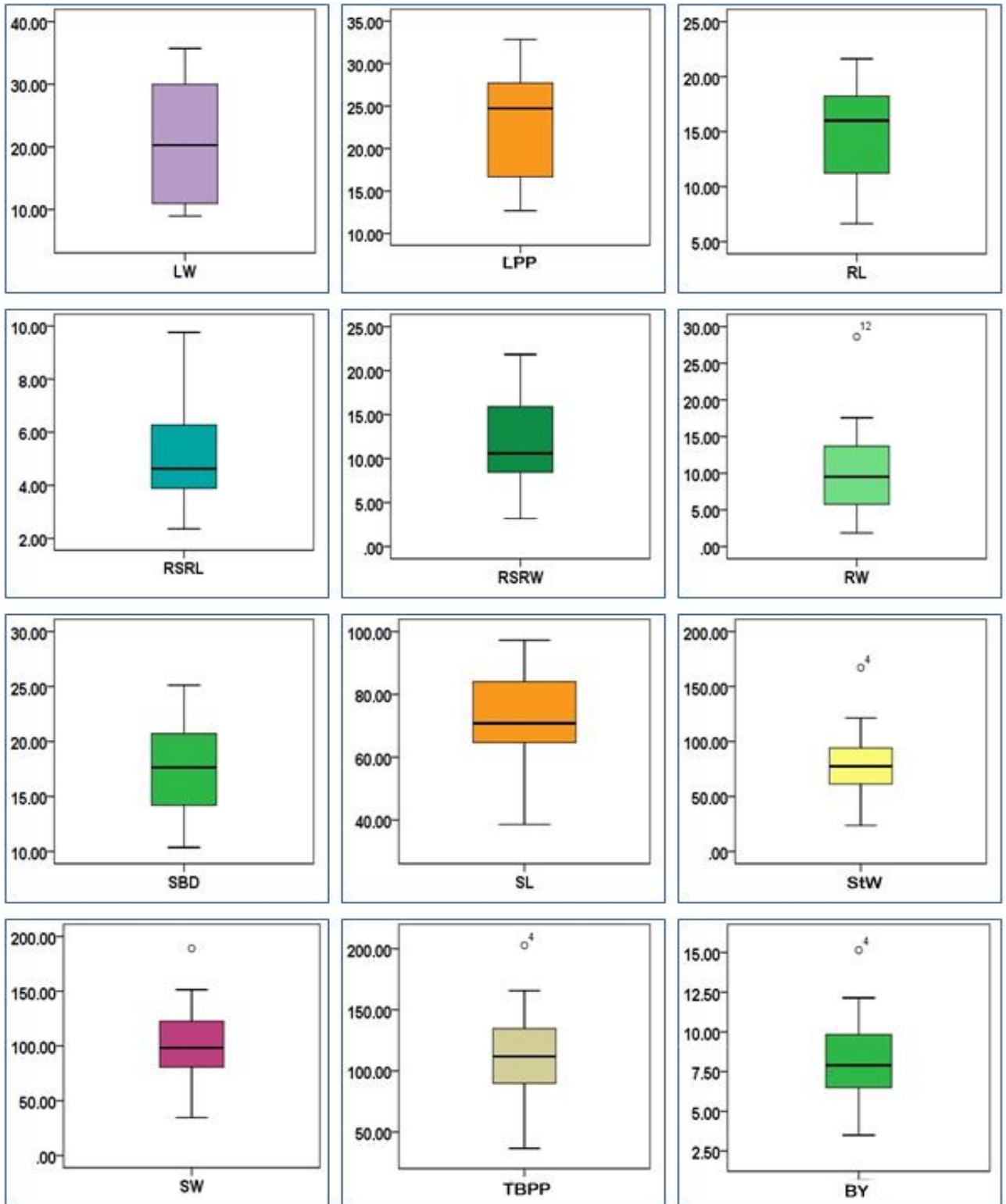
Figure 2. Box plots showing the deviations of the quantitative traits in the datashak. The 75th, 25th, and 50th percentiles of the datashak are characterized by the upper, lower, and median quartiles, respectively. The population variation is shown by the vertical lines. Dots show the outliers. SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).

average performance and six had below-average. The CV of the LPP was 1.66% (Table 3). The maximum SBD was observed in Payra (25.12) followed by Redtower (23.32 cm), and Data (cross) (21.91 cm). The mean SBD of fourteen green datashak ranged from 10.37 cm to 25.12 cm, with a grand mean performance of 17.71 cm (Table 3). RM had the shortest SBD (10.32 cm). Among the 14 datashak, 7 showed above-average performance. The CV of the SBD was 2.32%. The average TBPP of the 14 datashak ranged from 36.51 to 202.71 g, with a grand mean performance of 113.29 g (Table 3). The highest TBPP was recorded for Redtower (202.71 g). Among the 14 datashak, seven showed above-average mean performance and seven had below-average. The lowest TBPP (36.51 g) was recorded for RM. The CV of the TBPP was 3.34%. The ANOVA of the BY per hectare indicated a highly significant mean sum of squares at 1% significance level. This highly significant genotypic difference indicates that there was a wide range of variance in the BY per hectare across the genotypes. The mean BY per hectare of the 14 datashak ranged from 35.0 to 151.5, with a grand mean performance of 83.5 (Table 3). The maximum BY was recorded for Redtower (151.5), followed by Redforce (121.4 kg), Sabujshak (102.3 kg), and Data (cross) (98.3 kg), respectively. The lowest BY per hectare was recorded for RM (35.0 kg). Six of the 14 datashak exhibited above-average performance. The CV of the BY per hectare was 0.05%.

3.2. Variability and genetic parameters
In terms of morphological traits, the highest phenotypic variance (V_p) and genotypic variance (V_g) were documented for the TBPP (1784.74 and 1676.55) followed by the SW

(1528.64 and 1244.34), StW (1327.81 and 1249.65), and SL (202.86 and 184.47), respectively (Table 4). Moderate V_p and V_g were obtained from the LW followed by the number of LPP, RW, RSRW, and RW. Conversely, the SBD, RL, BY, and RSRL exhibited very low V_p and V_g. The highest PCV and GCV were found for the RW (62.34 and 58.05) followed by the LW (48.15 and 46.68), SW (38.14 and 34.41), and RSRW (43.20 and 37.85), respectively. Moderate PCV and GCV were obtained from the RSRL, SW, TBPP, and BY. The highest GAPM was documented for the LW (93.22) followed by the RW (91.35), and StW (86.47). The lowest GAPM was recorded for the SL (36.53) followed by the BY (38.92), SBD (40.12), and RL (41.05). The majority of the parameters showed high h²b as well as high to moderate GAPM.

3.3. Correlation analysis
The correlation study of the datashak genotypes revealed that all the traits, except for the RSRL and RSRW, displayed a significant correlation at the 1% level in a positive direction with the BY. Among them, the RL, SW, StW, LPP, SBD, and TBPP displayed a correlation in a positive direction with the BY at 1% probability, while for the SL, RW, and LW, the correlation was at 5% significance level at both levels (Table 5). The TBPP showed a significant positive correlation with the SL, RL, SW, SW, RW, and LW, and the LPP and SBD, but an association in a negative direction with the RSRL and RSRW at both levels. The RL also showed a positive association with the SW, SW, RW, LW, LPP, and SBD at both levels. The SW showed a nonsignificant association with the SL, RSRL, RW, RSRW, and RW, but a correlation in a positive direction with

Table 4. Determination of the hereditary parameters for the BY and the contributing agronomic traits of the 14 datashak genotypes.

Characters	V_p	V_g	V_e	PCV	GCV	h²b	GA	GAPM
SL	202.86	184.47	18.39	19.50	18.60	90.93	26.68	36.53
RL	19.22	13.21	6.01	29.00	24.04	68.73	6.21	41.05
RSRL	4.43	2.42	2.01	39.56	29.24	54.63	2.37	44.52
SW	1528.64	1244.34	284.3	38.14	34.41	81.40	65.56	63.96
StW	1327.81	1249.65	78.16	44.60	43.27	94.11	70.65	86.47
RW	45.24	39.23	6.01	62.34	58.05	86.72	12.02	111.35
RSRW	25.84	19.81	6.03	43.23	37.85	76.66	8.03	68.27
LW	100.41	94.36	6.05	48.15	46.68	93.97	19.40	93.22
LPP	45.61	39.46	6.15	29.58	27.52	86.52	12.04	52.72
SBD	19.34	15.17	4.17	24.83	21.99	78.44	7.11	40.12
TBPP	1784.74	1676.55	108.19	37.29	36.14	93.94	81.75	72.16
BY	8.65	4.64	4.01	35.22	25.80	53.64	3.25	38.92

Vp: phenotypic variance, Vg: genotypic variance, Ve: environmental variance, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, h²b: heritability (broad sense), GA: genetic advance, GAPM: GA in percent of the mean, SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP : total biomass per plant (g), BY: biological yield (ton/hectare).

Table 5. Genotypic (r_g) (lower side of the diagonal) and phenotypic (r_p) (upper side of the diagonal) correlations among the BY and its contributing agronomic traits of the 14 datashak.

Characters	SL	RL	RSRL	SW	StW	RW	RSRW	LW	LPP	SBD	TBPP	BY
SL	1	0.196NS	0.256NS	0.375*	0.272NS	0.427**	-0.364*	0.474**	0.470**	0.259NS	0.415**	0.383*
LR	0.197NS	1	-0.862**	0.504**	0.329*	0.737**	-0.675**	0.772**	0.555**	0.523**	0.584**	0.506**
RSRL	0.255NS	-0.863**	1	-0.360*	-0.257NS	-0.432**	0.440**	-0.472**	-0.296NS	-0.395**	-0.402**	-0.356*
SW	0.375*	0.505**	-0.361*	1	0.967**	0.401**	-0.086NS	0.384*	0.670**	0.721**	0.989**	0.997**
StW	0.272NS	0.329*	-0.257NS	0.967**	1	0.210NS	0.104NS	0.138NS	0.511**	0.633**	0.929**	0.969**
RW	0.427**	0.737**	-0.433**	0.401**	0.210NS	1	-0.767**	0.801**	0.565**	0.276NS	0.530**	0.383*
RSRW	-0.365*	-0.676**	0.440**	-0.086NS	0.104NS	-0.768**	1	-0.714**	-0.468**	-0.123NS	-0.201NS	-0.083NS
LW	0.474**	0.773**	-0.473**	0.384*	0.138NS	0.801**	-0.715**	1	0.757**	0.509**	0.483**	0.365*
LPP	0.471**	0.556**	-0.297NS	0.671**	0.512**	0.565**	-0.469**	0.758**	1	0.781**	0.710**	0.650**
SBD	0.260NS	0.525**	-0.396**	0.724**	0.637**	0.276NS	-0.123NS	0.511**		1	0.711**	0.701**
TBPP	0.415**	0.584**	-0.403**	0.989**	0.929**	0.530**	-0.202NS	0.483**		0.714**	1	0.983**
BY	0.384*	0.506**	-0.356*	0.997**	0.969**	0.383*	-0.083NS	0.365*		0.704**	0.983**	1

NS = nonsignificant, *, ** = Significant at a 5% and 1%. SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).

the rest of the traits at both levels. The LW displayed a correlation in a positive direction with most of the traits, except for the RSRL and SW at both levels. The RSRL and RSRW displayed significant and nonsignificant negative associations, respectively, with the SBD, TBPP, and BY at both levels. All the variables had strong correlations in a positive direction with the BY, except for the RSRL and RSRW.

3.4. Path analysis

Path analysis was utilized to investigate the link between the BY and the other yield-contributing traits, allowing for a deeper understanding of the interaction. The BY per hectare was measured as a resultant (dependent) variable and the SL, RL, RSRL, SW, StW, RW, RSRW, LW, LPP, SBD, and TBPP were causal (independent) variables. Using the genotypic path coefficient analysis, the indirect and direct path coefficients (PCs) (in bold) of 11 causative factors on the BY are illustrated in Table 6.

The SL displayed a direct PC in a negative direction (–0.034) with the BY (Table 6 and Figure 3). The indirect PC was negative for the SBD (–0.021), and TBPP (–5.88), while the rest of the traits showed positive indirect PCs, which were almost negligible in magnitude. As a result, the overall correlation (0.384*) between the BY and the other features was positive. Consequently, increasing the BY could be achieved by selecting the SL. Despite the direct PC in a positive direction for the RL (0.0318) on the BY, the SW (6.135), StW (0.605), RW (1.578), and LW (0.345) had strong indirect PCs in a positive direction, and consequentially, a statistically significant positive correlation with the BY (0.506**) (Table 6 and Figure 3). The SW had a direct PC in a positive direction (12.159) on the BY. The indirect PCs in a positive direction for the RL (0.160), StW (1.779), RW

(0.858), and LPP (0.019) on the BY were sizable, resulting in a high significant positive correlation (0.997). The indirect PCs were negative for the SL (–0.013), SBD (–0.059), and TBPP (–14.007), which were almost negligible in magnitude. Therefore, improving leaf production could be accomplished by directly selecting the SW. The StW had a direct and positive PC (1.839) on the BY. The indirect PC was negative for the SL (–0.009), RSRL (–0.051), SBD (–0.052), and TBPP (–14.007). The indirect impact of the RL (0.105), SW (11.761), RW (0.449), LW (0.061), and LPP (0.015) on the BY was positive, which caused the overall significant positive correlation (0.969) between the StW and BY (Table 6 and Figure 3). The RW had a direct PC (2.137) on the BY. The indirect PCs of this trait on the BY for the RL (0.234), SW (4.877), StW (0.386), LW (0.357), and LPP (0.016) were positive and considerable, making the total significant positive correlation (0.383). As a result, there was a significant positive correlation between the RW and BY (0.383). The LW and LPP had a direct positive (0.446 and 0.029) impact, respectively, on the BY. The indirect PCs of the LW and LPP on the BY via the RL (0.246 and 0.177), SW (4.675 and 8.164), StW (0.253 and 0.941), RW (1.714 and 1.210), and LPP (0.022 and 0.029) were positive, except for the SL, RSRL, and SBD, but almost negligible in magnitude. As a consequence, the total significant positive correlation (0.365 0.651) with the BY was positive (Table 6 and Figure 3).

The SBD had a minor adverse direct PC (–0.081) on the BY. The indirect PCs of this trait on the BY via the RL (0.167), SW (8.807), StW (1.171), RW (0.591), LW (0.228), and LPP (0.022) were positive and considerable, making the total significant positive correlation (0.704). Whereas the negative PCs observed via the SBD (–0.009), RSRL (0.079), and TBPP (–010.114) were marginal. As a result, there was a significant positive correlation between the SBD and BY

Table 6. Correlation (genotypic) with the BY partitioned to indirect and direct (in bold) components in the 14 datashak genotypes.

	SL	RL	RSRL	SW	StW	RW	RSRW	LW	LPP	SBD	TBPP	GCBY
SL	**−0.034**	0.063	0.051	4.563	0.501	0.914	0.003	0.211	0.013	−0.021	−5.880	0.384*
RL	−0.007	**0.318**	−0.173	6.135	0.605	1.578	0.005	0.345	0.016	−0.043	−8.273	0.506**
RSRL	−0.009	−0.274	**0.200**	−4.386	−0.473	−0.926	−0.003	−0.211	−0.008	0.032	5.702	−0.356*
SW	−0.013	0.160	−0.072	**12.159**	1.779	0.858	0.001	0.171	0.019	−0.059	−14.007	0.997**
StW	−0.009	0.105	−0.051	11.761	**1.839**	0.449	−0.001	0.061	0.015	−0.052	−13.148	0.969**
RW	−0.015	0.234	−0.087	4.877	0.386	**2.139**	0.006	0.357	0.016	−0.022	−7.509	0.383*
RSRW	0.013	−0.215	0.088	−1.041	0.192	−1.643	**−0.008**	−0.319	−0.013	0.010	2.853	−0.083^NS
LW	−0.016	0.246	−0.095	4.675	0.253	1.714	0.005	**0.446**	0.022	−0.042	−6.844	0.365*
LPP	−0.016	0.177	−0.059	8.164	0.941	1.210	0.004	0.338	**0.029**	−0.064	−10.072	0.651**
SBD	−0.009	0.167	−0.079	8.807	1.171	0.591	0.001	0.228	0.022	**−0.081**	−10.114	0.704**
TBPP	−0.014	0.186	−0.081	12.029	1.708	1.135	0.002	0.216	0.020	−0.058	**−14.158**	0.983**

NS = nonsignificant, *, ** = Significant at 5% and 1%. SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), GCBY: genotypic correlation with biological yield (ton/hectare).
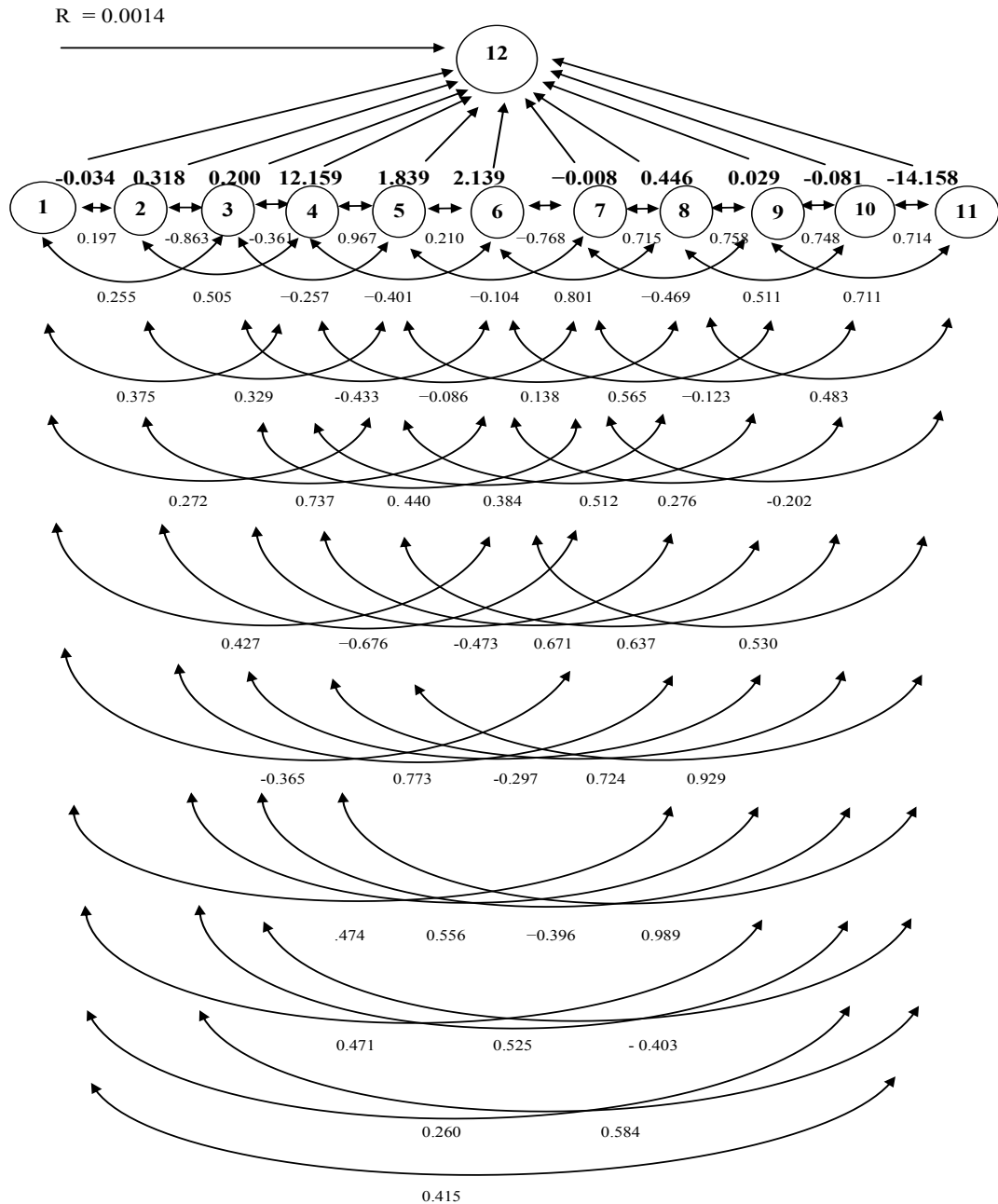
Figure 3. Genotypic path diagram for the BY per hectare of amaranth. 1 = SL, shoot length (cm), 2 = RL, root length (cm), 3 = RSRL, ratio of the shoot and RL, 5 = SW, shoot weight (g), 6 = StW, stem weight (g), 7 = RW, root weight (g), 8 = RSRW, ratio of shoot and root weight, 9 = LW, leaf weight (g), 10 = LPP, number of leaves per plant, 11 = SBD, stem base diameter (cm), 12 = TBPP, total biomass per plant (g), 13 = BY, biological yield (ton/hectare).

(0.704) (Table 6 and Figure 3). The TBPP displayed direct PC in a negative direction (–14.158) on the BY (Table 6 and Figure 3). The indirect PC was negative via the SL (–0.014), RSRL (–0.081) and SBD (–0.058), while the rest of the traits showed a positive indirect effect, which was almost considerable in magnitude. As a consequence, the

total significant positive correlation (0.983) with the BY was positive.

3.5. Heatmap and hierarchical clustering of the morphological traits of the 14 datashak genotypes
Heatmap analyses with double dendrograms were employed, where the dendrogram in the horizontal

direction indicates the datashak, and the second dendrogram in the vertical directions, presents the studied traits (Figure 4). The clustering of the datashak based on the 14 traits revealed the trait variability among the genotypes (Figure 4). The traits of the datashak were split into four distinct groups by hierarchical cluster analysis. Cluster 1 in the horizontal direction represents the high response to the morphological traits (RSR and RSRW) and also the lowest for the rest of the traits. The highest BY, SW, TBPP, and SW were found in cluster 3 (Figure 4). The cluster dendrogram of the datashak was divided into four distinct clusters. Among them, Panna, Altapati, Lolita, Lalgolapi, and BARI lalshak-1 belonged to the same cluster. Moreover, Sabujshak, Redtower, and Redforce were also observed in a separate cluster. However, RM formed a distinct individual cluster (Figure 4).

The accessions were grouped into four clusters. The distances of the inter and intracluster that were formed are shown in Table 7. The intercluster distance ranged between

4.75 and 7.30, with the shortest between clusters II and III, and the longest between clusters I and II. The intracluster distance ranged from 2.87 to 3.47. Cluster I consisted of 3 datashak accessions and displayed the greatest intracluster deviation (3.47), while cluster II (2.87) displayed the shortest distance. Cluster IV had no intracluster distances as it had only one genotype.

The datashak accessions were divided into four diverse clusters (Table 8). Among these, clusters I and III were the biggest with five datashak, followed by cluster II with three datashak, and cluster I with four datashak.

Based on the mean cluster values, the datashak in cluster IV demonstrated the lowest SL (64.70), while those in cluster III had the highest (78.94). The longest RL was in cluster II (17.91) and the shortest was in cluster IV (6.63) (Table 9). Cluster IV had the highest RSRL (9.76), while cluster II had the lowest (3.87). The SW ranged from 34.65 in cluster IV to 155.94 in cluster II. Similarly, the highest StW was in cluster II (1344.71) and the lowest was in cluster
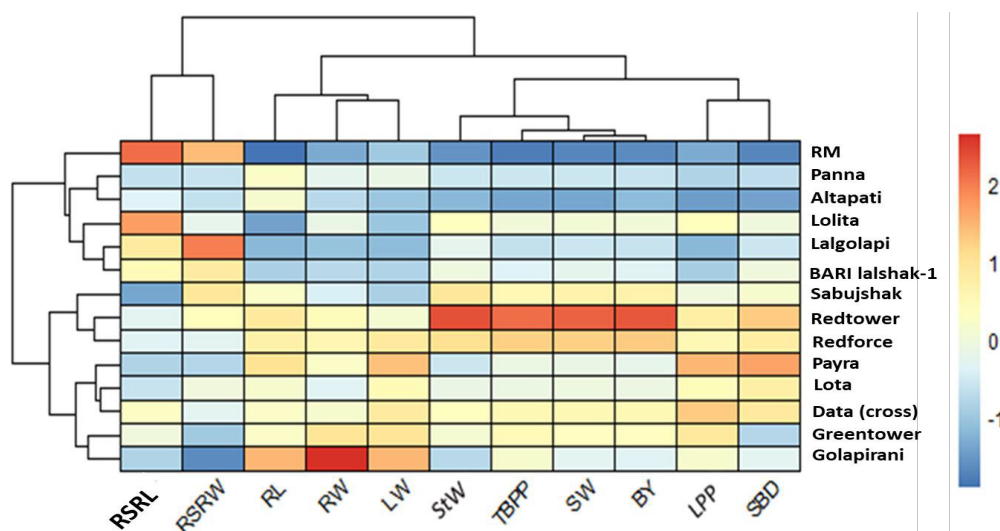

Figure 4. Heatmap and hierarchical clustering for the morphoagronomical traits. The relative abundance of each datashak genotype (columns) within each feature is described by the heatmap plot (rows). The color coding (blue to dark red) shows the row with blue representing low abundance and red representing high abundance. SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).

Table 7. Average intra and intercluster distances of the datashak accessions.

Cluster	I	II	III	IV
I	**3.47**			
II	**7.30**	2.87		
III	5.16	**4.75**	3.19	
IV	4.94	5.24	4.77	**0**

Values in bold indicate the shortest and longest intra and intercluster distances.

Table 8. Clustering of the 14 datashak germplasm for the yield and yield-related characters.

Cluster	Number of datashak	Datashak name
I	5	Lolita, Panna, Lalgolapi, BARI lalshak-1, and Altapati
II	3	Redtower, Sabujshak, and Redforce
III	5	Greentower, Lota, Data (cross), Payra, and Golapirani
IV	1	RM

Table 9. Mean cluster values of the yield and its component traits in the datashak.

Traits	Cluster			
	I	II	III	IV
SL	70.36	70.46	78.94	64.70
RL	12.35	17.91	17.90	6.63
RSRL	6.13	3.87	4.50	9.76
SW	81.22	155.94	105.29	34.65
StW	69.08	134.71	74.12	23.69
RW	6.84	11.91	15.85	1.86
RSRW	13.12	13.66	7.88	18.60
LW	12.15	21.23	31.18	10.96
LPP	17.32	25.46	28.57	13.73
SBD	15.31	21.04	19.61	10.37
TBPP	88.06	167.85	121.14	36.51
BY	6.72	12.51	8.45	3.50

SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).

IV (23.69). The highest RW was in cluster III (15.85) and the lowest was in cluster IV (1.86). The highest RSRW was in cluster IV (18.60) and the lowest was in cluster III (7.88). The highest LW was in cluster III (31.18) and the lowest was in cluster IV (10.96). The lowest NPP was in cluster IV (13.73) and cluster III had the highest (28.57). Cluster II had the longest SBD (21.04), while cluster IV had the shortest (10.37). The highest TBPP was in cluster II (167.85), while cluster IV had the lowest (36.51). Cluster II had the highest mean BY (12.51), while the lowest was in cluster IV (3.50).

3.6. PCA
The variation (%) explained by the first 10 principal components is shown in the scree plot (Figure 5), which revealed that the first three principal components explained the majority of the total variation expressed, with a maximum of 87.8% of the variability among the datashak. This was also shown by the eigenvalues and their contributions to the total variance. principal component 1 (PC1) displayed large values, although those of the subsequent principal components were small, indicating that PC1 expressed the maximum variation in the data set. PC1 explained 56.3% of the total variation, which was highly contributed to by the studied dependent variables of the TBPP, SW, BY, StW, and RSRW (Figure 6A). principal component 2 (PC2) contributed to 21.1% of the sum of variation, which was mainly attributed to the dependent variables of the RSRW, StW, BY, and SW (Figure 6A). In addition, the principal component-biplot analysis revealed the trait profiles of the studied datashak, particularly those that were distant from the origin, and the findings showed a correlation between the characteristics and the datashak. Consequently, the biplot assisted in the selection of suitable datashak for the traits that contributed to the yield or for those that improved the agronomic performance. Redtower was located in the far upper left side of the biplot due to its strong contribution to the SW, BY, and StW considering PC2. On the other hand, Payra and Greentower on the lower-right side of PC2 negatively contributed to the RW, RL, and LW. Meanwhile, among the studied datashak, Lalgolapi, Lolita, and BARI lalshak1 were more promising than the others with strong positive contributions in terms of the dimensions of both PC1 and PC2 for the traits of the RSRW and RSR (Figure 6B).

The ranking of the 14 datashak according to the MGIDI is shown in Figure 7. Redtower and Data (cross) could be chosen based on the MGIDI, which displayed stable parameters linked to the SW, StW, TBP, and BY, except for
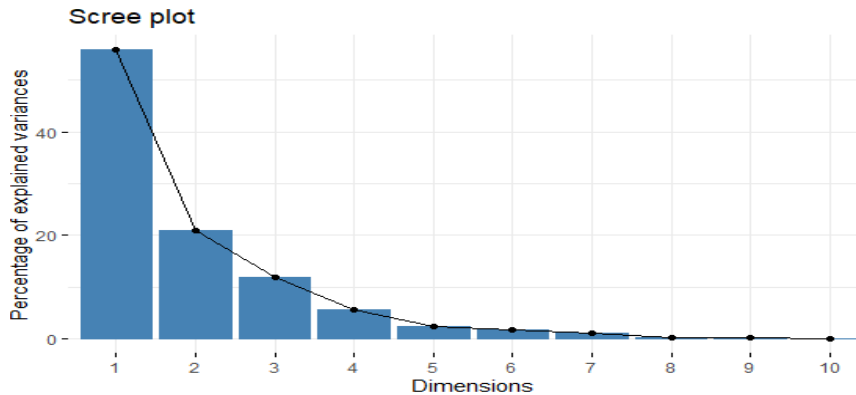
Figure 5. Scree plot constructed for the 14 morphoagronomical traits and percentage of the variance of the 10 PCs.

allocating the weights and they were multicollinearity free. As a result, they should be chosen as multitrait superior performer datashak. Redforce presented interesting features owing to the near selection intensity circle.

4. Discussion

Breeders must prioritize understanding the dimension and extent of genetic diversity among the datashak gene pool. The success of landraces for breeding programs may be improved by the phenotypic diversity of the current investigation of 14 datashak landraces using several BY criteria to estimate their yield potential. Because there is so much genetic variation in morphological traits, this is an important preliminary step in characterizing and identifying plant genetic resources (Carrillo-Perdomo et al., 2020).

4.1. Performance of the datashak

The datashak had highly noteworthy ANOVA (1% significance level) results for all the studied parameters. Jangde et al. (2017) reported a highly significant MS for the SW at a 1% significance level. These results are in line with those of previous studies on *Zea mays* (Azam et al., 2014), mung beans (Azam et al., 2022b), field pea (Azam et al., 2024), rice (Habib et al., 2024), and various *Amaranthus* species (Sarker et al., 2022c–2022e; 2023; 2024). The highly significant genotypic difference proved that there was a widespread difference for all the parameters among the datashak. The longest SL was observed for Data (cross). However, the longest RL was observed for Golapirani, which was longer than that reported in previous studies by Rashad and Sarker (2020) and Pharle et al. (2019). The maximum RSRL was recorded for RM, whereas Rashad and Sarker (2020) reported the highest RSRL in accession AA39. The 14 datashak genotypes herein exhibited greatly varied RSRL, SW, RW, StW RSRW, LW, LPP, SBD, TBPP, and BY. The range of the current findings was corroborated by the range of the RSRL, SW, RW, StW RSRW, LW, LPP,

SBD, TBPP, and BY for amaranths in previous works (Ahammed et al., 2012; Shankar et al. 2012; Sarker et al., 2015b; Chakrabarty et al. 2018; Pharle et al., 2019; Rashad and Sarker, 2020). The variations of some numerical values between the current and previous studies might have been due to the differences in the genotypes and their genetic makeup, growing environments, management practices, seasons, harvest time, etc. All the variables in the current study exhibited extensive differences, indicating a noteworthy variability across the datashak genotypes. The highest mean and range values were observed for the TBPP, followed by the SW, StW, SL, LPP, LW, SBD, RL, RSRW, BY, and RSRL. RM had the lowest BY per square meter, as well as the lowest mean values for the RL, SL, StW, RW, SBD, and TBPP. The study confirmed that six datashak, i.e. Redtower, Redforce, Sabujshak, Data (cross), Greentower, and Lolita, displayed above-average yield as well as most of the yield-related morphological traits over their corresponding grand means and can be used as preferable cultivars. Furthermore, eight datashak displayed below-average yields, and most of the yield-related morphological traits over the corresponding grand mean can be used in hybridization programs for the development of new future cultivars with desirable parameters with specific objectives. Redtower and Redforce had above-average mean values for the morphological traits, including a high BY, and would be more effective in breeding programs for BY improvement. All the agronomic traits significantly differed across the genotypes, which corroborated the results of different datashak genotypes in several studies (Pharle et al., 2020).

4.2. Variability of the studied parameters

Morphological markers can be used to highlight genetic changes in crop gene-pool resources quickly and straightforwardly. The initial stage in every breeding program is the evaluation of variability and correlations among the main agronomical and yield-related parameters
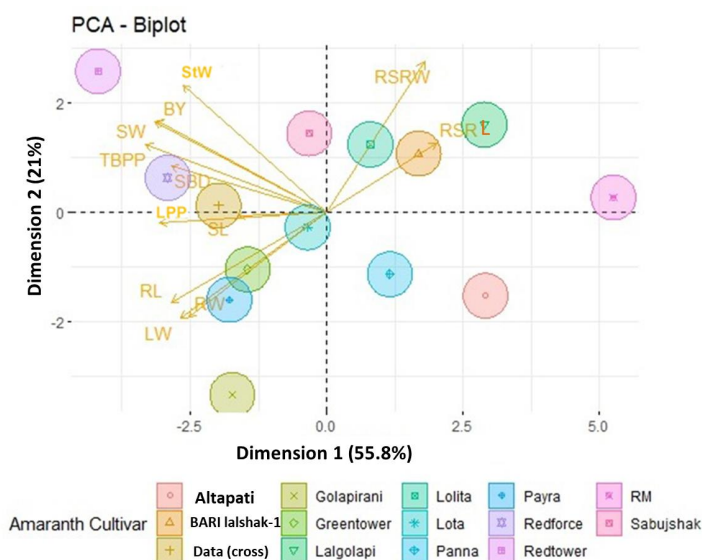
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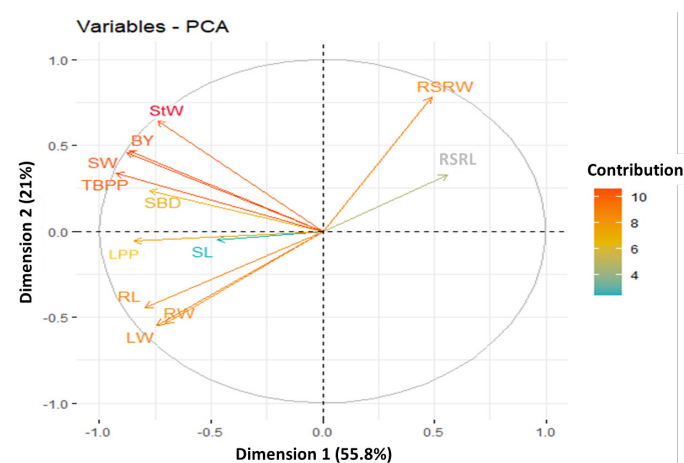
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Figure 6. A) Contribution of the traits on the variables via the PCA of the 14 datashak. The length and color intensity of a trait in the biplot shows how well the trait is represented and how much it contributes to the main components, respectively. Positive or negative interactions between the examined traits are shown by the angles between the traits derived from the midpoint of biplots. **B)** PC-biplot analysis of the datashak. Based on dissimilarity, the datashak accessions are scattered throughout several ordinates. On the biplot, the length and color intensity of a vector show how well the traits are represented and how much they contribute to each principal component, respectively. Positive or negative interactions between the traits under study are shown by the angles between the vectors produced from the midpoints of the biplots.

SL: shoot length (cm), RL: root length (cm), RSRL: ratio of the shoot and RL, SW: shoot weight (g), StW: stem weight (g), RW: root weight (g), RSRW: ratio of shoot and root weight, LW: leaf weight (g), LPP: number of leaves per plant, SBD: stem base diameter (cm), TBPP: total biomass per plant (g), BY: biological yield (ton/hectare).
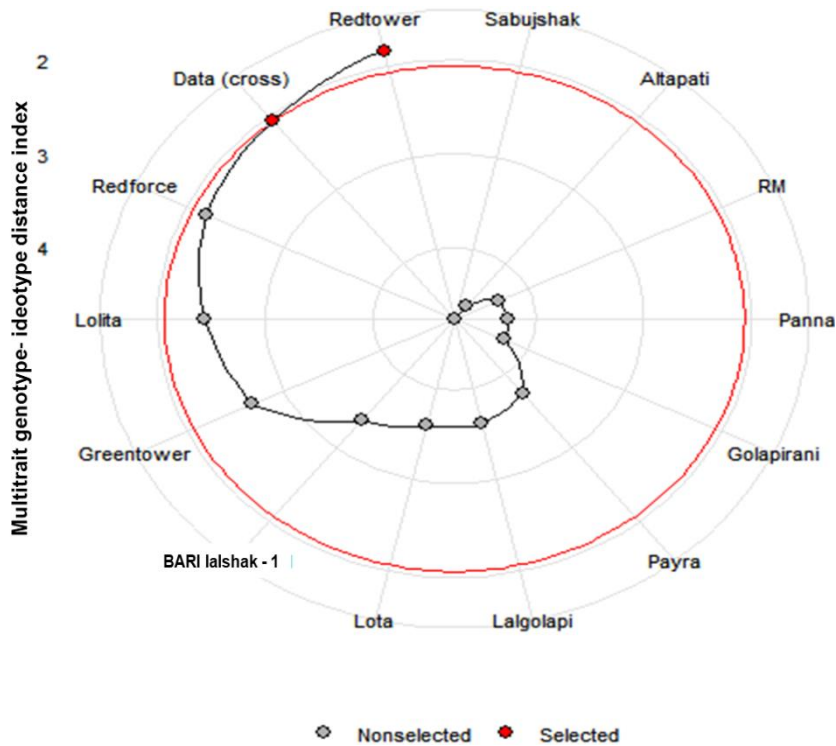
Figure 7. Ranking of the datashak and chosen datashak for the MGIDI index by 15% selection intensity (red circle).

(Wang, 2020). The main quantitative characteristics are influenced by both genetic and environmental variables which are the agronomic characteristics and yield attributes. Many crops have shown relationships between the genotype and the environment (Kovačević et al., 2019; Mwiinga et al., 2020). The PCV was greater than the GCV and displayed extremely modest variances, signifying that those genetic factors predominantly regulated these characters compared to factors regulated by the environment. Results from the current study indicated that all the examined traits had PCV values higher than the GCV values, indicating that all the attributes across the genotypes were equally influenced by the environment. The RW was followed by the LW, SW, RSRW, RSRL, SW, TBPP, and BY, all of which showed high to moderate GCV and PCV values due to the prevalence of additive gene action for these variables. This suggests that these traits have a scope for improvement through selection. Finding the heritable part of the variation is difficult to do based on variance alone. The RW, LW, and SW had higher GCV and PCV values than the other variables. The outcome showed that certain traits were marginally affected by environmental variables, suggesting that the selection might be fruitful for the next breeding initiatives.

In the current study, the h^2b and GA were high for the TBPP, SW, and StW, demonstrating the predominant

effects of the additive gene. A moderate GAPM was found for the SL, LW, LPP, and RW. The majority of the characters exhibited high h^2b as well as high to moderate GAPM. Therefore, selection based on the TBPP, SW, StW, and SL traits would economically be viable to improve the BY of datashak. In a selective breeding effort, the calculation of the h^2b using the GA might be a useful strategy (Sarker et al., 2015a). A trait driven by the additive gene action that has a high GA value and h^2b would be a very useful choice in breeding plans. For all the features, the GC coefficients were very close to the corresponding phenotypic values, indicating an additive type of gene action. Future breeding programs should give priority to traits with a high GCV, h^2b, and GA (Kuswantoro, 2017).

For the TBPP, SW, and StW in the current study, the h^2b and GA values were high, representing a predominance of additive gene effects. The SL, LW, LPP, and RW all exhibited a moderate GAPM. The majority of the attributes had a high to moderate GAPM and high to low h^2b. To increase the availability of datashak, selection based on the TBPP, SW, StW, and SL attributes might be viable economically. In a selective breeding effort, calculation of the h^2b using the GA might be fruitful (Sarker et al., 2015a). Additivity characteristics of a parameter may be principally useful for choosing and precision if it has a high GA and h^2b. For all the features, the GC coefficients were extremely

close to the corresponding phenotypic values, indicating an additive type of gene action. High GCV, h²b, and GA characteristics should be given priority in future breeding programs (Kuswantoro, 2017). Rashad and Sarker (2020) reported low V_g (3.57) and V_p (3.23) for the RL with very high h²b of 90.51%, but a low GA of 3.52. Chakrabarty et al. (2018) found high V_g (1070.20) and V_p (1056.76) for the SW with very high h²b of 98.74% and a high GA of 51.05. They found a close difference between the PCV and GCV for the RW and the h²b was high (98.81%) with a moderate GA (11.07). Ahammed et al. (2012) found very high V_g (5134.19) and V_p (6218.58) for the StW, with high h²b of 82.56% and a very high GA of 134.1. Hasan et al. (2013) studied 17 datashak accessions and found high h²b with high GAPM for the LPP, LW, and yield. Anuja and Mohideen (2007) reported a high GAPM and h²b for the LPP, RL, RW, LW, and SW. A high GAMP for the RSRW followed the SBD was reported by Sarker et al. (2015a). In some previous studies, for most of the phenotypic traits, there was significant PCV and GCV among the datashak species (Akaneme and Ani, 2013). A high V_g was found for the green yield per plant, StW, plant height, leaf area, and LPP among datashak species (Gerrano et al., 2015). Shukla et al. (2005) stated that the majority of the traits displayed high h²b. The foliage yield displayed the maximum GA, followed by the SBD and leaf size. Shukla et al. (2006) found high h²b and GA for the leaf–stem ratio, width of the leaf, total yield of the greens per plot, and length of the leaf, which were in agreement with the current study.

4.3. Association of the parameters

Significant choices using datashak that are exclusively based on the yield may not be advantageous because the environmental effect might influence polygenic traits. As a result, associated traits that increase production or plant morphology must be included in the selection process. Thus, correlation analysis was done using the yield, which provided 10 characters. As the yield is thought to be crucial to agricultural production, several researchers have begun to investigate the relationship between the yield and other yield-related traits in diverse crops. The GC coefficients for all the characteristics in the current study were extremely close to their corresponding phenotypic values, indicating additive gene action, that is, the minimal effect of the environment on the appearance of the traits. Table 5 shows that the BY had a statistically significant positive association with the SBD, SW, RW, and StW, indicating that the selection of stem amaranth based on these features would be very effective since they were strongly related to high BY. Ahammed et al. (2012) showed that the LPP, SBD, StW per plant, LW per plant, and plant height illustrated a positive and highly significant correlation with the yield per hectare at both levels. A significant association of TBPP and SW with the foliage yield per square meter was

reported by Rashad and Sarker (2020). Shukla et al. (2005) found that the plant height was positively associated with the foliage yield. Sarker et al. (2015a) noted that the BY displayed a strong association in a positive direction with the leaf area, SW, RSRW, and SBD. The SW exhibited a significant positive genotypic association with the RSRW (0.454), SBD (0.367), and BY (0.999). Shankar et al. (2012) stated that the yield per plot (g) had a significant positive association with the leaf length (0.44), leaf width (0.51), StW (0.98), LW (0.94), LPP, and SW (0.98). Anuja (2012) found that the RL was significantly and positively correlated with the BY. The leaf area was positively and substantially correlated with the LPP, plant height, leaf breadth, and leaf length. Showemimo et al. (2021) and Rana et al. (2005), documented a highly significant positive genotypic association between the plant height and seed yield per plant. Hailu et al. (2015) showed that the green leaf yield per plant had a positive and significant relationship with the SBD and plant height, as well as a highly significant relationship with the LPP and TBPP. The foliage yield had a highly significant and positive correlation with the plant height, leaf length, and number of leaves (Rana et al., 2005; Khurana et al., 2009), which conformed to the present findings.

4.4. Path analysis

The relationship between the BY and the other yield-related features was found using path analysis, which provided a more thorough understanding of the interaction. The SL, RL, RSRL, SW, StW, RW, RSRW, LW, LPP, SBD, and TBPP were independent factors in the current study, whereas the BY was assessed as a dependent variable. Table 6 shows the indirect and direct PCs (in bold) of 11 variables contributing to the BY using the genotypic path analysis. The most significant positive genotypic association to the BY was generated by the RL, LW, SW, and LPP, which showed the largest positive direct effect (DE) (Table 6). The SBD, RW, and SL had an adverse DE on the BY. Hasan et al. (2013) reported the greatest negative DE of the plant height on the yield and negative DE of the leaf length on the yield (–0.022). Chakrabarty et al. (2018) stated that the SW (0.9535) had the greatest and most positive DE on the BY. The RW (0.2039) and StW (0.0869) also showed a high and positive DE on the BY. Rashad and Sarker (2020) reported that the TBPP (–0.350) had a negative and high DE on the foliage yield, but the SW (1.19) displayed the greatest positive DE on the foliage yield. The fresh StW (1.100) and LPP (0.014) displayed the greatest positive DE on the plant height and leaf yield (–0.071) and a negative DE on the leaf yield in the study of Jangde et al. (2017). The greatest positive DE was reported by Dutta et al. (2002) for the plant height. Kendre et al. (2013) found that the SBD showed the maximum DE on the yield, followed by the leaf area and number of leaves.

4.5. Heatmap analysis

The heatmap showed the highest and lowest values for all the genotypes for all the comparable traits in a diversity of colors extending from hues to deeper intensities. The heatmap analysis revealed the hierarchical clustering based on the investigated datashak landraces, and morphological quantitative features, exhibiting four groups and highlighting the links between specific samples, as indicated by certain types of attributes (Figures 3 and 4, and Table 8). Landraces under cluster II for the RL, SW, StW, SBD, TBP, and BY were shown to be more genetically diverse when compared to the other 14 landraces. The relative pattern of a very abundant feature of the values under cluster III is represented by a heatmap feature with a high color consistency that corresponds to the characteristics of the SL, RL, RW, LW, LPP, and SBD. On the other hand, the RSRL and RSRW of the landraces in cluster IV were more dissimilar. The distribution of the landraces into several clusters suggests that genetic diversity may not always be connected to geographical diversity.

4.6. Cluster analysis based on the phenotypic characters

The datashak accessions can be roughly classified into four groups using the Euclidean distance and Ward's method using the 76.4% similarity coefficient, as shown in the dendrogram (Figure 4). Table 8 displays the average values of the datashak included in each cluster. The five accessions in Cluster III had the highest mean values for the SL, RW, LW, and LPP. The lowest mean values were found in this group for the RSRW. Three accessions made up cluster II. These accessions had high mean values for the RL, SW, StW, SBD, and TBP, and the lowest mean value for the RSRL. In Cluster IV, which consisted of one accession, the highest mean value was for the RSRW, whereas the lowest mean values were for the SL, RL, SW, StW, RW, LW, LPP, SBD, and BY. To improve desirable characteristics in component breeding, accessions with a high mean performance for those characters can be employed as contributor parents for crossbreeding (Terzieva et al., 2019).

4.7. PCA among the traits

A common method for exploring maximum variability from a large number of components through dimensionality reduction is PCA. In the present study, the eigenvalues for PC1, PC2, and PC3 were 56.3%, 21.1%, and 12.2%, respectively. They together accounted for 89.6% of the genotypic variability considered in the diversity study. Pokhrel et al. (2020) conducted PCA of 31 rice germplasm and revealed that the first four components accounted for 73.8% of the overall variance, which was quite similar to the current findings. PCA-biplots combine traits in two proportions and decrease contradictory variants, enabling the detection of the principal parameters in sets of data (Kose et al., 2018).

The biplot displays the loading of several variables depending on the first two main components. The biplots in Figures 6A and 6B, representing those variables, such as the SL, LPP, SBD, TBPP, SW, BY, StW, and RL are close enough and produce a slight angle, suggesting a positive interrelationship between two parameters. Due to Redtower's significant contributions to the SW, BY, and StW when PC2 was taken into account, this was evident in the upper left side of the biplot. Payra and Greentower, which were located on the lower-right side of PC2, had a detrimental influence on the RW, RL, and LW. Lalgolapi, Lolita, and BARI lalshak1 were more likely than the other datashak to have substantial positive contributions when taking into account the dimensions of both PC1 and PC2 for features of the RSRW and RSR (Figures 6A and 6B). Parallel findings have been reported by several researchers, such as Portis et al. (2006) for peppers and Koutsos et al. (2000) for okra.

4.8. MGIDI results

In the selection process, it is the main task of plant breeders to frequently assess multiple attributes (Santchurn et al., 2014). Plant breeders keep in mind that a model plant type suggests choosing plants with best performance. Breeders can improve plant performance by employing a stepwise trial-and-error methodology and adopting an ideotype as their final objective for selection (Van Oijen and Höglind, 2016). The selection depends on the ideotype procedure that should be used in breeding programs, Taking into consideration all the useful associations between the characteristics and the trait values. In the present study, ranking of the datashak landraces was performed using data from several attributes that were assessed (Figure 7). Redtower and Data (cross) were chosen based on the MGIDI; however, Data (cross) was very close to the cutoff point, suggesting that this germplasm may possess desirable characteristics and breeders should take special care when evaluating this datashak. Many studies have utilized the MGIDI for various crops, and it is an effective tool for creating improved recommendation techniques (Olivoto and Nardino, 2021).

5. Conclusion

The study assessed 14 red and green datashak genotypes and found that for the main yield-contributing features, the tested datashak had considerable genetic variability. The examination of the variance of each character examined revealed a large amount of variation among the 14 datashak. This indicated that there is the possibility of selecting promising genotypes from the present set of datashak for yield and other trait improvement. Considering the mean values and range, Redtower and Red force had the maximum performance, while that for Lolita, Green tower, Sabujshak, and Data (cross) was above

average. Significant correlation values were found for all the traits with the BY, except for the RSRL and RSRW. The path coefficients suggested that more priority should be given to choosing datashak with the SW, RL, LW, and SW. The datashak were divided into four clusters based on the Euclidean method distance and then hierarchical clustering was performed using Ward's method. The datashak in clusters II and III could be selected for future breeding programs based on the mean cluster values, as well as the intra and intercluster distances, as these two clusters displayed superior mean values for most of the traits. The heatmap-oriented cluster analysis grouped the 14 genotypes into 4 clusters, displaying the significant genetic variability among them. Redtower and Data (cross) can be carefully chosen as high-performing datashak based on the MGIDI, as they displayed balanced traits associated with the SW, StW, TBPP, and BY, without assigning weights, and were free from multicollinearity. According to the PCA, heatmap, and cluster dendrogram, Lalgolapi, Lolita, and BARI lalshak1 showed the greatest potential to make significant positive contributions, making them the datashak to choose for yield-related traits. These studied datashak accessions might be referred to as high yielding varieties with BY potential for future breeding operations.

Contribution of authors

Concept, software, resources, visualization, and supervision: US; methodology, investigation, data curation, and writing—original draft preparation: KGS and US; formal analysis: KGS, JH, and MGA; validation: US, JA, and SO; writing—review, revising and editing: US, JH, JA, MGA, RR, and SO. All the authors have read and agreed to the published version of the manuscript.

Data availability

All the tables and figures in the text contain the data that were used in the current research.

Conflict of interest

The authors have no conflicts of interest to declare.

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