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Morpho-agronomic and genetic evaluation of long day garlic (*Allium sativum*)

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ABSTRACT

In India, productivity of garlic (*Allium sativum* L.) is low due to non-availability of high yielding varieties for a particular province/state. In India, Himachal Pradesh is the major garlic producing state amongst the various hilly regions. In Himachal Pradesh, districts like Sirmour, Solan, Kullu, Mandi and Kangra are main garlic producer and meet the demand of garlic seed of whole state, but majority of varieties are low yielding. The present study was carried out during 2022–23 and 2023–24 at Dr. Y S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh to evaluate morphological and horticultural traits of garlic in mid-hill environments of Himachal Pradesh. Thirty-five genotypes of garlic including cultivar Solan Selection as check were evaluated for yield and yield contributing characters based on DUS guidelines notified by Protection of Plant Varieties and Farmer's Right Act (PPV&FRA). The experiment was laid out in a randomized complete block design (RCBD) with three replications. The results revealed that LGC–20, LGC–2, and LGC–22 performed better in terms of yield with 52.27%, 48.51% and 45.78% increase over check variety, Solan Selection, respectively. Furthermore, the DUS traits like leaf, stem, pseudo-stem, bulb, clove weight, clove size, bulb yield, maturity and incidence of rust, were also exhibited wide variation and found helpful in enhancing yield of garlic. Clustering analysis differentiated all the genotypes into four major clusters based on various traits studied. The Principal Component Analysis (PCA) represented a similar grouping of the genotypes which helps in the assessment of diversity in the multivariate analysis and indicated morphological variation of the germplasm under study. Therefore, based on present investigation, it is recommended that high yielding genotypes LGC-20 (259.45 q/ha), LGC-2 (240.25 q/ha) and LGC-22 (239.69 q/ha) with improved productivity and variable morphological traits were found promising genotypes and can be recommended for commercial cultivation to enhance the profitability of stake holders.

Keywords: Bulb yield, Diversity index, DUS traits, Garlic genetic diversity, Principal component analysis

In India, garlic (*Allium sativum* L.) is a widely cultivated bulb crop with a wide range of agro-climatic conditions. It is produced by small and commercial growers for various purposes, such as herbal medicine and flavouring traditional cuisines, and serving as a source of income for many stake holders. It is also rich in carbohydrates, sugar, dietary fibres, fat, protein, thiamine, riboflavin, niacin, vitamin C and calcium (Thakur *et al.* 2024). Additionally, garlic is recognized for its anticancer potential (Sharma *et al.* 2024) and have ability to lower blood cholesterol levels (Sunata *et al.* 2023). Worldwide, production is 30.7 million tonnes with a recorded land area of 1.6 million ha. China is the leading country in area and production of garlic followed by India and Egypt (FAOSTAT 2019). In India, it is cultivated over an area of 393 thousand hectares with production of 3208 thousand metric tonnes (NHB 2021). In Himachal Pradesh, garlic is grown over an area of 6.51 thousand ha with an annual production of 12.71 metric thousand tonnes (NHB 2021). Garlic cultivation is more popular amongst the farmers of Sirmaur, Kullu, Mandi and Kangra districts of Himachal Pradesh because of its higher profit margins and ease in production.

Despite being reproduced asexually, garlic cultivars showed inconsistent yield performance, and phenotypic traits across various locations (Yebirzaf *et al.* 2018, Getahun and Getaneh 2019, Tesfaye 2022). Evaluation of diversity in garlic is therefore important for selection and breeding purposes to improve yield and quality. An effective improvement programme in garlic, depends on clonal selection, availability of diverse genetic stock. For evaluation of genetic diversity, the distinctness, uniformity

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and stability (DUS) qualities are required to be used to morphologically separate distinct genotypes of garlic and to discern new plant varieties from commercial ones. However, the shortage of high yielding location specific varieties is the major constraint. To address this issue, the present study was undertaken to assess the nature and magnitude of diverse genetic diversity present in the genotypes based on morphological, multivariate analysis, DUS traits and on mean performance. In light of this, we conducted a study on 35 genotypes of garlic collected from various parts of the region, concentrating on morphological and horticultural traits in mid-hill environments of Himachal Pradesh.

MATERIALS AND METHODS

Experimental materials: The present study was carried out during 2022–23 and 2023–24 at Dr. Y S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh. In the present study, 35 genotypes collected from different parts of the country (Supplementary Table 1) were examined for morphological and horticultural characterization. Planting was done on 5th October, 2022 and harvested in first week of May 2023. In 2023, planting was done on 7th October, 2023 and harvested in first week of May 2024.

All the 35 genotypes including the check variety 'Solan Selection' were planted in the research farm adopting a randomised complete block design (RCBD) with three replications. The well sprouted cloves of each genotype were planted on a plot size of 1.20 m × 1.00 m accommodated 60 plants/plot with a spacing of 20 cm between rows and 10 cm between plants. The standard cultural practices including hoeing, weeding, irrigation was applied as recommended for healthy crop development of garlic given in the "Package of Practices for Vegetable Crops" by Dr. Y S Parmar, University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh. For 31 morphological traits, assessment in 35 garlic genotypes, the distinctiveness, uniformity, and stability (DUS) criteria was followed as outlined by the PPV& FRA (2001). The genetic divergence, principal component analysis (PCA) and diversity index was also worked out in the current research to assess the genetic diversity present in the material.

Morphological characterization: The data were recorded for 12 quantitative, and 21 qualitative traits of 35 genotypes as per the DUS guidelines for garlic during both years of study. The observations were recorded on ten randomly selected samples of each replication.

Data analysis: Beside visual observations of 31 traits based on DUS guideline, mean performance for different horticultural traits and incidence of rust (As per scale given by Koike *et al.* 2001) were also recorded for two years, 2022–23 and 2023–24. The results obtained with respect to morphological, agronomic traits characterization and the Shannon diversity index were also performed using variance analysis in the SAS version 9.3. The diversity analysis was done for observed traits by Mahalanobis D^2 statistics and the grouping pattern of the genotypes and estimated by principal component analysis (PCA) in PAST (Paleontological Statistics) software.

RESULTS AND DISCUSSION

DUS characterization of garlic genotypes: The observations recorded on different DUS characters has been present in Table 1. The frequency of the characterization of DUS traits is presented in (Supplementary Fig. 1) which depicts the data in the form of pie charts. There were significant differences in growth traits amongst studied genotypes. In the present study substantial variability in the qualitative traits in garlic was observed in respect to DUS traits which is influenced by environment and genotype. Similar results were also shown by other researchers, viz. Gupta and Mahajan (2018), Kohli and Prabal (2000), Prajapati *et al.* (2018), Benke *et al.* (2020), Pasupula *et al.* (2024) in garlic.

Table 1 Diversity indices of morphological descriptors in garlic genotypes

Trait	Class or scale of descriptor	Frequency	Relative frequency (100%)	Diversity index (DI)
Plant: Density of leaves	Sparse	7	20.00	1.02
	Medium	18	51.42	
	Dense	10	28.57	
Plant: Number of leaves/ pseudostem	Few (<9)	29	82.85	0.46
	Medium (9–12)	6	17.14	
	Many (>12)	0	0.00	
Foliage: Attitude	Erect	16	45.71	0.93
	Semi–erect	16	45.71	
	Drooping	3	8.57	
Leaf: Intensity of green colour	Light	10	28.57	1.09
	Medium	12	34.28	
	Dark	13	37.14	
Leaf: Waxiness	Absent	0	0.00	0.00
	Present	35	100	

Contd.

Table 1 (*Continued*)

Trait	Class or scale of descriptor	Frequency	Relative frequency (100%)	Diversity index (DI)
Leaf: Length	Short (<25 cm)	0	0.00	0.67
	Medium (25–35 cm)	14	37.14	
	Long (> 35 cm)	21	62.85	
Leaf: Width	Narrow (< 1.5 cm)	21	60.00	0.84
	Medium (1.5 – 2.5 cm)	12	34.28	
	Broad (>2.5 cm)	2	5.71	
Leaf: Shape in cross section	Flat	19	54.28	0.69
	Slightly concave	16	45.71	
	Strongly concave	0	0.00	
Pseudostem: Length	Small (<5 cm)	17	48.57	0.69
	Medium (5–10 cm)	18	51.42	
	Long (>10 cm)	0	0.00	
Pseudostem: Width of the base	Narrow (<1.0 cm)	21	60.00	0.84
	Medium (1.0–1.5 cm)	12	34.28	
	Broad (>1.5 cm	2	5.71	
Pseudostem: Intensity of anthocyanin colouration at base	Absent	13	37.14	0.66
	Present	22	62.85	
Flowering stem	Absent	18	51.42	0.69
	Present	17	48.57	
Flowering stem: Curvature	Absent	1	2.85	0.22
	Present	16	45.71	
Flowering stem: Bulbils	Absent	18	51.42	0.69
	Present	17	48.51	
Time of maturity (from date of planting)	Early (<130 days)	0	0.00	0.00
	Medium (130–160 days)	0	0.00	
	Late (>160 days)	35	100	
Bulb: Size (diameter)	Small (< 2.5 cm)	0	0.00	0.83
	Medium (2.5–3.5 cm)	4	11.42	
	Large (3.5–5.0 cm)	24	68.57	
	Very large (>5.0 cm)	7	20.00	
Bulb: Shape in longitudinal section	Elliptic	2	5.71	0.77
	Ovate	24	68.57	
	Circular	9	25.71	
Bulb: Shape in cross section	Elliptic	5	14.28	0.41
	Circular	30	85.71	
Bulb: Position of cloves at tip of bulb	Inserted	20	57.14	0.68
	Exerted	15	42.85	
Bulb: Position of root disc	Inserted	0	0.00	0.66
	At surface (flat)	13	37.14	
	Exerted	22	62.85	
Bulb: Shape of base	Recessed	23	65.71	0.88
	Flat	5	14.28	
	Rounded	7	20.00	
Bulb: Compactness of cloves	Loose	7	20.00	1.05
	Medium	14	40.00	
	Compact	14	40.00	
Bulb: Ground colour of dry external scales	White	4	11.42	0.35
	Yellowish white	0	0.00	
	Reddish white	0	0.00	
	Purple	31	88.57	

Contd.

Table 1 (*Concluded*)

Trait	Class or scale of descriptor	Frequency	Relative frequency (100%)	Diversity index (DI)
Bulb: Anthocyanin stripes on dry external scales	Absent	4	11.42	0.35
	Present	31	88.57	
Bulb: Number of cloves	Few (<10)	21	60.00	0.67
	Medium (11–20)	14	40.00	
	Many (>20)	0	0.00	
Bulb: Distribution of cloves	Radial	6	17.14	0.46
	Non–radial	29	82.85	
Bulb: External clove	Absent	34	97.14	0.13
	Present	1	2.85	
Bulb: Skin adherence of dry external scales	Weak	5	14.28	0.99
	Medium	17	48.57	
	Strong	13	37.14	
Clove: Size (diameter)	Small (<1 cm)	4	11.42	0.48
	Medium (1–2 cm)	30	85.71	
	Large (>2 cm)	1	2.85	
Clove: Colour of scale	White	3	8.57	0.64
	Cream	2	5.71	
	Pink	0	0.00	
	Brown	0	0.00	
	Purple	29	82.85	
	Any other i.e. Yellow	1	2.85	
Clove: Colour of flesh	White	0	0.00	0.00
	Yellowish	35	100	
Mean				0.67
Maximum				1.09
Minimum				0.00

Mean performance of garlic genotypes: The mean performance was recorded during 2022–23 and 2023–24 for different horticultural traits namely, number of leaves/pseudo stem ranged from 6.66–10.11. Maximum number of leaves (10.11) was found in LGC–22. Leaf length ranged between 25.55–50.66 cm, leaf width ranged between 0.96–3.86 cm. Substantial variability in the quantitative traits and for incidence of rust was also noticed. Earlier workers have also been reported substantial diversity for number of leaves, leaf length and leaf width in garlic. The findings of present study about traits namely, number of leaves, leaf length and leaf width were in agreement with Ranjitha *et al.* (2018), Tiwari *et al.* (2020), Dixit *et al.* (2021) and Anand *et al.* (2022). The significant variability for pseudo stem length and width was observed and it ranged between 3.90–9.12 cm and 0.47–2.31 cm respectively. Earlier Dixit *et al.* (2021), Anand *et al.* (2022) and Tesfaye (2022) also reported substantial diversity for pseudo stem length and width. Bulb equatorial diameter ranged between 2.58–5.93 cm and maximum was observed in LGC–2 (5.93 cm), whereas, bulb polar diameter ranged between 2.48–3.82 cm and maximum (3.82 cm) in LGC–22. The findings of the traits, viz. bulb equatorial diameter and bulb polar diameter in present study are in close conformity with the results of Ranjitha *et al.* (2018), Dixit *et al.* (2021) and Anand *et al.* (2022). Number of cloves/bulb is an important trait of garlic, for export purpose 10–15 cloves/bulb are required. In the present genotypes under study, it ranged from 7.67–13.33 and highest were in genotype LGC–20 (13.33). Earlier, Dixit *et al.* (2021) and Anand *et al.* (2022) reported the same results in garlic. Similarly, clove weight ranged between 1.03–5.33 g and was maximum in LGC–20 (5.33 g). Variability among genotypes for clove weight were also evaluated by Tiwari *et al.* (2020), Dixit *et al.* (2021) and Anand *et al.* (2022) in garlic, as present studies exhibited lot of variability for this trait. Clove diameter ranged between 0.67–2.33 cm with maximum value of 2.33 cm in LGC–22. These findings for clove diameter were in agreement with Tiwari *et al.* (2020) and Kumar *et al.* (2017) in garlic. Bulb weight is a significant quantitative trait of garlic which has direct influence on yield of garlic; it ranged between 8.98–64.86 g with maximum value of (64.86 g) in LGC–20 followed by LGC–2 (60.06 g), Earlier significant variability for bulb weight was also reported by Dixit *et al.* (2021) and Kumar *et al.* (2017) in garlic. High yield is the ultimate objective of cultivation of any crop. High yield will eventually lead to higher revenues and profitable to farmers. Yield/plot and per hectare ranged from 0.54–3.89 kg and 35.92–259.45 q respectively. Maximum yield/plot and hectare was exhibited by LGC–20 (3.89 kg and 240.25 q) followed by LGC–2, LGC–22 and LGC–15. Dixit *et al.* (2021) and Anand *et al.* (2022) reported significant variability among the genotypes for trait. Majority of genotypes under study were late in maturity and genotype LGC–13 took maximum days for maturity. These same findings in garlic were represented by Dixit *et al.* (2021), Anand *et al.* (2022) and Tesfaye (2022). The rust incidence ranged from 11.00–32.00 % and minimum incidence was recorded in genotype LGC–3 (11.00%). Therefore, on the basis of mean performance, genotypes LGC–20, LGC–2 and LGC–22 exhibited highest bulb weight, yield/plot and hectare, respectively (Table 2). Significant variations were also noted for other desirable traits, which are significantly linked to yield, viz. number of cloves/bulb, clove weight, clove diameter, bulb equatorial and polar diameter and days to maturity. This notable variability among the genotypes concerning these traits has been similarly observed by Bhatt *et al.* (2017), Prajapati *et al.* (2018), Jethava *et al.* (2018), Rathava *et al.* (2018), Benke *et al.* (2020), Tiwari *et al.* (2020), Dixit *et al.* (2021), Tesfaye (2022), Khadi *et al.* (2022), and Aswani *et al.* (2024) in garlic.

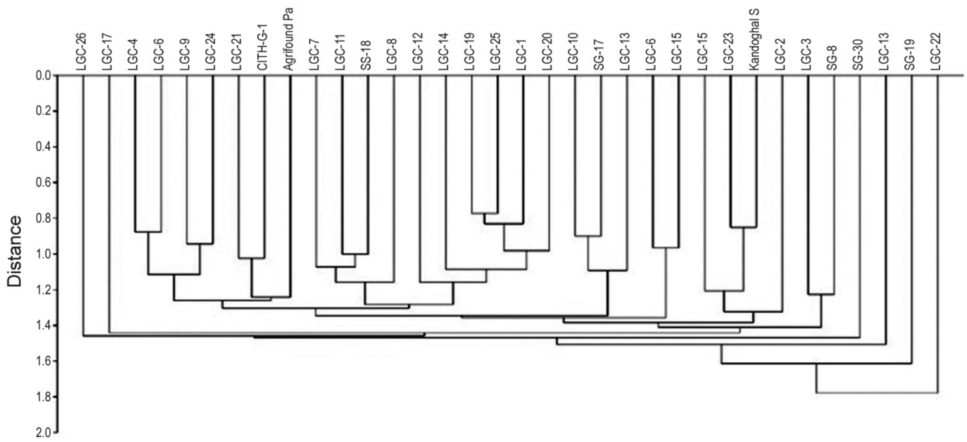

Fig. 1 Clustering pattern of garlic genotypes based on different traits.

Shannon diversity index: The Shannon Diversity Index (SDI) serves as a useful tool for capturing the degree of variability in different morphological characteristics. The diversity of each descriptor was quantified using the SDI, with values ranging from 0–1.09. Notably, descriptors such as leaf waxiness, time to maturity, and clove colour of flesh exhibited a diversity index of 0, suggesting little to no variation for these traits across the genotypes under study. On the other hand, traits like leaf intensity of green colour showed the highest diversity index of 1.09, followed by Bulb: Compactness of cloves having diversity index of 1.05 and Plant: Density of leaves having diversity index of 1.02 indicating substantial variation in these traits. Such morphological descriptors can help breeders select for traits of interest and develop improved varieties with specific attributes, such as disease resistance, yield potential, or quality. Similar results were also reported by Pasupula *et al.* (2024) in garlic.

Cluster analysis: The current investigation revealed that 35 genotypes were grouped into 4 clusters based on Mahalanobis D^2 values (Fig. 1). The cluster I was the largest group accommodated maximum (16) genotypes, cluster II contains three genotypes (LGC–2, LGC–20, LGC–15), characterized by the highest leaf length, bulb polar diameter, bulb equatorial diameter, clove weight, bulb weight, number of cloves/bulb, yield/plot and yield/ha. Hence this group may be used for the selection of genotypes for superior morphological and horticultural traits. Similarly, cluster III contains 15 genotypes, and cluster IV contains only LGC–22 genotype, being peculiar genotype had maximum number of leaves per plant, pseudostem width, clove size, leaf width along with desirable yield and yield related traits. The maximum inter cluster distance was between cluster III and cluster IV. The cluster having higher inter cluster distance showed the maximum divergence. Amongst traits, maximum contribution is made by bulb weight (34.45%) for divergence followed by clove weight (27.39%), bulb equatorial diameter (6.72%), leaf length and width (6.55%, 5.88%), days to maturity (5.88%), pseudostem width and length (5.71%, 5.04%), clove size (2.86%), bulb polar diameter (2.52%) and number of cloves (2.02%) while, minimum contribution was recorded by number of leaves/pseudostem (1.10%). Other studies, including those by Benke *et al.* (2020), Tesfaye (2022) and Pasupula *et al.* (2024), have also reported parallel findings on genetic clustering in garlic.

Principal component analysis: Principal component analysis (PCA) reflects the importance of the largest contributor to the total variations at each axis of differentiation. In the present investigation, PCA analysis represented a similar grouping of genotypes which helps in the assessment of diversity in multivariate scales (Fig. 2). This depicts the variations in morphological and horticultural traits among the various genotypes of garlic. Amongst 35 genotypes, genotype LGC–22 was most diverse one and grouped separately. This diverse nature of LGC-22 is due to morphological differences in number of leaves/plant, pseudo stem width, clove size, leaf width along with desirable yield and yield related traits from other genotypes. Similarly, genotype, LGC-20 and LGC-2 were separately grouped due to high values of various yield and yield related traits. The eigen value, variability (%) and cumulative (%) is given in Table 3. Maximum eigen value, variability (%) and cumulative (%) was found for trait number of leaves/plant i.e. 7.74, 55.3% and 55.3%, respectively. The PCA results from the current study align with the findings of Pasupula *et al.* (2024) and Aswani *et al.* (2024).

Table 2 Mean performance of different garlic genotypes for growth and bulb traits (Pooled data of 2022–23 and 2023–24)

Genotypes	NLPP	LL (cm)	LW (cm)	PL (cm)	PW (cm)	BED (cm)	BPD (cm)	CD (cm)	CW (g)	NCPB	BW (g)	YPP (kg/1.2 m^2)	YH (q)	DTM	RI (%)*
LGC–1	7.89^{b-h}	43.78^{a-f}	1.69^{cd}	5.17^{d-i}	1.44^{bc}	5.05^{a-f}	3.58^{a-g}	1.60^{b-f}	3.27^{c-f}	10.33^{cde}	49.51^{b-e}	2.97^{b-f}	198.05^{b-f}	206.67^{b-h}	16.87^{lm} (4.11)
LGC–2	8.55^{a-g}	39.33^{b-k}	1.44^{c-k}	4.44^{g-i}	0.70^{h-k}	5.93^{a}	3.61^{a-f}	1.37^{b-g}	4.63^{ab}	12.67^{ab}	60.06^{ab}	3.60^{ab}	240.25^{ab}	215.00^{a-d}	11.80^{u} (3.44)
LGC–3	7.45^{d-h}	36.33^{e-n}	1.38^{c-k}	5.64^{d-i}	1.10^{b-g}	5.82^{ab}	2.82^{i-m}	1.77^{a-e}	3.23^{c-f}	11.33^{a-d}	44.24^{def}	2.71^{d-g}	180.66^{d-g}	202.67^{d-h}	11.00^{v} (3.32)
LGC–4	8.11^{b-h}	33.11^{j-o}	1.33^{c-k}	5.23^{d-i}	0.70^{h-k}	3.74^{i-l}	3.68^{a-j}	1.53^{b-f}	2.37^{f-j}	9.33^{d-g}	17.13^{l-o}	1.03^{n-q}	68.52^{n-q}	206.33^{b-h}	23.11^{fg} (4.81)
LGC–5	6.66^{h}	30.77^{l-o}	0.99^{k}	5.89^{d-g}	0.47^{k}	3.86^{g-l}	2.99^{g-m}	1.27^{b-g}	2.23^{f-k}	9.33^{d-g}	16.59^{l-o}	1.00^{n-q}	66.36^{n-q}	200.67^{f-i}	17.67^{k} (4.20)
LGC–6	7.00^{fgh}	33.78^{i-n}	1.25^{d-k}	6.31^{c-f}	0.95^{e-j}	3.99^{g-k}	3.20^{b-k}	1.60^{b-f}	1.07^{l}	8.67^{e-g}	16.24^{l-o}	0.97^{n-q}	64.96^{n-q}	200.67^{f-i}	23.90^{f} (4.89)
LGC–7	7.55^{c-h}	25.55^{o}	0.96^{k}	5.00^{d-i}	0.83^{g-k}	4.11^{f-k}	3.21^{b-k}	1.60^{b-f}	2.13^{f-l}	10.00^{cde}	26.04^{i-l}	1.56^{k-n}	104.17^{k-n}	202.33^{e-h}	28.10^{d} (5.30)
LGC–8	8.55^{a-g}	38.35^{c-l}	1.68^{cd}	5.20^{d-i}	1.18^{b-g}	4.54^{c-j}	3.03^{f-m}	1.83^{a-d}	1.30^{jkl}	10.33^{cde}	23.89^{j-m}	1.43^{l-o}	95.56^{l-o}	215.67^{a-d}	22.17^{h} (4.71)
LGC–9	9.33^{abc}	37.66^{d-m}	1.22^{d-k}	4.77^{e-i}	0.87^{g-k}	3.91^{g-l}	3.62^{a-e}	1.50^{b-f}	2.40^{f-j}	11.00^{bcd}	25.76^{i-l}	1.55^{k-n}	103.05^{k-n}	218.33^{ab}	18.90^{j} (4.35)
LGC–10	7.66^{c-h}	30.00^{m-o}	0.98^{k}	7.74^{abc}	0.62^{i-k}	3.20^{k-m}	2.89^{h-m}	1.07^{efg}	1.03^{l}	8.33^{e-g}	11.36^{no}	0.68^{pq}	45.44^{pq}	200.00^{g-i}	26.73^{e} (5.17)
LGC–11	8.00^{b-h}	31.89^{k-o}	1.05^{i-k}	6.32^{c-f}	0.55^{jk}	3.58^{j-m}	3.00^{g-m}	0.97^{fg}	1.17^{kl}	11.67^{abc}	13.66^{m-o}	0.82^{o-q}	54.64^{o-q}	215.33^{a-d}	28.20^{d} (5.31)
LGC–12	8.66^{a-f}	44.11^{a-e}	1.77^{bc}	4.25^{g-i}	1.41^{bcd}	4.87^{b-g}	3.74^{ab}	1.53^{b-f}	2.93^{d-h}	10.33^{cde}	48.28^{cde}	2.90^{b-f}	193.13^{b-f}	207.33^{b-h}	27.17^{e} (5.21)
LGC–13	7.00^{fgh}	36.00^{f-n}	1.07^{h-k}	8.12^{ab}	0.84^{g-k}	3.66^{j-l}	3.07^{e-l}	1.27^{b-g}	1.97^{g-l}	9.67^{c-f}	29.42^{g-k}	1.77^{i-m}	117.69^{i-m}	204.00^{c-h}	16.70^{mn} (4.09)
LGC–14	8.89^{a-e}	45.66^{abc}	1.52^{c-j}	4.36^{g-i}	1.38^{b-e}	4.49^{c-j}	3.56^{a-g}	1.40^{b-f}	1.97^{g-l}	9.67^{c-f}	42.04^{def}	2.52^{e-h}	168.17^{e-h}	214.00^{a-e}	20.93^{i} (4.57)
LGC–15	8.11^{b-h}	30.44^{m-o}	1.22^{d-k}	4.03^{hi}	0.70^{h-k}	5.29^{a-e}	3.72^{abc}	1.67^{a-f}	1.80^{h-l}	11.00^{bcd}	59.36^{abc}	3.56^{abc}	236.65^{abc}	213.67^{a-f}	14.40^{qr} (3.79)
LGC–16	7.11^{e-h}	41.44^{b-i}	1.41^{c-k}	5.10^{d-i}	0.87^{g-k}	3.96^{g-k}	3.69^{a-d}	1.93^{ab}	1.16^{kl}	9.33^{d-g}	27.16^{h-l}	1.63^{j-n}	108.65^{j-n}	202.67^{d-h}	17.33^{l} (4.16)
LGC–17	9.22^{a-d}	35.11^{g-n}	1.30^{c-k}	5.44^{d-i}	0.65^{i-k}	3.80^{h-l}	3.39^{a-i}	1.80^{a-d}	1.33^{jkl}	11.33^{a-d}	19.65^{k-o}	1.18^{l-p}	78.60^{l-p}	207.67^{b-g}	29.07^{c} (5.39)
LGC–18	8.11^{b-h}	39.44^{b-k}	1.65^{cde}	5.65^{d-i}	0.93^{f-j}	3.91^{g-l}	3.15^{c-l}	0.67^{g}	2.97^{d-g}	11.00^{bcd}	24.89^{i-m}	1.49^{k-o}	99.56^{k-o}	196.33^{hij}	15.90^{o} (3.99)
LGC–19	7.55^{c-h}	44.33^{a-d}	1.60^{c-f}	5.73^{d-h}	1.14^{b-g}	4.33^{e-j}	3.39^{a-i}	1.53^{b-f}	2.37^{f-j}	11.67^{abc}	47.83^{cde}	2.87^{c-f}	191.33^{c-f}	215.33^{a-d}	17.30^{l} (4.16)
LGC–20	8.11^{b-h}	50.66^{a}	2.21^{b}	3.90^{i}	1.55^{b}	5.50^{abc}	3.71^{abc}	1.50^{b-f}	5.33^{a}	13.33^{a}	64.86^{a}	3.89^{a}	259.45^{a}	218.67^{a}	12.07^{tu} (3.47)

Contd.

Table 2 (*Concluded*)

Genotypes	NLPP	LL (cm)	LW (cm)	PL (cm)	PW (cm)	BED (cm)	BPD (cm)	CD (cm)	CW (g)	NCPB	BW (g)	YPP (kg/1.2 m^2)	YH (q)	DTM	RI (%)*
LGC–21	8.89^{a-e}	41.33^{b-i}	1.31^{c-k}	6.45^{b-e}	1.18^{b-g}	4.36^{d-j}	2.77^{k-m}	1.13^{d-g}	2.90	8.67^{e-g}	15.96^{l-o}	0.96^{n-q}	63.84^{n-q}	200.33^{f-i}	32.00^{a} (5.66)
LGC–22	10.11^{a}	44.55^{a-d}	3.86^{a}	3.92^{i}	2.31^{a}	5.82^{ab}	3.82^{a}	2.33^{a}	5.24^{a}	9.66^{c-f}	59.92^{abc}	3.59^{ab}	239.69^{ab}	203.00^{d-h}	15.03^{p} (3.88)
LGC–23	9.11^{a-d}	36.00^{f-n}	1.19^{e-k}	4.49^{g-i}	0.94^{f-j}	4.80^{b-h}	3.44^{a-h}	1.33^{b-g}	3.23^{c-f}	10.33^{cde}	44.04^{def}	2.64^{e-h}	176.17^{e-h}	204.67^{v-h}	13.73^{r} (3.71)
LGC–24	8.89^{a-e}	40.78^{b-j}	1.61^{c-f}	4.16 $^{g-i}$	1.10^{c-h}	3.82^{h-l}	3.28^{a-k}	1.33^{b-g}	3.63^{b-e}	11.67^{abc}	32.64^{f-j}	1.96^{h-l}	130.57^{h-l}	207.33^{b-h}	14.27^{q} (3.78)
LGC–25	7.78^{b-h}	46.55^{ab}	1.53^{c-i}	4.58^{f-i}	1.17^{b-g}	4.74^{c-i}	3.46^{a-h}	1.57^{b-f}	2.50^{e-i}	10.33^{cde}	55.94^{abc}	3.36^{a-d}	223.77^{a-d}	215.00^{a-d}	12.23^{t} (3.50)
LGC–26	8.11^{b-h}	30.11^{m-o}	1.13^{f-k}	4.44 $^{g-i}$	0.98^{d-i}	4.28^{e-j}	3.72^{abc}	1.93^{ab}	4.22^{abc}	12.67^{ab}	57.05^{abc}	3.42^{abc}	228.21^{abc}	211.00^{a-f}	16.83^{lm} (4.10)
SG–8	7.00^{fgh}	42.33^{b-g}	1.56^{c-g}	6.67^{bcd}	0.96^{e-j}	3.94^{g-k}	2.94^{h-m}	1.30^{b-g}	1.37^{i-l}	10.00^{cde}	22.59^{j-n}	1.36^{l-p}	90.36^{l-p}	193.67^{ij}	18.97^{j} (4.36)
SG–17	7.67^{c-h}	28.78^{n-o}	1.10^{g-k}	9.12^{a}	0.90^{g-k}	2.58^{m}	2.59^{lm}	1.30^{b-g}	1.47^{i-l}	7.67^{fg}	8.98^{o}	0.54^{q}	35.92^{q}	185.00^{j}	31.90^{a} (5.65)
SG–18	8.33^{a-h}	33.22^{j-o}	1.25^{d-k}	5.00 $^{d-i}$	0.99^{d-i}	3.59^{j-m}	3.11^{d-l}	1.27^{b-g}	1.37^{i-l}	11.00^{bcd}	18.47^{k-o}	1.11^{m-q}	73.88^{m-q}	206.67^{b-h}	22.87^{g} (4.78)
SG–19	6.78^{gh}	30.55^{l-o}	1.23^{d-k}	4.50^{g-i}	0.84^{g-k}	2.88^{lm}	2.48^{m}	1.40^{b-f}	1.57^{i-l}	7.33^{g}	9.95^{o}	0.60^{q}	39.80^{q}	187.33^{ij}	30.97^{b} (5.57)
SG–30	7.22^{e-h}	34.55^{g-n}	1.20^{e-k}	4.91 $^{d-i}$	0.59^{i-k}	4.06^{f-k}	2.84^{h-m}	1.17^{c-g}	1.47^{i-l}	8.67^{e-g}	29.64^{g-k}	1.78^{i-m}	118.57^{i-m}	216.33^{abc}	15.00^{p} (3.87)
Kandaghat Selection	9.55^{ab}	40.33^{b-j}	1.61^{c-f}	4.64^{f-i}	1.18^{b-g}	4.72^{c-i}	3.41^{a-h}	1.87^{abc}	2.27^{f-k}	10.33^{cde}	50.70^{bcd}	3.04^{b-e}	202.81^{b-e}	208.33^{b-g}	12.80^{s} (3.58)
Agrifound Parvati	9.22^{a-d}	33.89^{h-n}	1.09^{g-k}	4.77^{e-i}	1.36^{b-f}	4.87^{b-g}	3.46^{a-h}	1.60^{b-f}	4.77^{ab}	11.33^{a-d}	38.06^{e-h}	2.28^{f-j}	152.25^{f-j}	205.33^{b-h}	16.26^{no} (4.03)
CITH –G–1	9.11^{a-d}	41.66^{b-h}	1.54^{c-h}	4.09^{hi}	1.25^{b-g}	5.38^{a-d}	3.57^{a-g}	1.93^{ab}	3.97^{bcd}	10.00^{cde}	38.99^{efg}	2.34^{e-i}	155.97^{e-i}	212.67^{a-f}	17.83^{k} (4.22)
Solan Selection (C)	8.22^{b-h}	25.55^{o}	1.04^{jk}	4.23 $^{g-i}$	0.63^{i-k}	3.94^{g-k}	2.79^{j-m}	1.70^{a-e}	3.86^{bcd}	11.00^{bcd}	36.03^{f-i}	2.16^{g-k}	144.13^{g-k}	211.00^{a-f}	15.86^{o} (3.98)
Over all mean	8.15	37.08	1.43	5.27	1.01	4.33	3.27	1.50	2.59	10.31	33.76	2.03	135.60	207.17	19.60
Genotypes significantly superior than check	05	32	19	15	23	09	22	01	04	03	15	15	15	12	00
Genotypes statistically at par with best performing genotype	04	00	00	00	00	03	09	00	01	02	03	03	03	09	02
SEM	0.32	1.39	0.08	0.32	0.08	0.30	0.11	0.13	0.21	1.09	1.99	0.14	9.30	2.46	0.37
CD (p=0.05)	0.91	3.94	0.24	0.89	0.21	0.85	0.32	0.36	0.59	1.42	5.62	0.39	26.30	6.96	1.05

Means that do not share a letter are significantly different.

NLPP, Number of leaves/plant; LL, Leaf length; LW, Leaf width; PL, Pseudostem length; PW, Pseudostem width; BED, Bulb equatorial diameter; BPD, Bulb polar diameter; CD, Clove diameter; CW, Clove weight; NCPB, Number of cloves/bulb; BW, Bulb weight; YPP, Yield/plot; YH, Yield/ha; DTM, Days to maturity; RI, Incidence of rust.

Table 3 Eigen value and contribution of the principal component axes towards total genetic variation in garlic genotypes under study

Traits	Eigen value	Variability (%)	Cumulative (%)
Number of leaves/plant	7.74	55.3	55.3
Leaf length	1.76	12.6	67.8
Leaf width	0.97	7.0	74.8
Pseudostem length	0.90	6.4	81.2
Pseudostem width	0.77	5.5	86.8
Bulb equatorial diameter	0.43	3.1	89.9
Bulb polar diameter	0.36	2.6	92.4
Clove diameter	0.34	2.5	94.9
Clove weight	0.23	1.7	96.6
Number of cloves/bulb	0.19	1.4	97.9
Bulb weight	0.18	1.3	99.2
Yield/plot	0.11	0.8	100

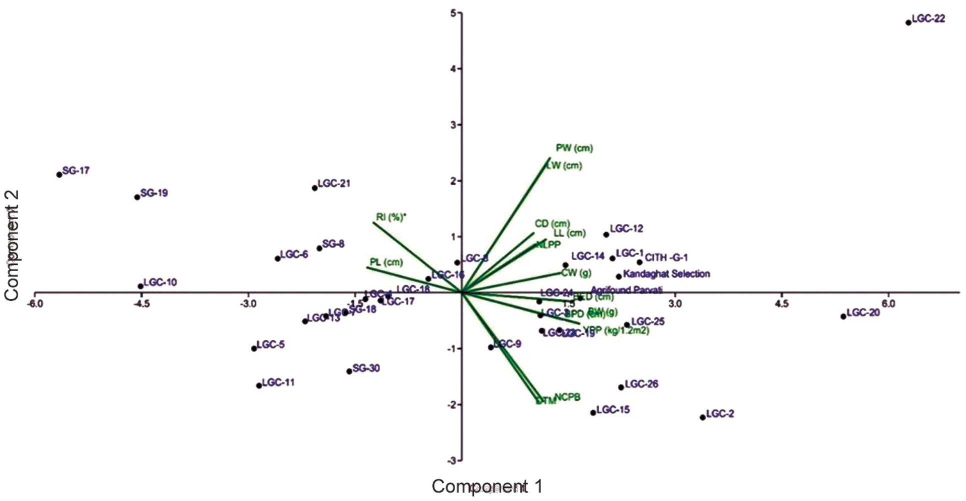

Fig. 2 Biplot generated by Principal Component Analysis of different qualitative and quantitative traits in garlic genotype.
NLPP, Number of leaves/plant; LL, Leaf length; LW, Leaf width; PL, Pseudostem length; PW, Pseudostem width; BED, Bulb equatorial diameter; BPD, Bulb polar diameter; CD, Clove diameter; CW, Clove weight; NCPB, Number of cloves/bulb; BW, Bulb weight; YPP, Yield/plot; YH, Yield/ha; DTM, Days to maturity; RI, Incidence of rust.

The studies reviewed in this discussion, highlights the significant variability for various morpho-agronomic and horticultural traits in different genotypes of garlic under study. Similarly, genotypes classified morphologically based on 31 DUS characters, exhibited enormous variability. On the basis of overall mean performance of 35 diverse genotypes, high values of bulb weight exhibited by LGC–20, LGC–2, LGC–22 and LGC–15 genotypes had direct as well as positive correlation with yield. Genotype, LGC–20 emerged as the top performer among all genotypes, demonstrating an impressive 80% increase in yield compared to the check "Solan Selection." Likewise, genotypes viz. LGC–2, LGC–22 and LGC–15 exhibited, 66.60%, 66.30%, and 64.20% increase respectively relative to check variety "Solan Selection." Overall, genotype, LGC–20, LGC–2 and LGC–22 unveiled notable variations among the garlic genotypes collected from the various part of country, holds a potential for further enhancements in the morpho–agronomic traits of garlic.

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