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Assessment of genetic diversity in coriander (*Coriandrum sativum*) germplasm

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ABSTRACT

The present study was carried out during the winter (*rabi)* seasons of 2019–20 and 2020–21 at Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, to examine the variability, correlation, path coefficient and genetic divergence among 275 coriander (*Coriandrum sativum* L.) accessions with four check varieties, viz. CO4, CO1, CO3, and CO2. The study utilized an augmented complete block design, which incorporated four checks. The study revealed significant variability among the coriander genotypes for key traits, indicating strong potential for improving coriander through selective breeding. High estimates of genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance were observed for the traits such as number of primary branches, number of secondary branches, number of umbels/plant, number of umbellets/plant, number of seeds/umbel, seed yield/plot and seed yield/plant. Correlation analysis showed a highly significant positive relationship between seed yield per plant and the number of seeds per umbel. Path analysis, however, suggested that both direct and indirect effects were relatively low, with the direct effect of the number of seeds per umbel being the most significant and positive. The genetic divergence analysis demonstrated that the accessions clustered into 10 distinct groups. Notably, cluster 4 contained highest number of accessions among all clusters, i.e. 48 and cluster 6 had only one accession. Principal component analysis revealed that PCA 1 showed maximum variances for yield traits while PC2, PC3 and PC4 showed maximum variances for yield attributing traits.

Keywords: Coriander, Correlation, Genetic divergence, Heritability, Path analysis, Principal component analysis

A significant spice crop in the Apiaceae family is coriander (*Coriandrum sativum* L.), also referred to as "Dhania". The coriander plant yields two primary products: fresh green herbs and dry spices. These items are utilized across a range of industries, including food, beverages, perfumery and pharmaceuticals, as well as in the production of essential oil and oleoresin (Tahraoui *et al.* 2007, Islam 2009, Aissaoui *et al.* 2011, Matsubara *et al.* 2011, Adams *et al.* 2012, Riella *et al.* 2012, Meena *et al.* 2014, Onder 2018, Scandar *et al.* 2023). Additionally, coriander leaves contains abundant flavonoids and carotenoids (Nambiar and Sharma 2014, Kamali *et al.* 2019, Mahleyuddin *et al.* 2022). Since ancient times, coriander has been grown all throughout the Mediterranean, Southern Europe and Asia where it is considered to have originated. India produces 111 lakh tonnes from 4.5 lakh hectares (Spice Board of India 2023). India is the world's top producer of coriander, followed by Russia (Anonymous 2020).

The coriander crop is cross-pollinated, which results in the high variation of genetic components. A crop's level of genetic variety is crucial for crop improvement because it mostly determines how effectively selection occurs. Breeding activities have made a significant contribution to the improvement of grain properties, tolerance, resistance, resilience and prospective yield. The degree of genetic improvement is determined by the quantum of genetic variability and the degree to which heritable and non-heritable variants are associated to the features. Every selection programme must start with an understanding of how various component characters relate to yield. The path analysis is used to categorize traits that can be applied as selection criteria to improve crop yield in the crop improvement (Dewey and Lu 1959). In order to find genetically varied parents for hybridization programmes, genetic diversity assessment is a prerequisite for each plant breeding operation. The diversity pattern created through cluster analysis can be confirmed using principal component analysis (Tomar *et al.* 2014, Dudekula *et al.* 2022). Therefore, using genetic variability measures,

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path coefficient analysis, hierarchical cluster analysis, and principal component analysis, the current study was conducted to evaluate the genetic diversity in coriander germplasm.

MATERIALS AND METHODS

The study was conducted during (*rabi*) seasons of 2019–20 and 2020–21 at Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu where augmented block design (ABD) was used for 275 coriander genotypes with four check varieties, viz. CO4, CO1, CO3, and CO2. The genotypes were collected from different states of the country as mentioned in Supplementary Table 1. Each genotype was planted in three rows of a 3 m × 2 m plot, spaced 30 cm × 15 cm apart. In each plot, five randomly selected plants from each of the eight agro morphological traits were examined. According to the recommendations of Mahmud and Kramer (1951), Comstock and Robinson (1952), Burton and Devane (1953), the pooled data from two years was evaluated for genetic variability parameters, such as genotypic variability (GV), phenotypic variability (PV), genotypic Cco-efficient of variability (GCV), phenotypic co-efficient of variability (PCV), broad sense heritability (h^2b), and genetic progress expressed as a percentage of mean (GAM). Following Panse and Sukhatme's (1967) investigation of phenotypic and genotypic correlation coefficients, path coefficient analysis (Dewey and Lu 1959) was used to distinguish the direct and indirect impacts of yield-related variables. Mahalanobis (1936) D^2 statistics were employed to calculate genetic divergence (1936). The observed features were analyzed using the average linage hierarchical approach of cluster analysis and principal component analysis to uncover a common pattern of variation among the accessions. GRAPES: General Rishney-Based Analysis Platform. Principal component analysis was performed using the Statistical Tool 1.0.0 (Gopinath *et al.* 2020).

RESULTS AND DISCUSSION

Per se *performance of coriander genotypes*: Assessing the variability and diversity of coriander genotypes forms the foundation for any crop improvement program. All the 271 coriander genotypes with four checks under study exhibited significant variation for all observed traits (Supplementary Table 2). With respect to the biometrical traits, plant height ranged from 24.75 cm in genotype CS162 to 68.37 cm in CS153, with an average of 51.71 cm. The number of primary branches/plant varied between 4.32 in CO3 to 14.33 in CS20, averaging 7.04 branches. The number of secondary branches/plant ranged from 5.33 in CS32 to 23 in CS196, with a mean of 12.48 branches. The number of umbels/plant varied from 9.67 in CS32 to 45 in CS135, with an average of 23.60 umbels. The number of umbellets/plant ranged from 3 in CS4 to 19 in CS32, with a mean of 6.07 umbellets. The number of seeds/umbel ranged from 7.33 in CS32 to 53.33 in CS159, averaging 29.59 seeds. Seed yield/plot ranged between 90 g in CS57 to 300.15 g in CO3, with an average yield of 159.21 g. Seed yield/plant varied from 4.95 g in genotypes CS57 and CS114 to 16.50 g in CS247,

Table 1 Variability among traits in coriander

Parameters	Mean	GCV (%)	PCV (%)	h^2b (%)	GA	GAM (%)
Plant height (cm)	51.71	16.76	16.82	99.28	17.79	34.40
Number of primary branches	7.04	44.66	44.73	99.70	6.47	91.87
Number of secondary branches	12.48	26.67	26.75	99.36	6.84	54.76
Number of umbels/plant	23.60	21.39	21.48	99.14	10.36	43.88
Number of umbellets/plant	6.07	21.90	22.14	97.84	2.71	44.63
Number of seeds/umbel	29.59	28.63	28.66	99.80	17.44	58.93
Seed yield/plot (g)	159.21	26.80	26.91	99.17	86.68	54.98
Seed yield/plant (g)	8.67	26.69	26.91	98.36	4.73	54.52

GCV, Genotypic co-efficient variability; PCV, Phenotypic co-efficient variability; h^2b, Broad sense heritability; GA, Genetic advance; GAM, Genetic advance as percent of mean.

Table 2 Correlation coefficient among various characters in coriander at genotypic and phenotypic level

Traits	PH	NPB	NSB	NUP	NUBP	NSU	SYP
PH	1						
NPB	0.180**	1					
NSB	0.446**	0.025	1				
NUP	0.402**	-0.044	0.552**	1			
NUBP	0.029	0.571**	-0.113	-0.117	1		
NSU	0.058	-0.137*	0.035	-0.020	0.325**	1	
SYP	-0.099	-0.071	0.021	-0.083	-0.154*	0.172**	1

PH, Plant height; NPB, Number of primary branches; NSB, Number of secondary branches; NUP, Number of umbels/plant; NUBP, Number of umbellets/plant; NSU, Number of seeds/umbel; SYP, Seed yield/plant.

with a mean yield of 8.67 g/plant. The wide range and mean values observed in the study revealed significant variability among the coriander genotypes for key traits, indicating strong potential for improving coriander through selective breeding. Similar findings were reported by Dhakad *et al.* (2017) and Sandhu *et al.* (2018).

Genetic variability: The estimates of genetic advance as a GAM, PV, GCV, PCV, and h^2b for various features are shown in Table 1. Higher estimates of GCV and PCV were observed in the following areas: no. of seeds/umbel (28.63 and 28.66%), seed yield/plot (26.80 and 26.91%), seed yield/plant (26.69 and 26.91%), umbels/plant (21.39 and 21.48%), umbellet/plant (21.90 and 22.14%), primary branch/plant (44.66 and 44.73%), secondary branches/plant (26.67 and 26.75%), umbels/plant (21.39 and 21.48%), and seed yield/plant (26.69 and 26.91%). Even though the disparities were not as great, the PCV for every feature was larger than the GCV. The small difference between PCV and GCV suggested that these characters were not much impacted by their surroundings (Hassan *et al.* 2018, Kumar *et al.* 2020). Genetic improvement through the selection of improved genotypes cannot be achieved just through heritability assessments. Thus, an estimate of GAM was made. The high estimates of h^2b and GAM were plant height (99.28 and 34.40%), no. of primary branches/plant (99.70 and 91.87%), no. of secondary branches/plant (99.36 and 54.76%), no. of umbels/plant (99.14 and 43.88%), no. of umbellets/plant (97.84 and 44.63%), no. of seeds/umbel (99.80 and 58.93%), seed yield/plot (99.17 and 54.98%), and seed yield/plant (98.36 and 54.52%). These traits are driven by additive genes, according to high heritability and GAM estimates, and selection may strengthen them. Singh *et al.* (2006) also demonstrated a comparable pattern of heritability.

The interactions of several characters' resulted in the yield of coriander. Selection that is based on the components of yield will be more effective for a rational approach to increasing yield. The degree and direction of the relationship between yield and its constituents as well as between them determines how effective yield selection is. The study found a positive and very significant correlation between the no. of seeds/umbel (0.172) and total no. of seeds yield/plant (Table 2 and Fig. 1). While the no. of umbels/plant (-0.154) shown a negative and significant correlation with seed yield/plant, plant height (-0.099), no. of primary branches/plant (-0.071), and no. of umbels/plant (-0.083) showed a negative and non-significant association with seed yield/plant. Sharma and Sharma (1989), Kumar *et al.* (2012) and Meena *et al.* (2014) have all observed similar correlations in coriander. Studies of correlation provide insight into the favourable and unfavourable relationships that various characteristics have with yield as well as with one another. Nevertheless, the precise impact and significance of these traits on crop yield remain elusive.

Path coefficient analysis offers a more realistic depiction of the correlations between various characters by taking into consideration both the direct and indirect influences of the various yield components. By understanding the correlations that exist between and among yield components and yield, plant breeders can more easily identify the qualities that have the greatest impact on yield. The number of seeds/umbel (0.326), number of primary branches/plant (0.208), and number of secondary branches/plant (0.078) had the most direct impact on seed yield, as indicated by the path coefficient analysis (Supplementary Table 3). On the other side, the quantity of seeds per umbel had the highest direct impact on seed yield and the strongest positive association (0.172). The above results are also in accordance with the findings of Singh *et al.* (2006). Hence, selection of coriander plants with the above positively associated biometrical traits will facilitate the seed yield improvement in coriander and could serve as a base material for further breeding programmes in coriander as suggested by Meena *et al.* (2014), Ram *et al.* (2017) and Sandhu *et al.* (2018).

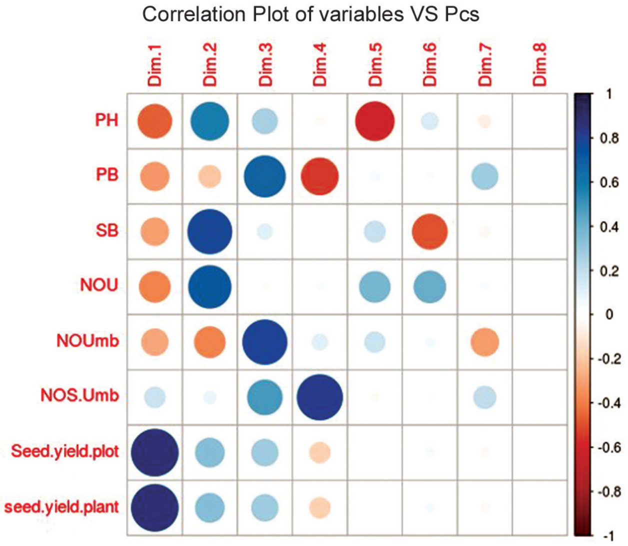

Fig. 1 The contribution of measured traits on extracted principal components based on square cosine and squared coordinates.

Genetic divergence: The 275 genotypes were divided into 10 clusters using cluster analysis, and each cluster contained accessions with lower values than the accessions from the other clusters (Table 3). With 48 genotypes (viz. CS5, CS21, CS27, CS50, CS90, CS95, CS97, CO1, CS112, CS117, CS 120, CS125, CS126, CS128, CS129, CS130, CS131, CS132, CS133, CS134, CS135, CS140, CS144, CS152, CS154, CS161, CS163, CS164, CS175, CS187, CS192, CS193, CS195, CS201, CS202, CS204, CS205, CS213, CS217, CS219, CS222, CS223, CS231, CS232, CS233, CS234, CS236, CS238), the largest cluster, cluster 4 (58.33%), displayed the least genetic variation or the most homogeneity among them. Following it were cluster 1, 3, 2, 7 and 5, with genotypes of 41 (CS1, CS2, CS9, CS10, CS12, CS16, CS17, CS18, CS23, CS24, CS25, CS26, CS28, CS29, CS32, CS33, CS34, CS35, CS36, CS38, CS39, CS40, CS41, CS44, CS45, CS46, CS48, CS52, CS53, CS54, CS55, CS57, CS59, CS64, CS65, CS68, CS74, CS118, CS249, CS251, CS253), 40 (CS4, CS6, CS7, CS8,

Table 3 Distribution of 275 coriander genotypes (including check) in different clusters

Cluster No.	No. of genotypes	Name of genotypes
1	41	CS1 CS2 CS9 CS10 CS12 CS16 CS17 CS18 CS23 CS24 CS25 CS26 CS28 CS29 CS32 CS33 CS34 CS35 CS36 CS38 CS39 CS40 CS41 CS44 CS45 CS46 CS48 CS52 CS53 CS54 CS55 CS57 CS59 CS64 CS65 CS68 CS74 CS118 CS249CS251 CS 253
2	38	CS3 CS30 CS37 CO2 CS51 CS56 CS58 CS60 CS63 CS66 CS67 CS70 CO3 CS83 CS84 CS86 CS87 CS88 CS94 CS114, CS148 CS165 CS167 CS170 CS172 CS178 CS180 CS184 CS198 CS224 CS225 CS226 CS245 CS247 CS248 CS250 CS258 CS269
3	40	CS4 CS6 CS7 CS8 CS11 CS13 CO(CR)4 CS15 CS19 CS20 CS47 CS73 CS77 CS78 CS81 CS89 CS91 CS98 CS104 CS107 CS109 CS110 CS113 CS115 CS119 CS141 CS147 CS149 CS151 CS169 CS176 CS179 CS185 CS188 CS194 CS203 CS206 CS208 CS216 CS218
4	48	CS 5 CS 21 CS 27 CS 50 CS 90 CS 95 CS 97 CO 1 CS 112 CS 117 CS120 CS125 CS126 CS128 CS129 CS130 CS131 CS132 CS133 CS134 CS135 CS140 CS144 CS152 CS154 CS161 CS163 CS164 CS175 CS187 CS192 CS193 CS195 CS201 CS202 CS204 CS205 CS213 CS217 CS219 CS222 CS223 CS231 CS232 CS233 CS234 CS236 CS238
5	33	CS22 CS42 CS43 CS61 CS71 CS79 CS80 CS92 CS93 CS96 CS99 CS101 CS106 CS121 CS136 CS139 CS146 CS150 CS155 CS156 CS157 CS158 CS160 CS173 CS177 CS181 CS189 CS196 CS211 CS235 CS241 CS254 CS267
6	1	CS 31
7	37	CS62 CS72 CS100 CS123 CS124 CS137 CS138 CS142 CS153 CS166 CS168 CS174 CS182 CS197 CS199 CS209 CS212 CS215 CS220 CS221 CS227 CS228 CS230 CS239 CS246 CS252 CS255 CS256 CS257 CS259 CS260 CS263 CS264 CS265 CS266 CS270 CS271
8	13	CS 69 CS75 CS76 CS85 CS102 CS103 CS108 CS116 CS122 CS127 CS159 CS171 CS207
9	11	CS105 CS143 CS145 CS183 CS186 CS190 CS191 CS200 CS210 CS229 CS272
10	13	CS162 CS214 CS237 CS240 CS242 CS243 CS244 CS261 CS262 CS268 CS273 CS274 CS275

CS11, CS13, CO(CR) 4, CS15, CS19, CS20, CS47, CS73, CS77, CS78, CS81, CS89, CS91, CS98, CS104, CS107, CS109, CS110, CS113, CS115, CS119, CS141, CS147, CS149, CS151, CS169, CS176, CS179, CS185, CS188, CS194, CS203, CS206, CS208, CS216, CS218), 38 (CS3, CS30, CS37, CO2, CS51, CS56, CS58, CS60, CS63, CS66, CS67, CS70, CO3, CS83, CS84, CS86, CS87, CS88, CS94, CS114, CS148, CS165, CS167, CS170, CS172, CS178, CS180, CS184, CS198, CS224, CS225, CS226, CS245, CS247, CS248, CS250, CS258, CS269), 37 (CS62, CS72, CS100, CS123, CS124, CS137, CS138, CS142, CS153, CS166, CS168, CS174, CS182, CS197, CS199, CS209, CS212, CS215, CS220, CS221, CS227, CS228, CS230, CS239, CS246, CS252, CS255, CS256, CS257, CS259, CS260, CS263, CS264, CS265, CS266, CS270, CS271), and 33 (CS22, CS42, CS43, CS61, CS71, CS79, CS80, CS92, CS93, CS96, CS99, CS101, CS106, CS121, CS136, CS139, CS146, CS150, CS155, CS156, CS157, CS158, CS160, CS173, CS177, CS181, CS189, CS196, CS211, CS235, CS241, CS254, CS267), respectively (Fig. 2). Cluster 9 comprised 11 genotypes, while cluster 8 and 10 both contained 13 genotypes each. The check variants for CO1, CO2, CO3, and CO (CR) 4 were separated into many clusters. In contrast, CO2 and CO3 were assigned to cluster 2, which contained 38 genotypes. The CO1 and CO (CR) 4 types were allocated to clusters 3 and 4, respectively. The observation was remarkable as only CS 31, with a seed yield of 6.33 g/plant, was present in cluster 6.

From the clustering pattern, it is evident that the genotypes studied are independent, unique and much reliable for further hybridization and selection. The selection of parental materials based on genetic divergence rather than geographical diversity would result in developing varieties of much desirable traits (Gothandan 2021). Cluster 4 exhibited higher mean values for most of the yield contributing characters indicating the importance of cluster genotypes in coriander seed yield improvement programs. Similar finding were reported Singh *et al.* (2006), Mengesha *et al.* (2011), and Kalidasu *et al.* (2015)

Principal component analysis: An experimental data set comprising 275 genotypes and eight growth and yield factors was subjected to Principal Component analysis (PCA). PCA reduces the dimensionality of the multivariate data, allowing for graphical visualization with minimal information loss. The results of the current investigation revealed the identification of four principal components (Supplementary Table 4), each with a cumulative variance of 84.39%, indicating a thorough comprehension of the structure underlying the variable being studied. Comparable outcomes were reported by Hemavathy *et al.* (2017) and Gopi Krishna *et al.* (2022). The largest percentage of the population's overall variance (27.63%) is explained by the first element, PC1, which is followed by PC2 (23.80%), PC3 (19.72%) and PC4 (13.23%). Therefore, PCA can be used to assess how much a specific attribute independently contributes to the overall variation of each component. The spatial distribution of all the coriander entries collected over several quarters is depicted in Fig. 3(a,b).

PC1, which accounted for 27.63% of the total variability, was influenced by plant height (0.309), number of primary

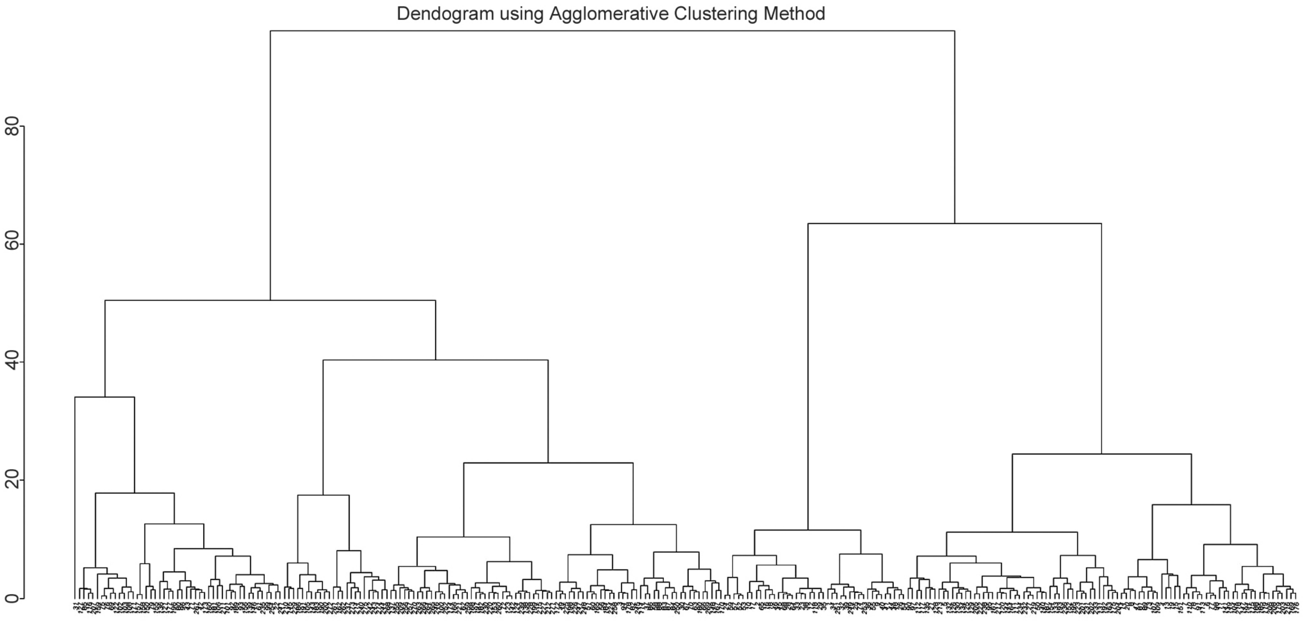

Fig. 2 Dendrogram based on quantitative characters for 275 genotypes of coriander (including check).

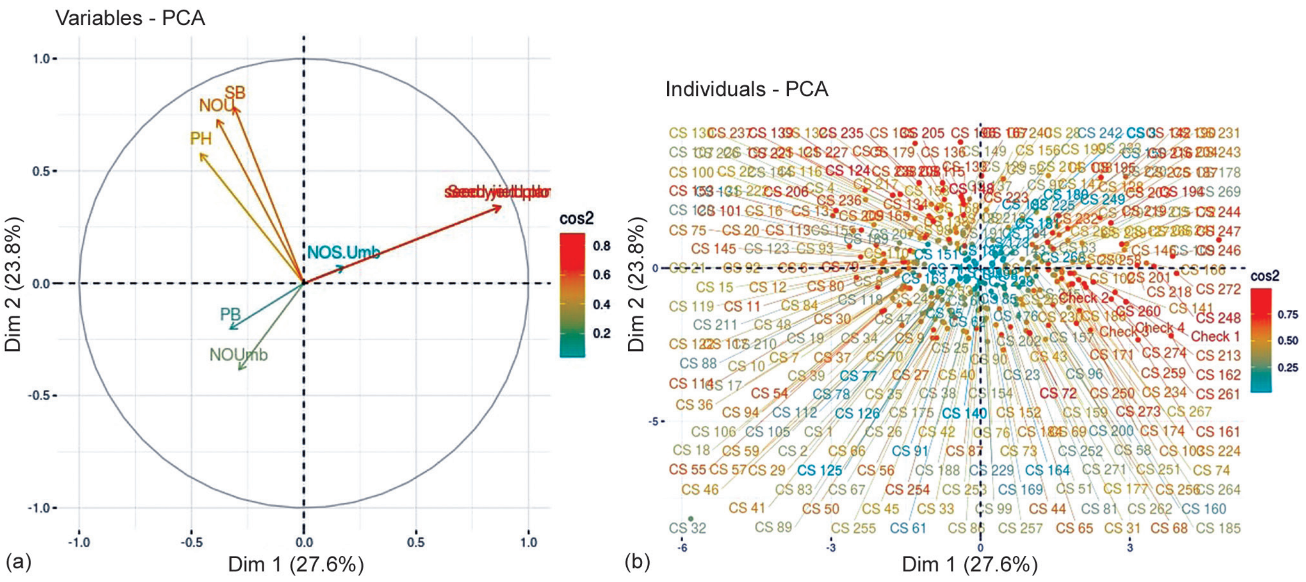

Fig. 3 Principal components of morphological traits (a); Genotype illustrating the relationship between PC1 and PC2 for 275 genotypes (including check) and eight traits of coriander (b).

branches/plant (0.221), number of secondary branches/plant (0.208), number of umbels/plant (0.259), and the seed yield/plant (-0.589) (Supplementary Table 4). Similarly, plant height (0.418), number of secondary branches/plant (0.568), number of umbels/plant (0.527), number of umbellets/plant (-0.279), and seed yield/plant (0.247) contributed to the overall variation of 23.80% from PC2. PC3 accounted for 19.72% of the variability and was correlated with plant height (-0.209), number of primary branches (-0.554), number of umbellets/plant (-0.630), number of seeds/umbel (0.388), and seed yield/plant (-0.231). Conversely, PC4 received 13.23% of the total variability from the number of seeds per umbel (-0.802) and the number of major branches (0.534). The cumulative variance of 76.9% of the total variation among 12 characters (Manyasa *et al.* 2009), the cumulative variance of 88.80% of the total variation among nine characters (Gopi Krishna *et al.* 2022), and the cumulative variance of 71.21% of the total variation among 12 characters (Vamsi Krishna *et al.* 2022) were findings that were extremely relevant to the current findings. PC1 contained the most variances for the yield characteristics, while PC2, PC3, and PC4 included the highest variances for the attributes that contributed to the yield. The differences that each character offered to the main components are listed in Supplementary Table 4.

There was a direct, positive, and statistically significant association between the quantity of seeds/umbellet and the seed yield/plant. As a result, selecting these traits helped the crop yield more seeds/plant. The accessions were categorized into 10 clusters, where cluster 4 having the highest no. of accessions (48), and cluster 8 having just one accession that was more divergent than the others. In the current investigation, PCA identified four main components with eigenvalues greater than one, representing an expressed cumulative variance of 84.39%. The factors that most contributed to the overall variability in yield traits were plant height (0.309), no. of primary branches/plant (0.221), no. of secondary branches/plant (0.208), no. of umbels/plant (0.259) and seed yield/plant (-0.589), as indicated by the maximum variances for PC1.

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