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## **ASSESSMENT OF GENETIC DIVERSITY IN SPINACH (*Spinacia oleracea* L.) USING SOME MORPHOLOGICAL TRAITS**

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**DOI: <https://doi.org/10.51193/IJAER.2022.8601>**

Received: 19 Oct. 2022 / Accepted: 01 Nov. 2022 / Published: 25 Nov. 2022

### **ABSTRACT**

Spinach is a leafy green vegetable cultivated in most part of the world due to its nutritive and medicinal value. Fifty-one germplasm of spinach (*Spinacia oleracea* L.) collected from diverse geographical region of Bangladesh were evaluated to assess their diversity using several qualitative and quantitative characters. Variation was found in all the characters except Inflorescence color and seed type. Leaf shape was exhibited as elliptic, broad elliptic, ovate and broad ovate where elliptic shape was found in maximum germplasm. The highest quantitative variation was observed in edible leaf weight per plant followed by petiole length and number of lateral branches. Germplasm TRMR-95, NT-34, TRMR-136, NRI-121 had longer leaf and NRI-121, TRMR-136, RC-139, TRMR-12 and NT-33 had broader leaf. Germplasm RC-139 had highest number of lateral branches. The germplasm NQ-68 required maximum days for bolting which was followed by TRMR-136 and RNF-126 that was most important characters for spinach. The dendrogram shown that the maximum thirty-six germplasm were grouped into cluster I and Cluster IV was occupied by only one germplasm. The maximum cluster mean value was observed in Cluster II for the characters leaf length, leaf width and edible leaf weight per plant. The first PC explained 37.10% of the total variability and the second PC explained 22.90% of the variation among fifty-one spinach germplasm. Populations with high scores for the first eigenvectors are leaf length (0.4860), leaf width (0.4827) and petiole length (0.4792) these traits were the most important contributors towards diversity of the germplasm in PC1. Considering

leaf characters and bolting time, germplasm TRMR-136, TRMR-144, R-342, RNF-26, NQ-68 and RC-139 were selected for future breeding program.

**Keywords:** Germplasm, Morphological variation, Diversity, Cluster analysis, Principal component analysis

## 1. INTRODUCTION

Spinach (*Spinacia oleracea* L.) is an edible vegetable belonging to the family *Amaranthaceae*. It was originated from Iran and first declared as an herb of Persia by the Chinese [1]. Currently, China, United States Turkey, Japan and Indonesia are considered the largest producers of spinach and in Bangladesh spinach production quantity was 59400 tons in 2020 FAOSTAT [2]. Leafy vegetables are an important part in the human diet and spinach is one of the dark green leafy vegetables among them. It has versatile used such as salad, a cooked vegetable or as a component of many other cooked meat and vegetable dishes [3]. Spinach is dioecious species with both male and female plants and its leaves are alternate, simple, from ovate to triangular-based, with larger leaves at the base of the plant and small leaves higher on the flowering stem [4]. A large number of nutrients have been reported in spinach including vitamins, minerals, antioxidants, carotenoids, steroids, apocyanin, flavonoids and p-coumaric acid [5]. Spinach contains highly active antioxidants that work against cancer and diabetes, nitrates for maintaining blood pressure and vitamin K<sub>1</sub> for blood clotting [6]. On the basis of its medicinal properties, a herbal product, namely Appethyl (Green Leaf Medical, Stockholm, Sweden), has also been designed specifically to suppress appetite and reduce weight [7].

In order to develop new genetically improved cultivars, a preliminary characterization and estimation of the genetic diversity among local spinach germplasm for agronomic performance could be useful for exploitation of this genetic material for breeding programs. Characterization of germplasm acts as a starting point for the establishment of “a core collection” where the whole variability in the collection is represented in a small subset of accessions [8]. PGRC collected spinach germplasm across the country. The value of germplasm collection depends not only on the number of accessions but also on the genetic diversity present in those accessions. Diversity in the gene pool of a species may affect the adaptability to a new environment as well as to develop new varieties more tolerant to stress and pathogens [9]. Hence, characterization of the collected germplasm is essential for easy and rapid evaluation of germplasm. Morphological traits are considered as the simplest marker for assessing the genetic diversity of species. Study of morphological diversity is mandatory before biochemical and molecular characterization [10]. Multivariate procedures are useful for characterization, evaluation and classification of germplasm collections when a large number of accessions are to be assessed for several traits [1] Sabaghnia, *et al.*, 2014). Information generated by multivariate analysis can be useful for

different germplasm identification which has explained traits for crossing, for planning efficient crop improvement program. Therefore, this study has sought to afford the opportunity to assess the genetic diversity of spinach germplasm by using agro-morphological traits and to detect groups of genetically distinct morphological types among the collected germplasm.

## **2. MATERIALS AND METHODS**

The study was done in the field area of Plant Genetic Resources Centre, BARI, Gazipur during rabi season 2021-22 at 23.988929 N latitude, 90.412393 E longitudes and 8.40 m above sea level. The soil in the test field was silty clay with a pH of 6. Fifty-one germplasm of spinach were used in this study. Seeds of fifty-one germplasm were obtained from seed gene bank of PGRC were arranged in a randomized complete block design. Line sowing was done in 3m long of 2 rows plot. Row to row distance was 50 cm and plot to plot distance was 100 cm. Direct seeding was completed with inside the well-organized plot on 22th November, 2021. Well-decomposed farmyard manure (FYM) at 10 t/ha and urea 180 kg/ha, TSP 125 kg/ha, MP 125kg/ha, gypsum 110 kg/ha, zinc 3 kg/ha and boron 1.5 kg/ha were applied [11]. Whole amount of farmyard manure (FYM), TSP and half amount of urea and MP were applied during land preparation. Urea and MP were applied in three equal installments at 10, 30 and 45 days after sowing. Plants were isolated with nylon net to control cross pollination and the seeds were collected from these plants. Normal cultivation techniques and standard intercultural operations were followed to have a good crop. Twenty-one observations on qualitative (13) and quantitative (8) characters were recorded in different stage of life cycle as per European Cooperative Program for Plant Genetic Resources (ECPGR) descriptors [12]. Qualitative data were represented in the form of frequency distribution. By simple descriptive statistics including mean, variance, standard deviation and coefficient of variation quantitative data were analyzed. Cluster analyses and Principle component analysis were performed by computerized software STAR 2.0.1 [13].

## **3. RESULTS AND DISCUSSION**

The agro-morphological study is the simplest and easiest way for the taxonomic description of plants [14]. The description of agro-morphological traits is an important prerequisite for efficient utilization of plant materials in every plant breeding program [15]. The characterization of landraces is essential for exploiting the variability of important traits such as yield potential and resistance to biotic and abiotic stresses [8]. In this study, fifty-one germplasm of spinach were characterized morphologically based on thirteen (13) qualitative and (8) quantitative traits. Twenty-one (21) morphological traits including six (6) quantitative and fifteen (15) qualitative of 200 spinach accessions were recorded by [9]. Fifty-four spinach landraces collected from diverse geographical regions of Iran were evaluated for ten (10) qualitative and nine (9) quantitative characters [1]. Divergence of forty-four spinach were estimated using twenty-one (21)

morphological characters by [16]. Variation were observed in respect of different morphological traits which shown the possibility to get desirable plant characters in selective accessions, in order to fulfill the demand of a plant breeder [8].

### **3.1 QUALITATIVE CHARACTERS**

Qualitative characters are considered as important markers in describing the physical appearance of a plant [17]. In this study a total of thirteen (13) qualitative characters including early plant vigor, stem anthocyanin content, leaf shape excluding basal lobes, leaf color, leaf blistering, leaf texture, leaf edge, petiole attitude, plant growth habit, inflorescence color, inflorescence shape, seed type and seed colour were evaluated to know the variability of the germplasm. [1] also recorded various qualitative traits consist on leaf texture, seed type, stem anthocyanin, petiole attitude and vegetative leaf shape. Qualitative characteristics of different germplasm of spinach are presented in Table 1. Considerable variation was found in studied characters except inflorescence color and seed type. Considerable variation was also observed among leaf features of accessions like anthocyanin, blistering and lobing by [9]. Poor, good and very good type early plant vigor were recorded as per descriptor states of which 25.49% of the germplasm had poor vigor, 43.14% germplasm had medium vigor and very good vigor in 31.37% germplasm. Among the fifty-one germplasm, only 1.96% germplasm had strong and medium anthocyanin content in stem rest 96.08% germplasm had no coloration in stem. Stem anthocyanin content was also recorded by [1] in two types i.e very low and strong. Leaf shape exhibited as elliptic, broad elliptic, ovate and broad ovate where elliptic shape was found in maximum germplasm (64.71%) where as 11.76% had broad elliptic leaf shape and 13.73% had ovate leaf shape. Leaf color was found in two categories such as yellow green (27.45%) and green (72.55%). Two types of leaf blistering i.e. weak, medium and strong were observed. 45.10% germplasm had weak leaf blistering, 29.41% had medium and 25.49% had strong leaf blistering. Leaf texture of the germplasm exhibited as smooth (90.20%) and slight crinkled (9.80%). The edge of leaf was observed in two categories. Leaf edge was smooth in 58.82% germplasm and ripple in 41.18% germplasm. Variation was not found in petiole attitude. Three types petiole attitude were found i.e. Erect (35.29%), semi spared (45.10%) and spared (19.61%). [9] also found variation in case of petiole attitude, most of the accessions were erect including the germplasm of India, Afghanistan, South Korea, Mongolia, Taiwan and Belgium. The semi-erect attitude was found mostly in the germplasm of Pakistan, Iran and Ethiopia and the US had all three types of petiole attitude in spinach. Plant growth habit was categorized in erect, semi spared and spared types. Inflorescence color was yellow in all germplasm. In case of inflorescence shape, 47.06% germplasm had globose shape, 45.10% had semi drooping and only 7.84% had completely drooping type. All the germplasm showed prickly type seed. Two types of seed color i.e. yellow (35.29%) and gray (64.71%) were observed among the accession.

**Table 1: Qualitative variations of different characteristics in spinach germplasm**

Characters	Descriptor states	No. of germplasm	Percent of germplasm
Early plant vigor	Poor	13	25.49
	Good	22	43.14
	Very good	16	31.37
Stem anthocyanin content	Absent	49	96.08
	Medium	1	1.96
	Strong	1	1.96
Leaf shape excluding basal lobes	Elliptic	33	64.71
	Broad elliptic	6	11.76
	Ovate	7	13.73
	Broad ovate	5	9.80
Leaf color	Yellow Green	14	27.45
	Green	37	72.55
Leaf blistering	Weak	23	45.10
	Medium	15	29.41
	Strong	13	25.49
Leaf texture	Smooth	46	90.20
	Slight crinkled	5	9.80
Leaf edge	Smooth	30	58.82
	Ripple	21	41.18
Petiole attitude	Erect	18	35.29
	Semi spared	23	45.10
	Spared	10	19.61
Plant growth habit	Erect	24	47.06
	Spreading	23	45.10
	Drooping	4	7.84
Inflorescence color	Yellow	51	100
Inflorescence shape	Globose	24	47.06
	Semi drooping	23	45.10
	Completely drooping	4	7.84
Seed type	Prickly	51	100
Seed color	Yellow	18	35.29
	Grey	33	64.71



### 3.2 Quantitative characters

Quantitative characters are also important markers, especially those which are showing high variability [18]. The present study was based on 8 quantitative traits including leaf length, leaf width, Petiole length, number of lateral branches, Edible leaf weight per plant, bolting time, days for 50% flowering and 100 seed weight. Some descriptive statistics including range, mean, standard deviation and CV% of the measured quantitative data of spinach is presented in Table 2. [8] also recorded descriptive statistics for 13 characters in the 121 spinach accessions. The highest quantitative variation was observed in edible leaf weight per plant (CV-30.59%) followed by petiole length (CV-22.21%) and number of lateral branches (CV-19.40%). The minimum CV was found for days to 50% flowering (CV-10.34%). Percent of coefficient of variation indicated the variability among the accessions comparing within the characters. The characters showing above 20% of the coefficient of variation could be used as reliable markers for the characterization of accessions [19]. [9] also found all quantitative characters had high values of CV ranging from 30.8% (leaf length) to 66.9% (plant height).

Leaf length ranged from 7.83-16.83 cm. On an average, leaf length was 13.08 cm. [8] also found the maximum leaf length was 15.98 cm; the minimum leaf length was 5.87 cm and the average leaf length was 10.16 cm. Leaf width ranged from 2.62-10.21 cm with an average of 7.75 cm. Based on leaf length and leaf width, it was evident that germplasm TRMR-95, NT-34, TRMR-136, NRI-121 had longer leaf and NRI-121, TRMR-136, RC-139, TRMR-12 and NT-33 had broader leaf. Petiole length was found minimum in germplasm KMR-332 (4.83 cm) and maximum TRMR-144 (13.30 cm). For the characters number of lateral branches, average value obtained 5.69. Germplasm RC-139 had highest number of lateral branches (9) whereas SNQR-28 had the lowest number (4). Edible leaf weight per plant ranged from 9.67-49.5 g with an average 27.55 g. Edible leaf weight per plant was found maximum in TRMR-136 (49.5 g), TRMR-144 (47.78 g) and RC-139 (41.33 g) and the minimum in M-35 (9.67 g), KAS-33 (11.30 g) and RNF-114 (13.0 g). In case of bolting time, it was observed that average time required for bolting was 61.27.

The germplasm NQ-68 required 85 days bolting followed by TRMR-136 (83 days) and RNF-126 which was most important characters for spinach. SNQR-28 had lowest bolting time. [9] also confirmed that the bolting period of accessions also varied greatly, as some of the accessions bolted very early, some very late. [20] also found considerable variation among bolting periods, representing it as one of the selection criteria for the assessment of spinach germplasms.

**Table 2: Quantitative variation of different characteristics in spinachgermplasm**

Characters	Range	Mean	SD	CV%
Leaf length (cm)	7.83-16.83	13.08	2.09	16.00
Leaf width (cm)	2.62-10.21	7.75	1.45	18.74
Petiole length (cm)	4.83-13.30	8.26	1.83	22.21
Number of lateral branches	4-9	5.69	1.10	19.40
Edible leaf weight per plant (g)	9.67-49.5	27.55	8.43	30.59
Bolting time	49-85	61.38	7.70	12.57
Days to 50% flowering	58-93	72.27	7.47	10.34
100 seed weight (g)	1.16-3.8	2.39	0.56	23.21

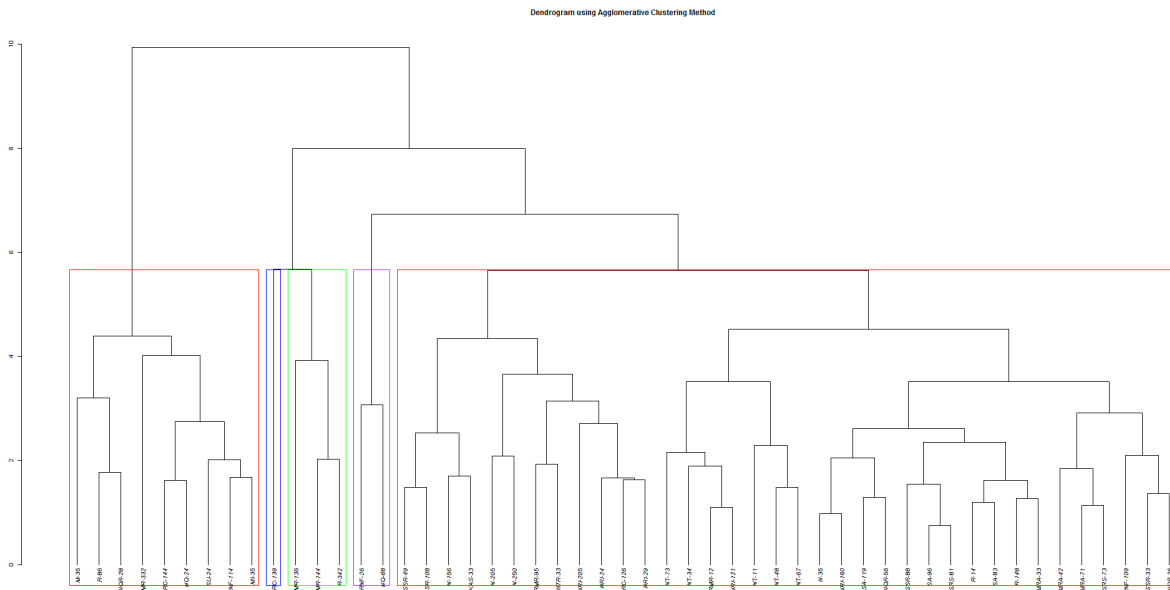
### 3.3 Germplasm distribution and dendrogram

Cluster analysis is a tool for classifying the materials into groups. On the basis of multiple variable grouping of a large number of accessions, is a reliable technique to determine the similarities and extent of differences among them [21]. The cluster analysis indicates the extent of variability that could be useful for future breeding programs [22]. Several authors have used this tool for morphological characterization of different species representing their intra specific relationship [8]; [20];[23]; [24]. On the basis of eight quantitative characters, fifty-one spinach germplasm were grouped into five clusters. The dendrogram (Fig.1) shown that the maximum thirty-six germplasm were grouped into cluster I indicating overall genetic similarity among them, followed by nine germplasm in cluster III. Cluster II and V composed of only 3 and 2 of each, respectively. Cluster IV was occupied by only one germplasm. Divergence of forty-four spinach landraces were estimated by [16]. Based upon cluster analysis, landraces were classified into four groups each with 14, 4, 19 and 7 landraces.[8] also reported 6 clusters for 121 spinach landraces.



**Table 3: Distribution of fifty-onegermplasmin five different clusters**

Cluster	Number of germplasm	Germplasm included in different clusters
I	36	NT-11, NT-34, NT-48, NT-67, NT-73, N-35, N-156, N-205, N-250, TRMR-12 TRMR-95, R-14, R-148, RC-126, SSR-33, SSR-49, SSR-88, RNF-109, SA-83, SA-96, SA-119, NRI-24, NRI-29, NRI-121, NRI-160, NRI-205, MRA-33, MRA-42, MRA-71, SNQR-56, SRS-73, SRS-81, NQR-26, NSR-108, NTR-33, KAS-33
II	3	TRMR-136, TRMR-144, R-342
III	9	R-86, RC-144, RNF-114, SNQR-28, NQ-24 , KMR-332, MI-35, SU-24, M-35
IV	1	RC-139
V	2	RNF-26, NQ-68



**Fig. 1: Cluster tree of fifty-one germplasm of spinach based on quantitative characters**

### 3.4 Cluster mean

The genetic differences between clusters were reflected by cluster means. Eight character's mean value studied in spinach germplasm for five clusters are presented in Table 4. Variations were observed in cluster mean for all characters. The maximum cluster mean value were observed in

Cluster II for the characters leaf length (cm), leaf width (cm) and edible leaf weight per plant (g).[1] also recorded the cluster C14 had the largest leaf width and the cluster C1 had the smallest leaf width. Both leaf length and leaf width are important characters for yield performance in spinach [25]. So, the germplasm belong to this cluster may be selected for leafy character. In cluster II petiole length was maximum. The long petiole length is essential for machinery harvesting and genetic improving for having long petiole length which is one of the breeding targets of spinach [16]. Number of lateral branches was highest in cluster IV. Bolting time and days to fifty percent flowering time observed maximum in cluster V, so the germplasm in this cluster is desirable for spinach due to longer bolting time and late flowering. These useful information on the clusters to which particular accessions with traits of interest belong will aid in researching more accessions with similar characteristics in breeding programs [26] and grouping of the germplasm to different clusters gives an opportunity to select germplasm to develop high yielding and good quality varieties.

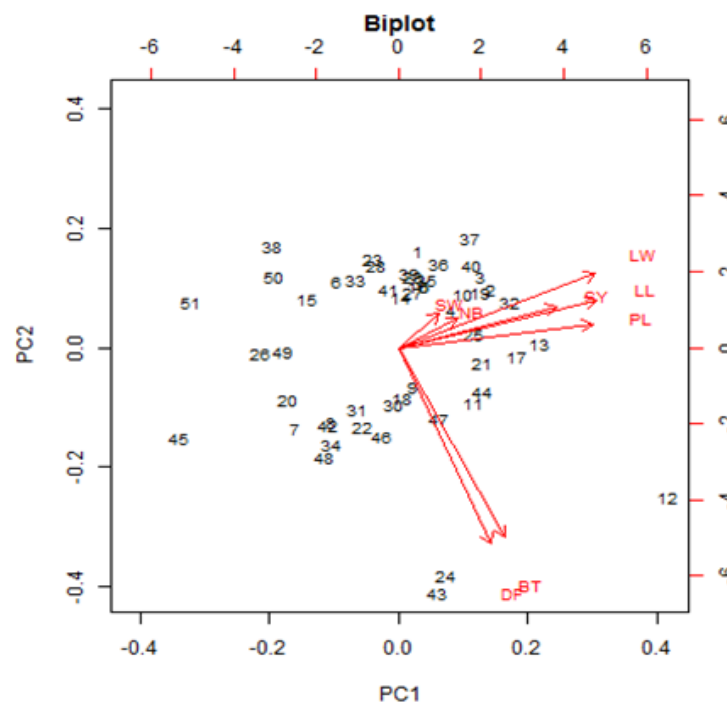
**Table 4: Cluster means for eight characters of fifty-one spinach germplasm**

Characters	I	II	III	IV	V
Leaf length (cm)	13.77	14.61	10.02	13.56	11.93
Leaf width (cm)	8.16	9.06	5.73	9.43	6.67
Petiole length (cm)	8.33	12.63	6.42	7.55	8.84
Number of lateral branches	5.53	6.33	5.67	9.00	6.00
Edible leaf weight per plant (g)	27.42	45.85	21.65	41.33	22.10
Bolting time	60.67	71.33	55.44	61.00	83.50
Days to 50% flowering	71.67	80.67	67.44	72.00	92.50
100 seed weight (g)	2.51	1.75	1.99	2.40	3.05

### 3.5 Principal component analysis (PCA)

Principle component analysis (PCA) is a reliable multivariate technique that converts a large data set in the form of a few factors which include several inter-correlated variables [27]. The analysis was carried out to determine the main differentiating characters that cause variation among fifty-one spinach germplasm by calculating the first two principal components which accounted for 60.00 % of the total divergence (Fig. 2). The overall data were reduced to five factors or principal components (PC) representing about 92.37% of the total variability. The first PC

explained 37.10% of the total variability and the second PC explained 22.90% of the variation among fifty-one spinach germplasm. Thus, the present study was revealed that the first PC was more important than the second PC for explaining the variability among the germplasm based on studied traits. Usually, the first component contributes toward maximum variance while the rest of the factors justify the remaining amount of variance [28]. The spinach germplasm RNF-26, NQ-68, TRMR-136, TRMR-144, R-342 and RC-139 were separately isolated from the others and they were away from centroid. This result showed the uniqueness and divergence of the germplasm. Each factor reflected the PC values of different traits, showing their importance towards the overall variability [9]. The eigen values and vectors of eight characters for a PCA of important traits for the first fifth principal components in fifty-one spinach germplasm was shown in Table 5. Populations with high scores for the first eigenvectors are leaf length (0.4860), leaf width (0.4827) and petiole length (0.4792) and overall variation 37.10% these traits were the most important contributors towards diversity of the germplasm in PC1. Similar to this, [1] also reported leaf trait as the most important factor contributing towards variability of spinach germplasm. The second eigen vector was mostly connected with scores of edible leaf weight per plant (0.3889) and number of lateral branches (0.1000), these traits were the second most important contributors among the eight characters for fifty-one germplasm. The plant breeders might select the combination of morphological characters through PCA and then by plotting the main components in a single plot, germplasms closed to the ideal could be indicated [29].



**Fig. 2: The plot of the first two PCA 1 and PCA 2 for spinachgermplasm**

**Table 5: Principal Components for eight traits of spinach germplasm**

Characters	PC1	PC2	PC3	PC4	PC5
Leaf length (cm)	0.4860	0.1608	0.2498	0.1398	0.1077
Leaf width (cm)	0.4827	0.2534	0.1207	0.0493	0.1730
Petiole length (cm)	0.4792	0.0783	0.1145	0.1616	0.2582
Number of lateral branches	0.1447	0.1000	-0.7036	-0.4856	0.4690
Edible leaf weight per plant (g)	0.3889	0.1395	-0.4592	0.0518	-0.7780
Bolting time	0.2605	-0.6454	0.0303	-0.0756	0.0581
Days to 50% flowering	0.2259	-0.6662	-0.0317	-0.0663	-0.0696
100 seed weight (g)	0.1006	0.1183	0.4496	-0.8387	-0.2415
Eigenvalue	2.97	1.83	1.21	0.95	0.42
Variability (%)	37.10	22.90	15.08	11.93	5.30
Cumulative (%)	37.10	60.00	75.08	87.01	92.37

#### 4. CONCLUSION

Characterization of fifty-one germplasm of spinach based on the qualitative and quantitative characters was suitable to assess the genetic diversity among collected spinach germplasm. Most of the qualitative traits showed distinct variations among the germplasm. Qualitatively, the maximum variation was observed in leaf shape, petiole attitude and leaf shape. According to PCA, leaf characters were found to be the important characters in contributing towards divergence. The present findings have a great genetic potential for the studied germplasm. In spinach breeding program these genetically diverse germplasm will be useful for screening the desirable traits. Concurrently, the promising germplasm identified in this present study might be used in future utilization to create new varieties with desirable traits for spinach improvement.

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