

# Assessing Genetic Diversity by Morphological Markers of Bean (*Phaseolus vulgaris* L.) Germplasm from Northeast Anatolia

Kuzeydoğu Anadolu Fasulye (*Phaseolus vulgaris* L.) Germplazmında Morfolojik Belirteçler ile Genetik Çeşitliliğin Değerlendirilmesi

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## ABSTRACT

The Northeast Anatolia Region of Turkey is a rich plant biodiversity spot including the common bean (*Phaseolus vulgaris* L.). This study was undertaken in order to collect, classify, and characterize bean landraces from the region. For this purpose, 256 common bean landraces were collected from 25 districts in 7 provinces and were grown in completely randomized block design with 3 replicates under the field conditions in Erzurum in Northeast Region, Turkey. Twenty-five qualitative and quantitative morphological markers were measured by International Plant Genetic Resources Institute and European Union Community Plant Variety Office criteria on the germplasm. Genetic variability was examined by path analysis, principal component analysis, Simpson's and Shannon and Weaver diversity indices, and UPGMA cluster dendrogram. A high level of polymorphism and genetic diversity was present within the germplasm for all the descriptors with the exception of bract color. Highest variation was recorded for seed yield, plant height, pod number per plant, and pod length. It was concluded based on findings that landraces in the collection may be used for breeding superior bean cultivars. Selection specifically for higher pod number per plant, longer pods, greater seed number per pod, and greater branch number per plant may be employed for breeding high-yielding robust cultivars.

**Keywords:** Characterization, common bean, genetic diversity, germplasm, morphology

## ÖZ

Kuzeydoğu Anadolu Bölgesi, fasulye (*Phaseolus vulgaris* L.) açısından zengin bir biyolojik çeşitliliğe sahiptir. Bu çalışma, bölgedeki yerel fasulye genotiplerini toplamak, sınıflandırmak ve karakterize etmek amacıyla yürütülmüştür. Bölgede yer alan 7 ildeki 25 ilçeden toplanan 256 yerel kuru fasulye genotipi Erzurum tarla koşullarında tesadüf blokları deneme deseninde 3 tekrarlamalı olarak denemeye alınmıştır. Yerel genotiplerin değerlendirilmesinde IPGRI ve EU-CPVO kriterlerine göre toplam 25 kalitatif ve kantitatif karakter dikkate alınmıştır. Genetik çeşitlilik path analizi (PA), temel bileşen analizi (PCA), Simpson's ve Shannon ve Weaver çeşitlilik indeksleri ve UPGMA küme dendrogramı (CA) ile incelenmiştir. Brakte rengi hariç, incelenen tüm karakterler açısından germplazmı içerisinde yüksek düzeyde polimorfizm ve genetik çeşitliliğin bulunduğu belirlenmiştir. En yüksek varyasyon tane verimi, bitki boyu, bitki başına bakla sayısı ve bakla uzunluğunda saptanmıştır. Koleksiyondaki yerel genotiplerin üstün fasulye çeşitlerinin geliştirilmesinde kullanılabileceği; özellikle bitki başına yüksek bakla sayısı, yüksek bakla uzunluğu, bakla başına yüksek tohum sayısı ve bitki başına yüksek dal sayısı yönünden yapılacak seleksiyonun, yüksek verimli ümitvar çeşitlerin geliştirilmesinde yararlı olabileceği sonucuna varılmıştır.

**Anahtar Kelimeler:** Karakterizasyon, fasulye, genetik çeşitlilik, germplazm, morfoloji

## Introduction

Common beans (*Phaseolus vulgaris* L.) are the most important source of major protein and mineral nutrients such as potassium, calcium, iron, and phosphorus for human nutrition in the world (Graham & Ranallin, 1997; Voysest & Dessert, 1991). Global production of dry beans reached 28.9 M tons in 2019 (FAOSTAT, 2019). In Turkey, dry beans rank third after chickpeas and lentils (TUIK, 2020) with production exceeding 279.518 tons.

The Northeast Anatolia Region of Turkey is a rich source of local landraces of common beans. Çoruh valley in Northeast Anatolia stretches along the Çoruh river that originates from high mountains in Erzurum and Bayburt provinces and passes through Artvin province until it reaches the Black Sea. Çoruh valley also stands along the border area between Eastern Anatolia and Black Sea Regions (Akpınar et al., 2011). Diverse climatic conditions, variable topography, and a transitional geographical zone from high altitude mountains to sea shore habitats confer the valley exceptionally rich plant biodiversity. Numerous small valleys stretching along the Çoruh river are also home to a rich bean diversity. Common beans are grown in the valleys stretching along the Çoruh river. The area is famous for its specialty beans traditionally grown for centuries. Specialty dry beans produced in the valley, known as İspir beans with geographical indication labeling, are much in demand in Turkey.

As part of a national plan, a series of 15 hydroelectric dams are currently being built to utilize the large hydroelectric power potential of the region (Akpınar et al., 2011). A project was therefore carried out in order to collect, characterize, and preserve bean germplasm in Çoruh Valley in Northeast Anatolia. This article investigated genetic diversity by morphological markers and identified individual landraces for breeding new bean cultivars.

## Methods

### Experimental Layout

Two hundred fifty-six bean (*Phaseolus vulgaris* L.) landraces were collected from 25 districts in 7 provinces in the Northeast Anatolia region and Çoruh valley, Turkey (Figure 1 and Table 1). The landraces were grown in comparison with two registered cultivars (Kantar-05 and Elkoca-05) as standard in Erzurum (latitude 29°55' N, longitude 41°16' E, altitude 1875 m) in Northeast Region of Turkey. The average temperature and annual rainfall are 5.7°C and 402.5 mm, respectively, and the growing season lasts 5 months (between May and October) in the region. The experimental soil was sandy loam with an organic matter content of 1.4%–1.8%, and pH of 7.0–7.8. Available P and K contents were 52–85 kg ha<sup>-1</sup> and 1815–2338 kg ha<sup>-1</sup>, respectively. N (40 kg ha<sup>-1</sup>) as ammonium sulfate and P (60 kg ha<sup>-1</sup>) as triple superphosphate were applied to the experimental field at sowing. Sowing was done by hand in rows of 4 m length with 45 cm inter-row spacing with 2 rows so as to give 30 seeds per m<sup>2</sup> in a completely randomized block design with 3 replications. Trifluralin (2 L ha<sup>-1</sup>) was applied for weed control 2 days after sowing. After emergence, weeds were also controlled by hoe if necessary. Plants were irrigated four times starting from mid-June until 4 weeks prior to harvest.

### Data Collection

Data on plant growth and morphological traits were made during the growth season by International Plant Genetic Resources Institute and European Union Community Plant Variety Office on ten randomly selected representative individual plants from each landrace. Agronomic and morphological descriptors were recorded for days to emergence (DE), standard color (SC), beak length, days to flowering (DF), wing color (WC), shape of pod curvature (SPC), growth type, opening of wings, pod width (PW), leaf color (LC), flower length (FL), plant height (PH), size of terminal



**Figure 1.** Map of Northeast Anatolia That Includes Çoruh Valley and Seven provinces from Which Common Bean Landraces Were Collected. Each Symbol Denotes Ten Accessions Represented by Different Symbols in Each Province on the Map.

**Table 1.** Provinces, Countries, Accession Numbers, and Altitudes from Where Common Bean Landraces Were Collected in Northeast Anatolia, Turkey

Province	County	Accession Number (ACN)	Altitude (m)
Erzurum	İspir	145, 146, 147, 148, 149, 150, 151, 152, 155, 156, 157, 159, 160, 161, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 193, 195, 196, 197, 199	1125–1650
	Pazaryolu	153, 158, 163	1350
	Olur	318, 319, 320, 321, 322, 323, 324, 325, 326, 329, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 380, 381, 382, 383, 390, 391, 392, 393, 394, 395, 396	1520–1900
	Narman	3, 4, 6, 13, 19, 26, 28, 31, 32, 33, 36, 42, 43, 44, 50, 58, 68, 70, 73, 74, 77, 82, 88, 94, 99, 100, 102, 103, 105, 106, 109, 110, 111, 117, 142, 236	1560–1885
	Oltu	8, 9, 21, 25, 29, 30, 35, 37, 38, 40, 41, 46, 47, 48, 52, 54, 57, 59, 65, 72, 76, 78, 79, 80, 81, 98, 101, 104, 107, 115	1390–1830
	Tortum	296, 301, 302, 303, 307, 308, 384	1315–1749
	Hınıs	20, 75, 238, 239, 242, 243, 244	1720–1905
	Karaçoban	51, 53, 55, 240, 241	1580
	Şenkaya	10, 56, 63, 69, 260	1550–1855
	Uzundere	250, 274, 275, 278, 280, 281, 282, 283	970–1205
Gümüşhane	Şiran	309	1400
	Torul	327, 328, 330, 331, 332, 343, 347, 348	1010–1335
	Merkez	344	1150
	Kürtün	368	1580
Erzincan	Refahiye	11, 64, 84, 89, 95, 97, 112, 113, 116, 123	1470–1720
	Üzümlü	61	1440
	Kemaliye	86	1285
	Kemah	1, 17, 85, 92, 93	1430–1500
	Otlukbeli	91, 114	1790
	Çayırlı	2, 67, 87, 90, 96, 108	1550–1750
Bayburt	Merkez	249, 252, 254, 257, 264, 268, 269, 272, 273, 405	1470–1620
	Aydıntepe	259	1545
Ardahan	Posof	5, 15, 16, 22, 23, 27, 62, 71	1360–1540
İğdir	Tuzluca	271, 402, 403	2125–2195
Kars	Kağızman	247, 248, 251	1215–1340

leaflet (STL), flower raceme length (FRL), branch number per plant (BN), leaf roughness (LR), intensity of pod ground color (IPGC), pod number per plant (PN), bract size (BSz), variegated color in pod (VC), pod length (PL), bract shape (BSH), curvature of beak, seed number per pod (SN), and seed yield (SY). A total of 25 qualitative and quantitative traits were observed for the evaluation of landraces based on cluster analysis. The mean, standard deviation, and range were calculated for quantitative descriptors, and the mode was determined for qualitative traits. Path analysis was performed to investigate the effect of the most important yield components on the SY. All traits were standardized before analysis by subtracting the mean value and dividing by the standard deviation in order to remove scale effects before calculating Euclidian distances. Principal component analysis (PCA) was performed on observed morphological traits after standardization. Based on standardized trait values, Euclidian distances between the lines were calculated. Using the matrix of Euclidian distances, a UPGMA (Unweighted Pair Group Method with Arithmetic mean) cluster analysis was performed producing a dendrogram depicting relationships among genotypes relative to their morphological characteristics. As for genetic similarity, the cophenetic correlation was calculated to measure the quality

of the clustering with regard to the original data. Genetic variability among the accessions with respect to the morphological descriptors was examined by calculating Simpson (1949) and Shannon and Weaver (1949) diversity indices. These indices give a measure of phenotypic diversity corresponding to the probability that two individuals randomly selected from a group of populations will have the same morphological feature. The formula to calculate both indices is presented below:

$$\text{Shannon-Weaver diversity } (H) = -\sum (p_i \log p_i) / \log p_i$$

$$\text{Simpson diversity index } (D) = 1 - \sum (p_i^2)$$

where  $i = 1$  to  $n$ , and  $p$  is the proportion of the total morphotypes made up of the  $i$ th morphotype.

### Statistical Analysis

The descriptive statistics, the correlation coefficients, analysis of variance, and the factor loadings were analyzed using Minitab version 17 statistical software (Minitab Inc., State College, PA, USA). The path coefficients of yield-related characteristics and correlation coefficients were analyzed using with Statistical Package for the Social Sciences 23 statistical package. Principal component analysis was performed using 12 characteristics in XLSTAT

software (2016.2 version). Components with greater than 1 Eigen value were taken into consideration. Agglomerative hierarchical clustering of landraces was produced with XLSTAT software. UPGMA cluster analysis was performed using the NTSYS-pc version 2.1 software.

## Results

### Morphological and Agronomic Characterization

Analysis of variance indicated that genotypic effects were statistically significant for all quantitative traits (Table 2). Considerable variability was also determined among the accessions for all morphological descriptors with the exception of solidly green bract color (Table 3).

The morphological and agronomic variables that showed high rates of polymorphism included the following:

**Days to emergence:** The average DE were 15.9 days, ranging from 12 to 22 days depending on the genotypes. The majority of the genotypes (78.9%) emerged between 12 and 17 days, and 60.9% of the genotypes (156 genotypes) emerged less than the average (Figure 2).

**Days to flowering:** The average DF were 63 days, ranging from 53 to 68 days in the majority (53.9%) of the genotypes (Figure 2). Only 42 genotypes (16.4%) had shorter days (37–52 days) of flowering than the other genotypes, whereas 29.7% of the genotypes had a longer time to flowering (69–92 days).

**Growth type:** Climbing growth habit was the most predominant (53.9%) followed by semi-climbing (34.0%). Bush growth habit was represented by a small number of genotype (12.1%) (Table 3).

**Leaf color:** Green LC was the most frequent (73.4%) followed by light green (20.3%). Dark green and very dark green were observed in only 10 genotypes (3.9%) and in 6 genotypes (2.4%), respectively (Table 3).

**Leaf roughness:** Only 18 out of 256 genotypes had less rough leaf surface. The other genotypes had moderate (73.8%) or strongly (19.2%) rough leaf surfaces (Table 3).

**Size of terminal leaflet:** Medium STL was the most frequent (69.1%) followed by the large size of the terminal leaflet (18.4%). Small STL was observed in only 32 genotypes (12.2%) (Table 3).

**Bract size:** Generally, small (32.4%) or medium (53.5%) and rarely large (14.1%) BSz was observed in landraces (Table 3).

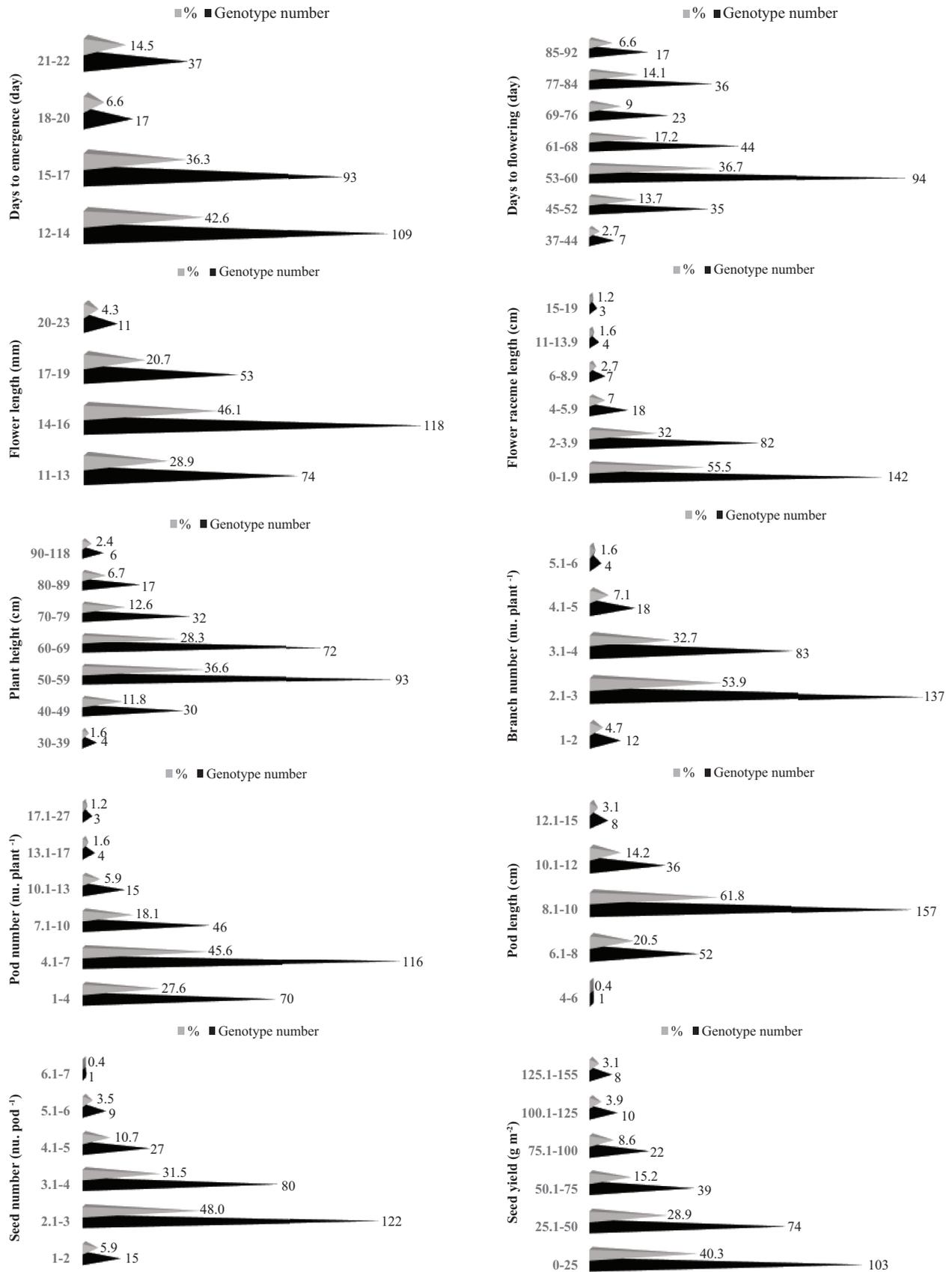
**Bract shape:** Bract shape was oval in only 9 out of 256 genotypes (3.5%) and intermediate in 57 genotypes (22.3%) with the rest of the genotypes (74.2%) having spear BSh (Table 3).

Traits	F Value	Traits	F Value
Days to emergence	1.75*	Branch number per plant	3.40**
Days to flowering	5.66**	Pod number per plant	2.49**
Flower length	7.48**	Pod length	2.46**
Flower raceme length	3.33**	Seed number per pod	2.36**
Plant height	5.37**	Seed yield	5.63**

\* $p < .05$ , \*\* $p < .01$ .

**Table 3.**  
Distribution of Morphological Characters in Bean Landraces Collected from Northeast Anatolia, Turkey, Based on IPGRI and EU-CPVO Criteria

Character	Classification	Number of Genotypes	Percent
Growth type	Bush	31	12.1
	Semi-climbing	87	34.0
	Climbing	138	53.9
Leaf color	Light green	52	20.3
	Green	188	73.4
	Dark green	10	3.9
	Very dark green	6	2.4
Leaf roughness	Weak	18	7.0
	Medium	189	73.8
	Much	49	19.2
Size of terminal leaflet	Small	32	12.5
	Medium	177	69.1
	Large	47	18.4
Bract size	Small	83	32.4
	Medium	137	53.5
	Large	36	14.1
Bract shape	Spear	190	74.2
	Intermediate	57	22.3
	Oval	9	3.5
Bract color	Green	256	100
	Other	0	0
Standard color	White	133	52.0
	Pink	29	11.3
	Violet	88	34.4
	Green	6	2.3
Wing color	White	139	54.3
	Pink	29	11.3
	Violet	88	34.4
Opening of wings	Closed	56	21.9
	Discrete	155	60.5
	Very discrete	45	17.6
Intensity of pod ground color	Light green	35	13.7
	Green	200	78.1
	Dark green	21	8.2
Variegated color in pod	Absent	149	58.2
	Present	107	41.8
Curvature of beak	Very weak	35	13.6
	Weak	156	61.0
	Medium	52	20.3
	Strong	12	4.7
	Very strong	1	0.4
Beak length	Short	108	42.2
	Medium	115	44.9
	Long	33	12.9
Shape of pod curvature	Straight	27	10.5
	Slightly curved	171	66.8
	Intermediately curved	54	21.1
	Strongly curved	4	1.6
Pod width	Narrow	97	37.9
	Medium	127	49.6
	Large	32	12.5



**Figure 2.** Distribution of Agronomic Characters in Bean Landraces Collected from Northeast Anatolia, Turkey.

**Standard color:** White SC was observed in the vast majority (52.0%) of the genotypes with violet (34.4%) being the second most common SC. A small number of genotypes had pink (11.3%) and green (2.3%) SC (Table 3).

**Wing color:** White (54.3%) and violet (34.4%) were the most common WC in the genotypes. Only 29 of 256 genotypes (11.3%) had pink WC (Table 3).

**Opening of wings:** Wings were discrete from each other in the vast majority of the genotypes (60.5%) followed by closed and more discrete wings by 21.9% and 17.6% of the genotypes, respectively (Table 3).

**Flower length:** Flower length in 46.1% of the genotypes varied from 14 to 16 mm, and the average FL was 15.4 mm with 111 genotypes (43.4%) having longer FL than the average. Eleven genotypes (4.3%) had the longest FL between 20 and 23 mm and followed by 53 genotypes (20.7%) with FL of 17–19 mm (Figure 2).

**Flower raceme length:** The average FRL was 2.5 cm and in the majority of genotypes (87.5%), FRL was less than 4 cm. On the other hand, 7 genotypes (accession number (ACN) 20, 75, 112, 179, 247, 329, and 303) had considerably longer FRL (11–19 cm) than the average and the other genotypes (Figure 2).

**Intensity of pod ground color:** Light green, green, and dark green pod ground colors were observed in 13.7%, 78.1%, and 8.2% of the genotypes, respectively (Table 3).

**Variiegated color in pod:** Variiegated color in the pod was observed in only 107 genotypes (41.8%) (Table 3).

**Curvature of beak:** The curvature of the beak was weak in 156 genotypes (61.0%), very weak in 35 genotypes (13.6%), medium in 52 genotypes (20.3%), and strong in 12 genotypes (4.7%). Only one genotype had a pod with a very strong convoluted beak (Table 3).

**Beak length:** Beak length was short (42.2%) or medium-long (44.9%) in the majority of the genotypes. Only 33 genotypes (12.9%) had long beaks (Table 3).

**Shape of pod curvature:** Pod was slightly curved in the majority (66.8%) of the genotypes followed by intermediately curved pods (21.1%). A very few of genotypes had straight (10.5%) or strongly curved pod (1.6%) (Table 3).

**Pod width:** The medium-large pod was predominant (49.6%) followed by the narrow pod (37.9%). The large pod was observed in only 12.5% of genotypes (Table 3).

**Plant height:** The average PH was 61.7 cm, ranging considerably from 29.6 cm (ACN 142) to 260 cm (ACN 260) depending on the genotypes. Approximately one-third of the genotypes (36.6%) were in the group with a PH between 50 and 59 cm. Plant height was between 60 and 69 cm in the second largest group (28.3%). Only 23 genotypes (9.1%) had a PH of 80–118 cm (Figure 2).

**Branch number per plant:** The average BN was 3.1 ranging between 1 (ACN 107) and 6 BN (ACN 22 and 116). The BN was between 2.1 and 3 in more than half (53.9%) of the genotypes and between 3.1 and 4 in about one-third (32.7%) of the genotypes. Only 1.6% of the genotypes (ACN 22, 54, 116, and 145) had 5.1–6 branches per plant (Figure 2).

**Pod number per plant (PN):** The average PN was 5.9 with 105 genotypes having higher pod numbers than average. In 45.6% of the genotypes, PN ranged from 4.1 to 7, and the genotypes that had 1–10 pods per plant made up 91.3% of the population (Figure 2). Accession number 87, 85, 160, 104, 54, 22, and 116 had the highest PN (13.4, 13.6, 14.8, 15.8 19.2, 20.8, and 27.0 number, respectively).

**Pod length:** The average PL was 9.0 cm ranging between 4.5 cm (ACN 150) and 15.0 cm (ACN 264). In 61.8% of the genotypes, PL varied between 8.1 and 10 cm. This was followed by 52 genotypes (20.5%) with PLs ranging from 6.1 to 8 cm (Figure 2). On the other hand, PL varied between 12.1 and 15 cm in only 8 (ACN 54, 62, 69, 248, 250, 264, 271, and 342) out of 256 genotypes.

**Seed number per pod:** The average number was 3.2 with 35.8% of genotypes having higher SN than average and 13 genotypes (ACN 61, 64, 84, 88, 91, 171, 181, 250, 273, 274, 342, 343, and 356) giving the highest SN (5.0–6.2 seeds) (Figure 2).

**Seed yield:** Seed yield in 69.2% of the genotypes varied from 0 to 50 g m<sup>-2</sup> and the average SY was 40.7 g m<sup>-2</sup>. The SY of 101 genotypes (39.5%) was higher than the average and 18 genotypes (ACN 29, 43, 46, 54, 56, 76, 84, 87, 90, 101, 104, 116, 246, 329, 390, 393, 395, and 403) had SY between 100.1 and 150 g m<sup>-2</sup> (Figure 2).

#### Path Analysis

Path analysis calculated on the bases of the quantitative characteristics shows direct and indirect effects on SY (dependent variable) among the quantitative characteristics (Table 4). The highest positive direct effect on SY was of PN (0.369\*\*) followed by FL (0.263\*\*) while DF (−0.435\*\*) and DE (−0.240\*\*) had negative effects on SY (Table 4). Branch number per plant, PL, and SN had the highest positive indirect effects on SY through PN

**Table 4.**

*Path Analysis for the Plant Growth Parameters and Morphological Traits Investigated of Common Bean Landraces from Northeast Anatolia, Turkey. Diagonal (bold) Values Indicate Direct Effects Whereas Values of Upper and Lower Diagonal Indicate Indirect Effects*

Plant Characteristics	DE	DF	FL	FRL	PH	BN	PN	PL	SN
Days to emergence (DE)	−0.240**	−0.395**	−0.124	−0.064	−0.181	−0.036	−0.105	−0.092	−0.178*
Days to flowering (DF)	−0.440**	−0.435**	−0.259**	−0.202*	−0.102	−0.214**	−0.203*	−0.215*	−0.221**
Flower length (FL)	−0.141	−0.265**	−0.263**	−0.478**	−0.101	−0.062	−0.010	−0.126	−0.033
Flower raceme length (FRL)	−0.063	−0.178*	−0.410**	−0.003	−0.059	−0.143	−0.038	−0.008	−0.016
Plant height (PH)	−0.150	−0.076	−0.074	−0.050	−0.113	−0.149	−0.010	−0.062	−0.073
Branch number per plant (BN)	−0.042	−0.226**	−0.064	−0.172	−0.211	−0.121	−0.471**	−0.139	−0.010
Pod number per plant (PN)	−0.106	−0.184*	−0.009	−0.039	−0.012	−0.405**	−0.369**	−0.026	−0.184*
Pod length (PL)	−0.103	−0.216*	−0.123	−0.009	−0.084	−0.133	−0.029	−0.039	−0.501**
Seed number per pod (SN)	−0.201*	−0.224**	−0.032	−0.019	−0.099	−0.010	−0.206*	−0.505**	−0.037

(0.471\*\*), SN (0.501\*\*), and PL (0.505\*\*), respectively. Conversely, DF had negative indirect effect on SY via FRL, PN, and PL.

**Principal Component Analysis**

The first 3 components with Eigenvalue above 1 explained 59.7% of cumulative overall variance (Table 5). Contributions of all characteristics in first component were positive. Branch number per plant (0.739), FL (0.628), and PL (0.604) had the highest Eigenvalues in the first component while SY (-0.779) and DF (-0.728) had the highest value in the second component. Flower raceme length had the highest value (0.687) in the third component (Table 5). Considering the strongest correlations and the contribution of each quantitative characteristic among the components, it is concluded that BN, FL, PL, PN, SN, and PH were positively correlated with first component. Seed yield, DE, and DF were negatively correlated with the second component. Flower raceme length was correlated with the third component (Table 5).

Of the variable loadings of the first nine PCs (Principal Component) (data not presented), SC, WC, and VC are the ones with the highest contribution to PC1. Therefore, PC1 could be termed the "color axis." Regarding PC2, the features related to DE and DF were the ones with the highest loadings (Table 5). Therefore, PC2 could be called the "time axis." Finally, the features related to the shape and size of morphological structures were the ones with the highest contribution to the loading of PC3, which included the SPC, the size of the terminal leaflet, PW, and LR. They are all qualitative features and hence the PC3 can be described as a "qualitative axis." Therefore, we could express that the PCA was able to discriminate and separate the accessions in terms of these three dimensions, represented by "color," "time," and "qualitative" axes.

The PCA diagram showed that PN had the highest positive and parallel effect on SY followed by PL, SN, PH, and BN (Figure 3a).

**Table 5.** Eigenvalues, Variability, and Component Loading of Ten Quantitative Traits in Common Bean Landraces Collected From Northeast Anatolia, Turkey

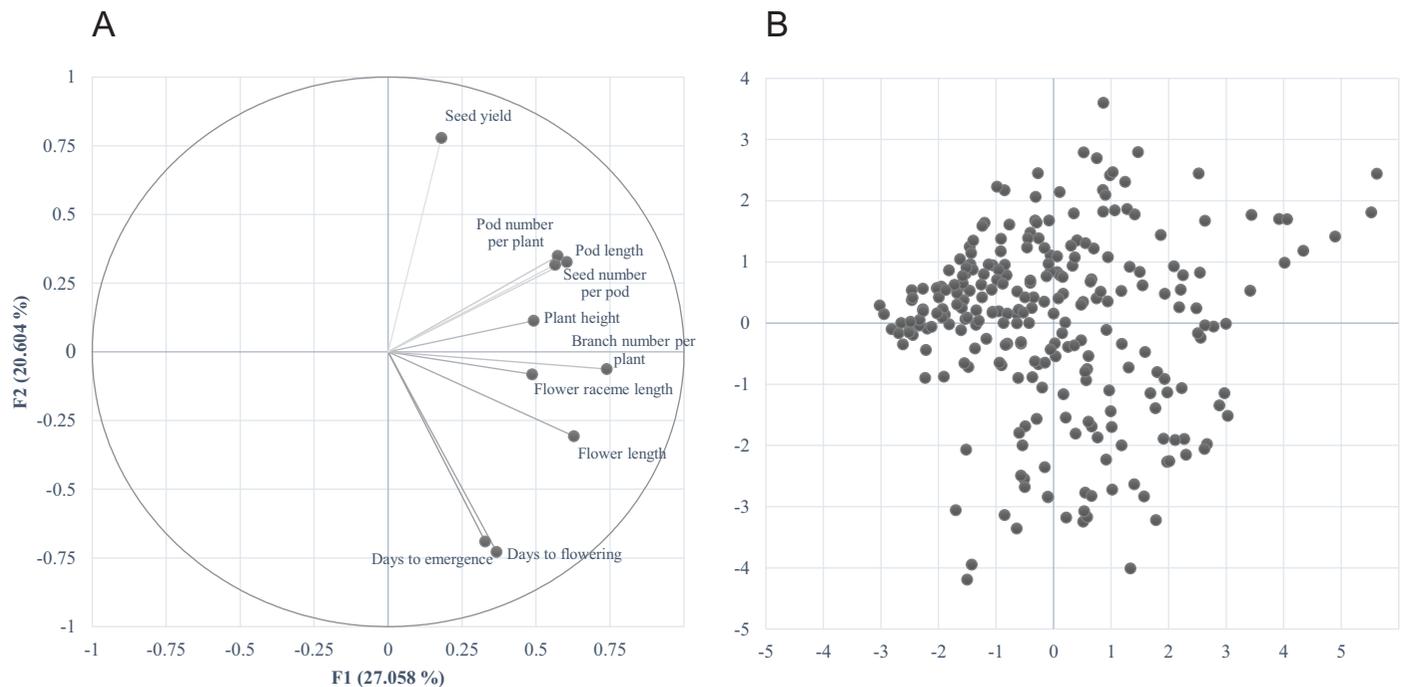
	PCAs Axis		
	PCA1	PCA2	PCA3
Eigenvalues ( $\geq 1$ )	2.706	2.060	1.209
Percentages of individual variation	27.058	20.604	12.091
Percentages of cumulative variation	27.058	47.662	59.753
Characteristics (factor loadings)			
Days to emergence	0.328	-0.691	-0.019
Days to flowering	0.367	-0.728	-0.288
Flower length	0.628	-0.307	0.447
Flower raceme length	0.487	-0.082	0.687
Plant height	0.492	0.113	-0.019
Branch number per plant	0.739	-0.062	-0.052
Pod number per plant	0.573	-0.349	-0.095
Pod length	0.604	-0.327	-0.306
Seed number per pod	0.564	-0.317	-0.489
Seed yield	0.180	-0.779	0.330

Note: PCA= principal component analysis.

Pod number per plant had a positive effect on SY in path analysis (Table 4). Days to emergence had in contrast the most negative effect on SY followed by DF, FL, and FRL (Figure 3a).

**Genetic Variability Based on Simpson and Shannon-Weaver Diversity Indices**

Diversity values were variable among traits, but in general, all morphological features expressed high genetic diversity. According



**Figure 3.** (A) Two-Dimensional Ordination of Ten Quantitative Traits in Common Bean Landraces on Principal Component Axes. (B) Scatter Plot of First Two Principal Components Contributing 47.66% of the Total Variation for Ten Quantitative Traits in 256 Common Bean Landraces Collected from Northeast Anatolia, Turkey.

**Table 6.**  
Simpson and Shannon–Weaver Diversity Indices for Morphological Characters of Common Bean Landraces Investigated

Morphological Variables	Shannon–Weaver Diversity Indices	Simpson Diversity Indices	Morphological Variables	Shannon–Weaver Diversity Indices	Simpson Diversity Indices
PH	4.92	0.99	BL	0.99	0.60
PN	3.96	0.98	BSz	0.98	0.59
PL	3.70	0.97	PW	0.98	0.59
FL	3.63	0.97	GT	0.96	0.58
FRL	3.48	0.96	OW	0.94	0.55
DF	3.43	0.96	SPC	0.83	0.48
SN	2.99	0.94	STL	0.82	0.47
BN	2.79	0.92	LC	0.77	0.42
DE	1.64	0.76	LR	0.72	0.41
SC	1.04	0.60	BSh	0.68	0.40
WC	1.04	0.60	VC	0.68	0.48
CB	1.04	0.56	IPGC	0.67	0.36
Total				1.82	0.67

Note: PH=plant height; PN=pod number per plant; PL=pod length; FL=flower length; FRL=flower raceme length; DF=days to flowering; SN=seed number per pod; BN=branch number per plant; DE=days to emergence; SC=standard color; WC=wing color; CB=curvature of beak; BL=beak length; BSz=bract size; PW=pod width; GT=growth type; OW=opening of wings; SPC=shape of pod curvature; STL=size of terminal leaflet; LC=leaf color; LR=leaf roughness; BSh=bract shape; VC=variegated color in pod; IPGC=intensity of pod ground color.

to Simpson's index, PH (0.99), PN (0.98), PL (0.97), and FL (0.97) were the descriptors with greatest diversity (Table 6). The lowest diversity values were related to IPGC (0.36), BSh (0.40), and VC (0.48). The total Simpson's index to all morphological descriptors was 0.67 (Table 6). Shannon–Weaver's diversity values were parallel but higher than Simpson's index in general. Higher values in Simpson's index were also higher in the Shannon–Weaver index. They were PH (4.92), PN (3.96), PL (3.70), and FL (3.63). Total genetic diversity was estimated as 1.82.

#### UPGMA Cluster Analysis

UPGMA cluster analysis showed two groups of landraces within the common bean germplasm with ten subgroups (Figure 4). Main groups numbered from C1 to C10 are shown in the inset of Figure 4. Genotypes of ACN 20, 303, 247, and 329 on the left of the X axis formed a subgroup (C4) that is distinctly different from genotypes with ACN 199, 149, 165, 161, 177, 113, and 183 on the right end of the X axis (C2). Most of the landraces were distributed in subgroups of C8, C5, C10, C6, and C7 (Figure 4).

### Discussion and Conclusion

Common bean germplasm from Northeast Anatolia showed high levels of polymorphism in all 25 qualitative and quantitative morphological characteristics investigated except for bract color. In other studies, conducted with different bean genotypes collected from Turkey, a wide range of variations were also reported for various qualitative and quantitative traits (Canci et al., 2019; Madakbaş & Ergin, 2011; Nadeem et al., 2020; Soydaş et al., 2021; Yeken et al., 2019). The PCA biplot based on the first two principal components showed genetically different genotypes by the pattern of scattering. The distribution of genotypes in the biplot demonstrated the existence of a reasonable amount of genetic diversity (Figure 3b). Shannon–Weaver's ( $H$ ) and Simpson's ( $D$ ) diversity indices calculated also indicated rich diversity within the germplasm investigated which may support a modest bean breeding program for local and regional use. These indices are important models to evaluate

the diversity in a given set as they distinguish the genetic variation in a germplasm (Kiwuka et al., 2012; Yıldız et al., 2020). Okii et al. (2010) used Shannon–Weaver diversity index on 284 bean accessions using 22 morphological descriptors and reported mean  $H$  of 0.56 and inferred moderate diversity among the bean accessions. Similarly, Arunga et al. (2015) also reported a mean  $H$  of 0.56 for a set of 36 French bean accessions. Compared to these studies, the higher mean  $H$  value (1.82) determined in our study indicated a rich diversity.

Khaidizar et al. (2012) investigated the genetic diversity with a simple sequence repeat marker system in 38 common bean germplasm including some landraces from this collection in comparison with 12 commercial cultivars. They determined a considerable level of polymorphism within the collection that can be exploited for breeding programs. They scored a total of 72 DNA fragments across all materials with 30 primer pairs. In their study, more than 97% of the amplification products showed polymorphism, indicating high variation at the DNA level also among these accessions. Findings presented here in our study indicate high levels of polymorphism in morphological traits in line with DNA level diversity in the core collection from the same germplasm (Khaidizar et al., 2012). The level of polymorphism represented in the germplasm was equal to or higher than in other germplasm collection from the Black Sea region (Balkaya, 1999; Balkaya & Yanmaz, 2002) and Van lake region (Sarıkamış et al., 2009). Northeast Anatolia including Çoruh Valley stands between the humid Black Sea Region in the North and the relatively dry Van Region in the South. The germplasm collected in Northeast Anatolia including Çoruh Valley bordering both regions may have therefore some common characteristics both from the Black Sea Region germplasm to the North and Van province germplasm to the south. Black Sea germplasm had predominantly climbing types whereas Van Province germplasm included bush and dwarf/bush types also. Geographical, edaphic, and climatic variations, different cultivation techniques, and selection for organoleptic

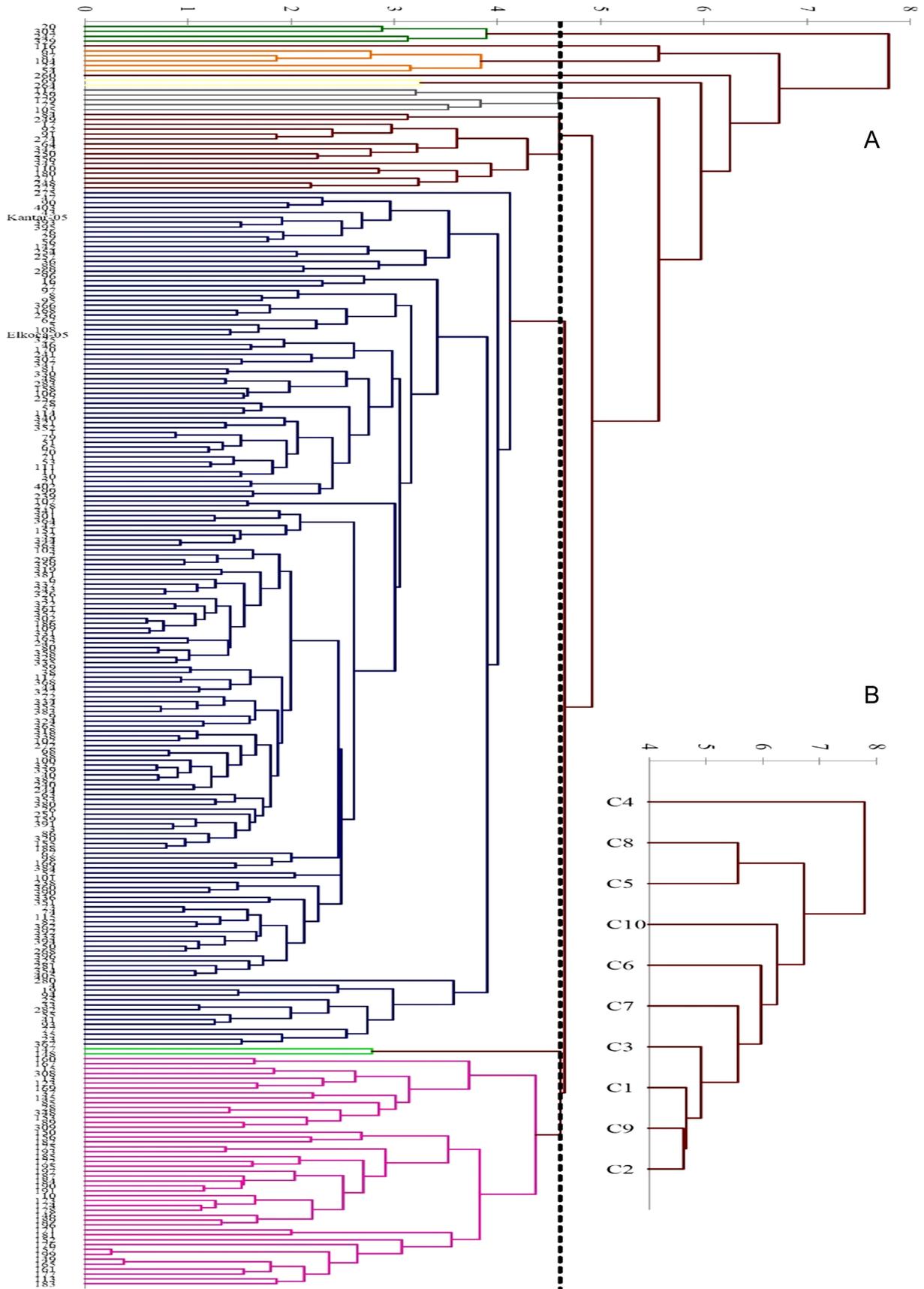


Figure 4. UPGMA Dendrogram of Common Bean Landraces Collected from Northeast Anatolia, Turkey.

preferences (Scarano et al., 2014) possibly contributed to rich bean plant diversity in these regions (Pekşen & Gülümser, 2005; Sözen et al., 2012).

The classification of genotypes in clusters reflects the relative distance of clusters and allows an appropriate selection group of genotypes with their overall phenotypic similarity for preparing breeding program. Generally, parents belonging to most distant clusters are beneficial for the development of new variety and to create wide variability in genetic structure (Panchbhaiya et al., 2017). Analysis of morphological markers here also laid a base for a breeding program using the germplasm of landraces collected from the region. Most distant landraces in UPGMA cluster dendrogram especially of ACN 20, 303, 247, and 329 in group C4 against ACN 183, 113, 177, and 161 in group C2 may also be used in hybridization and marker-assisted selection programs in order to develop superior cultivars.

The correlation coefficient can create deceptive results because the high degree of correlation between two traits may happen due to the indirect effect of a third one (Machado et al., 2017). Therefore, it is necessary to investigate the cause-and-effect relationship between variables. Path analysis splits the correlation coefficient between traits into direct and indirect effects using main and explanatory variables (Al-Ballat and Al-Araby, 2019). In our study, we considered SY as the dependent variable and the other traits as independent ones. The maximum positive direct effects were obtained by PN and FL which suggest the importance of these traits as selection criteria for high SY in common bean. On the contrary, DE and flowering had negative direct effects, which indicate that the selection based only on these traits will decrease the seed yield. Since BN, PL, and SN had high positive indirect effects on SY through PN, SN, and PL, respectively, these traits should be selected simultaneously for high SY.

Data obtained here from the path and PCA analysis show that PN, PL, SN, PH, and BN may be used as selection criteria in bean breeding programs. By recurrent selection for higher PN, longer pods, greater SN, taller plants, and greater branch number per plant may lead to higher-yielding robust bean plants. Bean plants with greater plant architecture may be also suitable for mechanical harvest for commercial scale bean production. Simpson and Shannon–Weaver diversity indices calculated also confirmed that PH, PN, and PL may be useful selection criteria in breeding programs for the development of superior cultivars.

In conclusion, the germplasm collected from Northeast Anatolia and Çoruh Valley comprised rich polymorphism. UPGMA dendrogram classified the landraces into two main groups and ten sub-groups. The germplasm investigated had also a high level of genetic diversity that could be exploited for the development of superior bean cultivars. Selection for higher PN, longer pods, greater SN, and greater BN may lead to high-yielding robust cultivars.

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