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Characterization of some local pea (*Pisum sativum* L.) genotypes for agromorphological traits and mineral concentrations

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Characterization of some local pea (*Pisum sativum* L.) genotypes for agro-morphological traits and mineral concentrations

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Abstract: The aim of the present study is to evaluate diversity among the Turkish local pea germplasm for mineral concentrations and agro-morphological traits for breeding programs. The experiment was conducted during 2018/2019 and 2019/2020 and arranged according to an augmented block design with 40 local genotypes and two standard check cultivars (Carina and Jof). Seed yield per plant was positively and significantly correlated with branches per plant, pods per plant, seeds per pod, harvest index, and 100-seed weight. The first three principal components (PC1) for agro-morphological traits accounted for 76.3% of the total variation. The principal first component was positively correlated with harvest index, seeds per pod, seed yield per plant and negatively correlated with first podding height and plant height. The PC2 was positively related to plant height, first podding height, branches per plant, pods per plant, seed yield per plant, 100-seed weight. Principal components analysis for mineral contents revealed that first three component accounted for 69.6% of total variability which was observed among the genotypes. PC1 was positively associated with protein, Cu, Zn, K, Mg, and P. PC2 was positively correlated with Mn and Ca, but negatively correlated with K. Hierarchical cluster analysis showed that genotypes were grouped into 5 main clusters for agro-morphological traits and mineral concentrations. The present study revealed that wide genetic variability among the various genotypes for these traits from different clusters can be exploited for selection or hybridization programs to improve with high-seed yielding pea genotypes.

Key words: Characterization, local pea genotypes, cluster analysis, principal component analysis, correlation

1. Introduction

Pea (*Pisum sativum* L.) is one of the most important grain legumes and widely grown for human or livestock feeding in the world. Pea seeds contain high levels of protein, carbohydrate and minerals and they also provide nitrogen and organic matter to the soil in crop rotation. The Mediterranean Region of Turkey has seed production potential for pea (Ceyhan et al., 2012; Ton and Anlarsal, 2013; Ton et al., 2018). Therefore, it is important that new pea cultivars with higher seed yield and mineral concentrations may be improved for our region conditions. Description of local genotypes for some traits is very important for cultivar breeding (Ceyhan et al., 2008; Ouafi et al., 2016; Kumar et al., 2018) and magnitude of genetic diversity in the different traits of studied genotypes is needed for successful breeding programs (Jukanti et al., 2015). Principal component analysis (PCA) and cluster analysis are called multivariate

statistical technique methods, and these methods revealed divergence among genotypes for traits (Manivannan et al., 2016; Güngör et al., 2021). Arif et al. (2020) reported that PCA and cluster analyses were used to occur Euclidean distance among landraces to distinguish the relation to most traits in pea. Turkey is rich in terms of local pea genotypes, and these are very important for improving new cultivars with high yielding because of a valuable resource for genetic variation in terms of agro-morphological traits and mineral composition (Karayel and Bozoğlu, 2015; Şimşek and Ceyhan, 2017; Demirbaş, 2018). Studies on characterization for morphological traits and mineral compositions in local genotypes using cluster and principal component analysis were considered in future pea breeding programs (Ouafi et al., 2016; Kumar et al., 2018). Many studies on the characterization of agro-morphological traits and mineral composition were carried out in pea (Demirbaş, 2018; Kumar et al., 2018;

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Hancı and Cebeci, 2019; Ada et al., 2019; Arif et al., 2020; Ceyhan and Şimşek, 2021) and various crops such as in chickpea (Cinsoy et al., 1997; Kahraman et al., 2015), lentil (Karaköy et al., 2012), faba bean (Karaköy et al., 2014), dry bean (Harmankaya et al. 2009; Ceyhan et al., 2014; Sözen et al., 2014), cowpea (Harmankaya et al., 2016), yardlong bean (Rambabu, 2016), safflower (Ali et al., 2020), and maize (Mustafa et al., 2015).

The aim of the present study is to estimate the diversity of agro-morphological traits and mineral concentrations in the local pea genotypes collected from different regions of Turkey for future pea breeding programs.

2. Materials and methods

2.1. Experimental conditions

This study was conducted in the research area of Field Crop Department of Agricultural Faculty, Çukurova University for a 2-year period between 2018/2019 and 2019/2020 under rain-fed conditions in Adana, which has an annual precipitation of 625 mm and a mean temperature of 18.7 °C according to long-term meteorological data. Some climatic values in the experimental years are given in Table 1. The texture of the research soil was sandy-loam and clay-loam. The values of pH and salt content were 7.78 and 0.33 mmhos cm⁻¹, respectively.

2.2. Plant material

In the present study, 40 local genotypes collected from various sites of Turkey by the National Plant Gene Bank included in Aegean Agricultural Research Institution and gene bank of ICARDA (International Center for Agricultural Research in the Dry Area) were used as plant material. Mentioned local genotypes were obtained from East Mediterranean Research Institution, Adana. Plant material is exhibited in Table 2.

The experiment was arranged according to an augmented block design with two standard check cultivars

(Carina and Jof). The experiment had four blocks and each block had ten local genotypes and check cultivars. Each plot consisted of two rows with 45 cm between rows and 10 cm spacing between plants. Fertilization was applied at a rate of 30 kg N ha⁻¹ and 76 kg P₂O₅ ha⁻¹ before sowing. The experiments were established on 26th of November 2018 and on 15th of November 2019. Field emergences were recorded on the 10th of December, 2018 and on the 7th of December, 2019. The plots were harvested on the 15th of May, 2019 and on the 21st of May, 2020.

Data for plant height (cm), number of main branches per plant, number of seeds per pod, number of pods per plant and first podding height (cm), seed yield per plant (g), harvest index per plant (%) were recorded on the individual five plants randomly selected from each plot. The 100-seed weight (g) was recorded from randomly selected samples of 100 grains from each plot. The seed yield (kg ha⁻¹) was estimated in total seed weight obtained from each plot.

Seed samples were milled for analysis. Nitrogen concentration was determined using the Kjeldahl method (Bremner, 1996). Crude protein content (%) was calculated by using the formula: CP = N% × 6.25. After milling, seed samples were ashed at 550 °C for 8 h and the ash was dissolved in 3.3% HCl (Kaçar and İnal, 2010). Macro- and microelements (K, Ca, Mg, Fe, Zn, Mn, and Cu) were measured by using an atomic absorption spectrophotometer (Varian FS220). Phosphorus was analyzed using the method declared by Barton (1948).

2.3. Statistical methods

Analysis of variance was performed for agro-morphological traits and mineral concentration over two years according to augmented block design. Data obtained from both of the years were also evaluated to calculate basic statistical parameters such as mean, minimum and maximum values,

Table 1. Some climatic values in the experiment years.

Meteorological parameters	Min temperature (°C)		Max temperature (°C)		Mean temperature (°C)		Relative humidity (%)		Total rainfall (mm)		
	Months	2018 2019	2019 2020	2018 2019	2019 2020	2018 2019	2019 2020	2018 2019	2019 2020	2018 2019	2019 2020
November		7.4	10.3	30.8	30.6	16.9	18.1	64.1	56.7	25.6	22.6
December		2.9	6.5	21.3	20.7	12.2	12.2	75.3	79.4	297.6	414.0
January		0.4	0.6	18.9	18.0	9.8	9.9	71.0	67.9	245.8	140.2
February		4.5	-2.1	21.2	22.8	11.8	10.4	72.1	67.1	89.8	93.0
March		2.3	5.8	26.4	27.6	13.8	15.3	69.0	69.3	94.8	47.4
April		7.0	8.3	32.0	29.9	17.0	18.3	67.0	70.2	59.4	21.4
May		11.8	12.9	39.4	40.3	24.1	23.3	57.6	61.0	2.6	66.6

Table 2. List of plant material.

Registration no	Local name/ institute	Registration no	Local name/institute
1101	Kars-49/ICARDA	2109	TR-54953 Tekirdağ/AARI
1102	Muğla-46/ICARDA	2111	TR-67094 Tekirdağ/AARI
1103	Antalya-13/ICARDA	2114	TR-77732 Muğla/AARI
1106	Antalya-104/ICARDA	2116	TR-26306 Muğla/AARI
1115	Konya-134/ICARDA	2401	Afyon 146
1116	Konya-155/ICARDA	2402	Antalya 100
1403	Bingöl -151/ICARDA	2403	Konya 153
1410	Unknown/ICARDA	2404	İzmir 108
1411	Unknown/ICARDA	2405	Unknown/Turkey
1412	Unknown/ICARDA	2406	Unknown/Turkey
1413	TR-33238 Çanakkale/AARI	2407	Unknown/Turkey
1701	TR-77737 Manisa/ AARI	2408	Unknown/Turkey
1702	TR-77737-1 Manisa/AARI	2409	Antakya -19
1707	TR-43509 İstanbul/AARI	2410	TR-30760 Adana/ AARI
1711	TR-53747 Çanakkale/AARI	2411	TR-77732 Muğla 2/ AARI
1715	TR-61266 Tekirdağ/AARI	2412	TR-49596 Antalya/ AARI
1716	TR-5478 Antalya/AARI	2413	TR-49598 Hatay/ AARI
2102	TR-61309 İzmir/AARI	2414	TR-64147 Çanakkale/ AARI
2103	TR-32230 Muğla/AARI	2415	TR-61284 Tekirdağ/ AARI
2108	TR-53749/Unknown/AARI	2416	TR-61301 Giresun/ AARI

AARI: Aegean Agricultural Research Institution

standard deviation and correlations, principal component analysis, cluster analysis, and biplot graphing using JMP (version pro 14 and 16).

3. Results and discussion

3.1. Basic statistical parameters

Basic statistical parameters for mean values of agromorphological traits and mineral compositions of 42 pea genotypes according to the mean of 2 years are shown in Tables 3 and 4.

As seen in Table 3, wide ranges were observed for plant height (65.3–191.8 cm), first podding height (24.1–74.5 cm), harvest index (16.6%–48.8%), pods per plant (13.7–40.8), seed yield per plant (6.5–30.3 g), and seed yield (1210–3225 kg ha⁻¹). Similar to our results, a large variation for the same traits was reported by some studies in pea (Ceyhan et al., 2008; Azmat et al., 2011; Karayel and Bozoğlu, 2015). This variability in the agro-morphological traits can be used in breeding programs. Hence, lower variability was found for days to 50% flowering in the present study (93.0–101.0). Gatti et al. (2011) reported that the values obtained from seeds per pod and 100-seed weight were similar to the values in the present study.

However, Kumar et al. (2018) found fewer pods per plant and seed yield per plant, shorter plant height and days to 50% flowering, but similar harvesting index and 100-seed weight compared to present data.

As seen in Table 4, great variation was found in Fe (53.8–75.4 mg kg⁻¹), Zn (39.6–59.5 mg kg⁻¹), Cu (10.7–17.8 mg kg⁻¹), P (0.32%–0.46%), Ca (0.07%–0.11%), Mn (16.6–21.3 mg kg⁻¹) concentrations. However, relatively low variability was observed in Mg (0.12%–0.16%), K (0.92%–1.18%), protein (21.7%–28.9%) in the studied genotypes (Table 4). This variability among the local genotypes can be used to improve new pea cultivars which have high mineral concentrations. Several studies reported that great variability was found for mineral concentration in pea germplasm (Harmankaya et al., 2010; Karaköy and Demirtaş, 2017; Ada et al., 2019; Ceyhan and Şimşek, 2021). Earlier studies reported that diversity in the chemical composition of various crop germplasm was a good source for improving new cultivar in the lentil (Karaköy et al., 2012; Sarker et al., 2017), bean (Harmankaya et al., 2009; Ceyhan et al., 2014), faba bean (Karaköy et al., 2018), cowpea (Harmankaya et al., 2016), and field pea (Demirbaş, 2018; Ceyhan et al. 2021) breeding.

Table 3. Basic statistical parameters for agro-morphological traits in pea genotypes.

Traits	Min	Max	Mean	SD	CV (%)
Days to %50 flowering	93.0	101.0	96.5	2.9	3.04
Plant height (cm)	65.3	191.8	146.1	13.6	9.3
First podding height (cm)	24.1	74.5	52.1	8.4	16.1
Branches per plant	1.80	4.10	2.64	0.78	29.6
Harvest index (%)	16.6	48.8	37.0	7.83	21.1
Pods per plant	13.7	40.8	25.0	8.55	34.1
Seeds per pod	3.2	6.1	4.61	0.54	11.8
Seed yield per plant	6.5	30.3	17.1	6.70	38.9
100 seed weight (g)	14.4	29.5	18.5	1.54	8.3
Seed yield	1210	3225	2028	627.2	30.9

Table 4. Basic statistical parameters for protein content and mineral concentrations of pea genotypes.

Traits	Min	Max	Mean	SD	CV (%)
Protein (%)	21.7	28.9	25.9	1.53	5.92
Cu (mg kg ⁻¹)	10.7	17.8	14.7	2.28	15.5
Zn (mg kg ⁻¹)	39.6	59.5	49.9	5.91	11.8
Fe (mg kg ⁻¹)	53.8	75.4	62.4	8.23	13.2
Mn (mg kg ⁻¹)	16.6	21.3	18.9	1.91	10.1
K (%)	0.92	1.18	1.02	0.06	6.66
Mg (%)	0.12	0.16	0.14	0.01	7.80
Ca (%)	0.07	0.11	0.09	0.01	11.0
P (%)	0.32	0.46	0.37	0.03	10.2

3.2. Correlation analysis

The correlation coefficients among the agro-morphological traits are presented in Table 5. Seed yield had a positive and significant association with harvest index, seed yield per plant, and 100-seed weight. Correlations between seed yield and days to 50% flowering, plant height, first podding height, and branches per plant were nonsignificant. Seed yield per plant was positively and significantly correlated with branches per plant, pods per plant, seeds per pod, harvest index, and 100-seed weight in the present study. Similarly to the present study, seed yield per plant exhibited a positive and significant correlation with these traits in pea (Parihar et al., 2014; Srivastava et al., 2018; Singh et al., 2017; Ton et al., 2018). Similar to our findings, Tofiq et al. (2015) declared that the weight of seeds per plant had a positively significant correlation with pods per plant and harvest index in pea genotypes. However, there was a negative correlation between seed yield per plant and first podding height. Therefore, the present study suggests that seed yield per plant can be improved throughout the

selection of these traits in local pea genotypes. Geogieva (2015) also reported that seeds per plant, pods per plant, and 1000-seed weight were considered for selection of high-yielding pea genotypes.

The correlations among the mineral concentrations are exhibited in Table 6. Protein content showed a positive and significant association with Cu, Zn, Fe, K, Mg, and P, but no correlation with Mn and Ca. This correlation revealed that genotypes with high mineral concentration may be also improved throughout the selection of genotypes with high protein content. Harmankaya et al. (2010) reported that correlations between protein and K, Zn concentrations were significant and negative. Özer et al. (2012) exhibited that positive and significant correlation between protein and Mg, P, Zn. In the present study, P was positively and significantly correlated with mineral concentrations except for Fe, Mn, and Ca. Thus, significant and positive associations with P and K, Zn, Cu have been reported in previous studies in pea (Karaköy and Demirtaş, 2017; Demirbaş, 2018). Phosphorus had

Table 5. Correlations among agro-morphological traits of pea genotypes.

Traits	1	2	3	4	5	6	7	8	9	10
1.DF	1									
2.PH	0.1139	1								
3.FPH	0.2921	0.8337**	1							
4.BPP	0.3096*	0.0049	0.0025	1						
5.HI	-0.3737*	-0.5011**	-0.5412**	0.1820	1					
6.PPP	0.1130	0.2411	0.0752	0.6491**	0.2827	1				
7.SPP	-0.4234**	-0.5638**	-0.5562**	-0.2923	0.6676**	-0.2409	1			
8.SYPP	-0.1677	-0.0915	-0.2019	0.4429**	0.7059**	0.6627**	0.3275*	1		
9.100SW	0.0441	0.0967	0.1202	0.2632	0.2150	0.1466	-0.0295	0.5461**	1	
10.SY	-0.2965	0.2568	0.1913	0.0708	0.4426**	0.2334	0.2551	0.4578**	0.3241*	1

DF: Days to flowering %50; PH: Plant height; FPH: First podding height; BPP: Branches per plant; HI: Harvest index; PPP: Pods per plant; SPP: Seeds per pod; SYP: Seed yield per plant; 100 SW: 100-seed weight; SY: Seed yield.

Table 6. Correlations among mineral concentrations of pea genotypes.

Traits	Protein	Cu	Zn	Fe	Mn	K	Mg	Ca	P
Protein	1								
Cu	0.6085**	1							
Zn	0.5610**	0.5196**	1						
Fe	0.4193**	0.1094	0.1309	1					
Mn	0.2943	0.2446	0.0688	0.1454	1				
K	0.5416**	0.3172*	0.4052**	0.4768**	0.1306	1			
Mg	0.6392**	0.5111**	0.4641**	0.2549	0.4566**	0.4084**	1		
Ca	0.2326	0.1391	0.1469	0.1000	0.3211*	0.0408	0.3741*	1	
P	0.5460**	0.3543*	0.5122**	0.2705	0.1754	0.6045**	0.5072**	0.2657	1

a positive and significant association with K, Fe, Mn, Cu, and Zn in faba bean landraces (Baloch et al., 2014) and lentil germplasm (Sarker et al., 2017). The results of the present study revealed that these traits can be used as selection criteria for pea breeding and new pea genotypes which have high protein and mineral composition suitable for Mediterranean climate conditions can be improved.

3.3. Principal component analysis

Principal component analysis (PCA) for agro-morphological traits of 40 local peas and two cultivars is presented in Table 7 and Figure 1. The first three principal components (PCs) accounted for 76.3% of total variation with >1.0 (33.5%, 27.2%, 15.6% for PC1, PC2, and PC3, respectively). Weight values of PCA of characters that are over ± 0.3 are considered to be significant (Brown, 1991). The first principal component (PC1) was positively correlated with harvest index, seeds per pod, seed yield per plant and negatively associated with first podding height and plant

height. The PC2 was positively related to plant height, first podding height, branches per plant, pods per plant, seed yield per plant, 100-seed weight. PC3 was negatively associated with days to 50% flowering, branches per plant and positively with plant height, first podding height and seed yield. Similar to our findings, Kumar et al. (2018) reported that the first three components explained 75% of the variation in pea genotypes and variation positively related to pods per plant in PC1, seeds per pod in PC3. Karaköy et al. (2014) found that the first six PCs accounted for 74.6% of cumulative variance for morphological traits in faba bean landraces. Espósito et al. (2007) reported that the first two PCs explained 67.7% and 69.8% variations for yield components in pea germplasm in different years. Similarly to our findings, PCA analysis revealed that pea genotypes showed a great genetic variability for similar traits (Azmat et al., 2011; Parihar et al., 2014). Ouafi et al. (2016) reported that PC1 was positively related to seeds

3.4. Cluster analysis

Hierarchical cluster analysis and the mean values of agro-morphological traits for each cluster are presented in Table 9 and Figure 3. Cluster analysis showed that 42 pea genotypes were grouped into 5 main clusters for these traits. Cluster 1 included 14 local genotypes and was characterized by maximum branches per plant with 3.1 and pods per plant with 33.5. Cluster 2 consisted of two local genotypes and was observed to have the highest values for harvest index with 44.4%, seed yield per plant with 27.2 g, and 100-seed weight with 28.9 g. The maximum seed yield (2523 kg ha⁻¹), medium values for

100-seed weight (19.1 g) and pods per plant (24.3), highest seeds per pod (4.9), lowest branches per plant (2.4), earliest flowering (95.0 days) were in cluster 3 consisted of 13 genotypes. Cluster 4 included 7 local genotypes and was characterized by maximum plant height with 99.5 cm, maximum first podding height with 64.4 cm, highest plant height with 173.9, and the lowest seeds per plant with 3.7 and seed yield with 1659 kg ha⁻¹. Cluster 5 contained 4 local genotypes and two cultivars showed the highest values for, seeds per pod (5.6) and the lowest value in first podding height (31.4), pods per plant (20.9), 100-seed weight (16.9 g). Similar to our results, previous

Table 9. Mean values of clusters for agro-morphological traits of pea genotypes.

Cluster	Count	DF	PH	FPH	BBP	HI	PPP	SPP	SYPP	100SW	SY
1	14	96.9	162.1	55.4	3.1	36.4	33.5	4.0	20.8	19.2	2094.6
2	2	98.8	146.2	59.5	3.1	44.4	25.2	4.6	27.2	28.9	2326.6
3	13	95.0	169.1	60.1	2.4	38.8	24.3	4.9	18.5	19.1	2523.6
4	7	99.5	173.9	64.4	2.5	26.1	21.1	3.7	9.9	17.0	1659.2
5	6	95.9	96.7	31.4	2.6	42.4	20.9	5.6	16.3	16.9	1801.6

DF: Days to %50 flowering; PH: Plant height; FPH: First podding height; BBP: Branches per plant; HI: Harvest index; PPP: Pods per plant; SPP: Seeds per pod; SYP: Seed yield per plant; 100 SW: 100 seed weight; SY: Seed yield.

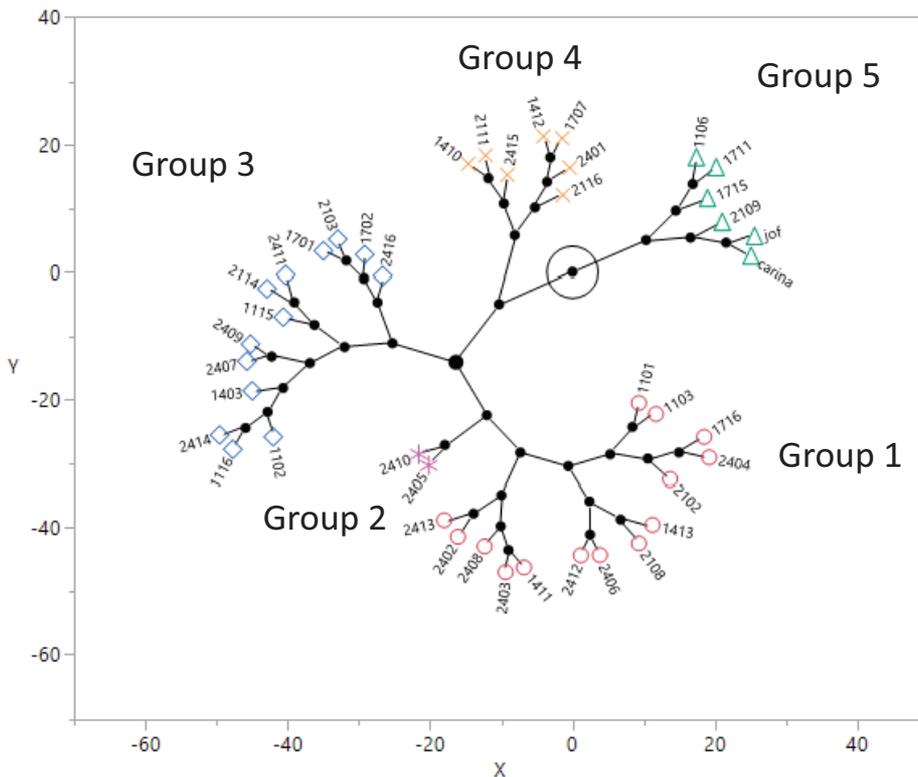


Figure 3. Hierarchical clustering analysis for agro-morphological traits in pea genotypes.

studies revealed that differences in intercluster was found for agro-morphological characters in pea genotypes (Gatti et al., 2011; Karayel and Bozoğlu, 2015; Khan et al., 2016; Prasad et al., 2018). Similar results were reported by some studies (Azmat et al., 2011; Parihar et al., 2014; Ouafi et al., 2016). The present study demonstrated that pea genotypes of different geographical regions were grouped in the same cluster in accordance with the previous reports (Azmat et al., 2011; Parihar et al., 2014; Srivastava et al., 2018). Clustering analysis revealed wide variation among the studied pea genotypes for agro-morphological characters. The present study showed that considerable variability among the local genotypes can be used for selection or hybridization programs among the various genotypes from distant clusters to improve high seed yielding pea

genotypes. So, this will be a good opportunity to obtain desirable recombinants in future pea breeding.

Hierarchical cluster analysis and the mean values of protein content and mineral concentrations for each cluster are demonstrated in Table 10 and Figure 4. Cluster analysis ranged pea genotypes into 5 main clusters for mineral composition. Cluster 1 contained 3 genotypes and had the lowest values for protein and all of the mineral concentrations (except for Fe, Mn). Cluster 2 was comprised of 16 genotypes and characterized by medium value of protein with 25.34%, Cu (13.99 mg kg⁻¹), Zn (49.23 mg kg⁻¹), Mg (0.14 mg kg⁻¹), K (1.01%), P (0.36%) and low Mn (18.14 mg kg⁻¹). Cluster 3 included six local genotypes and cluster 4 consists of 13 local genotypes and Carina. Both of the clusters showed medium values

Table 10. Mean values of clusters for protein content and mineral concentrations of pea genotypes.

Cluster	Count	Protein	Cu	Zn	Fe	Mn	K	Mg	Ca	P
1	3	22.40	11.47	42.44	57.76	18.34	0.94	0.13	0.09	0.34
2	16	25.34	13.99	49.23	63.19	18.14	1.01	0.14	0.09	0.36
3	6	25.51	15.58	46.91	57.35	19.92	0.95	0.14	0.10	0.34
4	14	26.28	15.60	51.06	63.83	18.95	1.05	0.15	0.09	0.40
5	3	28.56	16.15	56.89	67.05	20.18	1.07	0.16	0.11	0.42

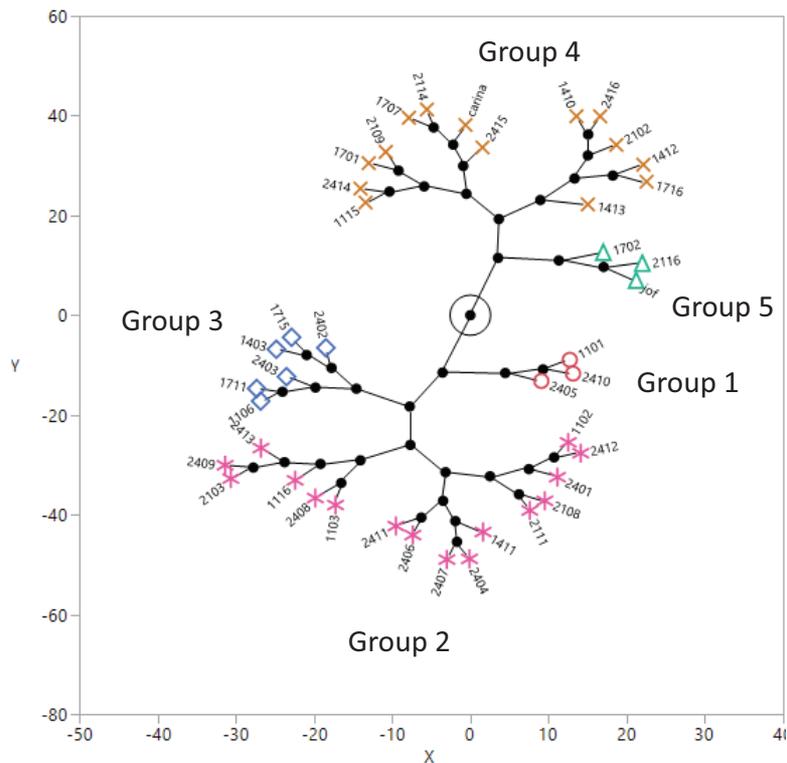


Figure 4. Hierarchical clustering analysis for protein content and mineral concentrations in pea genotypes.

for protein and almost all mineral concentrations (except for Ca). Cluster 5 included two local genotypes and jof. This group exhibited the highest value for protein with 28.56% and all mineral concentrations. Cluster analysis for nutrient composition exhibited that groups were not related to the geographical origins of local pea genotypes. Local genotypes were a good source for improving new pea cultivars with high nutrient concentrations. Present results were in agreement with Demirbaş (2018), who recorded that the same clusters included landraces from different geographical regions for various mineral concentrations in pea. Earlier studies reported in pea, lentil, and faba bean that landraces showed wide variations in mineral concentrations or quality traits which are important for crop breeding (Özer et al., 2012; Karaköy et al., 2014; Karaköy et al., 2018).

4. Conclusion

The present study revealed that agro-morphological traits such as seed yield per plant, pods per plant, harvest index, branches per plant 100-seed weight and nutrient contents can be exploited as selection criteria for improving new pea

cultivars. Wide variation among the studied pea genotypes was also found for agro-morphological traits and mineral concentrations. Local genotypes provided from different regions were grouped in the same cluster and Turkish pea germplasm is a good resource to improve new pea cultivars with seed yield and mineral contents. As a result, it suggests that new pea cultivars will be improved with hybridization among diverse local genotypes from different clusters for agro-morphological traits and mineral contents.

Contribution of authors

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All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare that they have no conflicts of interest.

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