

## Full Length Research Paper

# Agro-morphological diversity within field pea (*Pisum sativum* L.) genotypes

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Received 19 July, 2016; Accepted 15 September, 2016

The objective of this study was to analyze the genetic diversity present in twelve Algerian pea genotypes using 24 agro-morphological traits. The experiment was carried out during three growing seasons (2013 to 2014, 2014 to 2015 and 2015 to 2016). ANOVA analysis revealed the presence of a great genetic variability for all characters studied. This diversity might be used in breeding programs. Also, expression of characteristics is highly influenced by the environment. For quantitative traits, correlation studies showed that weight of 100 seeds was significantly and positively correlated with leaflet length. Number of pods per 1 m<sup>2</sup> has a positive significant correlation with leaflet width. Weight of pods per 1 m<sup>2</sup> was correlated with three characters: Stipule length, leaflet length and leaflet width. The principal component analysis revealed that three components explained 85.92% of variation. Two groups were noted by dendrogram. The first group (demchi 1, p069, bouch1, p539, p593, p595 and p596) was characterized by a high pod yield; the other group comprises the less productive genotypes (p071, sefrou, p072, p073 and p350). Otherwise, the genotype p593 produced the best results for pods yield.

**Key words:** Genetic diversity, agro-morphological traits, field pea, *Pisum sativum* L.

## INTRODUCTION

Pea (*Pisum sativum* L) is one of the oldest culture in the world with cereals and lens (Zohary et al., 2012). Field pea primarily is used for human consumption or as livestock feed. It is an important source of proteins (21 to 25%) and potential alternative to soybean in Europe (Barac et al., 2010). It contains high levels of carbohydrates and total digestible nutrients (86 to 87%), which makes it an excellent livestock feed (Enderes et

al., 2016).

According to Janzen et al. (2014), through symbiosis, pea can fix atmospheric nitrogen and therefore does not need nitrogen fertilizer especially since it provide nitrogen for the crop following it. Also, Pea tolerates drier growing season conditions and limited rainfall (Janzen et al., 2014).

Pea is a widely cultivated crop species and the second

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**Table 1.** List of genotypes and their origins.

N°	Code/name	Country
1	Demchi 1	Algeria
2	Bouch1	Algeria
3	P539	Algeria
4	p593	Algeria
5	p595	Algeria
6	p596	Algeria
7	p069	Algeria
8	p071	Algeria
9	p072	Algeria
10	p073	Algeria
11	p350	Algeria
12	Sefrou	Morocco

most important food legume worldwide after common bean (Esposito et al., 2007). Its global production reached 11 332 772 tons with an area of 6 868 131 ha (FAOSTAT, 2014). Canada is the leading producer with approximately 3 million metric tons in 2012 (Jansen et al., 2014) followed by France, Russian federation, China mainland and Ukraine. In 2014, approximately 45000 tons of pea were harvested in North Africa on an area of 63127 ha (FAOSTAT, 2014).

In Algeria, pea exists for a long time (INRAA, 2006). However, this heritage was largely lost. Indeed, in the past, Algeria introduced new performing varieties (Arbouche et al., 2011) and the landraces which presented a greater tolerance to the biotic and abiotic conditions were replaced by new varieties (Cupic et al., 2009). Thus, the local germplasm suffered great genetic erosion (Arbouche et al., 2011). Fortunately, many pea cultivars were preserved in gene banks (Hagenblad et al., 2014) or among farmers occupying marginal lands (FAO, 2011) and practicing family farming. The studies clearly demonstrate the importance of this crop diversity in counteracting the effects of droughts and other environmental hazards and in ensuring family food security (FAO, 2004).

Furthermore, Landraces can play a very important role in improvement works and selection, offering interesting characteristics for farming. However, the description and knowledge of these genotypes is a prerequisite for their use (Marchenay and Lagarde, 1987). So, several studies of pea germplasm using different approaches have been published in the world (Ali et al., 2007, Sarikamis et al., 2010, Ghixari et al., 2014) and in Tunisia and Morocco where interest was brought to the development of local varieties (Mani et al., 2007; Benbrahim and Gaboun, 2008). In Algeria, landraces are still neglected in favor of imported varieties of peas and then the number of local genotypes is much reduced.

Traditionally, germplasm diversity is assessed by morphological descriptors, which remain the only

legitimate marker type accepted by the International Union for protection of New varieties of plants (UPOV, 2009) (Ghixari et al., 2014).

The objective of this research was to determine genetic diversity among pea genotypes using morphological and agronomic traits in a goal of their valorization.

## MATERIALS AND METHODS

Search pea landraces from farmers was very difficult to do because of the priority given to the introduced varieties and thus, the number of cultivars collected was limited to twelve (Table 1).

Nine genotypes were obtained from ICARDA (International Center for Agricultural Research in Dry Areas), two genotypes (demchi1 and bouch1) were collected as part of this work, the first being cultivated in Adrar in southern Algeria and the second is harvested in Algiers (Bouchaoui). Sefrou is an introduced genotype (from Morocco) but has been long cultivated in Algeria, at the Technical Institute of Field Crops (TIFC-Sidibellabes).

The study was carried out during the winter seasons of 2013 - 2014, 2014 - 2015 and 2015 - 2016. The first experiment was conducted at the experimental station of ENSA (National Higher school of Agronomy) at El Harrach-Algiers. The second and the third experiments were carried out in the central farm of ENSA. The field trials were in a randomized complete block design with three replications. Seeding was done in a plot of 1.5x1.5 m. The seeds were sown in rows spaced 35 cm.

Observations were made for 24 agro-morphological characters described by UPOV Guidelines for the conduct of tests for distinctness, uniformity and stability. The qualitative traits are presented in Table 2. The quantitative characters were resumed in Table 3. The stem length; the number of pods per 1 m<sup>2</sup> and the weight of pods per 1 m<sup>2</sup> were measured only during the last season.

Statistical analysis was performed using the software StatView. The analysis of variance (ANOVA) was performed by Fisher's least significant difference (LSD) method to test the significance difference between means. Correlations were performed based on fifteen quantitative characters (AFF, SL, NNFFN, STL, STW, LL, LW, PL, MNFN, PLE, PWI, NGP, WTS, NPM2, WPM2). The principal component analysis and the cluster analysis were done using eleven characters (AFF, STL, STW, LL, LW, PLE, PWI, NGP, WTS, NPM2, WPM2). The cluster analysis was adopted with the Ward's method as a clustering algorithm (Ward, 1963).

## RESULTS AND DISCUSSION

### Qualitative traits

According to Solberg et al. (2015), a combination of morphological and genetic characterization can identify if the material is unique or just duplicates of gene bank material. In the other hand, Yirga and Tsegay (2013) characterized pea genotypes using only qualitative traits related to the color of flower and seed shape.

The results of qualitative traits are presented in Table 4. A polymorphism was found within the different genotypes. The presence of anthocyanin coloration of axil was evident in 58.33% of genotypes. Only three genotypes presented strong dentations on leaflets. Four genotypes (p593, p596, p072 and sefrou) have very

**Table 2.** Qualitative traits.

Qualitative trait	Polymorphism
Anthocyanin coloration of axil (ACA).	1-Present ; 2-absent
Dentation of leaflet (DL).	1-Absent or very weak, 2-weak, 3-medium, 4-strong, 5-very strong
Flecking on stipule (FS)	1-Present ; 2-absent
Stipule: density of flecking (DFS).	1-Very sparse, 2-sparse, 3-medium, 4-dense, 5-very dense
Flower : color of wing (CWI)	1-White with pink blush, 2-pink, 3-reddish purple
Flower : color of standard (CST)	1-White, 2-whitish cream, 3-cream, 4-pink, 5- light purple.
Shape of seed (SS).	1-Ellipsoid, 2-cylindric, 3- rhomboid, 4- irregular.
Seed : spot on testa (SST)	1-Absent, 2-faint, 3-intense
Seed : color of testa (CT)	1-Redish brown, 2-brown, 3-brownish green

**Table 3.** Quantitative traits.

Character	Descriptors	Code
Phenological character.	Appearance of the first flower	AFF
	Stem length	SL
	Number of nodes including first fertile node	NNFFN
	Stipule length	STL
	Stipule width	STW
Morphological characters.	Leaflet length	LL
	Leaflet width	LW
	Peduncle length from stem to first pod	PL
	Maximum number of flowers per node	MNFN
	Pod length.	PLE
	Pod width	PWI
	Number of grain per pod	NGP
Yield characters.	Weight of 100 seeds	WTS
	Number of pods per 1 m <sup>2</sup>	NPM2
	Weight of pods per 1m <sup>2</sup>	WPM2

**Table 4.** Qualitative characters of the 12 genotypes.

N°	Genotype	ACA	DL	FS	DFS	CWI	CST	SS	SST	CT
1	Demchi 1	1	2	2	-	3	5	2	2	3
2	Bouch1	1	1	2	-	3	5	3	3	3
3	P539	2	2	2	-	2	4	2	2	3
4	p593	2	1	1	1	2	4	2	2	3
5	p595	1	4	2	-	2	4	1	1	1
6	p596	2	2	1	1	3	4	2	1	3
7	p069	1	2	2	-	3	4	4	2	3
8	p071	1	1	2	-	3	5	4	1	3
9	p072	1	2	1	1	3	5	2	2	3
10	p073	1	2	2	-	3	5	2	2	3
11	p350	2	4	2	-	2	5	1	2	2
12	Sefrou	2	4	1	1	3	5	1	1	3

sparse flecking in stipule. For the color of wing (CWI), two types were observed: Reddish purple (66.66%) and pink

(33.33%). Light purple color was observed in standard of 58.33% of genotypes. Five genotypes presented a

Table 5. ANOVA.

Code	Mean±SD	Min.	Max.	CV	P (genotype)	P (year)	P (G xY)
SL	90.05±16.96	50.00	118.80	18.80	0.0003**	-	-
AFF	109.25±18.13	78.00	155.00	16.60	<0.0001***	<0.0001***	<0.0001***
NNFFN	16.57±3.14	10.20	21.75	19.00	<0.0001***	0.0040*	<0.0001***
STL	5.51±0.82	4.25	7.80	15.0	<0.0001***	<0.0001***	0.0422*
STW	2.81±0.54	2.00	4.32	19.50	<0.0001***	0.0004**	0.0111*
LL	3.81±0.67	2.35	5.73	17.60	<0.0001***	<0.0001***	0.0078*
LW	1.98±0.49	0.85	3.30	25.10	<0.0001***	<0.0001***	0.0307*
PL	6.05±1.57	3.10	9.75	25.90	0.0004**	0.6377 <sup>NS</sup>	0.0008**
PLE	5.19±0.64	4.00	7.03	12.50	<0.0001***	0.0116*	0.4965 <sup>NS</sup>
PWI	0.78±0.11	0.50	1.09	14.70	<0.0001***	<0.0001***	0.8168 <sup>NS</sup>
NGP	6.91±1.12	4.60	10.33	16.20	<0.0001***	0.2568 NS	0.0022 *
MNFN	1.91±0.27	1	2	14.50	<0.0001***	-	-
WTS	12.27±3.37	6.12	20.27	27.5	<0.0001***	-	-
NPM2	153.05±104.61	2	360	68.40	<0.0001***	-	-
WPM2	193.44±140.13	32	554.67	72.40	0.0002**	-	-

SD, Standard deviation/ Min, observed minimal value; Max, observed maximal value; CV: coefficient of variation, NS, not significant, \*significant at  $p < 0.05$ , \*\*significant at  $p < 0.001$ , \*\*\* significant at  $p < 0.0001$ .

cylindrical form of seed; however one genotype (bouch1) had rhomboid shape of seed. Bouch1 is the only genotype that had intense spots on testa. 83% of genotypes have a brownish green color of testa. According to Cupic et al. (2009), use of morphological traits is unavoidable for DUS (Distinctness, Uniformity and stability) testing and in the procedures for protection of varieties.

## Quantitative traits

### ANOVA analysis

ANOVA analysis revealed the presence of a great genetic variability for all characters studied (Table 5) in concordance with the works of Gixhari et al. (2014), Wani et al. (2013), Khan et al. (2013) and Gatti et al. (2011) who analyzed genetic diversity among different accessions of pea using the same traits and found significant differences.

This diversity might be used in breeding programs (Cupic et al., 2009) by selecting parental lines among accessions (Gatti et al., 2011). Also, the differences were significant for the factor year (except for two parameters which are peduncle length and number of seeds per pod in which non-significant differences were observed) (Table 4). This can be explained by a difference in environment between the three years of experimentation. Indeed, in the first test the soil was silty texture and rich in organic matter (5.53%) as against in the last two test soil (clay loam) was poor in organic matter. Also, monthly cumulative rainfall was an average of 46.3 mm in the first test and 49.89 mm in the second. This result is confirmed by the work of Habtamu and Million (2013) who found

that Ethiopian field pea genotypes were highly influenced by environment. Interaction genotype  $\times$  year revealed significant differences for parameters AFF and NNFFN, STL, STW, LL, LW, PL and NGP. While the differences were not significant for both parameters PLE and PWI.

### Phenological character

Phenology was represented by a single character which is the appearance of the first flower. This character is dependent on the environment. Flowering is considered very late when the number of days between sowing and appearance of the first flower exceed 60 days (Solberg et al., 2015). Thus, all genotypes which were the subject of our study are very late, with an average of 109.25 days. Similar results were obtained by Gatti et al. (2011) who observed the first flower after an average of 105.64 days.

### Morphological characters

The highest plant height was taken from genotype p593 (111.33 cm), while p350 showed the lowest (63.66 cm) plant height (Table 6). Researchers obtained lengths varying between 65.67 and 132 cm (Ceyhan and Avci, 2015), 51.20 and 111.30 cm (Georgieva et al., 2016), 65.67 and 126 cm (Khan et al., 2013). On the other hand, the average (63.64 cm) reported by Habtamu and Million (2013) is lower than that obtained in the present work (90.05 cm). Difference in plant height might be due to genetic characteristic of genotypes and adaptability to a particular environment (Khan et al., 2013), especially that this character is dependent on the environment (Solberg et al., 2015).

**Table 6.** Means of different genotypes.

Code	Demchi1	Bouch1	p539	p593	p595	p596	p069	p071	p072	p073	p350	Sefrou
SL	95.85 <sup>cde</sup>	80.15 <sup>abc</sup>	109.68 <sup>e</sup>	111.33 <sup>e</sup>	96.93 <sup>cde</sup>	72.95 <sup>ab</sup>	89.81 <sup>bcd</sup>	87.48 <sup>bc</sup>	79.35 <sup>abc</sup>	87.6 <sup>bcd</sup>	63.66 <sup>a</sup>	105.8 <sup>de</sup>
AFF	102.66 <sup>c</sup>	130.16 <sup>e</sup>	102.66 <sup>c</sup>	94.66 <sup>a</sup>	118.5 <sup>d</sup>	94.66 <sup>a</sup>	91.33 <sup>a</sup>	106 <sup>c</sup>	118 <sup>d</sup>	101.16 <sup>b</sup>	122.16 <sup>d</sup>	120 <sup>d</sup>
NNFFN	11.49 <sup>a</sup>	18.75 <sup>gh</sup>	17.46 <sup>fg</sup>	18.56 <sup>gh</sup>	18.37 <sup>gh</sup>	14.52 <sup>bc</sup>	15.38 <sup>cde</sup>	13.5 <sup>b</sup>	16.52 <sup>ef</sup>	18.46 <sup>gh</sup>	15.22 <sup>b</sup>	19.25 <sup>h</sup>
STL	5.61 <sup>cde</sup>	5.36 <sup>bcd</sup>	6.07 <sup>e</sup>	6 <sup>de</sup>	5.27 <sup>bc</sup>	6.2 <sup>e</sup>	5.94 <sup>de</sup>	5.79 <sup>cde</sup>	4.55 <sup>a</sup>	4.76 <sup>ab</sup>	5.39 <sup>bcd</sup>	5.17 <sup>abc</sup>
STW	3 <sup>cd</sup>	2.55 <sup>ab</sup>	3.15 <sup>de</sup>	2.96 <sup>bcd</sup>	2.62 <sup>abc</sup>	3.57 <sup>e</sup>	3.07 <sup>d</sup>	2.84 <sup>abcd</sup>	2.4 <sup>a</sup>	2.47 <sup>ab</sup>	2.55 <sup>ab</sup>	2.51 <sup>a</sup>
LL	4.2 <sup>def</sup>	3.53 <sup>abc</sup>	4.21 <sup>def</sup>	3.92 <sup>cde</sup>	3.76 <sup>bcd</sup>	4.09 <sup>def</sup>	4.47 <sup>f</sup>	4.33 <sup>ef</sup>	3.11 <sup>a</sup>	3.4 <sup>ab</sup>	3.27 <sup>ab</sup>	3.46 <sup>abc</sup>
LW	2.37 <sup>ef</sup>	1.96 <sup>cd</sup>	2.2 <sup>def</sup>	1.98 <sup>ce</sup>	1.89 <sup>cd</sup>	2.4 <sup>f</sup>	2.52 <sup>e</sup>	2.22 <sup>def</sup>	1.45 <sup>ab</sup>	1.64 <sup>abc</sup>	1.35 <sup>a</sup>	1.74 <sup>bc</sup>
PL	5.91 <sup>bcd</sup>	5.25 <sup>ab</sup>	6.92 <sup>de</sup>	5.98 <sup>bcd</sup>	7.15 <sup>de</sup>	6.59 <sup>cde</sup>	5.95 <sup>bcd</sup>	7.26 <sup>e</sup>	5.4 <sup>abc</sup>	6.86 <sup>de</sup>	4.19 <sup>a</sup>	5.17 <sup>ab</sup>
NGP	6.84 <sup>c</sup>	6.65 <sup>c</sup>	7.42 <sup>de</sup>	7.46 <sup>e</sup>	7.18 <sup>cde</sup>	7.09 <sup>cde</sup>	6.48 <sup>b</sup>	5.77 <sup>a</sup>	6.86 <sup>cd</sup>	6.66 <sup>c</sup>	9.94 <sup>f</sup>	6.90 <sup>cde</sup>
PLE	5.39 <sup>cd</sup>	4.71 <sup>ab</sup>	5.19 <sup>bcd</sup>	5.35 <sup>cd</sup>	5.04 <sup>bcd</sup>	4.79 <sup>abc</sup>	4.88 <sup>abc</sup>	5.49 <sup>d</sup>	5.25 <sup>cd</sup>	4.43 <sup>a</sup>	6.62 <sup>e</sup>	5.19 <sup>bcd</sup>
PWI	0.81 <sup>bc</sup>	0.85 <sup>bc</sup>	0.79 <sup>b</sup>	0.81 <sup>bc</sup>	0.76 <sup>b</sup>	0.77 <sup>b</sup>	0.82 <sup>bc</sup>	0.86 <sup>c</sup>	0.78 <sup>b</sup>	0.68 <sup>a</sup>	0.65 <sup>a</sup>	0.79 <sup>b</sup>
WTS	13.81 <sup>g</sup>	13.81 <sup>g</sup>	13.20 <sup>fg</sup>	11.61 <sup>e</sup>	11.35 <sup>de</sup>	10.63 <sup>cd</sup>	15.51 <sup>h</sup>	18.64 <sup>i</sup>	12.88 <sup>f</sup>	8.99 <sup>b</sup>	8.04 <sup>a</sup>	10.48 <sup>c</sup>
NPM2	223.66 <sup>de</sup>	247.00 <sup>de</sup>	223.33 <sup>de</sup>	291.66 <sup>e</sup>	171.33 <sup>cd</sup>	156.66 <sup>bcd</sup>	253.33 <sup>de</sup>	86.33 <sup>abc</sup>	58.66 <sup>ab</sup>	67.00 <sup>abc</sup>	2.00 <sup>a</sup>	87.00 <sup>abc</sup>
WPM2	288.22 <sup>def</sup>	266.66 <sup>def</sup>	339.55 <sup>ef</sup>	408.89 <sup>f</sup>	181.33 <sup>bcd</sup>	220.44 <sup>cde</sup>	261.33 <sup>def</sup>	149.33 <sup>abcd</sup>	45.33 <sup>ab</sup>	58.66 <sup>ab</sup>	32.00 <sup>a</sup>	96.00 <sup>abc</sup>

To get an idea of the variability of stipule and leaflet, we studied traits related to their sizes (length and width of stipule, length and width of leaflet). The results obtained showed a high level of variation. For example, we find that width of leaflet which showed an important CV (25.10%) exhibit averages ranging from 1.35 to 2.52 cm (Table 6).

As regards the size of the pod, genotype p350 had the longest pod (6.62 cm), the lowest pod length was found in genotype p073 (4.43 cm). In general, pod size is a varietal character, but it is also affected by vigor of plant (Khan et al., 2013).

A wide range of variation was noticed for peduncle length (3.10 - 9.75 cm) (Table 5).

**Yield characters**

In order to estimate yields, we measured the number of grain per pod, weight of 100 seeds, number of pods per 1 m<sup>2</sup> and weight of pods per 1 m<sup>2</sup>.

For the parameter number of grain per pod, the

genotype p350 differed significantly from the other genotypes with an average of 9.94 grain per pod (Table 6) which represented the high value. P071 showed the minimum value (5.77 grain per pod). The results we have obtained are higher than those (2.87 and 5.73 grain per pod) obtained by Ceyhan and Avci (2015). This character can be used in breeding programs to improve yield.

For the weight of 100 seeds, the means varied between 8.04 g (p350) and 18.64 g (p071). The most productive genotype was p593 (Table 6) (408.89 g per 1 m<sup>2</sup> for weight pods per 1 m<sup>2</sup> and 291.66 per 1 m<sup>2</sup> for number of pods per 1 m<sup>2</sup>). This value is high compared to that obtained by Wozniak (2013) who studied the yielding of pea under different tillage conditions and had results varying between 243 and 320 pods per 1 m<sup>2</sup>.

**Correlation matrix**

Table 7 represents the correlation coefficients

among all the quantitative traits. The appearance of the first flower was significantly and negatively correlated with three characters which are: Stipule width, leaflet length and leaflet width. Characters of yield were significantly and positively correlated with the traits related to size of stipule and leaflet, for example a significant correlation was found between leaflet length and weight of 100 seeds. Number of pods per 1 m<sup>2</sup> has a positive significant correlation with leaflet width. Weight of pods per 1 m<sup>2</sup> was correlated with three characters: Stipule length, leaflet length and width. This can be explained by photosynthesis which is more important when the size of stipules and leaflets are large, therefore the yields are higher. Basaran et al. (2012) and Basaran et al. (2013) noted a strong correlation between leaflet length and weight of 100 seeds in grass pea. Number of seeds per pod was negatively correlated to weight of 100 seeds. A negative significant correlation between these two characters was found by Gati

**Table 7.** Correlation matrix on fifteen traits.

	SL	AFF	NNFFNN	STL	STW	LL	LW	PL	MNFP	PLE	PWI	NGP	WTS	NPM2	WPM2
SL	1.00														
AFF	-0.29 <sup>NS</sup>	1.00													
NNFFNN	0.35 <sup>NS</sup>	0.34 <sup>NS</sup>	1.00												
STL	0.23 <sup>NS</sup>	-0.59 <sup>NS</sup>	-0.33 <sup>NS</sup>	1.00											
STW	0.11 <sup>NS</sup>	-0.73*	-0.45 <sup>NS</sup>	0.89**	1.00										
LL	0.35 <sup>NS</sup>	-0.70*	-0.49 <sup>NS</sup>	0.83**	0.79*	1.00									
LW	0.29 <sup>NS</sup>	-0.65*	-0.45 <sup>NS</sup>	0.78*	0.82*	0.94***	1.00								
PL	0.38 <sup>NS</sup>	-0.50 <sup>NS</sup>	-0.06 <sup>NS</sup>	0.28 <sup>NS</sup>	0.39 <sup>NS</sup>	0.56 <sup>NS</sup>	0.50 <sup>NS</sup>	1.00							
MNFP	-0.12 <sup>NS</sup>	0.14 <sup>NS</sup>	0.64	-0.06 <sup>NS</sup>	-0.17 <sup>NS</sup>	-0.27 <sup>NS</sup>	-0.33 <sup>NS</sup>	0.05 <sup>NS</sup>	1.00						
PLE	-0.25 <sup>NS</sup>	0.27 <sup>NS</sup>	-0.35	0.07 <sup>NS</sup>	-0.14 <sup>NS</sup>	-0.16 <sup>NS</sup>	-0.37 <sup>NS</sup>	-0.52 <sup>NS</sup>	-0.11 <sup>NS</sup>	1.00					
PWI	0.40 <sup>NS</sup>	-0.12 <sup>NS</sup>	-0.13	0.39 <sup>NS</sup>	0.29 <sup>NS</sup>	0.56 <sup>NS</sup>	0.64 <sup>NS</sup>	0.26 <sup>NS</sup>	-0.15 <sup>NS</sup>	-0.31 <sup>NS</sup>	1.00				
NGP	-0.33 <sup>NS</sup>	0.27 <sup>NS</sup>	0.04	0.00 <sup>NS</sup>	-0.11 <sup>NS</sup>	-0.41 <sup>NS</sup>	-0.51 <sup>NS</sup>	-0.59 <sup>NS</sup>	0.08 <sup>NS</sup>	0.73*	-0.71*	1.00			
WTS	0.30 <sup>NS</sup>	-0.26 <sup>NS</sup>	-0.26	0.35 <sup>NS</sup>	0.20 <sup>NS</sup>	0.69*	0.64 <sup>NS</sup>	0.34 <sup>NS</sup>	-0.07 <sup>NS</sup>	-0.21 <sup>NS</sup>	0.82**	-0.69*	1.00		
NPM2	0.57 <sup>NS</sup>	-0.44 <sup>NS</sup>	0.05	0.61 <sup>NS</sup>	0.53 <sup>NS</sup>	0.63 <sup>NS</sup>	0.70*	0.26 <sup>NS</sup>	-0.24 <sup>NS</sup>	-0.38 <sup>NS</sup>	0.60 <sup>NS</sup>	-0.30 <sup>NS</sup>	0.45 <sup>NS</sup>	1.00	
WPM2	0.59 <sup>NS</sup>	-0.49 <sup>NS</sup>	-0.03	0.75*	0.64 <sup>NS</sup>	0.68*	0.70*	0.29 <sup>NS</sup>	-0.24 <sup>NS</sup>	-0.22 <sup>NS</sup>	0.57 <sup>NS</sup>	-0.19 <sup>NS</sup>	0.38 <sup>NS</sup>	0.95***	1.00

et al. (2011). Stipule length and width, leaflet length and width were correlated between themselves. The same result was obtained by Gatti and al (2011). Number of grain per pod was correlated positively and significantly with pod length. Ali et al. (2007) and Tofiq et al. (2015) found also a significant positive correlation between these two characters. Pod length and width were correlated between themselves. Avci and Ceylan (2006) and Pal and Singh (2012) showed a high positive correlation between these traits.

### Principal component analysis

Principal component analysis was performed based on eleven characters (Table 8). The first three principal components (PC) accounted for 85.92% of the variation (56.86, 19.08 and 9.95%

for PC1, PC2 and PC3 respectively). The first component was negatively related to STL, STW, LL, LW, PWI, WTS, NPM2 and WPM2, while AFF showed positive correlation.

The second component was associated with NGP. The PLE contributed to the third component. These results are confirmed by Gixhari et al. (2014) who studied PCA on pea and noted that some of these characters as leaflet length and width, number of seed per pod, weight of 1000 seeds and yield per genotype contributed to a great part of variability. In the work of Esposito et al. (2007) on pea genotypes, the two first components explained 67.7% of variability in the first season of experiment and 69.8% in the second one. According to the same author, length and width of stipule, length and width of leaflet, length and width of pod, number of days to flowering explained most of the variability. The study conducted by Umar et al. (2014) on pea

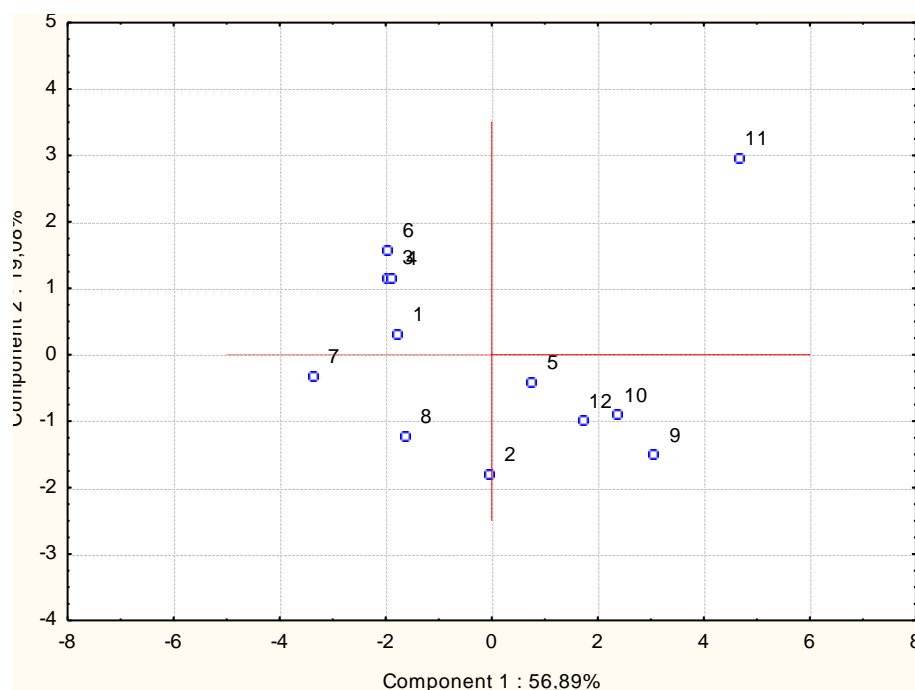
genotypes from different origins showed that the two parameters: Pod length and width are related to the first component which explained 40.29% of variation.

### Cluster analysis

As was the case for the principal component analysis (Figure 1), cluster analysis ranged pea genotypes into two different groups (Figure 2). The first cluster which is characterized by a greater yielding (NPM2 and WPM2) includes demchi 1, p069, bouch1, p539, p593, p595 and p596. The second cluster which could be defined as the low-yielding group contains p071, sefrou, p072, p073 and p350. These results were in concordance with the work of Esposito et al. (2007) who identified two groups, the first one contained genotypes with low yielding, the second

**Table 8.** Principal component analysis (PC) of 12 pea genotypes based on eleven traits.

Parameter	PC 1	PC 2	PC 3
Eigen values	6.26	2.09	1.09
% of variance	56.89	19.08	9.95
Cumulative %	56.89	75.97	85.92
Characters	Eigenvector		
AFF	0.681	-0.294	0.477
STL	-0.801	0.521	0.143
STW	-0.787	0.482	0.212
LL	-0.927	0.139	0.072
LW	-0.958	0.021	-0.052
PLE	-0.374	0.584	0.646
PWI	-0.717	-0.498	0.407
NGP	0.531	0.793	0.189
WTS	-0.679	-0.481	0.396
NPM2	-0.817	0.015	0.054
WPM2	-0.828	0.196	0.119



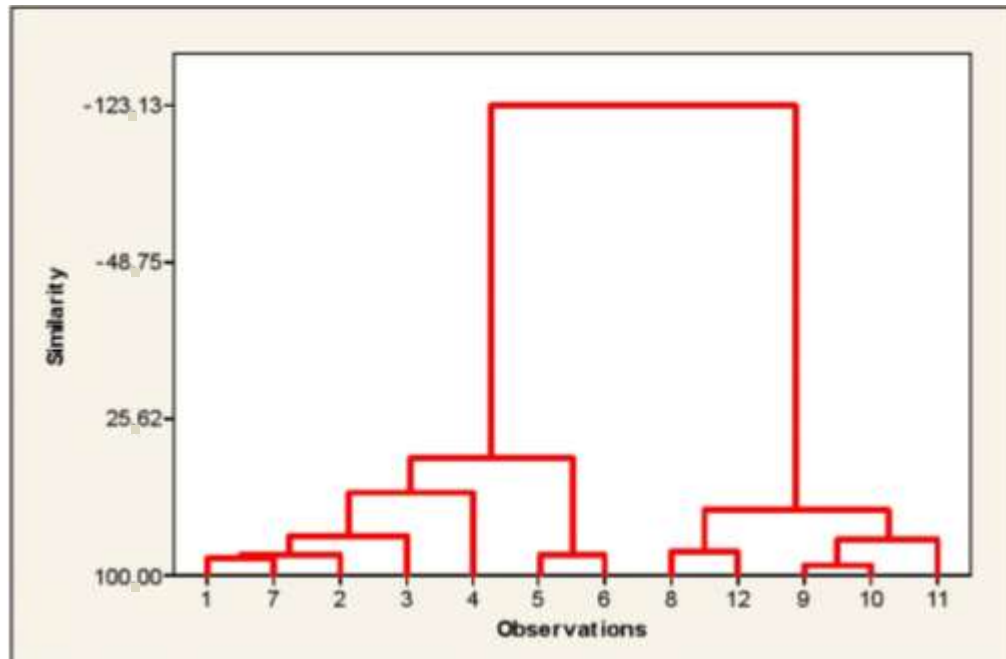
**Figure 1.** Distribution of pea landraces based on the first two components.

group comprises high yielding genotypes. Two clusters were revealed in the study of Georgieva et al. (2016), one of the two groups includes the low grain yield genotypes, the other group contains high yield genotypes.

**Conclusion**

The genetic diversity of Algerian pea genotypes was

studied using different agro-morphological traits. The results showed the existence of a great variability within the studied genotypes of pea. This variability can be used in the work of selection and improvement is observed on the level of precocity to flowering but also for other qualitative and quantitative traits. On the other hand, expression of characteristics is highly influenced by the environment. Two groups were noted by dendrogram. The first group (demchi 1, p069, bouch1, p539, p593,



**Figure 2.** Dendrogram of twelve genotypes based on morphological data.

p595 and p596) was characterized by a high pod yield; the other group comprised less productive genotypes (p071, sefrou, p072, p073 and p350). Otherwise, the genotype p593 produced the best results for pods yield.

### Conflict of Interests

The authors have not declared any conflict of interests.

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