Journal of Horticulture and Postharvest Research

University of Birjand

Morphological evaluation of Tunisian garlic (*Allium sativum* L.) landraces for growth and yield traits

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A B S T R A C T

Purpose: Despite the significance of garlic as a food product and high annual income, until now there are no local commercialized Tunisian cultivars with registered names, which lead to the lack of recommended varieties of high yielding. This work is aimed to create the first garlic gene bank collection in Tunisia, evaluate the variation, identify yield related traits and structure genetic diversity among them. **Research method:** Thirty six local garlic landraces from the main production regions of Tunisia were collected and recorded in the National Gene Bank of Tunisia database, then grown in a gene bank field for multiplication. The phenotypic diversity was conducted on the basis of fourteen quantitative characteristics add to flowering ability. **Findings:** High diversity among Tunisian garlic landraces was detected. The bulb weight and bulb diameter explain the most significant variation of the yield. The cluster analysis sorted the 36 genotypes into three main groups as cluster 1 (11 accessions), cluster 2 (20 accessions), and cluster 3 (5 accessions). However, the grouping of genotypes did not correspond with their geographic origin. The highest genetic distance was reported between NGBTUN442 and NGBTUN452, however NGBTUN429 and NGBTUN434 found to be most similar with the lowest dissimilarity. **Research limitation**: Morphological traits need to be investigated overtime. **Originality/Value:** This study is interesting since it presents the first creation of the garlic gene bank in Tunisia. The results will provide basis information for the efficient use of the local garlic germplasm and help breeders to easily select out the desirable materials.

INTRODUCTION

Allium is a species-rich and taxonomically complicated genus. In fact, modern classifications accept more than 750 species and about 60 taxonomic groups (Fritsch & Friesen, 2002). Garlic (*Allium sativum* L.) is an important vegetable crop for its culinary and medicinal properties (Petropoulos et al., 2018), grown worldwide and has a wide range of climatic and soil adaptation (Yeshiwas et al., 2018). Although it is an asexually propagated crop, and reproduces only by vegetative way, a large-scale diversity of different ecotypes has been established over time in various cultivation areas (Panthee et al., 2006; Stavělíková, 2008; Volk & Stern, 2009). Biodiversity plays a great role in human existence and in healthy function of natural systems although it is on the way of depletion dominantly due to anthropogenic activities. This requires the conservation of biodiversity either *in situ* or *ex situ* or both methods in combination based on the conservation situation and its objective (Kasso & Balakrishnan, 2013). Several countries, including United States, United Kingdom, Japan, Germany, Italy, Australia, Chile, Czech Republic, and Brazil, have created Germplasm Banks for the conservation of garlic accessions due to limited species recombination (Stavělíková, 2008). These include seed banks (for seeds), field gene banks (for live plants), *in vitro* gene banks (for plant tissues and cells), and cryopreservation. The principal aim of gene bank conservation is to maintain genetic diversity alive as long as possible and to reduce the frequency of regeneration that may cause the loss of genetic diversity. Plants that cannot be conserved as seeds because of their recalcitrant nature or are clonally propagated are traditionally conserved as live plants in ex situ field gene banks (Kasso & Balakrishnan, 2013). In addition, the phenotypic variability in these banks should be quantified in order to allow an effective use of accession collections, and this warrants the need for studies on the morphological characterization of cultivars (Silva et al., 2014). Morphological traits diversity of crop germplasm resources plays a significant role for breeding program (Panthee et al., 2006). In fact, choosing suitable genotypes should be done to achieve an economic yield with good quality (Abdel-Rasheed & Moustafa, 2016). Therefore, the knowledge of genetic association between garlic yield and its components would improve the efficiency of breeding programs by identifying appropriate indices for selecting garlic varieties (Al Gehani & Kanbar, 2013) and understanding the variation between accessions (Wang et al., 2014).

In Tunisia, local garlic is rich in organo-sulphur compounds (Jabbes et al., 2012). It is the most expensive local vegetable at mid-season and occupies nearly 3% of the total vegetable area. However, despite its significance as a food product and its high annual income, the genetic background and diversity of Tunisian garlic landraces has not been well characterized. Indeed, local and most south Mediterranean garlic are not classified horticulturally (Jabbes et al., 2011). Farmers are using garlic cloves from a previous crop as seeds in a household small-scale production system (Ayed et al., 2018). Tunisian garlic is threatened by genetic erosion, uncontrolled introduction of foreign germplasm and is under-exploited which may lead to its loss and the extinction of the local breed (Jabbes et al., 2011). Although the morphological, biochemical and molecular characterization of some Tunisian garlic landraces was obtained by Jabbes et al. (2011; 2012). Unfortunately, the collection was not preserved subsequently for future improvement programs. So, until now there are no local commercialized Tunisian cultivars with registered names, which lead to the lack of recommended or released variety of high yielding. In view of this, programs to produce certified virus-free materials of popular cultivars are, recently, being carried out in Tunisia in collaboration with the National Gene Bank (Ayed et al., 2018). The present study is the first step of this program, aimed to (1) collect and record the local garlic germplasms in the National Gene Bank of Tunisia database, (2) evaluate the phenotypic diversity among Tunisian garlic germplasms, to understand the

genetic background, (3) identify yield related traits which could be suitable descriptors in future clonal selection programs, and (4) structure the collection on the basis of agro morphological traits.

MATERIAS AND METHODS

Plant material and field experiments

This study included Thirty six local garlic landraces including all major garlic-growing regions in Tunisia. The bulbs were collected, during 2012-2013 seasons, from growers in 21 localities, 9 provinces of Tunisia and were recorded in the National Gene Bank of Tunisia database (Table 1). In fact, the first step of description of garlic collection genetic resources comprises the morphological characterization in association with passport data (Stavělíková, 2008).

Table 1. Origin of the Tunisian local garlic (*Allium sativum*) collection

Accessions code	Province	Locality	Latitude (N)	Longitude (E)
NGBTUN405	Nabeul	Fernine	36.15324	10.49260
NGBTUN406	Nabeul	Oued El Khatf	36.186720	11.11220
NGBTUN407	Nabeul	Oued El Khatf	36.186720	11.11220
NGBTUN408	Béja	Ksar Mezouara	36.53100	9.169920
NGBTUN409	Béja	Faouar	36.179100	9.205980
NGBTUN410	Béja	Faouar	36.63960	9.166440
NGBTUN411	Béja	Faouar	36.139560	9.159300
NGBTUN412	Béja	Faouar	36.139560	9.159300
NGBTUN413	Béja	Amdoun	36.45780	9.198180
NGBTUN414	Béja	Zahrat Maydan	36.204300	9.61500
NGBTUN416	Béja	Ayaida	36.118380	9.83280
NGBTUN417	Kairouan	Batan	35.76444	9.99083
NGBTUN419	Kairouan	Batan	35.76444	9.99083
NGBTUN421	Kairouan	Sbikha	35.93325	10.02081
NGBTUN425	Kairouan	Sbikha	35.93325	10.02081
NGBTUN429	Bizerte	Bakarya	37.151200	9.174780
NGBTUN430	Bizerte	Bou Mkhila, Mateur	37.97200	9.84900
NGBTUN431	Bizerte	Bou Mkhila, Mateur	37.82800	9.12900
NGBTUN432	Bizerte	Henchir El Ghelta	37.151200	9.174780
NGBTUN433	Bizerte	Borj El Dhahab	37.29100	9.192660
NGBTUN434	Bizerte	Ferdawin Ghezala	37.83040	9.109980
NGBTUN435	Sidi Bouzid	Om Ladham	35.136980	9.127320
NGBTUN436	Sidi Bouzid	Om Ladham	35.190980	9.26520
NGBTUN437	Sidi Bouzid	Om Ladham	35.72240	9.174060
NGBTUN438	Sidi Bouzid	Om Ladham	35.72240	9.174060
NGBTUN439	Sidi Bouzid	Om Ladham	35.29040	9.130860
NGBTUN440	Sidi Bouzid	Om Ladham	35.29040	9.130860
NGBTUN441	Sidi Bouzid	Ksar Mzara Bir Hefey	35.126000	9.155940
NGBTUN442	Sidi Bouzid	Ksar Mzara Bir Hefey	35.126000	9.155940
NGBTUN443	Kasserine	Rahmet-Sbitla	35.14640	9.162780
NGBTUN444	Kasserine	Rahmet-Sbitla	35.14640	9.162780
NGBTUN446	Kasserine	Ghara-Sbitla	35.14640	9.162780
NGBTUN451	Mahdia	--	--	--
NGBTUN452	Kebili	Etarfaya-Douz	33.84480	8.140220
NGBTUN454	Kebili	Nefzaoua-Douz	33.19740	9.63000
NGBTUN456	Gabes	Chénini	33.57120	10.3840

The accession number serves as a unique identifier for accessions within a genebank collection, and is assigned when a sample is entered into the genebank collection. Once assigned this number should never be reassigned to another accession in the collection. Even if an accession is lost, its assigned number should never be re-used (IPGRI, 2001). Then, the collection was grown in the research farm of the High Agronomic Institute of Chott Mariem in the province of Sousse (Tunisian coastal city 35° 54' 55" N and 10° 33' 37" E), for multiplication. Field experiment was conducted using complete randomized block design with three replicates with a density of 33 plants/m^2 (330.000 plants/ha). Garlic was planted in field in the autumn time, namely at mid-November and harvested at the end of June.

Agro-morphological traits
Morphological traits were measured at various growth stages according to descriptors for garlic developed by International Plant Genetic Resources Institute (IPGRI, 2001) and International Union for the Protection of New Varieties of Plants (UPOV, 2001). Totally, fourteen quantitative traits add to the ability to produce flower stalk were investigated. The first set of morphological characteristics, relating to leaves, pseudostems and collet, was measured at the end of the growth stage, 145 days after planting. The traits related with bulb, like bulb height, bulb diameter, bulb weight, clove diameter, clove number per bulb, mean clove weight and yield were recorded two months after harvesting. The bulbs were stored traditionally at ambient temperature in a well-ventilated room. Fifteen plants from each replicate were randomly chosen and measured.

Data analysis
Basic statistics including mean, maximum, minimum and coefficient of variation (CV) were applied to compare genetic variation of quantitative traits among accessions. Analysis of variance (ANOVA), as confirmatory analysis, was performed and then the means of results were compared by LSD analysis. Following correlation analysis were used to estimate the relationship between garlic yield and other evaluated variables. The 36 garlic ecotypes were clustered by the Ward method clustering procedure. Statistical analyses are done using the software SPSS (Inc., ver. 20.0).

RESULTS AND DISCUSSION

Phenotypic variation
The results demonstrate existence of high diversity among Tunisian garlic landraces (Table 2). The variability between accessions is statistically significant for the fourteen agro-morphological characters, which indicated the presence of wide spectrum of variability among the local garlic accessions. It spite of exclusively propagated by vegetative method, crop shows wide variation in agromorphological traits (Benke et al., 2018). Similar results have been reported by AlGehani & Canbar, Panse et al. (2013), Wang et al., (2014) and Yeshiwas et al., (2018). Whereas, Baghalian et al. (2005) report that Iranian garlic ecotypes were significantly different for the weights of bulbs and cloves, but non different for the number of cloves/bulb. Evaluation in post-harvesting traits showed that bulb weight was the character with the highest coefficient of variation (CV = 56.54) followed by the clove number (CV = 34.82). Whereas, in the pre-harvesting stage, the highest and lowest genetic variation was related to leaf length (CV = 27.41) and leaf width (CV = 0.19), respectively. The findings of Baghalian et al., (2006) are in contrast to that of the present findings, since they scored the clove number as the highest coefficient of variation (CV = 10.38) in the post-harvesting stage, and they founded the highest and lowest genetic variation related to leaf width (CV = 11.55)

and leaf number (CV = 1.99), respectively. The mean yield (Yi) of the collection is almost 6.94 T/ha. The maximum yield (10.65 T/ha) was recorded in NGBTUN409 from Beja and the minimum (4.43 T/ha) was observed in NGBTUN444 from Kasserine. In contrast, Jabbes et al. (2012) were detected the highest yield in KS11 from Kasserine and the lowest one in BJ16 from Beja with an average 4 T/ha. NGBTUN405 from Nabeul showed the lowest leaves/plant (7.48), leaf length (47.53 cm), pseudostem diameter (6.15 mm) and collet diameter (6.55 mm). While, the highest leaves/plant (NL) (14.05), leaf length (LL) (47.53 cm), and pseudostem diameter (10.56 mm) was exhibited in NGBTUN452 from Kebili, NGBTUN456 from Gabes, and NGBTUN430 from Bizerte, respectively. The highest and narrow leaf width (WL) was found in NGBTUN439 and NGBTUN435, respectively, from the same locality in Sidi Bouzid. Thus, significant differences were observed not only between the different provinces but also between the genotypes of the same locality. This could be attributed to different cultivation practices and soil properties (Petropoulos et al., 2018). The clove average weight (CW) is 2.25 g; it ranges from 1.15 g (NGBTUN419 from Kairouan) to 4.65 g (NGBTUN435 from Sidi Bouzid). The mean weight of the bulb (WB) was found of 21.04 g, it varies from 13.43 g (NGBTUN444 from Kasserine) to 32.29 g (NGBTUN409 from Beja). The average clove number (NC) by bulb is 11.75. The accession NGBTUN435 from Sidi Bouzid has the lowest NC (4.67) whereas NGBTUN452 from Kebili has the highest one (27.81). These findings are in agreement with Jabbes et al. (2012) who detected the highest NC (38.7) in KB6 from Kebili. A wide range of variation was recorded for growth characters like pseudostem length (LPT) (14.81-31.75 cm) with an average of 20.61 cm, bulb equatorial diameter (DB) (31.36-44.52 mm) with an average 38.25 mm, and clove length (LC) (20.9-32.57 mm) with an average of 26.79 mm. In the same context, Kaushik et al. (2016) explained the variation observed in morphological characters among the genotypes by the difference in genetically constituents as well as environmental effects. Findings of divergence study of all the 36 accessions suggested that genetic material have sufficient amount of diversity on morphological basis which can be helpful for breeder and researchers to comprehensively understand the genetic background of the collection and more easily select the target accessions, especially those with high yield (Wang et al. 2014).

About the qualitative trait of scape presence/absence, only eight accessions presented scapes in this collection. In fact, NGBTUN417 from Kairouan, NGBTUN434 from Bizerte, and NGBTUN441 from Sidi Bouzid showed 4.76% flowering plants. NGBTUN419 from Kairouan, NGBTUN437 from Bizerte and NGBTUN443 from Kasserine showed 9.52% flowering plants. Whereas, NGBTUN454 from Kébili and NGBTUN456 from Gabes showed 19.05% and 33.33% flowering plants, respectively. In the same context, Jabbes et al. (2012) presented 7 accessions with flower stems among 31 Tunisian accessions. In fact, the accessions K1, SBZ4, JND14, JND15, and BJ18 presented some flower scape, when G5 and BZT26 showed high frequency of flower scape. Garlic has low flowering ability. The emission of floral stalks presents in garlic an aspect very related to the varietal characters, the most usual classifications being based on the presence or not of flower stalk (Etoh & Simon, 2002). Thus, the accessions studied can be classified, according to their ability to form or not a flowering stem, in the botanical group *Allium sativum* ssp. *sativum*. This group presents two types under Tunisian conditions: the intermediate type including the eight accessions mentioned above, and the type without flowering stem which includes the rest of the accessions. The information related to flowering would benefit the study on true seed production and future sexual breeding programs. This result need to be confirmed by future investigation overtime.

Table 2. Mean performance of thirty-six Tunisian garlic for fourteen morphological characters.

Acc	NL	LL	WL	LPT	DPT	DC	DB	IB	WB	NC	LC	WiC	CW	Yi
405	7.48	34.61	1.32	16.38	6.15	6.55	34.00	0.2	17.52	10.48	25.80	11.42	1.70	5.78
406	7.57	38.51	1.61	18.34	6.79	7.04	34.30	0.21	17.38	11.33	23.98	10.63	1.88	5.74
407	7.90	38.82	1.43	18.07	6.48	6.96	31.36	0.22	13.52	9.95	27.59	11.89	1.32	4.46
408	9.71	42.16	1.75	18.43	9.24	10.70	37.92	0.28	22.69	10.48	27.84	14.07	2.17	7.49
409	9.67	43.44	1.9	19.60	9.61	10.88	43.46	0.25	32.29	12.90	31.55	14.13	2.65	10.65
410	10.86	44.19	1.95	21.31	10.28	12.00	37.11	0.33	23.05	9.67	32.57	14.16	2.70	7.61
411	9.37	42.88	1.91	15.78	8.13	8.97	36.40	0.25	20.29	9.00	26.43	12.10	2.50	6.69
412	9.48	43.34	1.85	17.62	8.86	10.40	36.09	0.29	22.38	11.10	26.63	13.22	2.08	7.39
413	11.14	43.45	1.80	20.12	9.30	11.43	36.76	0.31	21.77	11.05	29.35	12.87	1.99	7.19
414	11.14	45.56	1.98	20.60	9.76	11.61	41.95	0.28	26.95	12.24	28.14	13.90	2.45	8.89
416	10.81	42.50	1.73	18.52	8.44	10.60	35.52	0.3	16.43	10.29	23.83	10.52	1.53	5.42
417	9.52	44.26	1.98	18.24	8.70	8.85	41.52	0.21	22.76	10.57	30.75	13.39	2.24	7.51
419	11.05	39.64	1.20	27.55	7.19	8.58	37.52	0.23	15.10	20.29	20.90	9.46	1.15	4.98
421	10.19	42.81	1.82	20.48	8.73	10.30	36.82	0.28	19.57	12.00	26.77	11.34	1.74	6.46
425	9.90	42.02	1.74	19.45	8.30	9.42	36.88	0.26	20.52	10.00	25.28	11.74	2.06	6.77
429	9.95	43.32	1.76	21.07	8.56	9.79	37.77	0.26	22.71	11.71	27.60	11.73	2.09	7.50
430	11.14	46.80	2.06	22.12	10.56	12.58	40.75	0.31	25.90	11.38	29.25	12.36	2.42	8.55
431	10.10	42.40	1.68	20.02	8.27	9.26	41.25	0.23	22.29	11.62	27.10	12.38	2.24	7.35
432	8.86	44.16	1.82	20.31	8.26	10.08	38.14	0.27	20.48	11.81	28.55	13.59	1.81	6.76
433	9.10	42.35	1.76	18.83	7.52	8.49	38.74	0.22	22.24	12.00	26.02	11.29	1.92	7.34
434	9.52	43.88	1.81	19.64	8.82	9.46	38.08	0.25	21.76	12.00	26.26	12.41	1.92	7.18
435	10.95	39.74	1.07	28.81	6.34	7.15	35.08	0.21	17.00	4.67	24.40	14.66	4.65	5.61
436	8.67	43.87	1.87	17.69	8.20	8.17	36.79	0.23	18.71	9.86	25.87	12.26	1.88	6.18
437	10.10	39.14	1.08	26.31	6.50	7.60	43.23	0.18	24.14	19.86	25.80	9.64	1.64	7.97
438	10.71	38.98	1.13	25.81	6.88	7.89	41.57	0.2	22.67	17.33	23.61	9.88	1.81	7.48
439	9.81	46.78	2.19	17.19	8.54	9.92	44.52	0.27	29.29	11.48	28.01	13.70	2.98	9.66
440	9.33	46.53	1.96	19.33	8.09	8.54	36.97	0.23	18.95	9.86	26.66	13.69	1.93	6.25
441	10.10	38.51	1.19	25.68	6.34	7.21	38.99	0.19	17.29	6.24	26.20	13.60	3.71	5.70
442	9.35	41.74	1.79	14.81	7.06	7.18	36.38	0.2	17.43	7.33	27.18	14.17	2.81	5.75
443	9.67	45.73	1.95	19.33	7.60	8.18	38.50	0.21	20.90	7.43	28.56	14.74	2.96	6.90
444	10.24	38.69	1.09	26.45	6.17	7.01	33.30	0.21	13.43	10.07	23.74	9.54	4.20	4.43
446	9.67	45.03	2.10	18.38	8.59	8.71	40.79	0.21	24.38	10.52	28.14	13.69	2.38	8.05
451	10.81	37.93	1.62	16.29	6.78	7.57	35.79	0.21	16.29	9.19	26.34	12.29	1.77	5.37
452	14.05	39.83	1.30	31.75	7.20	8.87	42.03	0.21	22.19	27.81	23.81	8.53	1.46	7.32
454	11.30	42.58	1.68	22.63	7.61	8.71	38.73	0.23	19.19	19.43	24.48	10.93	1.68	6.33
456	11.29	47.53	2.01	19.64	9.16	10.41	40.45	0.26	25.38	9.48	28.33	14.19	3.17	8.38
Min	7.48	34.61	1.07	14.81	6.15	6.55	31.36	0.18	13.43	4.67	20.9	8.53	1.15	4.43
Max	14.05	47.53	2.19	31.75	10.56	12.58	44.52	0.33	32.29	27.81	32.57	14.74	4.65	10.65
Range	6.57	12.92	1.12	16.94	4.41	6.03	13.16	0.15	18.86	23.14	11.67	6.21	3.5	6.22
Mean	10.01	42.32	1.69	20.61	8.03	9.09	38.25	0.24	21.04	11.75	26.79	12.37	2.25	6.94
SE	0.07	0.19	0.02	0.17	0.07	0.09	0.2	0.002	0.27	0.22	0.14	0.11	0.05	0.09
CV	3.71	27.41	0.19	23.1	3.62	6.01	31.38	0.005	56.54	34.82	14.31	9.79	1.97	6.16
	**	**	**	**	**	**	**	**	**	**	**	**	**	**

NL: leaf number, LL: leaf length, WL: leaf width, LPT: pseudostem length, DPT: pseudostem diameter, DC: collet diameter, DB: bulb diameter, IB: bulbing index, WB: bulb weight, NC: cloves number/bulb, LC: clove length, WiC: clove width, CW: clove weight, Yi: yield.

Correlation between characters

Significant positive correlation of bulb yield per hectare was observed with clove length, bulb diameter, and bulb weight (Table 3). The more these variables are maximized the higher will be the yield. Choosing genotypes with high levels of these characteristics, and application of appropriate agronomical techniques will guaranty higher yield (Panthee et al., 2006). These findings corroborated with the earlier findings of Jabbes et al. (2012), Panse et al. (2013), and Sabir et al. (2017). The highest correlation was found positively among bulb yield with bulb weight (r = 1) and bulb diameter (r = 0.87), respectively. Obviously, if there is bigger bulb diameter or higher weight bulb, higher yield could be expected. The findings were quite similar as reported by Panthee et al. (2006), Wang et al. (2014), and Yeshiwas et al. (2018). The clove length is moderately positively correlated (r = 0.41) with the yield. This finding is

in good consistent with the findings of Sabir et al. (2017), while Wang et al. (2014) were found a low positive correlation coefficient. In the other hand, there was a strong positive correlation (r = 0.87) between bulb weight and bulb diameter, and between length and width of leaves (r = 0.76). Whereas, cloves number was moderately negatively correlated (r = -0.4) with cloves weight but positively correlated with pseudostem length (r = 0.34), and bulb diameter (r = 0.36). Similar results have been reported by Baghadian et al. (2005).

Table 3. Simple correlation between values of the garlic ecotypes for different botanical *Ex situ* traits

	NL	LL	WL	LPT	DPT	DC	DB	IB	WB	NC	LC	WiC	CW	Yi
NL	1													
LL	0.26	1												
WL	0.12	**0.76**∗∗	1											
LPT	0.47∗∗	0.09	-0.28	1										
DPT	0.33∗∗	0.58∗∗	0.64∗∗	0.05	1									
DC	0.38∗∗	0.5∗∗	0.54∗∗	0.12	0.83∗∗	1								
DB	0.17	0.2	0.16	0.14	0.2	0.17	1							
IB	0.27	0.36∗∗	0.41∗∗	0.06	0.66∗∗	0.85∗∗	-0.34∗∗	1						
WB	0.09	0.24	0.27	0.01	0.29	0.26	**0.87**∗∗	-0.19	1					
NC	0.24	-0.002	-0.12	**0.34**∗∗	0.01	0.04	**0.36**∗∗	-0.14	0.23	1				
LC	-0.08	0.21	0.3∗∗	-0.2	0.25	0.19	0.25	0.04	0.4	-0.19	1			
WiC	-0.12	0.12	0.16	-0.18	0.12	0.07	0.12	0.01	0.23	-0.42∗∗	0.59∗∗	1		
CW	-0.01	-0.01	-0.02	0.04	0.002	-0.01	0.09	-0.04	0.19	**-0.4**∗∗	0.2	0.37∗∗	1	
Yi	0.09	0.24	0.27	0.01	0.29	0.26	**0.87**∗∗	-0.19	**1**∗∗	0.23	**0.41**∗∗	0.23	0.19	1

NL: leaf number, LL: leaf length, WL: leaf width, LPT: pseudostem length, DPT: pseudostem diameter, DC: collet diameter, DB: bulb diameter, IB: bulbing index, WB: bulb weight, NC: cloves numer/bulb, LC: clove length, WiC: clove width, CW: clove weight, Yi: yield.

Table 4. Inter cluster mean performance of yield and contributing traits of Tunisian local garlic.

Ward method	Total No. of accessions	NL	LL	WL	LPT	DPT	DC	DB	IB	WB	NC	LC	WiC	CW	Yi
Cluster I	11	9.39	39.80	1.51	19.71	6.99	7.67	35.26	0.22	16.84	8.95	25.58	12.10	2.54	5.56
Cluster II	20	10.00	44.29	1.89	19.58	8.84	10.05	39.22	0.26	23.31	10.96	28.17	13.13	2.29	7.69
Cluster III	5	11.44	40.03	1.28	26.81	7.08	8.33	40.62	0.21	20.66	20.94	23.72	9.69	1.55	6.82
		∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗∗	∗	∗∗

NL: leaf number, LL: leaf length, WL: leaf width, LPT: pseudostem length, DPT: pseudostem diameter, DC: collet diameter, DB: bulb diameter, IB: bulbing index, WB: bulb weight, NC: cloves numer/bulb, LC: clove length, WiC: clove width, CW: clove weight, Yi: yield.

Cluster analysis

Cluster analysis based on morphological traits is an older breeding tools to get understand genetic resource needed to select genotypes for large scale multiplication and planning crop improvement program (Benke et al., 2018). The cluster analysis (Ward 1963 method) based on fourteen agro-morphological traits was shown as a dendrogram of dissimilitude representing the closest accessions in homogeneous groups. It sorted the 36 Tunisian garlics into three main groups (Fig. 1). The first group was formed by eleven accessions (4 from Sidi Bouzid, 3 from Nabeul, 2 from Beja, 1 from Kasserine and 1 from Mahdia), that are characterized by a lower production in the main agro-morphological characters except the clove weight. Whereas, the second group was constituted by the most important garlic landraces (6 from Bizerte, 6 from Beja, 3 from Kairouan, 2 from Kasserine, 2 from Sidi Bouzid and 1 from Gabes) that are characterized by the highest yield (7.69 T/ha), bulb weight (23.31 g), clove weight and length, leaf dimension, and pseudostem diameter (8.84 mm), which might be exploited for these several traits. The latest group had only five accessions (2 from Sidi Bouzid, 2 from Kebili and 1 from Kairouan) having the maximum bulb diameter (40.62 mm), leaf number (11.44), pseudostem length (26.81 cm) and the minimum bulbing index (0.21) (Table 4). Thus, cluster analysis based on morphological traits performed on genetic resources make breeder easier to understand the germplasm and select the potential

material among large-scale accessions with high efficiency (Wang et al., 2014). The highest genetic distance (D^2 = 837.282) was reported between NGBTUN442 from SidiBouzid (cluster I) and NGBTUN452 from Kebili (cluster III), however the lowest dissimilarity (D^2 = 6.195) corresponded to the most related accessions, was founded between NGBTUN429 and NGBTUN434 (cluster II) from the two localities of Bizerte, Bakarya and Ferdawin Ghezala, respectively. Generally, the grouping of genotypes did not correspond with their geographic origin, as accessions from same locality were clustered into different groups and accessions originated from different localities clubbed in one cluster. The present results are in accordance with the findings of Benke et al. (2018), Jabbes et al. (2012), and Panthee et al. (2006). It seems that these germplasms have been exchanged among farmers from different areas, so it is likely that garlic ecotypes were conserved under combined effect of natural and human selective pressure (Baghalien et al., 2006).
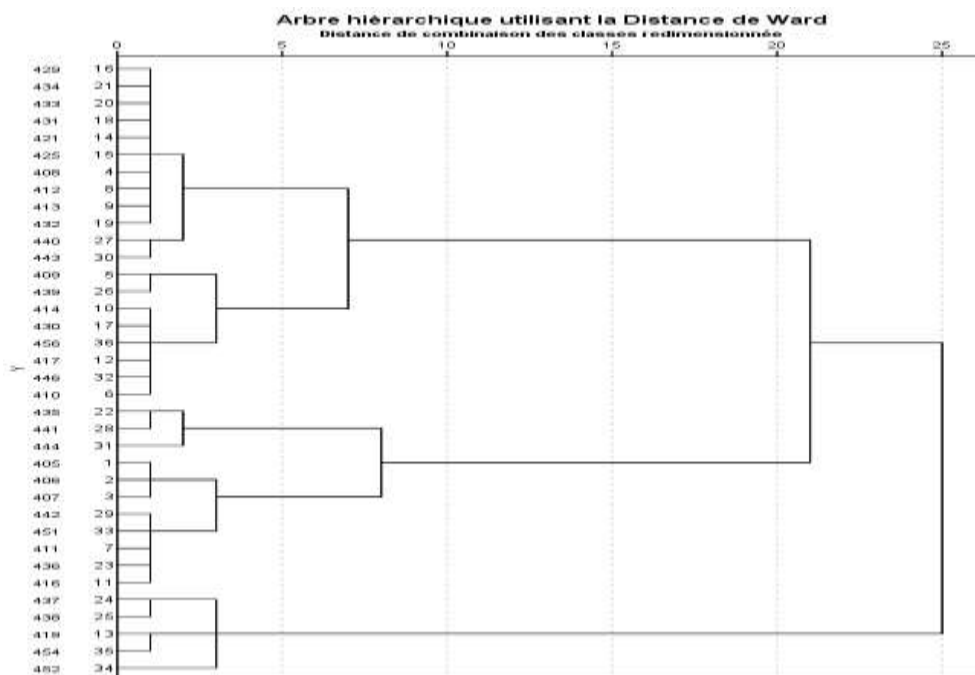
Fig. 1. Dissimilarity dendrogramme generated by HCA using SPSS.20. Software showing three major clusters on the basis of morphological traits of 36 Tunisian local garlics.

CONCLUSION

The first step of description of Tunisian garlic genetics resources including the morphological characterization in association with passport data was established. This collection presents the first garlic gene bank in Tunisia. The result will obviously be helpful for breeder and researchers to comprehensively understand the genetic background of the garlic collection and more easily select the target accessions, especially those with high yield and provide flower scape.

ACKNOWLEDGMENTS

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ارزیابی مورفولوژیکی ارقام سیر تونسی برای ویژگی‌های رشد و عملکرد

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چکیده:

با وجود اهمیت سیر به عنوان یک محصول غذایی و درآمد سالانه بالا، تاکنون هیچ رقم تجاری تونسی با نام ثبت شده وجود ندارد، که موجب شده است واریته‌های توصیه شده با عملکرد بالا موجود نباشند. این کار با هدف ایجاد اولین کلکسیون بانک ژن سیر در تونس، ارزیابی تغییرات شناسایی صفات مرتبط با عملکرد و ساختار تنوع ژنتیکی در میان آنها است. ۳۶ گیاه سیر محلی از مناطق عمده تولیدی تونس جمع آوری و ثبت شده در پایگاه بانک ژن ملی تونس انتخاب و سپس در مزرعه بانک ژن برای تکثیر پرورش یافتند. تنوع فنوتیپی بر اساس ۱۴ ویژگی کمی مربوط به توانایی گلدهی انجام شد. تنوع زیادی در میان گیاهان سیر تونس شناسایی شد. وزن پیاز و قطر پیاز بیشترین تغییر عملکرد را موجب شدند. تجزیه کلاستر ۳۶ ژنوتیپ را به سه دسته اصلی به عنوان خوشه ۱ (۱۱ پیوست)، خوشه ۲ (۲۰ پیوست) و خوشه ۳ (۵ پیوست) طبقه بندی کردند. با این حال، گروه بندی ژنوتیپ‌ها با خاستگاه جغرافیایی آنها مطابقت ندارد. بیشترین فاصله ژنتیکی بین NGBTUN442 و NGBTUN452 حاصل شد. اما GBTUN429 و NGBTUN434 بیشترین تشابه با کمترین تفاوت را دارند. این مطالعه جالب است زیرا ایجاد اولین بانک ژن سیر در تونس را ارائه می‌دهد. نتایج حاصل اطلاعات پایه برای استفاده کارآمد از ژرم پلاسم سیر محلی را مهیا کرده و به اصلاح کنندگان برای گزینش مواد مطلوب کمک می‌کند.

کلمات کلیدی: وزن پیاز، گلبرگ، حفاظت، بانک ژن، تنوع مورفولوژیک