

## Univariate and Multivariate Analysis of Agronomical Traits of Preselected Argan Trees

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### Abstract

A collection of thirty argan trees (*Argania spinosa* (L.) Skeels), representing the Aoulouz provenance in southwest of Morocco were used to study genetic variability and selection for three years. In this study, the genetic diversity of thirty genotypes (tree mothers) of argan (*Argania spinosa*) collected from Aoulouz was evaluated using agro-morphological characters. The main objective of the study was to assess and describe with multivariate analysis the genetic diversity in order to select good candidate trees for a future breeding program. The results obtained showed a large variation for all the traits examined. Analysis of variance using general linear model provided a significant variation between genotypes. Furthermore, genotypic and phenotypic variances for quantitative traits, particularly for seed length, seed width, almond length and oil content were higher. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters. High heritability was recorded for oil content (97.90%), seed width (72.68%) and seed length (57.55%) respectively, indicating the additive gene action. In addition, a three dimensional plot based on principal coordinate analysis method was used to evaluate the performance genotypes as to the production of oil for three years. The genotypes 'Ao-12R', 'Ao-7R', 'Ao-4R', 'Ao-4V', 'Ao-11R', 'Ao-8V' and 'Ao-7V' were found to be the best for high oil content. Identification and selection with superior agronomic traits may be an effective method for genetic improvement of argan trees, and a first step for further breeding studies.

**Keywords:** *Argania spinosa*, genotype, heritability, oil content, selection

### Introduction

Argan (*Argania spinosa* L. Skeels, Fam. Sapotaceae) is one of the most important oil seed plants in the world. It is native to Morocco, where is naturally distributed mainly in arid and sub arid of Southern - West areas. Due to their useful products (i.e., wood collection, grazing, oil), argan tree is one of the most economically and socially important tree species for the local population (Lybbert *et al.*, 2011). It is a long-lived tree, growing widely under different architecture forms. The seed of mature tree is a source of excellent vegetable oil. This oil is very stable due to the high percentage of polyunsaturated fatty acids. Several studies of lipid composition of argan seeds have been published (Charrouf and Guillaume, 1999, 2002; Gharby *et al.*, 2011; Nerd *et al.*, 1994). Furthermore, it is one of the most expensive oils in the world markets, used for food, pharmaceutical and cosmetic industries (Lybbert *et al.*, 2011). Moreover, drought stress, high exploitation and strong demand of oil contribute to the degradation, yield reduction and regression of surfaces of argan trees (Nouaim *et al.*, 2007). Degradation of the argan trees is a serious problem for the south west of Morocco and it becomes necessary to develop conservation programs. Tree improvement is a stepwise process involving exploration, collection, evaluation, breeding, multiplication, distribution and conservation of genetic resources (Mishra, 2009). In the aim to

meet the requirement of massive exploitation of oil argan, evaluation of good yielding argan tree is directly needed to select highly productive individuals. The selection is the most important activity in all tree breeding programs (Zobel and Tolbert, 1984), and variability is a key factor for selection programs. Therefore, it is necessary to detect the existing variation between the genotypes. So, in parallel with this approach, a guide to the genetic selection is examining the tree-to-tree variability in a number of relevant traits and identifying elite trees (White *et al.*, 2007). Thus, several studies have examined the potential of argan by estimating genetic variability in different sites of argan tree (Ait Aabd *et al.*, 2011; Bani Aameur and Ferradou 2001; Nouaim *et al.*, 2007; Zunzunegui *et al.*, 2010). The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection (Falconer and Mackay, 1996; Maniee *et al.*, 2009; Silva *et al.*, 2009; Volker *et al.*, 2008), and are strategic parameters for genetic improvement. Hence, genotype-environment or genotype-year interactions are important to decide a possible breeding method to improve cultivars with adequate adaptation to environments (Fox *et al.*, 1997; Jenni and Hayes, 2010). However, such genetic gain from multi-trait selection depends upon the level of additive genetic variability in each trait, the selection intensity and the genetic correlations among traits (Falconer and Mackay, 1996).

A number of studies have been initiated to assess variation in fruits, nuts and kernels of some important indigenous African tree species such as *Adansonia digitata* (Assogbadjo *et al.*, 2006; Sanchez *et al.*, 2011), *Tamarindus indica* (Fandohan *et al.*, 2011), *Balanites aegyptiaca* (Abasse *et al.*, 2011), *Irvingia gabonensis* (Leakey *et al.*, 2000) and *Sclerocarya birrea* subsp. *caffra* (Gouwakinou *et al.*, 2011; Leakey *et al.*, 2005:). Most of these studies have documented a continuous variation between and within studied populations for the investigated traits and have highlighted the possible ability to derive improved cultivars from the wild populations for the purposes of domestication (Sanchez *et al.*, 2011). Besides, the first step in the plus tree selection is to state the selection criteria. So, previous studies carried out in oleaginous plant have found correlations among some fruits, seed traits related to the oil content and other factors such as moisture and soil nutrient (Iqbal *et al.*, 2009; Kaushik *et al.*, 2007a; Nehdi *et al.*, 2012; Rao *et al.*, 2008; Yadav *et al.*, 2011) and several studies have been done on selection for high oil yield (Divakara *et al.*, 2010; Kaushik *et al.*, 2007b; Mishra, 2009). The aim of this study was to evaluate levels of genetic diversity in thirty argan trees of Aoulouz region, and to evaluate agronomic and morphological traits for a future breeding program. In this way, it might be possible to select the genotypes that show the most interesting characteristics and a quality product.

## Materials and methods

### Study area

Field expeditions were carried out in summer 2008, 2009 and 2010 in Aoulouz region (Province of Taroudant). The sampling site is located approximately at latitude 30°43' N, longitude 08°09' E and at an altitude of 730-850 m. The site features a semi-continental climate.

Annual precipitation is very irregular and ranges from 123 to 587 mm, whilst the mean annual temperature is around 21°C. Thirty trees were selected and geographical data including altitude, latitude and longitude were recorded for each tree, using a GPS device and projected on map after transformation using Global Mapper V.13 (Fig. 1). For each tree, 90 mature fruits were randomly collected and evaluated to select the superior genotypes.

### Morphological characterization

Each year, ten morphological traits related to fruit, seed and almond were recorded for each tree. The measured characters were: fruit weight (g), seed weight (g), seed length (mm), seed width (mm), carpel number, almond number, almond weight (g), almond length (mm), almond width (mm) and oil content (%). The oil content was estimated by Soxhlet method; it was determined using the formula given by Khalil and Manan (1990).

### Statistical analysis

After evaluation of the investigated characters, an analysis of variance was performed using general linear model procedure of the software package Statistica V.6. Both univariate and multivariate analyses were performed on the data. The means were subjected to further statistical and genetically analysis. All statistical parameters: mean, range over years, variance and coefficient of variation were analyzed.

The mean square was used to estimate genetic variability parameters for the studied traits. Phenotypic and genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense, genetic advance as percent of mean, were worked out for fruit, seed, almond traits and oil content as suggested by Lush (1940), Johnson *et al.* (1955) and Toker (1998).

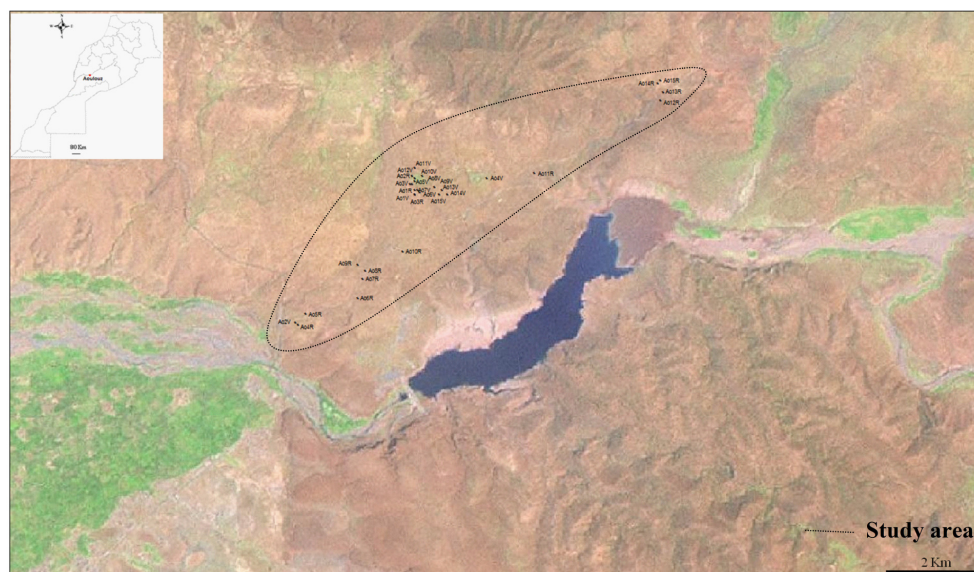


Fig. 1. Geographical distribution of the thirty trees selected in Aoulouz provence

The repeatability was estimated for observations both within and among individuals using the formula given by Falconer and Mackay (1996).

The data matrix was then prepared to be used in the subsequent multivariate analyses and genetic divergence analysis. The selection of number of performing genotypes for three years (2008-2010) was based on the criterion of oil content using the three dimensional plot based on principal coordinate analysis. Grouping of genotypes into different clusters was carried out following Tocher's procedure (Rao, 1952), and principal component analysis was done according to Rao (1964). The intra and inter-cluster distance and the relative contribution of different characters towards total divergence was calculated using the formula given by Singh and Choudhary (1977). Average

intra-cluster  $D^2 = \Sigma D^2_i/n$ , where,  $\Sigma D^2_i$  = Sum of distances between all possible combination ( $n$ ) of the varieties/lines included in a cluster,  $n$  = all possible combinations (Rahman and Al Munsur, 2009).

## Results

### Morphological analysis

Mean values of the studied morphological characters, tested each year (2008 to 2010) showed considerable variations between genotypes for fruits, seeds and almonds characters studied (Tab. 1, Fig. 2). All the genotypes displayed considerable differences in their mean performance. The maximum weight of fruit (5.61 g) and seed (3.38 g) were observed in 'Ao-10R', and the minimum value was re-

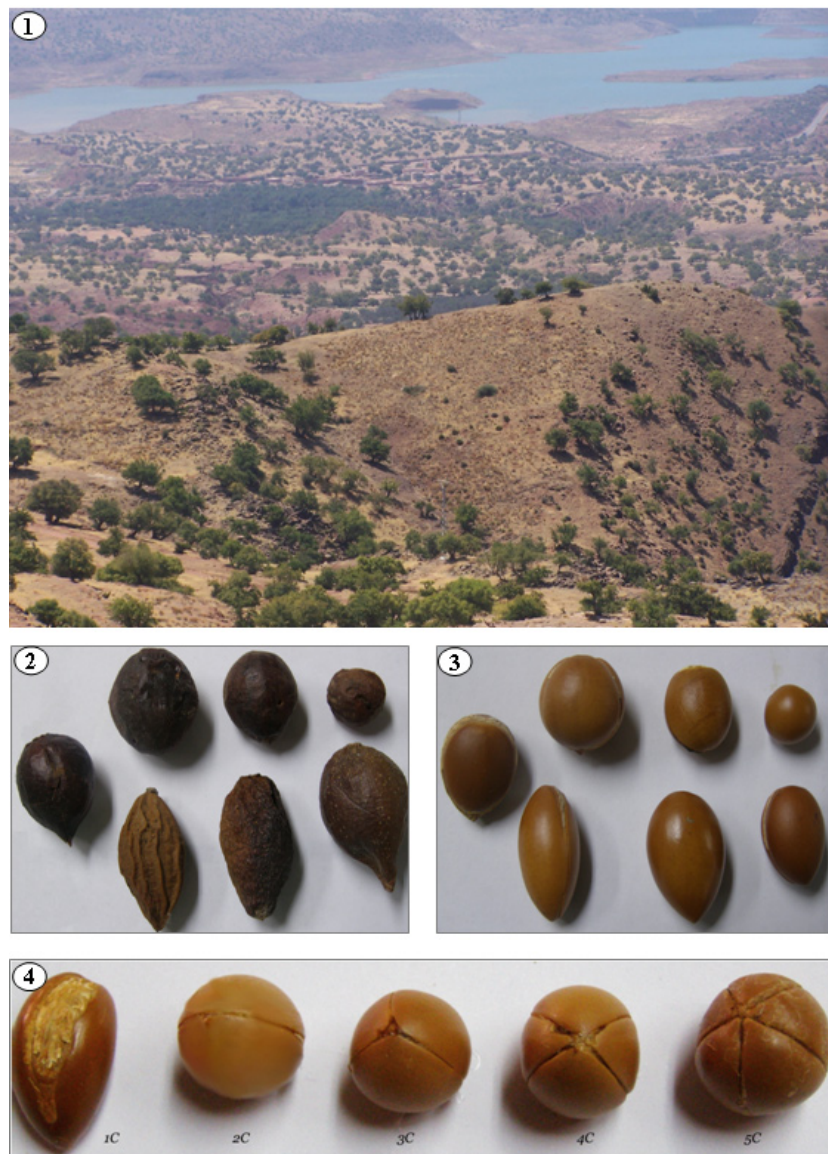


Fig. 2. Habitat and morphological variability of fruits and seeds of *Argania spinosa*: (1) naturally growing trees, (2), (3) fruits and seeds of argan tree with distinct morphological variations (results from 5 populations of Morocco), (4) number of carpels per seed (1C; 2C; 3C; 4C; 5C)

Tab. 1. Mean values for various characters studied of different genotypes over three years

Arbre N°	Fruit trait		Seed trait				Almond trait			Oil content
	FW	SW	SL	SWi	CN	AN	AW	AL	AWi	
'Ao-1V'	2.95	1.62	19.04	12.08	2.49	1.14	0.20	15.09	7.62	52.70
'Ao-2V'	3.56	2.01	20.83	12.92	2.20	1.04	0.23	18.81	8.78	51.17
'Ao-3V'	3.24	1.87	25.89	12.46	2.11	1.08	0.28	20.36	8.09	53.13
'Ao-4V'	3.21	2.00	20.31	13.68	2.46	1.15	0.23	17.19	8.83	55.03
'Ao-5V'	4.91	2.85	22.07	15.26	2.12	1.25	0.31	18.99	9.80	52.97
'Ao-6V'	3.52	2.09	20.51	13.26	2.05	1.21	0.28	16.17	8.34	52.68
'Ao-7V'	3.95	2.21	21.72	13.35	2.43	1.13	0.26	17.33	8.33	53.92
'Ao-8V'	3.15	1.82	18.94	13.14	2.12	1.18	0.24	15.55	8.55	54.72
'Ao-9V'	5.28	2.77	25.36	14.17	2.11	1.14	0.35	19.38	9.49	53.38
'Ao-10V'	2.48	1.58	17.77	12.61	1.78	1.03	0.19	13.54	7.61	52.93
'Ao-11V'	3.22	1.82	22.08	12.43	2.63	1.37	0.25	18.08	8.18	53.42
'Ao-12V'	2.49	1.45	16.13	12.47	2.11	1.06	0.17	12.86	8.03	52.57
'Ao-13V'	3.10	1.87	19.40	13.44	2.18	1.12	0.24	14.94	8.65	52.32
'Ao-14V'	4.36	2.65	23.44	14.67	1.92	1.12	0.34	18.50	9.43	51.57
'Ao-15V'	3.76	2.03	19.96	13.83	2.14	1.11	0.27	15.34	8.98	51.66
'Ao-1R'	4.58	3.08	25.82	16.64	2.22	1.15	0.31	19.05	8.93	53.06
'Ao-2R'	3.89	2.17	20.94	13.83	2.54	1.27	0.26	16.22	8.40	51.81
'Ao-3R'	3.38	1.99	21.88	13.25	2.20	1.11	0.25	17.52	8.77	50.50
'Ao-4R'	3.42	2.17	20.63	13.82	2.40	1.06	0.25	15.63	8.20	53.90
'Ao-5R'	4.06	2.44	20.10	15.31	2.08	1.07	0.23	15.58	9.55	52.85
'Ao-6R'	3.65	2.27	20.59	13.73	2.43	1.17	0.24	15.43	8.18	52.76
'Ao-7R'	3.71	2.25	20.08	14.52	2.29	1.16	0.29	16.30	9.57	55.07
'Ao-8R'	3.56	2.19	21.22	13.34	2.77	1.16	0.32	17.73	8.59	52.45
'Ao-9R'	2.49	1.48	17.86	11.83	2.57	1.18	0.26	15.05	8.27	52.44
'Ao-10R'	5.61	3.38	24.26	16.32	2.29	1.04	0.23	18.05	9.05	51.77
'Ao-11R'	4.50	2.14	23.61	13.21	2.31	1.08	0.31	18.38	8.51	54.33
'Ao-12R'	3.09	1.92	20.22	13.56	2.07	1.15	0.29	16.01	8.91	56.22
'Ao-13R'	3.39	1.70	21.41	13.06	2.16	1.16	0.30	17.49	9.59	52.86
'Ao-14R'	4.06	2.29	24.31	13.80	2.27	1.30	0.39	18.93	9.11	52.47
'Ao-15R'	4.53	2.60	21.94	14.76	2.34	1.11	0.28	15.90	9.02	50.36
LSD at 5%	0.009	0.004	0.02	0.02	0.002	0.001	0.06	0.01	0.001	0.82

FW: Fruit weight, SW: Seed weight, SL: Seed length, Swi: Seed width, CN: Carpel number, AN: Almond number, AW: Almond weight, AL: Almond length, Awi: Almond width, OC: Oil content (%)

corded in 'Ao-10V' (FW = 2.48 g) and 'Ao-12V' (SW = 1.45 g). 'Ao-12V' showed the lowest values for the almond weight. Seed length varied from 16.13 mm to 25.89 mm and almond length varied from 12.86 mm to 20.36 mm. So, the highest seed and almond length was recorded in 'Ao-3V' and smallest in 'Ao-12V'. Oil content expressed in percentage had a range of 50.36-56.22%, with the lowest value in 'Ao-15R' genotype and the highest one in 'Ao-12R'. Moreover, significant differences among genotypes were found for all traits studied.

#### Variability and genetic parameter estimates

The results of the analysis of variance, evaluation of mean and coefficient of variation over three years for the traits: fruit weight, seed weight, seed length, seed width, carpel number, almond number, almond weight, almond length, almond width and oil content are shown in Tab. 2. Significant variations among all the wild genotypes were found. A combined analysis of variance over three years

indicated that year, genotype and genotypes x year interaction were highly significant ( $p < 0.01$ ) for most of the tested characteristics.

The results showed a great phenotypic variation, mainly between genotypes, and revealed the existence of a potential for selection of genotypes under these environments.

Genotypic variance, phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance, and genetic advance in percent of mean for 10 different characters are presented in Tab. 3. The phenotypic variance and phenotypic coefficient of variation were higher than the genotypic variance or genotypic coefficient of variation for all the characters, suggesting the presence of environmental influence to some extent in the expression of these characters.

Higher values of genotypic and phenotypic variances were found for seed length, seed width, almond length, oil content. The highest phenotypic and genotypic coefficients of variation were found for the weight of fruit, seed and al-

Tab. 2. Analysis of variance (GLM) of some characters for thirty argan trees studied during 2008 to 2010

Variation sources	D.F	FW	SW	SL	SWi	CN	AN	AW	AL	AWi	OC
Years	2	320.67**	152.01**	6015.07**	2.84**	2.01***	9.66**	2.67**	4207.31**	435.48*	36.44***
Genotype	29	163.79**	56.80**	1493.06**	28.24**	12.61***	1.64**	0.62**	884.73**	91.02***	10.41***
Genotype × years	58	36.91**	11.77**	353.17**	4.05**	6.33***	0.65**	0.23**	353.02**	54.06***	4.19*
Range over years	-	2.48-5.61	1.45-3.38	16.13-25.89	11.83-16.64	1.78-2.77	1.03-1.37	0.17-0.39	12.86-20.36	7.61-9.80	50.36-56.22
Mean	-	3.70	2.16	21.28	13.69	2.26	1.14	0.27	16.85	8.71	52.90
CV%	-	21.04	21.26	11.11	8.34	9.57	6.85	17.98	10.74	6.67	2.49

\*, \*\*, \*\*\*significant at 0.05, 0.01 and 0.001 probability levels, respect. FW: Fruit weight, SW: Seed weight, SL: Seed length, Swi: Seed width, CN: Carpel number, AN: Almond number, AW: Almond weight, AL: Almond length, Awi: Almond width, OC: Oil content (%)

Tab. 3. Estimates of genetic variables for fruit, seed and almond traits in argan tree

Traits	Variance		Coefficient of variation (%)		Heritability (%)	Repeatability	Genetic advance as % mean
	Phenotypic	Genotypic	Phenotypic	Genotypic			
Fruit weight	1.26	0.75	29.70	22.91	59.52	0.76	0.94
Seed weight	0.50	0.30	33.04	25.59	60.00	0.74	0.59
Seed length	8.18	6.18	13.43	11.68	57.55	0.88	3.03
Seed width	3.88	2.82	14.45	12.32	72.68	0.75	2.00
Carpel number	0.26	0.11	22.46	14.61	42.30	0.47	0.30
Almond number	0.12	0.01	30.93	8.93	8.33	0.10	0.04
Almond weight	1.21	0.21	40.41	16.73	17.35	0.38	0.27
Almond length	5.10	2.76	13.43	9.88	54.11	0.74	1.71
Almond width	1.31	0.46	13.11	7.77	35.11	0.50	0.56
Oil content (%)	3.34	3.27	3.48	3.44	97.90	0.62	2.50

mond, indicating a higher degree of genetic variability for these characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for carpel number, almond number, almond weight, almond width, suggesting the presence of environmental influence in the expression of these characters. A higher heritability (broad sense) associated with high genetic advance in the fruit weight, seed weight, seed length, seed width, almond length and oil content (%), suggested an additive genetic effect. The improvement of these characters would be effective for phenotypic selection.

#### Genetic divergence analyses

The genetic divergence among thirty argan genotypes was studied in order to know the extent of divergence in the genotypes, to identify the superior genotypes for utilization in improvement program and to find out the contribution of different characters towards genetic divergence in argan tree. The hierarchical clustering analy-

sis technique performed on the thirty trees produced six groups (Tab. 4). Maximum number of genotypes (8 genotypes) was grouped in cluster VI. Cluster I consists of 6 genotypes followed by clusters II, III, IV, V with 4 genotypes for each cluster.

Inter and intra cluster distance ( $D = \sqrt{D2}$ ) values were worked out from divergence analysis and are presented in Fig. 3. The analysis showed homogeneity within groups with significant differences between mean values of traits from distinct groups.

Thus, the genotypes included within a cluster had less diversity among genotypes. The maximum intra-cluster distance was observed in cluster VI followed by cluster I, V, IV and III. The cluster II contained four genotypes and hence, its intra cluster distance was the lowest among the clusters. The highest inter cluster distance was observed between cluster VI and V, followed by clusters VI and III, VI and II, V and I, VI and IV and V and IV, suggesting more variability in genetic makeup of the genotypes

Tab. 4. Hierarchical clustering of argan tree based on measured agro-morphological traits

Cluster number	Number of genotypes	Genotypes included in clusters
I	6	'Ao-2V' - 'Ao-7V' - 'Ao-11V' - 'Ao-3R' - 'Ao-8R' - 'Ao-13R'
II	4	'Ao-6V' - 'Ao-13V' - 'Ao-4R' - 'Ao-6R'
III	4	'Ao-4V' - 'Ao-8V' - 'Ao-7R' - 'Ao-12R'
IV	4	'Ao-15V' - 'Ao-2R' - 'Ao-5R' - 'Ao-15R'
V	4	'Ao-1V' - 'Ao-10V' - 'Ao-12V' - 'Ao-9R'
VI	8	'Ao-3V' - 'Ao-5V' - 'Ao-9V' - 'Ao-14V' - 'Ao-1R' - 'Ao-10R' - 'Ao-11R' - 'Ao-14R'

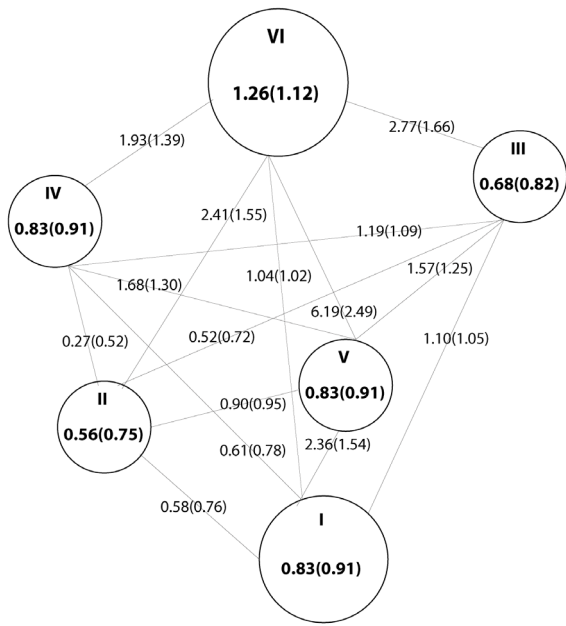


Fig. 3. Cluster divergences among six clusters of thirty genotypes of argan based on intra and inter distance

included in clusters V and VI. The intra cluster distance ranged from 0.56 to 1.26. Cluster II showed minimum intra-cluster distance (0.56) and maximum intra-cluster distance was exhibited by cluster VI (1.26) followed by cluster I, IV and V (0.83) (Fig. 3). Maximum inter cluster distance was found between clusters VI and V (6.19). Minimum inter-cluster distance was found to be minimum between clusters IV and II (0.27), suggesting a close relationship between them and a low degree of diversity among the genotypes.

Cluster means values of the ten characters are presented in Tab. 5. A perusal of results of cluster means revealed that cluster VI with eight genotypes exhibited the highest mean value for fruit weight (4.57), seed weight (2.63), seed length (24.34), seed width (14.57), almond weight (0.32),

almond length (18.96), almond width (9.05), and the lowest mean value for number of carpel per seed (2.17).

However, cluster V, with four genotypes, recorded the lowest mean for fruit weight (2.60), seed weight (1.53), seed length (17.70), seed width (12.25), number of almond per seed (1.10), almond weight (0.20), almond length (14.14) and almond width (7.88). Cluster III had genotypes with a high oil yield; contrary, the genotypes with the lowest oil content were grouped in cluster IV. In the case of mean number of carpel and almond per seed, cluster I had the highest number (2.40).

These findings of genetic divergence analysis were exploited to range the variability between genotypes for different traits in cluster.

The results on the contribution of individual characters towards the total divergence (Tab. 5) indicated that the contribution was the highest for oil content expressed in percentage (16.02) and volume (15.99), followed by number of almond per seed (12.15), and number of carpel per seed (10.84).

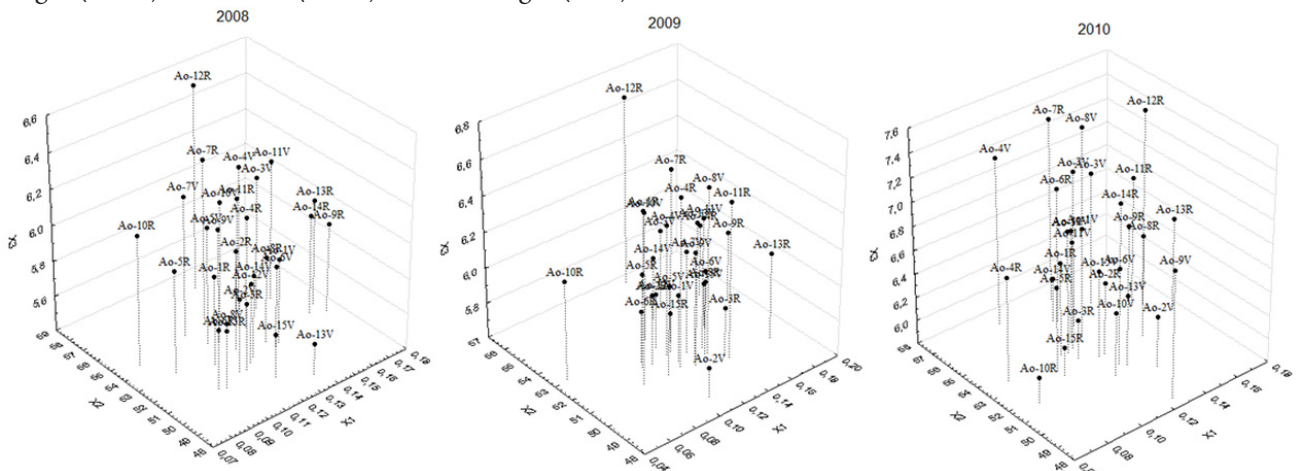
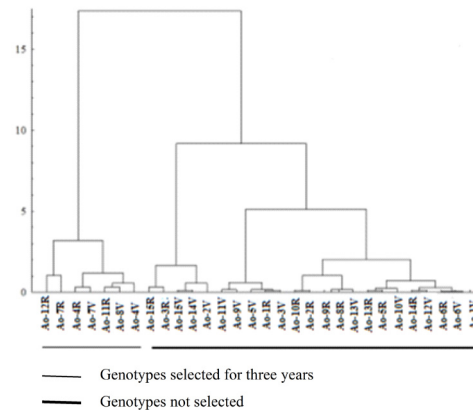


Fig. 4. Use of triplot analysis and hierarchical cluster analysis according to Ward method and generalized Euclidian distances for the investigation to identify the superior genotypes based on oil content data. Name of the genotypes are shown at the top of each bar for each years. The dendrogram grouping the genotypes selected and not selected based on the mean data for three years

Tab. 5. Cluster means and percent contribution of different characters in thirty genotypes of Argan

	FW	SW	SL	SWi	CN	AN	AW	AL	AWi	OC(%)	OV(ml)
Cluster I	3.51	1.99	21.52	13.06	2.40	1.16	0.27	17.83	8.71	52.39	6.19
Cluster II	3.42	2.10	20.28	13.56	2.26	1.14	0.25	15.54	8.34	52.92	6.23
Cluster III	3.29	2.00	19.89	13.73	2.23	1.15	0.26	16.26	8.96	55.26	6.68
Cluster IV	4.06	2.31	20.74	14.43	2.28	1.14	0.26	15.76	8.99	51.67	6.05
Cluster V	2.60	1.53	17.70	12.25	2.24	1.10	0.20	14.14	7.88	52.66	6.19
Cluster VI	4.57	2.63	24.34	14.57	2.17	1.15	0.32	18.96	9.05	52.84	6.27
Contribution of individual character towards total genetic divergence (%)	6.35	6.64	6.02	7.65	10.84	12.15	6.69	6.72	4.93	16.02	15.99

Genetic divergence existing in this studied population helps in the selection of suitable genotypes for utilization in breeding programs. Fig. 4 presented the genotypes selected in a collection of argan tree studied for three years (2008, 2009 and 2010).

The tri-dimensional triplot and dendrogram graphical method (Fig. 4) enabled the visual comparison of the genotypes studied and their interrelationships, and showed that the genotypes 'Ao-12R', 'Ao-7R', 'Ao-4R', 'Ao-4V', 'Ao-11R', 'Ao-8V', and 'Ao-7V' appear to be the best in each considered year and could be good candidates in a future breeding program. Therefore, these genotypes considered for genetic improvement of oil yield was clustered through the hierarchical cluster analysis (Fig. 4).

## Discussion

Evaluation program of various argan genotypes is essential to understand patterns of variability. The results showed a great variability of agro-morphological data, revealed the existence of a potential for selection and this quantification is important for tree improvement programs. Similar studies based on analysis of morphological characters have been carried out in the recent years (Ait Abd *et al.*, 2011; Bani Aameur and Ferradous, 2001; Zunzunegui *et al.*, 2010). Therefore, the existence of variability in traits is essential for domestication purpose. Hence, in the similar studies, the domestication utilizes the variability within species to select trees with desirable traits (Atangana *et al.*, 2002; Sanchez *et al.*, 2011; Silva *et al.*, 2009). This variability could offer some possibilities to identify the best genotypes. So, the agro-morphological characterization of plants is a common step in plant breeding for selection of parents and it also represents the first choice used for describing and classifying the germplasm (Gouwakinnou *et al.*, 2011). Improvement of argan oil production might be an important criterion of selection during domestication process. Means of quality traits of the genotypes show that the highest value for oil content was recorded by genotypes: 'Ao-12R', 'Ao-7R', 'Ao-4R', 'Ao-4V', 'Ao-11R', 'Ao-8V', and 'Ao-7V' which could be used as parental material for improvement of oil production. Oil content was an important contributor to the genetic divergence. Anuradha *et al.* (2004), Mohan and Seetharam (2005) and Loganathan *et al.* (2006) reported that oil con-

tent was the main contributor towards genetic divergence in sunflower.

The results indicated that there was significant variation between genotypes the traits varied also significantly yearly. These variations can be attributed to genetic characteristics of trees and environmental conditions, similar to what has been reported in other studies (Abasse *et al.*, 2011; Barracosa *et al.*, 2007; Fandohan *et al.*, 2011; Gouwakinnou *et al.*, 2011; Sidina *et al.*, 2009). Although, selection for morphological characters is a possible approach, an understanding of the inheritance of these characters, their genotype - environment interactions, and their correlation is needed to determine the validity of the breeding approach (Jenni and Hayes, 2010).

Multivariate analysis of genetic divergence among genotypes has resulted in the formation of six clusters and showed the existence of adequate genetic variation for further selection and breeding. Therefore, significant genetic distances between most clusters were observed from which selection of parents may be done. Parental material for improvement of argan oil production may be obtained from those genotypes which have high oil content in cluster III. Based on the results of this study, further restoration of argan genotypes selected from this population, through the assessment of genetic diversity should be practiced using progeny tests and cloning from mother plus tree, to test their adaptability under favorable and stress environments in diverse site conditions.

## Conclusions

The study revealed considerable phenotypic diversity among the argan genotypes analyzed based on their agro-morphological characters, which varied significantly yearly, probably as a result of the different environmental conditions. Evaluation of this diversity with uni and multivariate analysis indicated the most performing genotypes for improvement programs. Considering the overall results of the present study, argan trees from Aoulouz provenance evaluated in three years reveal a considerable range of diversity and a strong genotype and yearly interactions for several quantitative traits. Therefore, divergence analysis used to cluster the genotypes was an effective method in grouping these genotypes. It could be used to improve quantitative traits and thereby develop superior genotypes

with desirable traits, and facilitate the management and utilization in trees improvement by selecting a workable collection. Higher heritability of oil content might be a key option for the improvement of these traits through selection. Hence, it was found to be important as the major contributor for genetic divergence. The genotypes included in clusters I and III are those suitable for selection for higher oil content. With divergence analysis we have shown that, it is possible to find genotypes with valuable morphological traits interesting for improvement programs. So, the genotypes 'Ao-12R', 'Ao-7R', 'Ao-4R', 'Ao-4V', 'Ao-11R', 'Ao-8V' and 'Ao-7V' are recommended for best oil production and could be better exploited for future domestication. The success of sampling strategies for *ex-situ* conservation and breeding is to test the stability and adaptability to different cultivation conditions using progeny and seed clone. This management approach appears to be recommended to help delineate future strategies for the conservation of this species, to capture genetic diversity existing in argan population and to assure high yield performance under different environments.

#### Acknowledgements

This work was carried out with financial support from the European Union and Social Development Agency of Morocco (Project no. APLARG no. 03\_07) as well as the in kind support of the Association Agrotechnology for Souss Massa Draa. The authors express their sincere thanks for Association Agrotechnology for Souss Massa Draa, for Amehdar Mustapha and El Asbahani Abdelhafid for their technical assistance and rural women cooperatives for their help to choose the trees and the anonymous reviewers for specific comments.

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