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VARIATION OF SPECIFIC MORPHOLOGICAL TRAITS AND PLOIDY LEVEL OF FIVE *AEGILOPS* L. SPECIES IN MOROCCO.

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ABSTRACT. *Variation of specific morphological traits and ploidy level of five Aegilops L. species in Morocco.*The genus *Aegilops* L. represents an important natural source of useful genes for wheat breeding, with particular emphasis on biotic and abiotic stress resistance. For successful crosses, the primarily step is to select appropriate *Aegilops* accessions. In this paper, we studied five Moroccan species of an *Aegilops* collection on the basis of spike structure and chromosome number. Twenty-eight specific morphological characters were used to differentiate the species. Statistical analyses, in particular the DFA, allowed the characterization of the genetic variability of the species; the two first standardized axes explained 96,2% of the total variability and 100% of the entities were classified within their own group. In addition, the dendrogram constructed using morphological data reveals a significant variability within and between species. Cytogenetic study revealed four species, *A. geniculata* Roth, *A. triuncialis* L., *A. ventricosa* Tausch and *A. peregrina* Maire & Weiller, to be tetraploid. However, *A. neglecta* Req. ex. Bertol., where only two accessions are represented in the collection, revealed to be hexaploid, and can then be classified as *A. neglecta* subsp. *recta* Chennav.

Key words. *Aegilops*, Variation, Morphology, Ploidy, Morocco.

RÉSUMÉ. *Variation des caractères morphologiques spécifiques et niveau de ploïdie de cinq espèces Aegilops L. au Maroc.* Le genre *Aegilops* L. représente une importante source de gènes, potentiellement utilisables dans l'amélioration des blés cultivés (*Triticum spp.*) notamment pour la résistance aux stress biotiques et abiotiques. Le choix des accessions *Aegilops* à employer, dans un programme d'hybridation interspécifique, nécessite une caractérisation taxonomique et une évaluation préalables. L'objectif de ce travail a été d'étudier des accessions, appartenant à 5 espèces marocaines constituant une collection d'*Aegilops*, sur la base de caractères morphologiques spécifiques de l'épi et du niveau de ploïdie. La caractérisation phénotypique a été basée sur l'étude de 28 caractères morphologiques qui discriminent entre les espèces. Les résultats des analyses statistiques, en particulier de l'AFD, ont permis de caractériser la variabilité génétique de ces espèces et ont donné un pourcentage d'appartenance à l'espèce de 100%. Aussi, les deux premiers axes standardisés expliquent 96,2% de la variabilité totale. Un dendrogramme a été aussi construit, révélant une variabilité interspécifique. L'étude cytogénétique a révélé une tétraploïdie pour *A. geniculata* Roth, *A. triuncialis* L., *A. ventricosa* Tausch et *A. peregrina* Maire & Weiller. Quant à *A. neglecta* Req. ex. Bertol., une hexaploïdie a été mise en évidence pour les deux uniques accessions disponibles dans la collection, permettant de leur attribuer le nom *A. neglecta* subsp. *recta* Chennav.

Mots clés. *Aegilops*, Variation, Morphologie, Ploïdie, Maroc.

INTRODUCTION

The genus *Aegilops* L. has been one of the most intensively studied group among grasses, especially since it was confirmed to have a close relationship with cultivated wheat. *Aegilops L.* belongs to the family of *Poaceae* (Gramineae), first group described by Jussieu

in his book "Genera Plantarum" (Jussieu, 1789). Since then, several authors have concentrated their studies on this genus (Boissier, 1884; Zhukovsky, 1928; Eig, 1929; Sears, 1941; Kihara, 1946; Bor *et al.*, 1968; Hammer, 1980; Baum *et al.*, 1987; Perino & Prceddu, 1990 and Van Slageren, 1994).

Aegilops species are widely represented in Mediterranean and West Asian regions (Sakamoto & Kobayashi, 1980). They are well adapted to diverse disturbed environments, pastures, edges and within cultivated fields; which translate a huge morphological variability of the spike.

According to the classification of Van Slageren, the *Aegilops* genus comprises 22 diploid, tetraploid and hexaploid species (Van Slageren, 1994). The genus would probably originate from Transcaucasia (Hammer, 1980). All species are annual and autogame. The diversity of *Aegilops* make its taxonomy especially difficult. Therefore, for a proper evaluation of the species, it is necessary to check the ploidy level and the chromosome morphology. Indeed, an unacquainted observer may fail to distinguish between certain *Aegilops* species with different ploidy levels (tetra- vs hexaploid) if the observations are based only on morphological characteristics.

Cytogenetic studies of this genus have been especially used to establish genetic relationships in biosystematics research, and for assisted crop improvement programs. It is known that *Aegilops* species forms series of allopolyploids ranging from diploids (2n= 4x= 14) to hexaploids (2n= 6x= 42), with a basic set of chromosomes x= 7 (Sakamura, 1918). Senjaninova – Korczagina was probably the first author who worked on chromosome morphology in *Aegilops* (Senjaninova – Korczagina, 1932). Chennaveeraiah described the chromosomes morphology of 21 *Aegilops* diploids and polyploids (Chennaveeraiah, 1960). Despite this large amount of works (Zurabishvili *et al.*, 1978; Wains & Barnhart, 1991), there is still a need to extend cytogenetic investigation to further geographical areas. However, the majority of these studies were criticized for their limitation to few accessions of each species.

In Morocco, it has been reported, in an old herbarium database, seven tetraploid species of *Aegilops* (Kimber & Feldman, 1987; Van Slageren, 1994). Only five species were collected in 1994 - 1995 and identified on the basis of the morphological features of their inflorescences (Benlhabib et al., 2001). According to Kihara (1946) and Kimber (1983), their genome formula has been determined as: *A. geniculata* Roth (MU), *A. triuncialis* L. (UC), *A. ventricosa* Tausch (DN), *A. neglecta* Req. ex. Bertol. (UM or UMN) and *A. peregrina* Maire & Weiller (SU). They were distributed mainly in the northern area of the Rif mountains, the Central Plateaus of Saïs and Zaeir, the High and Middle Atlas mountains and the western coastal area from south of Tanger to north of Agadir. The first two species are widely distributed throughout the country. *A. ventricosa* grows on intermediate to high altitudes sites in humid and cold areas. *A. neglecta* seems to prefer littoral zones and never grows on dense surfaces but rather as loosely dispersed population (Benlhabib *et al.*, 2001). *A. peregrina* was recently collected in Rabat areas; it has been mentioned in Morocco previously in the "Flore de l'Afrique du Nord" (Maire, 1955), in the "Nouvelle flore d'Algérie et des régions désertiques méridionales" (Querzel & Santa, 1962-1963) and in the "Catalogue des plantes vasculaires du Nord du Maroc incluant des clés d'identification" (Valdés *et al.*, 2002).

In order to understand the taxonomic position of those *Aegilops* species growing in Morocco, a biosystematic study with several approaches was conducted. The present work deals with specific morphological traits and ploidy level. This characterization would allow us to confirm the diagnose of the prospectors

and to study the phenotypical variability within three of the five species of the collection.

MATERIALS AND METHODS

Plant Material

The morphological characterization was performed on dried plants belonging to the genus *Aegilops* that have been collected during summer seasons of 1994 and 1995 from different regions of Morocco. These plants were collected from natural populations growing on roadsides, pastures and edges of cultivated fields. Benlhabib *et al.* (2001) have described in detail these collection sites and populations. On the other hand, cytogenetic study was carried on root tips of some seedling samples of the collection.

The entire collection enclosing 151 accessions is maintained, by the Cereal Cytogenetic and Biotechnology Laboratory at the Agronomy Plants Breeding Department; I.A.V. Hassan II, as herbarium and stored seeds at –20°C. It is composed by 115 *A. geniculata*, 25 *A. triuncialis*, 7 *A. ventricosa*, 2 *A. neglecta* and 2 *A. peregrina* accessions.

Morphological data

One hundred thirty nine accessions among the 151 collected were characterized using 28 specific morphological traits. The traits studied included characteristics of the spike, spiklets, glume, lemma, palea and awns (tab. 1). Three to six representative spikes were used in this investigation.

Statistical analysis

The variance analysis was used to test the significance of the variation among accessions for the 28 traits studied. The correlation coefficients between traits were estimated by the mean value of accessions over locations. Analysis of variance, means and coefficient of variation for traits were calculated with the SAS program (SAS institut, 1989).

A discriminate factorial analysis (DFA) was also carried out on the correlation matrix of the traits using the STATITCF program.

Characters	Abbreviation
Spike length	SL
Spike wide	SW
Spiklets number	SN
Number of steril spiklets	NSS
Number of rudimentary spiklets	NRS
Awns number on lower glumes	ANLG
Awns number on upper glumes	ANUG
Teeth number on lower glumes	TNLG
Teeth number on upper glumes	TNUG
Length of lower glumes	LLG
Length of upper glumes	LUG
Wide of lower glumes	WLG
Shortest awns of the lower glumes	SALG
Longest awns of the lower glumes	LALG
Shortest awns of the upper glumes	SAUG
Longest awns of the upper glumes	LAUG
Length of lower lemmas	LLL
Length of upper lemmas	LUL
Awns number on lower lemmas	ANLL
Awns number on upper lemmas	ANUL
Teeth number on lower lemmas	TNLL
Teeth number on upper lemmas	TNUL
Shortest awns of the lower lemmas	SALL
Longest awns of the lower lemmas	LALL
Shortest awns of the upper lemmas	SAUL
Longest awns of the upper lemmas	LAUL
Length of lower palea	LLP
Length of upper palea	LUP

Table 1. Morphological traits studied on the *Aegilops* collection. Measures in mm. *Caractères morphologiques étudiées sur la collection d'Aegilops. Measures à mm.*

Euclidean distance was calculated upon the three first standardized principal components, this distance called "Mahalanobis generalized distance" was used (Llauradó & Moreno-Gonzalez, 1993).

Cluster analysis using the unweighted pair group method (UPGMA) based on arithmetic averages were carried out using the Cluster procedure of SAS Software 1987 (SAS institut, 1989). The euclidean distances among populations calculated on the first three standardized axes were computed in this procedure. Dendrograms showing the phenotypic relationships were obtained by the TREE procedure of SAS (SAS institut, 1989).

Cytological data

The five *Aegilops* species collected in Morocco were used for chromosomal analysis. Two to four accessions per species were analyzed with the cytological method described by Sharma (1982). Sterilized seeds were germinated in Petri dishes at room temperature. Young root tips were pre-treated with 2 or 4% alpha-bromonaphtalene solution for 24 hours, then fixed in a mixture of ethanol and glacial acetic acid (3:1, v/v) before their storage at 4°C. Fixed root tips were hydrolyzed in 1N hydrochloric acid at 60°C for 10 min, stained in 1% carmine solution for 1 to 2 hours, then squashed in 4% acetic acid. Cells with well-spread chromosome complements were scored and photographed for chromosomal morphology determination. Photographs were taken with an Olympus micromaster camera at 400x magnification.

RESULTS AND DISCUSSION

Ploidy level

The observation of somatic metaphase plates of each species shows a constant chromosome number between scored cells. Table 2 summarized the ploidy levels of Moroccan *Aegilops* studied and the genomic constitution (column 5) as established by Kihara (1946) and Kimber (1983) on the base of meiotic chromosome pairing in hybrids.

We have been able to confirm the tetraploid level (2n= 4x = 28) of the four species: *A. geniculata* (fig. 1), *A. triuncialis, A. ventricosa* and *A. peregrina* (*A. variabilis* Eig.) as have been mentioned by several authors (Chennaveeraiah, 1960; Gupta & Baum, 1986 and Kimber & Feldman, 1987). Both accessions of *A. neglecta* presented however a hexaploid number of chromosomes (2n =6x= 42). It can be then classified as *"A. neglecta* subsp. *recta* Chennav" or *"A. recta"* according to Kimber and Feldman (1987) (fig. 2). The hexaploid form of *A. neglecta* species has not been mentioned by Kimber and Feldman (1987) neither in Morocco nor in North Africa. Kimber & Feldman (1987) have reported that this hexaploid cytotype or race is relatively common in Greece and western Turkey and is found in Portugal, Spain, France, Yugoslavia and Italy. Van Slageren (1994) was however astonished that the hexaploid form *A. neglecta* is present in those countries without mentioning Algeria from where the lectotype specimen of *A. neglecta* subsp. *recta* is originates. In Morocco, Kimber & Feldman (1987) reported the tetraploid form of *A. neglecta*, which doesn't exist within the studied collection. This cytotype has certainly not been crossed during the *Aegilops* prospecting trip.

The two forms of the *A. neglecta* constitute a taxonomic difficulty since they cannot be distinguished on the basis of their phenotype. In fact, when based only on the morphological traits of the spike, spiklets, sterile glumes, lemmas and paleas, both 52 and 66 accessions are classified as *A. neglecta* with no regards to the cytotype group. Kimber & Feldman (1987) described the hexaploid form with a fertile terminal spiklet whereas the tetraploid form with sterile spiklet; they specified that the plants were growing under controlled

Species	Number of Accession	Accession reference	Origin	Genome	ploidy level
A. geniculata	4	24	Oujda 3 km from Beni Drar	MU	2n=4x=28
		51	Larach-Ksar al kebir 8 km to Ksar al kebir		
		70	15 km from Aguelmous to Kénifra (467°, 273°, 1000m)		
		80	13 km from Aïn louh to Azrou		
A. triuncialis	4	1	14 km from Rabat to Meknès	UC	2n=4x=28
		7	2 km from El Hajeb to Azrou		
		30	1 km from Ben abdellah to Targoust		
		120	20 km from Aït Atab to Ouzoud		
A. ventricosa	4	12	1 km to Azrou	DN	2n=4x=28
		15	10 km of Ifrane to Azrou		
		20	Sefrou, Station expérimentale Annacer		
		68	6 km from Oulmes to Aguelmous (444,310,1000)		
A. neglecta ssp. *recta*	2	52	17 km from Ksar El Kebir to Souk Al Arbaa	UMN	2n=6x=42
		66	6 km from Oulmès to Aguelmous		
A. peregrina	2	151	Rabat road to Casablanca	SU	2n=4x=28
		152	Rabat to Casablanca, ceinture verte		

Table 2. Ploidy level of species and their origin. *Niveau de ploïdie des espèces et leurs origines.*

conditions. Van Slageren (1994) thinks that the fertility of upper spiklet cannot be a discriminat character between the two species. His justification is that under favorable conditions, the upper spiklet of the tetraploid species can carry seeds. On the other side, terminal spiklet of hexaploid form can be sterile as is the case of our two Moroccan accessions of *A. neglecta*. Therefore, the examination of the ploidy is indispensable to confirm the cytotype group. Then, more investigation between both tetraploïd and hexaploïd forms of *A. neglecta* is needed as prospecting sites in the North part of Morocco where the tetraploid

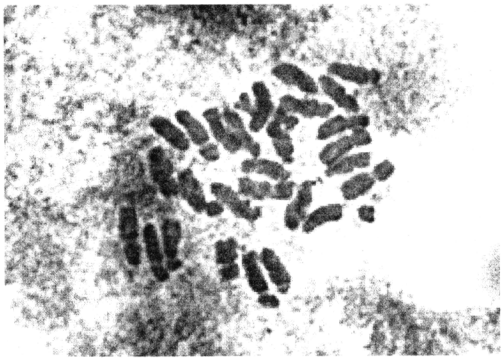

Figure 1. *A. geniculata* Roth.

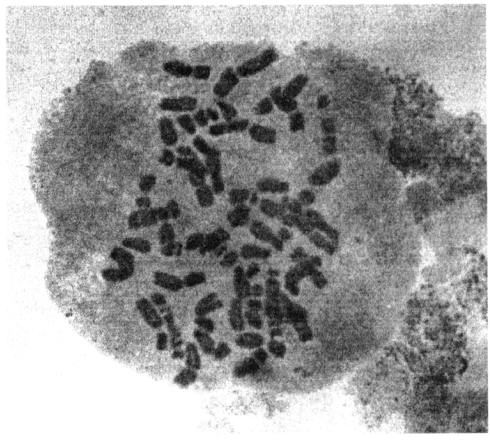

Figure 2. *A. neglecta* subsp. *recta* Chennav.

A. neglecta has been reported (Valdés *et al.*, 2002).

The cytological analysis of natural populations remains an effective tool to check the taxonomic classification of a specie (Davis & Heywood, 1973). Nevertheless, the chromosome number, is generally not enough to establish the relationship between species. According to Chennaveeraiah (1960), morphological characterization of the chromosomes shows differences that influence plant shape, which make it tool useful in some systematical works. The wide variations in the chromosome morphology explain the huge morphological variation found among accession originated from different geographical areas of a same polyploid specie (Zohary & Feldman, 1962).

In addition, diversity in chromosome shape (length, width) has been observed while studying the genomes (result not shown). Two explanations to this variation are plausible, either chromosome have different sizes and/or forms, or the method of preparing slides causes heterogeneity in chromosome compaction. Therefore, using other cytological methods, such as the binding techniques or the *in situ* hybridization, could help in producing accurate data.

Morphological characterization

a) Morphological variation:

The variance analysis performed on 28 quantitative morphological descriptors showed that the differences between species are statistically significant (tab. 3). Most coefficients of variation were ranged between 0- 30%. The number of teeth on upper and lower glumes (TNUG, TNLG) and the number of teeth on upper lemma (TNUL) reached 90, 129, and 257 % of variation, respectively. Few traits presented less than 10% of variation, such as the number of rudimentary spiklets (NRS). They do not discriminate between species but stand for specific descriptor of the genus. Slight variations can be of particular value for some species diagnostic; for instance the presence of teeth on lower and upper glumes (TNLG, TNUG), one awn on lower and upper lemmas (ANLL, ANUL) and one awn on upper glume (ANUG), which are all specific to *A. ventricosa*.

A. neglecta and *A. peregrina* data couldn't be analyzed by the statistical methods, because they were only two accessions within the collection.

A. geniculata species presented the largest number of significant traits. This variation is related to the diversity of its habitats (Allard, 1988). In fact, *A. geniculata* was collected from different environments in Morocco, from

	Aegylops		*A. geniculata*		*A. triuncialis*		*A. ventricosa*	
Characters	**Mean**	**cv inter**	**Mean**	**CV intra**	**Mean**	**CV intra**	**Mean**	**CV intra**
SL	34,35	28,8 ***	24,9	14,6 ***	59,2	10,3 ***	85,1	16,23 ***
SW	5,10	25 ***	5,32	25,5 ***	4,36	19 NS	3,65	21,5 NS
SN	4,32	15 ***	3,67	15 NS	5,06	10,5 NS	9,60	9,5 ***
NSS	1,00	**56** ***	1,03	54 NS	0,80	**75** ***	1,00	0 -
NRS	1,35	2 ***	1,03	18 NS	2,77	16,5 NS	0,34	132 NS
ANLG	3,56	28 ***	4,09	22 ***	2,82	13,5 NS	0,13	264 NS
ANUG	4,14	22 ***	4,78	22 ***	3,00	0 NS	1,00	0 -
TNLG	0,16	129 ***	0,03	548 NS	0,08	310 **	1,86	18,5 NS
TNUG	0,11	90 ***	0	- NS	0,00	- NS	1,78	23,5 NS
LLG	4,00	23 ***	4,13	23 **	3,50	20 NS	3,73	23 NS
LUG	4,55	24,5 ***	3,96	28 **	6,87	13,5 NS	5,69	24 NS
WLG	2,00	31,5 ***	1,97	34,5 **	2,45	16,5 NS	2,19	33 *
SALG	14,95	40 ***	14,26	36 NS	22,91	40,5 NS	0,00	- -
LALG	21,80	25,5 ***	21,42	24,5 **	30,15	24 NS	0,00	- -
SAUG	21,39	33 ***	15,3	34,5 NS	50,98	25 NS	9,69	48 NS
LAUG	29,97	22 ***	24,27	21 **	62,00	17,5 NS	9,69	48 NS
LLL	8,25	9 ***	7,93	10 NS	9,65	6,5 NS	7,39	14 NS
LUL	4,79	27 ***	3,86	31 NS	8,09	11 NS	6,04	36 NS
ANLL	2,14	29,5 ***	2,30	30 ***	2,06	12 *	1,00	0 -
ANUL	2,74	27 ***	2,86	28 ***	3,00	0 NS	1,00	0 -
TNLL	0,79	66 ***	0,67	75 ***	0,98	38 *	1,13	30,5 NS
TNUL	0,14	**257** ***	0,08	**429** *	0,00	- NS	1,08	54 NS
SALL	7,86	**60,5** ***	9,33	**54** ***	2,27	74,5 NS	9,21	36 NS
LALL	13,86	30 ***	16,58	27 **	5,43	34,5 *	9,21	36 NS
SAUL	10,90	**65** ***	10,87	51 ***	7,77	117 NS	25,34	32 ***
LAUL	22,15	34 ***	18,83	28,5 **	38,65	31 NS	25,34	32 ***
LLP	8,39	10 ***	8,11	10 **	9,88	7 NS	6,69	19 NS
LUP	4,97	30 ***	3,94	38,5 **	8,51	10 NS	6,08	22 *

NS: no significant; *: significant at 5%; **: significant at 1%; ***: significant at 1‰.

Table 3. Means and coefficients of variation of morphological traits studied. *Moyennes et coefficients de variation des caractères morphologiques étudiés.*

over 1700m of altitude, down to coastal zones such as Rabat and Kenitra area.

The studied descriptors were related; many were significantly correlated (tab. 4). The highest correlations was those between spike length SL and the number of spikelets SN (r= 0.866), and between the longest LAUG and shortest awn of the upper glume SAUG (r=0.93). The correlation between both traits is expected since they are biologically dependent. In fact, these correlations indicated probably that two linked genetic factors are controlling both traits. Less predictable correlation are those between the number of rudimentary spiklets NRS and the shortest and longest awns of upper glumes (SAUG and LAUG). Negative correlations were those between awns number on lower ANLG or upper ANUG glumes from one side and the number of spiklets SN or the spike length SL from the other side.

b) Discriminate factorial analysis:

Genetic distances between groups are based on similarities and give good picture of the relationship between accessions. Mahalanobis distance estimated through calculation showed that the closest two species are *A. geniculata* and *A. triuncialis* (d = 2,61) while the farthest species are *A. recta* and *A. peregrina* (d = 7,79). This statement confirms Benlhabib *et al.*'s results when using

	SL	SN	ANLG	ANUG	SAUG	LAUG	LAUL
SL	1.000						
SN	0.866	1.000					
ANLG	-0.674	-0.709	1.000				
ANUG	-0.681	-0.649	0.802	1.000			
SAUG	0.523	0.154	-0.196	-0.335	1.000		
LAUG	0.453	0.069	-0.052	-0.192	0.930	1.000	
LAUL	0.593	0.320	-0.174	-0.208	0.745	0.802	1.000

Table 4: Correlation coefficients between some traits in *Aegilops*. *Coefficients de corrélation entre quelques caractères chez les Aegilops.*

agromorphological traits of the same collection (2001).

Plotting accessions in new groups showed that they were assembled within their own species. The discriminate analysis confirm that all the 28 traits used in this study are characteristic to the species and are therefore useful for classification. In Benlhabib et al.'s investigations, where agro-morphological criteria were used, only 86,6 % of the variation could be explained by the same analysis method. For instance, 13.4 % of *A. geniculata* accessions was misclassified. This dispersion is explained by the morphological and phenological diversity within this species as stated by Zaharieva while describing Bulgarian collection (Zaharieva, 1999).

The discriminate factorial analysis (DFA) evaluates the discriminating degree of the used traits. The analysis computes new homogeneous groups with optimal similarities. A such method was largely used by several authors when studying *Aegilops* and *Triticum* genus (Baum, 1977).

Hackel, (1887), Pilger (1945) and Maire (1955) classified the *Triticeae* genera on morphological traits. Stebbins and Crampton (1959) have evaluated the usefulness of many characters specific to *Triticeae* of North America. Later on, various numerical techniques were used on different morphological characters of *Triticeae* by Baum (1978a, 1978b) and Baum et al. (1987) in order to define an "Operational Taxonomic Units" (OTUs). They evaluated the significance of 45 traits and their relationships for the classification and diagnosis purposes.

The first three principal axes accounted for 98,7% of the total variation. Axis 1 alone accounts for 68,6% variation. The relative magnitude of eigenvectors from the first axes (tab. 5) indicates that the lengths of upper glume (LUG), lemma (LUL) and palea (LUP), the shortest awns of upper glume (SAUG), the wide of lower glume (WLG) and the longest awns of upper lemma (LAUL) and shortest awns of lower lemma (SALL) were determinant for the affectation of the accession within the clusters. The second axis, which accounted 13,48% of variation, is significantly linked to three criteria, the awns number of the upper lemma (ANUL), the longest awns of the lower glumes (LALG) and the shortest awns of the upper lemma (SAUL). This analysis underlines that the shape of upper and lower glumes and the awn length of upper lemma are the traits, which have the largest contribution in the phenotypic variation observed among *Aegilops* accessions and between the species.

Plotting the accessions along the two first axes differentiates clearly between the five species (fig. 3). In spite of the high number of accessions studied, *A. geniculata* was projected on the positive side of the first axis forming a consistent group. All the others species, was projected on the negative side of the same axis. This shows the discriminating capacity of the morphological traits used. *A. geniculata* is

	DISCRIMINANT AXES			
Traits	**Axis 1**		**Axis 2**	
SL	-0.8750	0.7656	0.4842	0.2344
SN	-0.5898	0.3478	0.8004	0.6407
NRS	-0.8389	0.7037	-0.5270	0.2777
ANLG	0.6894	0.4753	-0.7168	0.5138
ANUG	0.8227	0.6768	-0.5477	0.2999
LLG	-0.8829	0.7795	-0.2648	0.0701
LUG	**-0.9642**	**0.9297**	0.0262	0.0007
WLG	**0.860**	**0.7407**	-0.0172	0.0003
SALG	-0.4950	0.2451	-0.8278	0.6853
LALG	-0.3229	0.1042	**-0.9200**	**0.8464**
SAUG	**-0.9011**	**0.8119**	-0.4152	0.1724
LAUG	-0.8386	0.7033	-0.5225	0.2730
LLL	-0.8271	0.6842	-0.5165	0.2667
LUL	**-0.9968**	**0.9937**	-0.0395	0.0016
ANUL	0.1114	0.0124	**-0.9798**	**0.9600**
SALL	**0.9501**	**0.9027**	0.2772	0.0768
LALL	**0.9389**	**0.8815**	-0.066	0.0044
SAUL	0.1549	0.0240	**0.9478**	**0.8984**
LAUL	**-0.9083**	**0.8251**	-0.1546	0.0239
LLP	-0.6886	0.4742	-0.7113	0.5060
LUP	**-0.9949**	**0.9897**	-0.0822	0.0068

For every axis: Column one: correlations between classes. Column two: correlations square

Table 5. Eigenvectors of axes 1 and 2 in the FDA. *Contribution des variables à l'explication des axes 1 et 2 de l'AFD.*

characterized by an ovoid shape of the spike with 3-4 spiklets. The lower spiklets is subventricose. Most of the characters studied were variable except the length of lower glumes, lemmas and paleas. This variation is in agreement with other investigations (Zaharieva et al, 1999) which reported a large variation in relation to the growing environment and to the specific adaptation of this species. The distinctive characters of *A. geniculata* from the four others species were ANUG and ANLL. The number of awns on the upper glume of *A. geniculata* is generally 3 but can vary from 2 to 6 and the number of awns on the lower lemma is 2 plus one tooth.

A. ventricosa was projected on the extreme positive side of axis 2 which separate it from *A. triuncialis*, *A. peregrina* and *A. reta*. *A. ventricosa* is characterized by its highest spiklets number (SN) and the only one awn on the upper glume and lemma (ANUG, ANUL). It also has a long spike, an oval spiklets, a strongly overlapping glumes and thick tips with two teeth separated with a broad sinus.

A. triuncialis was projected at the negative sides of the two axes not far from *A. peregrina* and *A. recta* confirming the close relationship between those three species. *A. triuncialis* is characterized by a subcylindrical spike. Its glumes are coriaceous with 2-3 awns. The central awn of the glumes of lower spiklets is shorter than the laterals. The central awn of the glumes of the terminal spiklets is contrarily longer and wider than the laterals and is often the longest awn on the spike.

A. peregrina and *A. recta* both were represented by only 2 accessions which were projected on the negative side of axis 1. *A.*

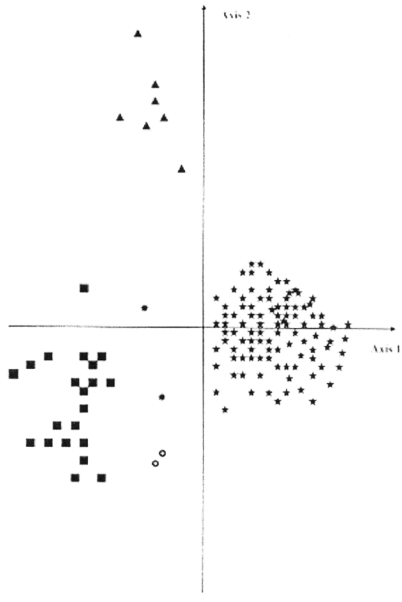

Fig 3. Plot of the discriminant scores of the 28 characters of on the first two axes. Legend: ★ *A. geniculata*; ✘ *A truncalis*; ▲ *A. ventricosa*; ○ *A. triaristata*; ✷ *A. peregrina.Projection des accessions Aegilops sur les deux premiers axes sur la base des 28 caractères.*

recta has a lanceolate spike, narrowly ovoid in the upper part. Its glumes are coriaceous, broad and shorter than the lemma which separate the hexaploid from the tetraploid forms according to Kimber & Feldman (1987). *A. peregrina* has a broad spike with 2 to 3 rudimentary spiklets. Its glumes are tough and rough with equally long, wide and parallel nerves.

c) Cluster analysis:

In order to establish the relationship between *Aegilops* species collected in Morocco, a dendrogram was constructed based on the similarity matrix (fig. 4). This tree shows a good separation between five clusters each corresponding to a define species. This dendrogram is in perfect agreement with the DFA analysis, but also provides additional information concerning the relationship between the accessions. *A. geniculata* and *A. peregrina* were close to each others with 50 % similarity; both of them were close to *A. recta* which was in turn more close to *A. triuncialis*. The four former species are forming a cluster with 25% similarity and are sharing together the U genome, which has probably a specific effect. Such similarity has been mentioned in a study based on RAPD markers (Monte et al., 1999). The last sub cluster corresponds the *A. ventricosa* group, which is clearly dissimilar from the other species which are not carrying D genome. It is established that D genome has undergone during its evolution few changes in comparison to other genomes, and seems therefore to be more homogeneous and have better distinctiveness within the *Triticeae* genus (Badaeva et al., 1996 and Damania, 1993).

CONCLUSION

The cytological investigation indicates that the studied collection of Moroccan *Aegilops* contains four tetraploid (*A. geniculata, A. triuncialis, A. ventricosa and A. peregrina*) and one hexaploid (*A. neglecta subsp. Recta*) species. The study of the morphological traits carried on a set of 28 discriminating characters, confirmed a large phenotypic variation both between and within species. Through numerical analysis, specific traits were clearly justified to be useful for the species identification.

The approch used in this study was however insufficient to establish the genetic structure of the Moroccan *Aegilops*. Therefore, DNA analyses combined with morphological and cytogenetic techniques is needed for such objective. The genetic resources, their classification, conservation and utilization are essential for sustainable agriculture and crop improvement. For effective plant germoplasm exploration, one must link between classical and new molecular techniques. In coming paper, we will be reporting more details about

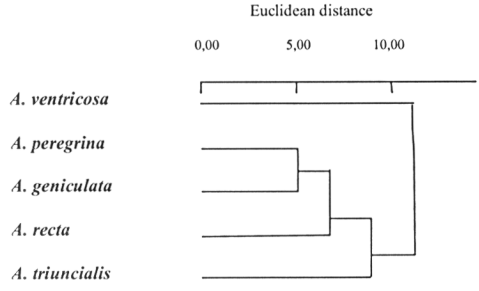

Fig 4. Dendrogram of 139 Moroccan *Aegilops* accessions obtained by analysis of 28 specific morphological traits. *Dendrogramme de 139 accessions Aegilops Marocaines obtenues par analyse de 28 caractères morphologiques spécifiques.*

genetic structure of the whole collection of Moroccan *Aegilops* where molecular markers are being used. Studying the genetic variability within the Moroccan *Aegilops* collection should be potentially of great value for the wheat improvement programs within the country and worldwide.

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