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Morphological and phylogenetic study of the Barbary sheep (Ammotragus lervia) at the Tlemcen hunting reserve.

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Abstract

The Barbary sheep (Ammotragus lervia) is a hoofed animal ranked globally as a vulnerable species. The Tlemcen hunting reserve is one of the structures that aims to protect, preserve and develop this species in ex-situ, but the problem is that the reserve does not have the history of its provenance; On the basis of this observation, we have highlighted our study, which is divided into two parts. The first part focus on a morphometric study targeting 42 adult individuals, 18 of which were imported from the United Arab Emirates and 24 developed in Algeria; this study focused on 18 variables including 15 quantitative and 3 qualitative. The data collected were subjected to a statistical analysis by the software R which; the principal component analysis (PCA) and the ascending hierarchical classification that the two populations are distinct from each other without significant separation since the work has was conducted on the same species. In addition, we have been able to identify specific subjects of each population that can be used as breeders. As for the second part, it is a phylogenetic study targeting the population of Algeria only, in which a molecular analysis of 6 collected samples has allowed us to obtain a partial DNA sequence of cytochrome b. We subsequently retrieved the nucleotide sequences of cytochrome b from the same taxonomy from the GenBank database and processed all the sequences by the MEGA software, after alignment by the ClustalW method. The phylogenetic tree showed that the barbary sheep population of the Tlemcen hunting reserve is a North African subspecies.
Keywords: Barbary sheep; RCT; UAE; morphometry; phylogeny; cytochrome b.

Introduction

North-West Africa is one of the regions that deserves to be investigated by ecological research because, on the one hand, it is a biogeographic crossroads between the Palearctic and Afro-tropical regions (Olson et al., 2001), and on the other hand, it belongs to the Mediterranean region, one of the world's most important biodiversity hotspots (Myers et al., 2000). Extended on a surface of 2.381.741 km ², being spread out of in West over 1622 km and North towards the South on nearly 2.000 km, Algeria is stretched is one of the most original countries of the palearctic western area from the geographical, climatic and ecological point of view and, consequently, it is one of the richest countries in biological diversity in the Mediterranean. The bioclimatology and extent of Algeria's geographical area is at the root of the existence of significant ecosystem diversity. The combination of all these factors has only resulted in an even greater variability of the environments which results in a diversity in terms of: physiognomy of vegetation formations, habitats and biotopes, landscapes and natural resources (Abdelguerfi et al., 2009).

This positive observation, however, is nuanced, because the current situation appears less brilliant. Indeed, this exceptional natural wealth has for several decades been subject to increasing pressures from a society in full development, plus the hazards of years of drought. It therefore undergoes alterations often serious, and as in many other countries around the Mediterranean, is today seriously threatened. The Algerian mammalian population is not immune to these threats; in fact, Algeria currently has 108 mammal species

(Stork and Samways, 1995; Abdelguerfi et al., 2009). As regards the protection of the mammalian fauna of the 108 mammal species in Algeria, 47 species are protected under Algerian law or 43.92% of the total. However, this list is also expected to be revised upwards (Abdelguerfi et al., 2009).

Protected species, one of the most notable is the barbary sheep (*Ammotragus lervia*) whose range and population numbers have been reduced by habitat degradation and poaching. The barbary sheep are now found in small populations in the steppe and pre-desert environments (Benkheira, 2006). The conservation of different species of wildlife is a huge job for any state. It requires a lot of time, material, financial resources and qualified personnel. However, the survival of an animal species does not have to be assured in situ. Conservation in ex-situ conditions (biological reserves, hunting centers, protected areas ...) is often beneficial to the species and prevents its extinction.

The Tlemcen hunting reserve (**Figure 1**) is part of this infrastructure that deals with the conservation of animal biodiversity. Its objective is to protect and develop wildlife and to develop the biotope of the species that live there.

The Barbary sheep is part of this fauna which the hunting reserve of Tlemcen is occupied with the aim of developing this species and making releases later on-site in order to reinforce the natural populations. The Tlemcen hunting reserve, after many years of work, has been able to reach a number of males with over one hundred sheep. For this purpose, the pre-release of this species remains essential given the number compared to the area. However, the problem is that the species remains genetically unrecognized, hence the return of these specimens to nature can cause enormous problems on biodiversity.

As a result, this work is structured around two main axes; the first is a study on phenotypic and morphometric characteristics, using biometric profiling; as for the second; a genetic identification of the Barbary sheep in the Tlemcen hunting reserve and the study of a database of molecular biology of the barbary sheep in order to position on the phylogenetic tree the population of the hunting reserve of Tlemcen compared to other populations of mouflon already studied.

Material and methods

Presentation of the Tlemcen hunting reserve

The Tlemcen hunting reserve is located in the northern part of Algeria, 26 km southwest of the city of Tlemcen and about 10 km from the capital of the Daïra Sabra. The reserve, part of the Hafir State Forest, occupies the highest and most forested area of the Tlemcen Mountains. It is located between a latitude of 34°43'45, 27¨N at 34°47'28, 22¨N and a longitude of - 1°26'32, 55¨E at -1°30'21, 62”N. It occupies an area of 2156 Ha surrounded by Zimmerman on a perimeter of 25.04 Km. It presents as limits:

- To the north, the agricultural lands of the Sidi Ouriache valley,
- To the south, the ridges and southern slopes of Ras Moutas mountain, up to the arable land of El Menakher,
- To the west, Djorf-El-Abiod, the slopes of Jebel Boumedrer to the bottom of the western slope of Djorf-El Guelâa,
- To the east, the summit of Ain-Djadj.

It is one of the four major reserves established throughout the country and currently operational (Zeralda, Djelfa, Mascara and Tlemcen) (RCT, 2018).

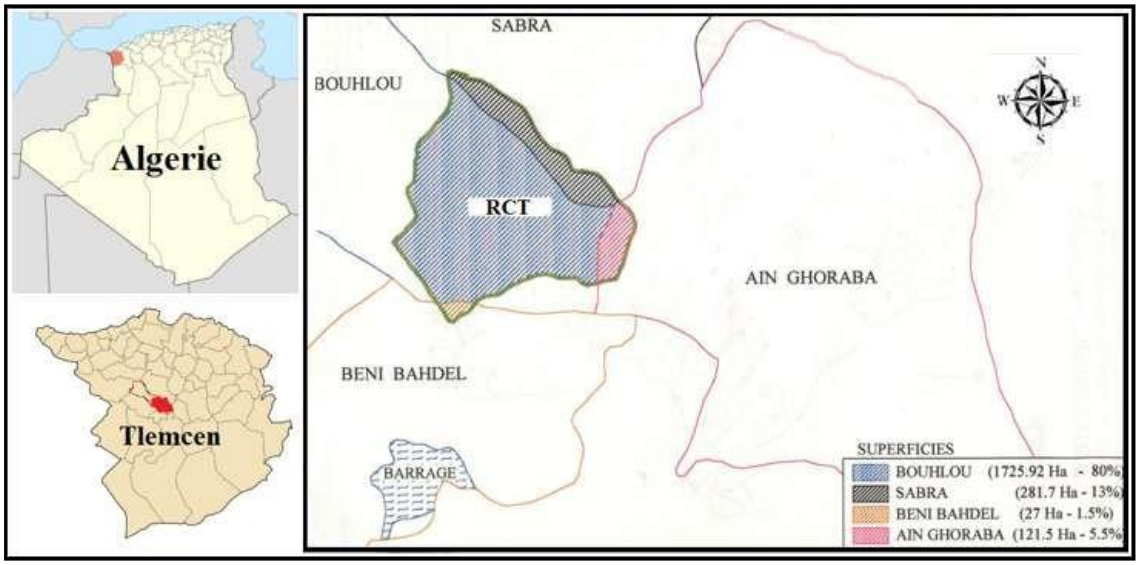

Figure 1: Location map of Tlemcen hunting reserve and delimitation by municipality (**RCT:** Tlemcen hunting reserve).

Morphological study

Biological material

Our study has targeted the barbary sheep population present at the Tlemcen hunting reserve (Moutas), which has evolved into a locally developed population since 2003 and another population imported from the United Arab Emirates in 2016. Sampling was done on individuals of both sexes, males and females, adults over two years of age, all individuals at the time of study were healthy. A total of 42 individuals were sampled including 20 males and 22 females divided into two populations 24 from Algeria (ALG) and 18 from the United Arab Emirates (UAE).

Non-biological material

- An animal capture and restraint device.
- Tape graduated 200 cm for body measurements.
- Marking material (earring and clip).
- Data sheet to fill containing the morphological characters to study.
- Camera for pictures taking.
- Statistics Software and Data Science R (3.5.0).

Experimental approaches

Capture and restraint of the animals

For the population of Algeria and the UAE, we used the same method of mechanical capture. Namely a capture device was built on an area of 500 m^2 surrounded by a fence (type Zimmerman), a height of 2 m covered with a tarp with two gates. The barbary sheep at the 40- hectare Toriche Reenactment Pad were turned down and led to the 7-hectare adaptation pen. Thirty subjects were trapped inside the capture device attracted by the food bait (barley). From there we follow the capture and the contention of the mouflons to realize the individual capture with the help of capture nets handled by qualified personnel. For the UAE population that lives in a 1 ha enclosure, the catch nets were used directly.

Data collection

Qualitative data: Using visual examination, 3 qualitative variables were studied (Table 1).

Table 1: Qualitative variables.

Variables	Abbreviations	Modalities
Age	Age	Dental estimation
Sexe	Sexe	1= male; 2= female
Coat color	CR	1= Light brown (MC) 2= Dark brown (MF)

Quantitative data: Using the tape measure each animal was subjected to 15 body measurements (Table 2) (Figure 2)

Table 2: Quantitative variables.

Measure*	Abbreviation	Principal
Body length	Lcp	tance from the tip of the shoulder to the ischium.
Withers height	HG	size from the lower part of the front foot to the highest point of the shoulder on the withers.
Sacrum height	HS	Distance from the sacrum to the ground.
Hip length	LH	Distance between the points of the hip's angles
Chest circumference	TP	The circumference of the body behind the scapula in a vertical plane, perpendicular to the longitudinal axis of the body.
Anterior cannon circumference	TCA	Anterior cannon circumference
Tail length	LQ	e point of attachment of the tail to the end.
Neck circumference	TL^2	The complete circumference of the neck
Length of the front neck	LLD	etween the roots of the horns and the beginning of the withers.
Length of the distal neck	LLF	throat and the beginning of the sternum.
Horns length	LC	its outer side, from its root to the tip.
Ears length	LO	Length of the outer ear from its base to the end.
Frontal head length	LTF	From the beginning of the forehead to the muzzle.
Distal head length	LTD	The length from the mouth to the throat.
Distance between eyes	EY	Distance between the eyes.

All measurements are in centimeters.

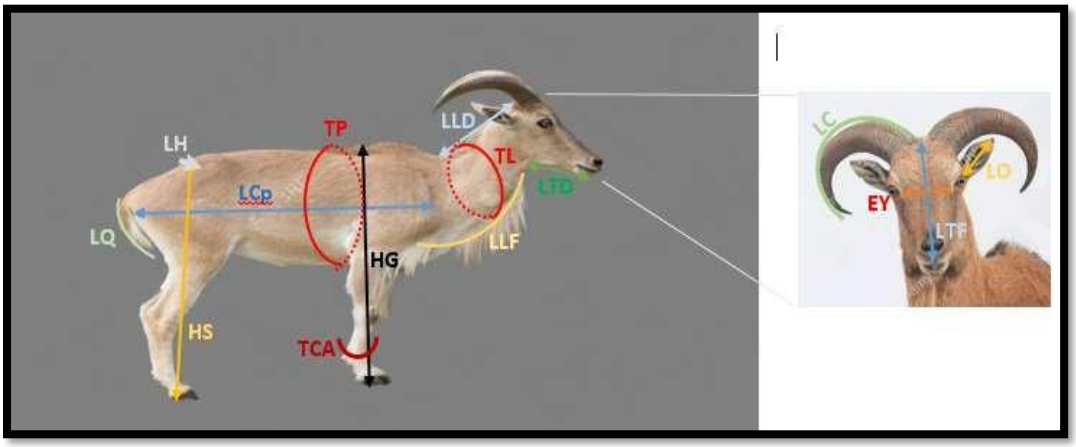

Figure 2. Graphical representation of quantitative variables.

Data analysis

The data processing was carried out by the software R (3.5.0). The statistical analysis is conducted in the following stages: The Shapiro-Wilk test was conducted on the quantitative variables to test the normality of the distributions. A descriptive analysis of the qualitative and quantitative variables: in this analysis we will focus on the mean, median, minimum, maximum and standard deviation. The correlation coefficient of Pearson was studied between the body measurements. Principal component analysis (PCA): the principal component analysis method allows the description of proximities between individuals on whom several quantitative characteristics have been measured (Pierre et al., 2011; Kassambara, 2017). Hierarchical Ascending Classification (CAH): aims at obtaining a simple schematic representation of a rectangular table of data whose columns, according to the usage, are descriptors of the set of observations, placed in lines. The simplest objective of the (CAH) is to divide the sample into groups of homogeneous observations, each group being well differentiated from the others (Roux, 1970).

Molecular analysis

The samples used to extract the DNA consisted of tissues (4 samples) and faecal material (2 samples); which have been preserved in 96° alcohol.

Total genomic DNA was extracted from tissue samples using the EZNA Tissue DNA kit (Omega Bio-Tek). To monitor for potential contamination, we included a negative extraction control at each extraction session. We amplified a fragment of cytochrome b (cytb) with the primers Bovidae Cyt b F and Bovidae Cyt b R.

Polymerase Chain Reactions (PCR) were carried out in volumes of 15 µl with 1.5 × PCR Buffer (Finnzymes), 1µl of each dNTP (Bioline), 0.15µl of each primer, 0.25 µl Phire® Hot Start DNA polymerase (Finnzymes), and 0.8µl of DNA extract. The thermal cycling conditions consisted of an initial denaturation at 95°C for 5 minutes, followed by 55 cycles of 30 seconds at 94°C, 30 seconds at 55°C and 30 seconds at 72°C, followed finally by an extension of 7 minutes at 72°C. The PCR products were purified with an Exo-SAP protocol (Hanke and Wink, 1994) and sequenced in Macrogen Inc. The sequences were edited, assembled and aligned using Sequencer 4.7 (Gene Codes Corporation). The final result obtained is a partial DNA sequence of cytochrome b of 376 bp.

Using GenBank data

All studied sequences of the genus *Ammotragus* in this work were downloaded from GenBank. Regarding the other group, it is a cervid (*Cervus duvauceli*), it was chosen using the web blast (nucleotide blast) of GenBank, it is identical to 89%.

Treatment of DNA sequences and obtaining the phylogenetic tree

To realize a phylogeny, a good number of computer programs are available, to treat the sequences about 92 packages of phylogeny and 54 free web servers among these we chose the software MEGA version 5 (Tamura et al., 2011). MEGA is designed to perform various statistical analyzes in a program and to produce results in publication-quality output (Kumara et al., 1994). The construction of phylogenetic trees was made by one of the distance-based methods, the UPGMA method, based on the assumption that the mutation rates and therefore the evolution rates are identical on the different branches of the tree, using the Kimura 2-parameter model. The transitions and transversions are not equivalent in terms of proportions and their reliability has been evaluated by the program "Bootstrap" which has been applied with a number of repetitions equal to 1000. The replications are reduced in percentages and are indicated at some knots.

Results and discussion

Results and statistical study

Quantitative variables

Before starting the descriptive statistics, we must first test the normality of the distributions of each variable, this will help us to better establish the next analyzes. The normality of the distributions is analyzed by the Shapiro-Wilk test. The alpha risk (α) for the Shapiro-Wilk test is fixed at 0.05%, knowing that the null hypothesis is that the population is normally distributed, if the p-value is lower than the chosen alpha level, then the null hypothesis is rejected and if the p-value is greater than the chosen alpha level, then we cannot reject the null hypothesis and therefore our distribution tends to normality. The results for our variable are in the following Table 3.

Table 3 : Les résultats du test Shapiro-Wilk.

Variable	p-Value	Variable	p-Value
LCp	0.70	LLF	0.25
HG	0.11	LLD	0.89
HS	0.72	LC	0.02
LH	0.10	LO	0.04
TP	0.32	LTF	0.10
TCA	0.01	LTD	0.15
LQ	0.12	EY	0.09
TL	0.01		

From the above table it can be concluded that the variables: TAC (anterior cannon circumference); TL (neck circumference); LC (horn length); LO (ear length) do not have a normal distribution while the rest of the variables tend to normality to different degrees. The total descriptive statistics of the measurements are shown in Table 4 for the Algerian population and Table 5 for the UAE population.

Table 4: Descriptive analysis of body measurements in the Algerian population.

	Mean	Standard deviation	Median	Min	Max
LCp	83,71	7,17	82,00	74,00	100,00
HG	89,71	7,64	88,00	78,00	107,00
HS	89,25	5,42	89,50	78,00	101,00
LH	16,96	1,97	17,00	12,00	21,00
TP	103,38	10,76	103,50	83,00	122,00
TCA	10,67	1,01	11,00	9,00	12,00
LQ	17,08	2,41	16,50	14,00	22,00
TL	49,25	8,55	47,50	36,00	66,00
LLF	36,50	4,71	36,00	28,00	49,00
LLD	30,71	3,56	30,50	26,00	38,00
LC	48,38	12,83	42,00	33,00	83,00
LO	13,33	1,61	13,00	11,00	17,00
LTF	27,96	2,12	27,50	24,00	32,00
LTD	17,92	1,74	18,00	14,00	21,00
EY	14,42	1,50	14,00	13,00	18,00

Table 5: Descriptive analysis of body measurements in the UAE population.

	Mean	Standard deviation	Median	Min	Max
LCp	74,50	7,60	74,00	59,00	90,00
HG	80,61	6,68	79,50	68,00	99,00
HS	82,94	7,14	80,50	72,00	101,00
LH	16,44	1,95	16,50	12,00	20,00
TP	88,28	9,44	89,00	72,00	111,00
TCA	8,56	1,04	8,00	7,00	11,00
LQ	18,22	2,02	19,00	13,00	21,00
TL	37,94	5,37	36,50	28,00	51,00
LLF	32,78	5,16	31,00	26,00	45,00
LLD	26,61	3,60	27,00	19,00	32,00
LC	33,56	9,83	37,00	18,00	56,00
LO	12,61	1,61	12,50	10,00	16,00
LTF	26,00	3,45	26,50	20,00	31,00
LTD	18,56	2,41	18,00	14,00	24,00
EY	12,39	1,75	12,00	10,00	16,00

Qualitative variables

Sexe: The same number of females was sampled for both populations; it represents 46% of the Algerian population and 61% of the UAE population, while in the Algerian population males represent 51% and 39% of the UAE population (Figure 3).

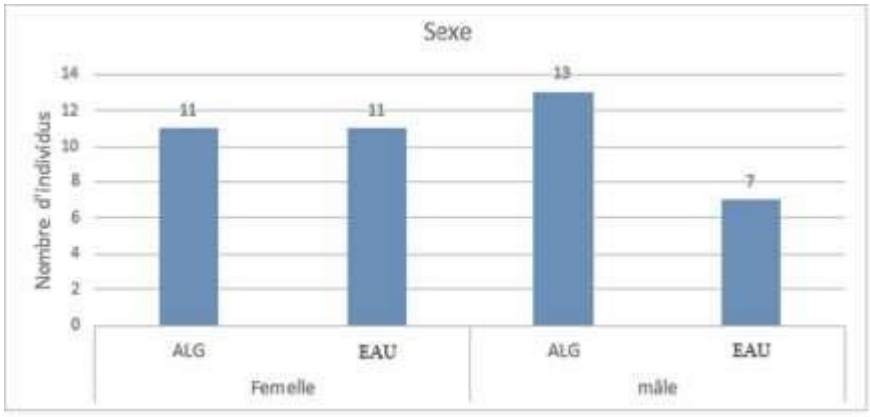

Figure 3: Sex distribution in our sample.

Age: The age of the majority of individuals sampled from the Algerian population is between 3 and 5 years (Figure 4).

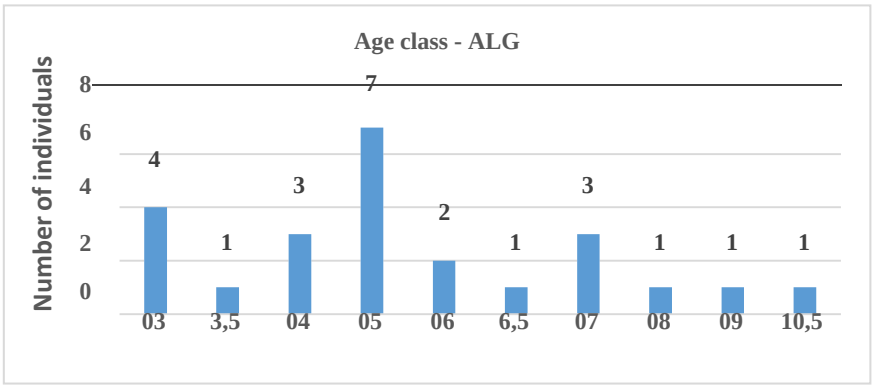

Figure 4: Age distribution in the Algerian population.

Moreover, in the UAE population, the age of the majority of individuals is 3 years (**Figure 5**).

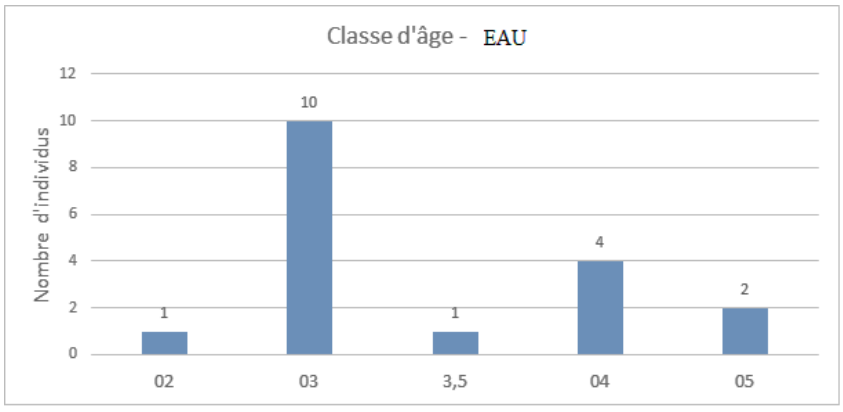

Figure 5: Age distribution in the UAE population.

Coat color

The light brown color of the dress is the most dominant between the two populations, for the UAE population light brown is the only color found while the dark color is present only in the Algerian population and represents 50% of the population.

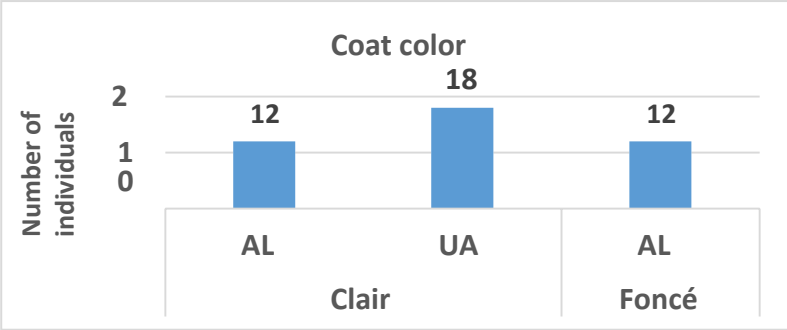

Figure 6: Distribution of the coat color in our sample.

The value α is set to 0.05. The eigenvalues measure the amount of variance explained by each main axis. We examine the eigenvalues to determine the number of principal components to retain. The results are in Table 6.

Table 6: Description of three axes PCA.

Component (Axe)	Eigen value	% variance	% cumulative variance
comp 1	9,28	61,87	61,87
comp 2	1,52	10,13	72,00
comp 3	1,09	7,26	79,26

We note that the first three components account for 79% of the variance; and according to Jollife (2002) and Peres-Neto (2005) the number of axes is determined by the point, beyond which the remaining eigenvalues are all relatively small and of comparable sizes. As a result, the number of axes retained is two and this is axis 1 and axis 2. Principal component analysis (PCA) was performed on the variables studied. The results of this analysis showed that these variables accounted for 72% of the total inertia on both axes, which is really very interesting statistically.

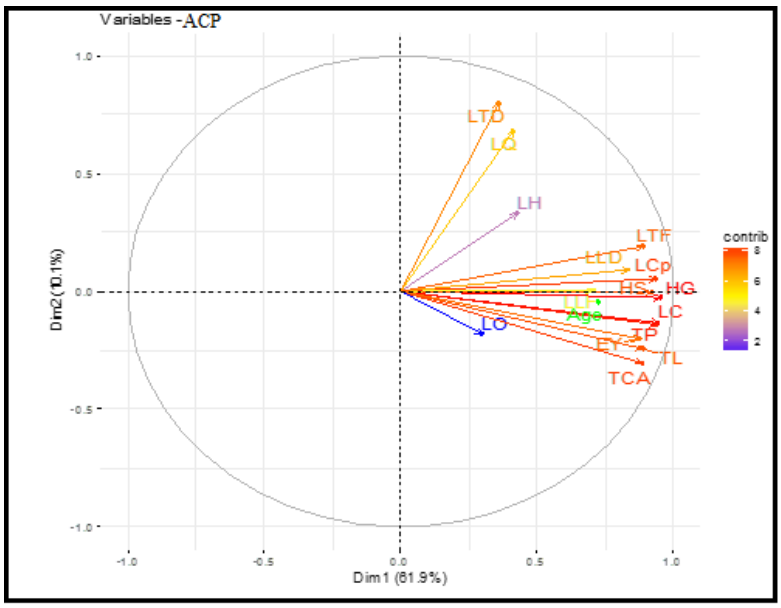

Figure 7: Circle of correlation according to the contribution of the PCA.

The graph above (Figure 7) is also known as the correlation graph of the variables. It shows the relationships between all the variables.

According to Kassambara (2017) in the circle of correlation:

- Positively correlated variables are grouped together.
- Negatively correlated variables are positioned on opposite sides from the center of the circle (opposite quadrants).
- The distance between the variables and the center of the circle measures the quality of representation of variables. Variables that are far from the center are well represented by the PCA.

The information to note from our correlation circle that is presented in figure 7 are:

- No negative correlation is observed.
- The variables LC, HG, LCp, TP and TCA are the closest to the periphery of the circle and therefore the best represented.
- The variables LTF, LLD, LCp, HS and HG are well correlated with each other; and they are well correlated with axis 1 and form a group.
- The variables, LC, TP, EY, TL and TCA are well correlated with each other; and they are well correlated with axis 1 and form a group.
- The LO and LH variables are closest to the center; correlate very weakly with each other and weakly correlate with the other two groups.
- The LTD and LQ variable has a low correlation with all the variables but it should be noted that it has a strong correlation with the axis 2.
- In conclusion:
- The HG, LCp, HS, LC, TL, TP, LTF, LTD and TCA variables have a high representation quality and the LQ, LLD, LLF and EY variables have just above average contribution.
- All the characters (LC, HG, LCp, TP, TCA, LC, TP, EY, TL, TCA) of the two groups are positively correlated between them because they are controlled by a large number of genes that are in common.

Principal component analysis of individuals (**Figure 8**) clearly distinguished the Algerian population from that of the UAE with an overlap zone between the two populations. The common area between the two populations indicates that there are a number of individuals who are alike; which is normal because we are studying the same species *Ammotragus lervia*.

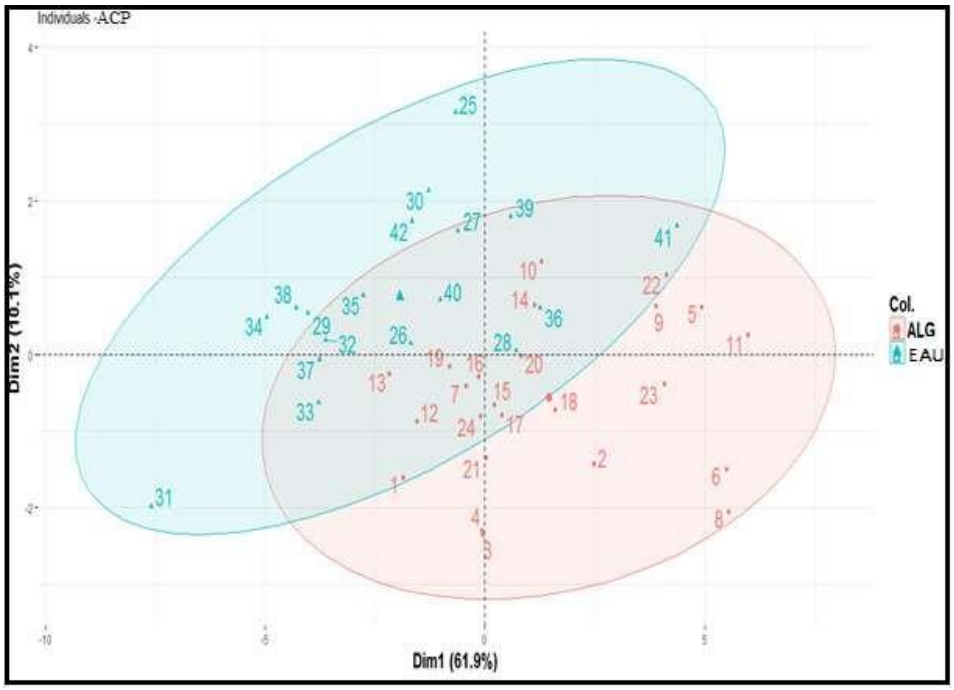

Figure 8. Principal component analysis (distribution of individuals).

The hierarchical ascending classification (CAH) of our sample reflects the same results from the principal component analysis of individuals and distinguished three classes (**Figure 9**) based on the different body measurements performed during our experiment.

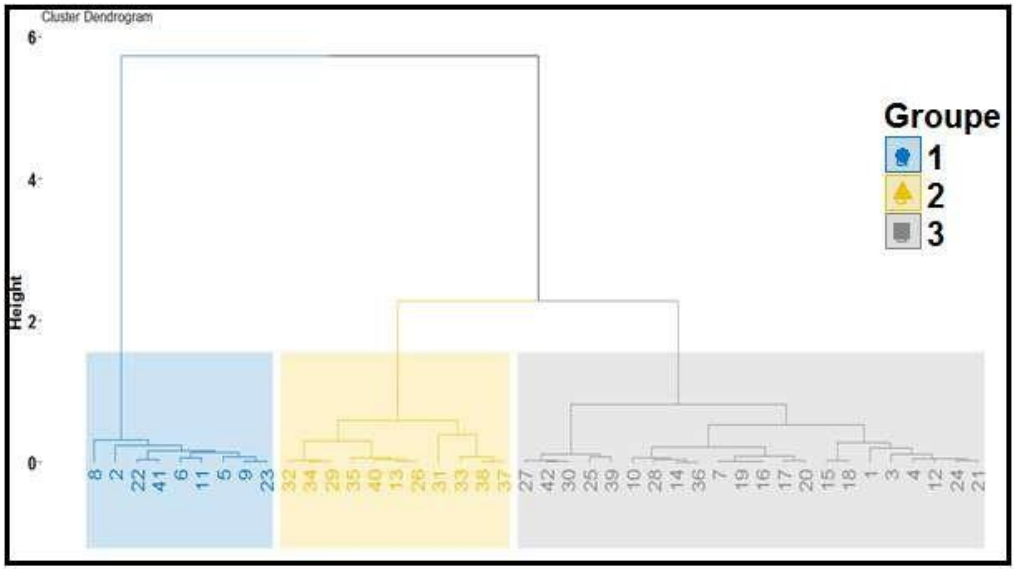

Figure 9: Dendrogramme de la classification ascendante hiérarchique.

The morphological study allowed us to distinguish clearly the two populations studied and -Identify the specific individuals that represent the Algerian subspecies to use as breeders such as males N° 2, 6 and 4.

Results of the phylogenetic study

Results of the GenBank

Our study is based on phylogenetic reconstruction from 48 sequences of the genus "*Ammotragus*" recovered from GenBank.

- Genomic DNA Sequences: ND1, Kcas, HBB, PRNP, HSP90AA1,… etc.
- 17 Mitochondrial DNA sequences predominantly cytb (11 cytb sequences).

We have chosen the mitochondrial gene, cytochrome b (cytb) to establish the phylogenetic tree because it is very widely used in phylogenetic studies and is therefore well documented for many mammal groups (Bradley and Baker, 2001; Delsuc et al., 2003). The cytb is a gene present in many copies in the cell, it is considered clonal and rarely or never subjected to recombination; it is transmitted maternally (cytoplasmic inheritance) (Gyllensten et al., 1991), it has a higher mutation rate than nuclear genes.

On the other hand, the study of previously published articles on these genes allowed us to identify the countries from which the sample comes from and consequently the subspecies according to the bibliographic study.

The eighth N° FJ556577 and fifteenth N° KM582126 sequence were expurgated because during the alignment it was noticed that they occupy a very minimal part of the part of the points of convergence.

Table 7. Mitochondrial DNA (cyt b) sequences extracted from GenBank for the genus *Ammotragus*; the sequences of the RCT and Out group.

N°	Locus	Gene	Country	Subspecies
01	/	cytb	RCT Algeria	/
02	KM582125	cytb	North Africans (Senegal, Mauritania, Morocco, Algeria, Tunisia, Niger, Chad, Trinidad and Tobago)	*Ammotragus lervia* (*lervia, angusi, sahariensis*)
03	KM582124	cytb	North African (Senegal, Mauritania, Morocco, Algeria, Tunisia, Niger, Chad, Trinidad and Tobago)	*Ammotragus lervia* (*lervia, angusi, sahariensis*)
04	KM582123	cytb	North African (Senegal, Mauritania, Morocco, Algeria, Tunisia, Niger, Chad, Trinidad and Tobago)	*Ammotragus lervia* (*lervia, angusi, sahariensis*)
05	FJ207522	cytb	France Muséum	*Ammotragus lervia*
06	AF034731	cytb	France Muséum	*Ammotragus lervia*
07	EU878385	cytb	Direct submission	*Ammotragus lervia*
08	FJ556577	cytb	Not published	*Ammotragus lervia*
09	FJ556568	cytb	Not published	*Ammotragus lervia*
10	EF466060	cytb	Zoo of Mansourah (Egypt)	*Ammotragus lervia ornata*
11	KU165683	cytb	Not published	*Ammotragus lervia*
12	NC_009510	cytb	Zoo of Mansourah (Egypt)	*Ammotragus lervia ornata*
13	EU878386	cytb	Direct submission	*Ammotragus lervia*
14	DL132334	cytb	Municipal Zoo (Japan)	*Ammotragus lervia*
15	KM582126	cytb	North African countries (Spain, Morocco, Algeria, Tunisia, Niger)	*Ammotragus lervia (lervia, sahariensis, angusi)*
16	AY607041	cytb	Out groupe	*Cervus duvaucelii*

Constructing of the phylogenetic tree

The construction of the phylogenetic tree (Figure 10) was carried out using the MEGA5 program. We chose the representative sequences of cytb, based on their geographical origins.

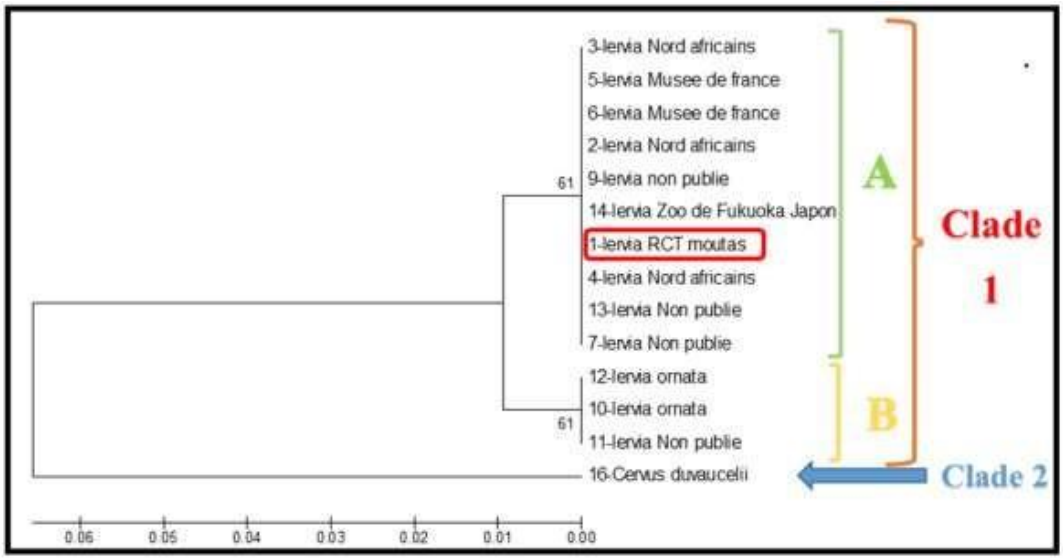

Figure 10: Phylogenetic tree reconstructed by the UPGMA method based on 14 cytochrome b sequences of the *Ammotragus* genus using MEGA5.

Analysis of the phylogenetic tree

According to the tree, the cytb sequences are divided into two main clades:

Clade 1: It includes all processed *Ammotragus lervia* sequences and this clade is subdivided into two subclades.

- Sub-Clade A: It contains the subspecies of our population of the Tlemcen hunting reserve, those of the North Africans, the France Museum, the Fukuoka Zoo and unpublished subspecies.
- Sub-Clade B: It corresponds to the subspecies *Ammotragus lervia ornata* and an unpublished sequence.

It includes the out group used (*Cervus duvaucelii*) which is a cervid from India and Nepal.

In general, the resulting tree shows that *Ammotragus lervia* is monophyletic, absence of nodes means that there is not a clear separation of subspecies, so they are very close subspecies, from a matrix of processed sequences (cytb) with the UPGMA method.

Subclade A is found to be attributed to the North African sub-species; since there are North African sequences (Silva et al., 2014), and those of the France Museum which were probably taken from the colonized countries of North Africa, and especially Algeria because according to Kowalski (1991) *Ammotragus lervia lervia* is the subspecies that was imported into European zoos at the end of the last century and from there to American zoos around 1900. On the other hand, even the unpublished sequences and that of the Fukuoka Zoo (Japan) are most likely from North Africa. Since the sequence of the Tlemcen hunting reserve is in subclade A, it is a North African sub-species.

On the other hand, subclade B is attributed to the subspecies *Ammotragus lervia ornata*; since the sequences composing this clade originate from the zoological garden of Mansourah (Egypt) (Mereu et al., 2008).

On the other hand, clade 2 is the external group and serves as a point of comparison for the group and specifically allows to root phylogeny.

The phylogenetic study allowed us:

- To affirm the results of morphological study by the absence of nodes which means that there is not a net separation of the subspecies, so they are subspecies very close.
- To identify the barbary sheep population of the Tlemcen hunting reserve as a North African subspecies.

Conclusion

In this study, we discussed the phenotypic and genotypic aspect of the Barbary sheep (*Ammotragus lervia*) in the Tlemcen hunting reserve; 42 adult barbary sheep were sampled belonging to two unrelated populations, one Algerian composed of 24 individuals and the other, imported from the United Arab Emirates in 2016 with 18 individuals.

The morphometric study is conducted by 15 quantitative variables and 3 qualitative variables; this was done primarily by descriptive analysis of the variables and a study of the correlations between the quantitative variables, followed by a principal component analysis and lastly an ascending hierarchical classification. Descriptive analysis revealed that individuals in the Algerian population are larger than the UAE population; the light brown color of the coat is more dominant and unique for the UAE population. Principal component analysis (PCA) distinguished the two populations studied with the presence of an overlap zone, which is normally explicable since it's the same species is studied. It also allowed us to identify the specific individual's representative of each subspecies. The hierarchical ascending classification (CAH) demonstrated the same results of the PCA and made it possible to distinguish 3 classes.

The phylogenetic study was devoted to the population of Algeria only for lack of data and means; this part of the study is conducted primarily by the molecular analysis of 6 samples taken; followed by the extraction and collection of data from GenBank. Finally, the treatment of the mitochondrial cytochrome b DNA sequences using MEGA5, gave us the phylogenetic tree. By molecular analysis; after sampling, extraction, DNA amplification, and sequencing, the partial DNA sequence of the 376 pb cytb of the RCT barbary sheep subspecies was obtained.

The exploitation of the NCBI gene bank and the taxonomy research (*Ammotragus*) enabled us to identify the 48 nucleotide sequences of the species and to conclude that the cytb gene is the most studied (14 sequences).

The use of the MEGA software and after the introduction and multiple alignment of the sequences by the ClustalW program, it was possible to obtain the phylogenetic tree which is divided into two clades; the first grouping together all the sequences of *Ammotragus lervia* is subdivided in turn into two sub-clades, the first contains the North African subspecies to which our population belongs, while the other subclade corresponds to the subspecies *Ammotragus. Lervia ornata*; the second clad includes the out group used as a point of comparison.

The assembly and comparison of both morphological and phylogenetic studies allowed us to deduce that:

The two populations studied are very close to what has been revealed by the statistical analysis (PCA and CAH).

- Specific barbary sheep subject's representative of each population can be used as specific breeders of each subspecies of which they belong.
- The Algerian barbary sheep population of the Tlemcen hunting reserve is a North African subspecies.

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