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Genetic characterization of four Algerian goat breeds assessed by microsatellite markers

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ABSTRACT

Genetic characterization and diversity of local goat breeds (Naine de Kabylie, Arbia, Mekatia, and M'zabite) raised in Algeria (n = 224) were investigated by eighteen microsatellite markers recommended by FAO (2011). A total of 450 alleles were detected in this study. The mean values of polymorphic information content, observed heterozygosity and expected heterozygosity were 0.93, 0.84, 0.94, respectively. The mean number of alleles per population ranged from 12.94 (M'zabite) to 16.39 (Arbia). The highest values of FIS, FST and FIT known as Wright F-statistics were 0.179, 0.087 and 0.219, respectively. Although a total of 118 private alleles was observed in this study, only frequency of six allele in M'zabite goat breed was greater than 5%. Mekatia and Arbia goat populations were genetically closest to each other according to dendrogram. Obtained GST value from the present study indicated that 4.00% of total genetic variation resulted from the differences between the breeds. This study indicates that the four studied Algerian native goat breeds are classified into distinct breeds with a good level of genetic diversity. Indeed, our results showed that the used microsatellite markers were adequately polymorphic and that they can be successfully used to investigate genetic diversity in Algerian goat populations.

1. Introduction

As in most countries of the Mediterranean region, the Goat (Capra hircus) is considered the most prolific ruminant among all domesticated ruminants especially under harsh climatic conditions. This is due to their ability of adapting to different environmental conditions, nutritional fluctuations, disease resistance and capacity to survive under low input systems (Serrano et al., 2009).

In Algeria native goat breeds, play a major role in using resources available under extensive production systems and marginal areas and thus contributing for environmental and socio-economic stability. In Algeria, there are approximately 4 million goats that are a source of income for about 800.000 small farmers. Goats are in second place with 13 percent of which does comprise half. Algeria located in north-west of African continent has a significant traditional background for goat breeding. Average annual milk production during the past decade has been about a billion liters of which 60% are from cows, 26% from ewes and 13% from goats (Nedjraoui, 2006). Arbia (AR), Mekatia (ME), M'zabite (MO) and Naine de kabylie (NK) which are native goat breeds of Algeria are important for milk quality and meat yield (Table 1). Indigenous breeds, which are the basic elements of animal breeding, have adapted very well to the ecological, sociological and economic conditions of different geographies. Culture breeds or crosses replace native breeds due to changing consumer habits, economic expectations of farmers and desire to work with highly productive animals that can respond to the demands of the growing population (Criscione et al., 2016). Variation, which is a fundamental characteristic of biological systems, is significantly reduce due to many factors such as species, breed or gene loss. The conservation of animal genetic resources is becoming an increasingly important issue in the world.

The inbreeding levels, genetic diversity and admixture in populations should be clearly addressed in conservation and breeding programs to be constructed. Microsatellites markers are very important and efficient tools for genetic diversity analysis because of their high degree of polymorphism, random distribution across the genome, co-dominance, possibility of automated scoring of genotypes and neutrality

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Table 1
Sample size and main characteristics (Kerba, 1995) of four goat breeds raised in Algeria.

Breeds	Number of samples		Height cm*		Mature weight*		Majors purpuses*		Hair lengh*	Hair colors*	Horns*	Ears*
	Bucks	Goats	Bucks	Goats	Bucks	Goats	Milk (liters)	Meat quality				
AR	63	16	70	67	60	32	0,5 to 1	Medium	Long	Black, Grey, Brown	Presence	Long, Large, Pending
ME	32	19	72	63	60	40	1 to 2	Medium	Short	Grey Brown	Presence	Long, Pending
NK	44	15	68	55	60	47	0,5 to 1	Appreciated	Long	Black, White, Brown	Presence	Long
MO	13	22	68	65	50	35	2 to 2,56	Medium	Short	Chamois, Brown, Black	Presence	Long, Falling

AR: Arbia, ME: Mekatia, NK: Naine de Kabylie, MO: M'zabite *Kerba (1995).

with the selection (Ligda et al., 2009). Due to the fact that there is an increasing interest in the genetic characterization by microsatellites markers, several studies are conducted in Algerian farm animals such as sheep (Gaouar et al., 2005; Gaouar et al., 2012; Gaouar et al., 2014; Gaouar et al., 2015a,b; Gaouar et al., 2017; Djaout et al., 2017; Ayachi et al., 2017; Ameur Ameur et al., 2017), camels (Cherifi et al., 2013; Harek et al., 2015; Cherifi et al., 2017; Holl et al., 2017), chickens (Mahammi et al., 2014; Mahammi et al., 2016) and horses (Berber et al., 2014). But until today genetic diversity studies have not been conducted on the Algerian goat populations.

It could be considered that the introduction of foreign goat breeds such as Saanen, Alpine and Chami goat breeds into the country in recent years may lead to the loss of some important characteristics of Algerian native goat breeds. Identification of the genetic diversity population is the most fundamental step in conserving and using biological diversity (Iamartino et al., 2005). Because of the absence of studies that demonstrate genetic diversity in the goats, the realization of this study has met an important information need. The aim of presented study is investigate genetic diversity and population structure of four goat breeds from Algeria by using 18 microsatellite markers.

2. Materials and methods

2.1. Breeds, sampling strategy and DNA extraction

Animal material for the study consisted of a total of 224 animals belonging to four local goat breeds raised in Algeria (Table 1). Samples from the breeds were collected from unrelated animals and different regions (Fig. 1). Blood samples were collected from the jugular veins of the animal material using vacutainer tube containing K3EDTA. Genomic DNA was extracted from blood samples according to the salting out protocol (Miller et al., 1988). Afterward, quantification and qualification of DNA were controlled using NanoDrop 2000 (Thermo Scientific, USA).

2.2. PCR and fragment analysis

Eighteen microsatellites markers were used according to recommendation of FAO (2011). Three multiplex groups were created according to fragment length of microsatellites (Table 2). Polymerase chain reaction (PCR) amplifications were carried out in 25-µL total volumes, containing 0.10 µM of primers (forward and reverse), 0.20 mM dNTPs, 2.0 mM MgCl2, 1X PCR buffer, 1U of Taq DNA polymerase, and ~50 ng of DNA. Touchdown PCR protocols was used for amplification of specific genomic regions (Table 3). Capillary electrophoresis was used for the separation of the PCR fragments labeled with fluorescent dye in the Beckman Coulter GeXP genetic analyzer (Beckman Coulter, Inc., USA). Genome Lab™ DNA Size Standard Kit 400 was used for the determination of the fragment size.

2.3. Statistical analysis

Number of alleles per locus (Na), mean number of alleles (MNa), effective number of alleles (Ne), polymorphic information content (PIC), observed heterozygosity (Ho), expected heterozygosity (He), average heterozygosity ($\hat{H}$), Hardy–Weinberg equilibrium, Wright's F-statistics (FIT, FIS, FST) (Wright, 1931; Weir and Cockerham, 1984) and null allele frequencies were calculated using GenAlEx (Peakall and Smouse, 2006, 2012), POPGENE (Yeh et al., 1997) and CERVUS 3.0.3 (Marshall, 2006; Kalinowski et al., 2007). The genetic distance dendrogram for the breed was drawn with Population 1.2.31 (Langella, 1999) and FigTree 1.4.2. (Rambaut and Drummond, 2015) software according to Nei's minimum genetic distance matrix (Nei, 1972), the bootstrap resampling methodology (1000 replicates) was performed to test the robustness of the dendrogram topology. Nei's gene diversity (HT), diversity between breeds (DST), and coefficient of gene

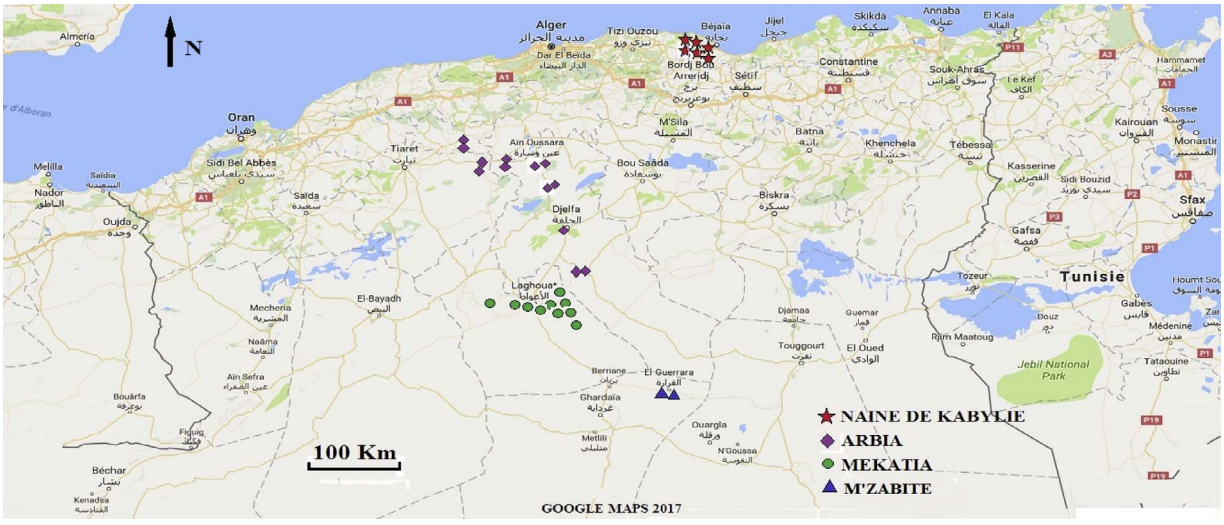

Fig. 1. Representative distribution of the sites sampled in the national scale.