



Contribution of microsatellites markers in the clarification of the origin, genetic risk factors, and implications for conservation of Tunisian native sheep breeds

Y. Ben Sassi-Zaidy^{1,2}, F. Maretto², F. Charfi-Cheikhrouha¹, A. Mohamed-Brahmi³ and M. Cassandro²

¹UR 11ES11 Bio-Ecologie et Systématique Evolutive, Faculté des Sciences de Tunis, Université de Tunis El Manar, Tunis, Tunisie

²Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Legnaro, Italy

³Laboratoire d'Appui à la Durabilité des Systèmes de Production Agricole dans la Région du Nord-Ouest, Département de la Production Animale, Ecole Supérieure d'Agriculture du Kef Boulifa, Le Kef, Tunisie

Corresponding author: Y. Ben Sassi-Zaidy
E-mail: bensassizaidyyousra@yahoo.fr

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ABSTRACT. The genetic diversity and genetic relationship of the two main groups of African sheep, thin-tailed and fat-tailed sheep, represented by the indigenous Tunisian sheep breeds “Barbarine” (BAR, fat-tailed) and “Queue Fine de l’Ouest” (QFO, thin-tailed) were investigated. The genotypes of 110 animals belonging to these two breeds and their crossbreed (CRO) were assessed using 17 microsatellite markers. The results showed high levels of genetic diversity and a total of 256 alleles were identified in the whole population. The mean values of observed and expected heterozygosity were 0.719 and 0.789, respectively, and the mean allelic richness estimate was 10.89. The average F_{IS} (0.112) and F_{IT} (0.118)

values over all loci indicated a notable level of inbreeding within the whole population. However, the F_{ST} value (0.007) showed a low level of genetic differentiation between these two native breeds. The high level of both gene flow and molecular coancestry coefficient detected between the two breeds and their CRO revealed an old miscegenation between the BAR and QFO breeds. The clustering analysis performed with the STRUCTURE software confirmed gene flow between these two breeds. Results arising from this study provide evidence regarding the genetic structure and variability of the two main local sheep breeds, and the implications of their actual management, which indicates the need for an urgent conservation strategy in order to prevent significant gene flow and preserve the remaining breed specificity for future generations.

Key words: Tunisian indigenous sheep; Microsatellite markers; Genetic variability; Population structure