

Article

Genetic Variation in the Prion Protein Gene (*PRNP*) of Two Tunisian Goat Populations

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Simple Summary: Goat production is contributing to the economic and social development of rural areas in arid lands, within harsh conditions of Southern Tunisia. In this geographic zone, there are two caprine populations: the native goat population and the crossed goat population. Genotyping goats for the prion protein gene (*PRNP*) allows us to estimate their level of genetic susceptibility to scrapie disease. In the present work, the Sanger sequencing method of the entire *PRNP* coding sequence was used to determine the different *PRNP* genotypes and haplotypes in two populations (116 animals). This study represents the first investigation on goats' *PRNP* genetic variability in Tunisia, and the results are useful in the design of national breeding programs.

Abstract: Scrapie is a fatal prion disease. It belongs to transmissible spongiform encephalopathies (TSEs), and occurs in sheep and goats. Similarly, to ovine species, the prion protein gene (*PRNP*) plays a major role in conferring resistance or susceptibility to TSE in goats. This study assesses the variability of *PRNP* in native and crossed-breed goat populations raised in the Southeast of Tunisia and provides information on the distribution of *PRNP* haplotypes and genotypes in these goat populations. A total of 116 unrelated goats including 82 native and 34 crossed-breed goats were screened for *PRNP* polymorphisms using Sanger sequencing. Sequence analysis revealed 10 non-synonymous polymorphisms (G37V, M137I, R139S, I142M, H143R, N146D, R154H, R211Q, Q222K, and S240P), giving rise to 12 haplotypes and 23 genotypes. Moreover, four silent mutations were detected at codons 30, 42, 138, and 179; the former was reported for the first time in goat (nucleotide 60 c→t). Interestingly, the PrP variants associated with resistance (D146 and K222) or with a prolonged incubation time of goat to scrapie (M142, R143, H154, Q211) were absent or detected with low frequencies except for H154 variant, which is present with high frequency (1%, 1%, 4%, 0%, 88%, and 6%, respectively, for native goats, and 0%, 1%, 0%, 1%, 78%, and 1%, respectively, for crossed goats). The analysis of *PRNP* polymorphisms of goats raised in other regions of the country will be useful in getting a global view of *PRNP* genetic variability and the feasibility of goat breeding programs in Tunisia.

Keywords: *PRNP*; polymorphism; goat; South-East; Tunisia



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1. Introduction

The transmissible spongiform encephalopathies (TSEs) or prion diseases occur in several mammal species such as humans (Creutzfeldt–Jakob disease or CJD), cattle (bovine spongiform encephalopathy or BSE) and small ruminants (scrapie of sheep and goats). These are fatal neurodegenerative disorders characterized by an accumulation of a patho-