

Genomic inbreeding and population structure in rams of Tunisian D'man sheep

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Abstract – D'man sheep is a minority breed in Tunisia that was established nearly two decades ago from a small Moroccan flock. Tunisian D'man is an isolated population which has experienced no gene flow since its introduction. Currently, this population is suffering from an increased incidence of stillbirths and recurrent abortions caused by inbreeding. The availability of dense SNP markers has facilitated the quantification of genomic inbreeding in farm animals. The aim of the present study was to estimate the kinship between the six D'man rams of a Tunisian breeding station and to assess their genomic structure using the Illumina OvineSNP50 BeadChip and comparisons with the French Lacaune and the Tunisian west thin tail breeds. We found moderate to high levels of inbreeding between the old rams ranging from 0.0069 to 0.1202 and low level of genetic diversity (expected heterozygosity ~ 0.26). Substantial level of west thin tail introgression was detected in the young D'man rams although these were supposed to be purebred. Analysis of runs of homozygosity (ROHs) showed that all individuals had at least one ROH > 10 Mb. ROH islands identified within the D'man rams harbored genes whose mutation leads to stillbirth, dystocia, embryo quality reduction and fleece phenotype variation. Our study demonstrates the usefulness of molecular markers in the management of inbreeding in small isolated populations and would be very helpful in the implementation of planned mating scheme based on sire genotypes.

Keywords: D'man sheep, Inbreeding, Single nucleotide polymorphism, Runs of homozygosity.

1. Introduction

The D'man sheep breed originated in the southern part of the Maghreb region (southwestern Algeria and southeastern Morocco). This breed was introduced for the first time in Tunisia in 1994 from a Moroccan founder flock composed of 200 ewes and 25 rams (Rekik *et al.* 2005). D'man population expanded widely in the country (particularly in the Tunisian oases) since its earliest introduction as it was appreciated by the breeders for its high prolificacy. A recent study showed that the high prolificacy of D'man is mainly due to the segregation of a major prolificacy locus, named FecL within the Tunisian D'man population (Ben Jemaa *et al.* 2019). This locus was originally shown to have a major effect on the prolificacy of the French Lacaune sheep and to be in complete linkage disequilibrium with a single nucleotide polymorphism (SNP) located in the intron 7 of B4GALNT2 gene (OAR11:36938224T>A) (Drouilhet *et al.* 2013). The estimated mutated allele effect of the FecL^L locus on litter size was +0.4 to +0.5 lambs per lambing (Martin *et al.* 2014). Currently, the Tunisian D'man breed can be considered as an island population as it is isolated and it has a small size. Indeed, for sanitary reasons, Tunisian D'man has experienced no gene flow from neighboring countries since its establishment nearly two decades ago thus leading to an increase in the level of inbreeding within this population. Consequently, a frequent onset of lethal genetic disorders in new born lambs was observed within many farms. The inbreeding problem is made worse by the absence of a National pedigree and performance recording system allowing the use of optimal mating strategies. However, the problem is less marked within the state flock of the breeding station of Chenchou which belongs to the Livestock and Pasture Office of Tunisia (OEP) which possesses a pedigree recording system allowing a planned mating scheme based on sire rotation across the seven family lines forming the flock. Chenchou breeding station is the leading supplier of rams for most of the small farmers of Southern Tunisia.