

Genetic diversity loss due to selection for scrapie resistance in the rare Spanish Xalda sheep breed

I. Álvarez^a, L.J. Royo^a, J.P. Gutiérrez^b, I. Fernández^a, J.J. Arranz^c, F. Goyache^{a,*}

^a SERIDA-Somió, C/ Camino de los Claveles 604, E-33203 Gijón (Asturias), Spain

^b Departamento de Producción Animal, Facultad de Veterinaria, Avda, Puerta de Hierro s/n, E-28040-Madrid, Spain

^c Departamento de Producción Animal I, Universidad de León, E-24071 León, Spain

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Abstract

The effect of selection for scrapie resistance on genetic variability in the rare Xalda sheep breed was studied. Pedigree information comprised 1851 animals (1444 alive) at the moment of sampling. A total of 304 reproductive (or selected for reproduction) Xalda individuals were sampled and genotyped for 14 microsatellites. Genetic variability was assessed using: gene diversity ($1 - \text{average kinship}$, GD), mean average relatedness (AR) and self-coancestry (c_i) at the genealogical level; and expected heterozygosity (H_e), molecular mean kinship (Mk), molecular self-coancestry (s_i) and rarefacted average number of alleles per locus (A) at the molecular level. Two breeding strategies were evaluated: a) use of only young rams with genotype ARR/ARR and young ewes with low to moderate risk (risk groups R1 to R3); b) breeding without selection for PrP genotypes. The major cause of losses of genetic variability in the Xalda breed is the drift that occurs when a new group of reproductive individuals is selected. The loss of genetic variability is small in females compared to the males, where it is considerable. However, losses at the molecular level for young females with respect to adult females were above 5%. Young male individuals also retained most of the genetic variability assessed in adult rams. Selection against susceptibility to scrapie produced additional losses of more than 2% for H_e and A when rYF individuals are considered. As regards males, the situation becomes critical because of the scant number of available ARR/ARR young rams. The consequences for the management of the Xalda breed are discussed.

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1. Introduction

Scrapie is one of the diseases of the group of transmissible spongiform encephalopathies, which also includes Creutzfeldt–Jakob disease in humans and bovine spongiform encephalopathy (BSE) in cattle (Hunter, 1997; Prusiner, 1998).

In the light of scientific evidence relating mutation in the codons 136, 154 and 171 of the third exon of the PrP gene to the degree of susceptibility to scrapie in sheep (Hunter, 1997; Elsen et al., 1999; O’Doherty et al., 2002), the European Union has classified the alleles and the genotypes for scrapie in five categories from highly resistant (R1) to highly sensitive (R5) and has decided that breeding programs aimed at decreasing susceptibility to scrapie should be implemented in all the sheep breeds in its territory (European Commission, 2003; see also Gama et al., 2006, for a review). The goals of these programmes

* Corresponding author. Tel.: +34 985195303; fax: +34 985195310.
E-mail address: fgoyache@serida.org (F. Goyache).

must include increasing the frequency of the ARR allele and the ARR/ARR homozygous genotype, which are considered highly resistant to scrapie, and the elimination of the VRQ allele, which has been shown to be highly sensitive to clinical scrapie (Hunter, 1997; Elsen et al., 1999; European Commission, 2003). These kinds of breeding programmes are criticised because they unavoidably reduce the available genetic variability in a breed, thus affecting selection and conservation programmes in sheep.

The protection of the genetic base of a population in risk has usually been measured by the rate of inbreeding (Windig et al., 2004). However, the computation of the individual coefficient of inbreeding is highly sensitive to the quality of the available pedigree information, thus making this parameter difficult to interpret (Goyache et al., 2003). Consequently, a number of recent studies (Caballero and Toro, 2000, 2002; Fernández et al., 2005) have used expected heterozygosity (Nei, 1987), usually called gene diversity (GD), as a criterion for quantifying genetic variability. In addition, recent studies (Caballero and Toro, 2002; Eding and Meuwissen, 2001) have formalised the way in which it is possible to obtain coancestry coefficients from molecular information by applying Malécot's (1948) definition to the marker genes, though referring to identity by state instead of identity by descent. Owing to its straightforward relationship with genealogical coancestry, this parameter has been shown to be useful for conservation purposes (Toro et al., 2002, 2003; Royo et al., 2007). From a molecular perspective, another important measure of variability is allelic richness or average number of alleles per locus (A ; Hurlbert, 1971; Fernández et al., 2005).

Several studies analysed how selection for scrapie resistance can affect performance traits (Brandsma and Visscher, 2004; De Vries et al., 2005; Vitezica et al., 2005). However, the assessments of the effect of such breeding programmes on the genetic variability in small-rare sheep breeds are scarce and have been only conducted at the genealogical level (Windig et al., 2004). Here, the effect of selection for scrapie resistance on genetic variability in the rare Xalda sheep breed is assessed, using theoretically equivalent parameters at the genealogical and molecular level. The study is done assuming the actual selective policy carried out by the Xalda breeders. The consequences on the management of the Xalda breed will be discussed.

2. Materials and methods

2.1. Flockbook information and risk groups

The Xalda (Álvarez Sevilla et al., 2004) is an endangered sheep breed mainly located in Asturias

(Northern Spain) that can be included within the Spanish Celtic sheep breeds including Churra and Latxa breeds (Álvarez et al., 2004). During the 1990s, a conservation program commenced with the foundation of a flockbook, the recovery of reproductive individuals in isolated flocks and the implementation of pure breed mating policy (Álvarez Sevilla et al., 2004; Goyache et al., 2003). Apart from preservation, breeders select individuals for reproduction by their accordance to the breed standard (Álvarez Sevilla et al., 2004; Goyache et al., 2003) and a significant number of individuals (especially males) born each lambing season do not remain in the flocks.

The information registered in the Xalda flockbook since its foundation to June 1st 2005 was obtained from the breeders association (ACOXA). The flockbook included a total of 1851 animals (217 males) and more than 100 small sized flocks. The total number of flocks registered in the flockbook is significantly higher than the number of active flocks each year due to the short duration of some of them. Up to 1444 individuals (134 males) were alive at the moment of sampling and a total of 58 flocks were active. Flocks are of small size and usually have only one ram. Though the number of founders is large (325) the pedigree knowledge at population level is high (79.8% of the fathers and 55.1% of the mothers known). No Xalda individual can be traced more than nine generations back in its pedigree. From the living reproductive individuals over 39% aged between 2 and 3 years old and 43% aged between 4 and 6 years old. Rams have usually a large reproductive life and are commonly exchanged between flocks. In this respect, over 28% of the available rams is 7 or more years old.

PrP genotypes, analysed at the Central Veterinary Laboratory of the Spanish Ministry of Agriculture, corresponding to the individuals born in the last lambing season were also provided by ACOXA. Individual genotypes were classified in five risk groups (European Commission, 2003) from R1 (very low) to R5 (greatest risk). A more detailed description of the risk groups can be found in Table 1.

2.2. Definition of breeding groups and breeding strategies

In order to define breeding groups for genetic analyses, the living individuals registered in the flockbook were grouped in the following groups according to age and sex: a) adult males (AM); b) adult females (AF); c) young males (YM); and d) young females (YF). The AM and AF groups were formed by, respectively, 123

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