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Genetic connections among herds in a selection nucleus of mutton type Merino sheep in Spain: A case of indirect connections through a connector herd in an extensive production system

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ABSTRACT

A study was conducted to quantify the levels of connection among herds, reached through a connector herd, in the Selection Nucleus of the Mutton Merino breed of sheep in Spain. The database, provided by the Asociación Nacional de Criadores de Ganado Merino (National Association of Spanish Merino Sheep Breeders), contained 86,773 lambing and weight records and pedigree records of 110,510 animals (86,879 lambs progeny of 2011 rams and 40,257 ewes) registered between 2000 and 2011 in 47 herds which constitute the Selection Nucleus of the breed. The ratios of genetic similarity (GS) between herds and the comparison of the means of the coefficients of determination (CD), a measure of the degree of connection of two herds through common ancestors, obtained using an animal model and the *Criterion of Admission to the Group of Connected Herds* (CACO) methodology, were used to quantify the levels of connection among herds and to cluster them. A direct genetic connection between herds of 55.3%, an indirect connection reached through the connector herd of 95.7%, twenty nine herds (61.7%) sharing parents with any other herd, 14 herds (28.6%) sharing paternal grandfathers and 27 herds (57.4%) sharing maternal grandfathers, were the main results of the GS analysis. The CACO analysis showed that the estimated values of the CD strongly depended on the heritability of the trait and the number of offspring per sire. Relatively high average values (0.548, 0.678 and 0.745) of the CD of contrasts, clustering 86.0%, 98.3% and 100% of the herds in the SN, were obtained under the low (0.10), moderate (0.25) and high (0.40) heritability scenarios was another result obtained with this method. For the main selection criterion presently being used in this breed (75 day-weight with $h^2 = 0.356$) the average CD of contrasts was 0.729, with a minimum value of 0.436 and a maximum value of 0.940, connecting 100% of the herds. Assessment of connections based on reproduction systems for natural mating using the animal model for 75-days weight in Merino lambs, provides high reliability in comparing the breeding values, despite the low use of artificial insemination in this breed. Results obtained in this work show that, for the purpose of estimating the BV for the main selection criterion of the breed (weight at 75 days), most Merino flocks in the SN are genetically well connected and unbiased EBV can be obtained through the use of the connecting herd, despite of lacking A.I. sires.

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1. Introduction

The animal model provides unbiased estimations of breeding values (BV) for all animals in a population as far as they have phenotypic records or their kinship to animals with known records (Henderson, 1973). Correction of fixed non-genetic effect included in the animal model enables the comparison of the estimated breeding values (EBV) of animals under different environmental conditions. However, comparison of EBV of animals in herds with different average BV may be biased, unless sufficient known reproductive connections exist among them (Kennedy and Trus, 1993; Lewis et al., 1999; Kuehn et al., 2007, 2008). A broad network of connections among herds even enables the comparison of BV estimated in different countries (Thorén et al., 2008).

Merino sheep in Spain are raised under a predominantly extensive system and the breed is distributed throughout a wide geographical area. As a consequence, animals in herds are subjected to very different environmental conditions. This, together with the broad genetic diversity existing among herds, generates large phenotypic differences both in respect to type and growth traits. The artificial insemination (A.I.) is scarcely used and moving rams from herd to herd in order to connect them is not feasible due to farmers' rejection to use rams from other herds as a sanitary precaution. Therefore, sires in the SN are tested within their own herd through their lambs issued from mating a random set of 40–45 ewes. The best sire from each herd is moved to an experimental farm (connector herd) where it is progeny tested again as all the other selected rams, all of them under the same conditions. These rams act, therefore, as indirect connectors of all herds through their kinship to the rams remaining in their original herds (Spanish Merino Breeding Program, 2011).

To evaluate the degree of connection among herds, we used methods already employed for other species like cattle and pigs, raised under similar conditions of relatively low genetic connection among herds (Kennedy and Trus, 1993). These methods are either graphic (representing the paths of connections among herds) or they compute an index based on the kinship among the animals or on the reliability of the EBV. One of these index based on kinships uses the genetic similarity (GS) to quantify the degree of connection between herds, considering that a herd belongs to a certain cluster of herds if it connected to at least one of the herds in the cluster even if it is not connected to the others. The methods based on the reliability of the EBV compare the connection index (CI), the predictions of the error variance (EVP) or the coefficient of determination (CD), a measure of the degree of connection of two herds through common ancestors. Laloë (1993) equated lack of connection between herds to a null CD. This parameter has been found to better define data structure and level of information (Laloë et al., 1996). It also provides a balanced measure of the decrease of EVP and the loss of genetic variability due to inbreeding. The CD is the best parameter to evaluate the reliability of the genetic evaluations (Kuehn et al., 2007) because it takes into account the relationship matrix and not only the sharing of parents or grandparents between herds (Laloë and Phocas, 2003). A low CD indicates a certain level of confounding between environmental and genetic differences (Kennedy and Trus, 1993).

Fouilloux and Laloë (2001) developed the method known as *Criterion of Admission to the Group of Connected Herds* (CACO) to compare the average CD values of every couple of herds. This methodology has been used to determine the degree of connection among herds in the routine genetic evaluation of the French cattle (IBOVAL) and dairy goat breeds (Fouilloux et al., 2008). In cattle breeds reproduced only via a natural service, connections through reference sires are weak. In order to apply this method, connections through maternal and paternal grandparents are taken into account (Fouilloux et al., 2008; Tarrés et al., 2009). This method has been recently applied to the genetic evaluation of the Spanish bovine breed Bruna dels Pirineus (Tarrés et al., 2010).

The study was to assess the level of connection among herds included in the SN of Merino sheep in Spain, by means of the proportions of genetic similarities between herds and to compare the CD between herds using CACO methodology, in order to cluster them according to their connection level.

2. Materials and methods

2.1. Animal material

Data from the Asociación Nacional de Criadores de Ganado Merino (National Association of Spanish Merino Sheep Breeders) were used for this study. The database contained 86,773 lambing and weight at 75 days records and pedigree records of 110,510 animals (86,879 lambs issued from 2011 rams and 40,257 ewes) registered between 2000 and 2011 in 47 herds, which constitute the SN. Lambing takes place throughout all months of the year, although they are less frequent in summer (Spanish Merino Breeding Program, 2011).

2.2. Methods

2.2.1. Connection through a connector herd of the SN

Two herds were considered directly connected when they shared descendants from at least 4 rams, with a minimum number of 25 offspring for each ram in both herds. Furthermore, indirect connections through a connector herd were ascertained.

2.2.2. Genetic similarity between herds

The genetic similarity (GS), defined as the proportion of descendants sharing common parents in two production units (or regions) with respect to the total number of descendants in both units (Rekaya et al., 2003), was computed with the following formula:

$$GS(i,j) = \frac{\sum_{r=1}^{2}\sum_{k=1}^{C(i,j)} ND_{kr}}{\sum_{r=1}^{2}\sum_{k=1}^{T(i,j)} ND_{kr}}$$

where $C(i,j)$ is the number of common parents in both herds i and j; $T(i,j)$ is the total number of common parents in both herds, and ND_{kr} is the number of descendants of parents k in herd r ($r = 1.2$).

A high value for GS between production units indicates a strong genetic link between them as well as a high degree of genetic connection (Thorén et al., 2008).

The genetic similarities via sires (GSs) were obtained with 21,253 records from 156 rams descending from common sires in two herds. To calculate the genetic similarities via paternal grandfathers (GSss) 15,446 records from 99 rams (those with half sibs issued from the same sire in other herds) were used. With 19,646 records from 1721 ewes with half sisters mothers issued from the same sire in some other herds the genetic similarities via maternal grandfathers (GSds) were computed.

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