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Genetic characterization of endangered Spanish horse breeds for meat production

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The horse breeds raised for meat production in Spain are located in the north of the country and all of them are endangered breeds. The aims of this study is to know the genetic variability of these horse breeds and their genetic relationship in order to assist in their breeding programs for meat production. We amplified 15 polymorphic microsatellite markers in 120 unrelated horses belonging to four breeds, 30 horses per breed (Jaca Navarra (JAC), Burguete (BUR), Hispano Bretón (HB) and Agrupación Hiperométrica del Pirineo (AHP)). The observed and expected heterozygosity ranged from 0.645 and 0.719 in AHP to 0.807 and 0.788 in JAC respectively. Average number of alleles per locus was 7.00 in AHP, 8.13 in BUR, 8.4 in HB and 8.06 in JAC. Only 7.18% of the total genetic variability could be attributed to differences between breeds ($F_{ST} = 0.0718$). The highest effective number of migrants per generation ($Nm = 16.11$) was between the BUR-HB pair.

Session 30

Theatre 1

Crossbreeding in New Zealand dairy cattle

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Heterosis effects for traits of economic importance in New Zealand (NZ) dairy cattle have been reported to be (in phenotypic sd): 0.27, 0.38 and 0.38 for lactation yields of milk, fat and protein, 0.20 for cow live weight, 0.09 for cow fertility, -0.05 for somatic cell score and 0.25 for longevity. Simulation shows that a two-breed rotation with straightbred Holstein-Friesian and Jersey bulls had highest net income per hectare (NZ\$1068) followed by the synthetic Holstein-Friesian×Jersey (NZ\$1047). The Holstein-Friesian herd had lowest net income per hectare (NZ\$993). These results agree well with Production Worth or overall merit expressed in profit per 4.5 t dry matter produced by the national genetic evaluation. The ranking of alternate crossbreeding systems is however sensitive to relative values of milk volume, fat and protein. Crossbreeding in NZ has increased the proportion of Holstein-Friesian×Jersey crossbred cows to 30% of the national herd in 2006. Three major changes in the industry have been required or have resulted from adoption of crossbreeding: implementation of an across-breed database and across-breed genetic and economic evaluation systems, modification of the selection scheme to progeny test crossbred as well as straightbred bulls and significant shifts in industry production of milk components and mix of dairy products.

Genetic characterization of endangered Spanish horse breeds for meat production: Hispano Bretón, Jaca Navarra, Burguete and Agrupación Hiperométrica del Pirineo

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ABSTRACT

The horse breeds raised for meat production in Spain are located in the north of the country and all of them are endangered breeds. The aim of this study is to know the genetic variability of these horse breeds and their genetic relationship in order to include them in their breeding programs for meat production. We amplified 16 polymorphic microsatellite markers in 120 unrelated horses belonging to four breeds: 30 horses per breed (Jaca Navarra (JAC), Burguete (BUR), Hispano Bretón (HB) and Agrupación Hiperométrica del Pirineo (AHP)). The observed and expected heterozygosity ranged from 0.846 and 0.718 in AHP to 0.807 and 0.732 in JAC respectively. A average number of allele per locus was 6.700 in AHP, 5.43 in BUR, 5.4 in HB and 5.08 in JAC. Only 7.13% of the total genetic variability could be attributed to differences between breeds ($F_{ST} = 0.07$). The highest effective number of migrant per generation ($N_m = 18.11$) was observed between BUR-HB pair.

Introduction

The number of equids slaughtered in Spain in 2008 was 26,484 and they produced 4,387 Tm of meat. Most of them are exported to France or Italy. Twelve horse breeds are recognized as endangered by Spanish Government in Spain and they are included in the FAO list of domestic animals to be protected.

Only three of these breeds are principally raised for meat production (Hispano Bretón, Jaca Navarra and Burguete). In addition there are other populations raised for meat production but they are not recognized as a breed. This population is the Agrupación Hiperométrica del Pirineo. All these populations are localized in north of Spain.

The molecular characterization and the genetic variability of the horse breeds and to know their genetic relationship is essential in order to include them in their conservation and breeding programs for meat production.



| Breed | HB | JAC | BUR | AHP | Total |
|---------|----|-----|-----|-----|-------|
| Samples | 30 | 30 | 30 | 30 | 120 |

The samples were collected in Iberian and Pyrenean mountain ranges (EDFA). Genomic DNA was extracted from whole blood using the salting out procedure of Miller et al. (1988). We amplified the following 16 microsatellite markers:

| Microsatellite | Reference | Microsatellite | Reference |
|----------------|--------------------|----------------|---------------------|
| ASB17 | Shaker et al. 1991 | BT54 | Carric et al. 1994 |
| ASB18 | Shaker et al. 1991 | BT55 | Carric et al. 1994 |
| ASB19 | Shaker et al. 1991 | BT56 | Shogren et al. 1992 |
| ASB20 | Shaker et al. 1991 | BT57 | Shogren et al. 1992 |
| ASB21 | Shaker et al. 1991 | BT58 | Shogren et al. 1992 |
| ASB22 | Shaker et al. 1991 | BT59 | Shogren et al. 1992 |
| ASB23 | Shaker et al. 1991 | BT60 | Shogren et al. 1992 |
| ASB24 | Shaker et al. 1991 | BT61 | Shogren et al. 1992 |
| ASB25 | Shaker et al. 1991 | BT62 | Shogren et al. 1992 |
| ASB26 | Shaker et al. 1991 | BT63 | Shogren et al. 1992 |
| ASB27 | Shaker et al. 1991 | BT64 | Shogren et al. 1992 |
| ASB28 | Shaker et al. 1991 | BT65 | Shogren et al. 1992 |
| ASB29 | Shaker et al. 1991 | BT66 | Shogren et al. 1992 |
| ASB30 | Shaker et al. 1991 | BT67 | Shogren et al. 1992 |

The Genesys program (Belkhir et al. 2001) was used to compute the following parameters as usual in a population: allele frequency, number of alleles per locus, observed heterozygosity (H_o) and expected heterozygosity (H_e). This program was also used to compute Wright's F_{ST} coefficient in the form proposed by Weir and Cockerham (1984).

We also used the Genesys program to compute the among population Reynolds distance matrix and the effective number of migrants per generation (N_m). The N_m can be interpreted as the upper limit of a number of migrant sperm/ova per generation for the maintenance of the observed genetic differentiation between the breeds; the more divergent the population the lower the N_m value. Individual multilocus genotypes were also included by carrying out a factorial analysis of correspondence to obtain an unbiased interpopulation structure.

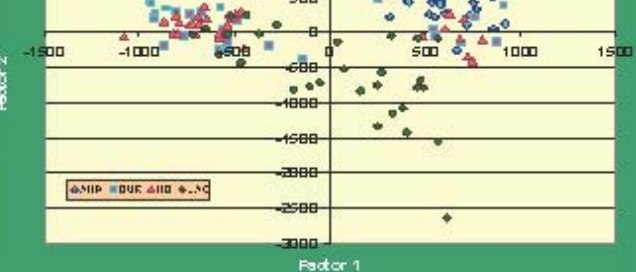


Figure 1. Correspondence analysis using individual multilocus genotypes in the horse breeds analyzed

The polymorphism of the microsatellites reported in the literature for other horse breeds mostly range from 0.65 to 0.75 for H_o and from 0.64 to 0.77 for H_e (Wimmer et al. 2003; Borralho et al. 2000; Cunningham et al. 2007; Lusa et al. 2002; Abate et al. 2008; Schumann et al. 2003; Galbraith et al. 2005; Hoye et al. 2005).

Table 1. Number of samples (N), average number alleles per locus and breed (k), observed (H_o) and expected heterozygosity (H_e)

| Population | N | k | Heterozygosity | |
|--------------------------------------|----|-----|----------------|----------|
| | | | Observed | Expected |
| Hispano Bretón | 30 | 8.4 | 0.641 | 0.788 |
| Jaca Navarra | 30 | 8.0 | 0.671 | 0.789 |
| Burguete | 30 | 8.1 | 0.685 | 0.772 |
| Agrupación Hiperométrica del Pirineo | 30 | 7.0 | 0.645 | 0.719 |

F-Statistics

| Between Breeds | F_{ST} | F_{IS} | F_{IT} |
|----------------|-----------------|-----------------|-----------------|
| | (0.060 - 0.229) | (0.049 - 0.096) | (0.111 - 0.211) |

Only 7.1% of the total genetic variability could be attributed to differences between breeds.

The overall F_{ST} value for our whole data set was similar to, but slightly lower than the 8% reported by Azor et al. (2008) for three balanced horse breeds (Spanish Trotter horse, Zamorano and Embury) breeds and Spanish Purebred (Andalusian Horse). The F_{ST} values were slightly lower than 10% reported by Azor et al. (2008) for some Turkish breeds. The 10% reported by Lusa et al. (2002) for the Apurimac, Curdo and the Argentinian and the 11% reported by Lopez and Moran (2003) for the Brazilian breeds. It has been pointed out by some authors that the typical high within-population variability in microsatellites may result in low discrimination values (Hedrick 1999; Ballou and Lugon-Moulin 2002). Thus, the order of magnitude of genetic differentiation between breeds assessed by F_{ST} estimators seems to be always low and rather consistent regardless the species (Hedrick et al. 1993; Lusa et al. 2000; Anzures et al. 2007).

In general, the highest N_m values were for the HB-BUR and the highest F_{ST} values were for the BUR-AHP pair of breeds.

The location of the analyzed breeds in the bidimensional space formed by the two vectors explaining the total variance is represented in figure 1. The first dimension clearly discriminates the AHP breed from the others breeds, the second dimension separates the JAC breed from the HB and BUR showing no clear discrimination between breeds.

Table 2. Reynolds distance Matrix (upper diagonal) and effective number of migrants per generation (N_m ; lower diagonal) for the four horse population analyzed

| | Hispano Bretón | Jaca Navarra | Burguete | Agrupación Hiperométrica del Pirineo |
|--------------------------------------|----------------|--------------|----------|--------------------------------------|
| Hispano Bretón | | 0.021 | 0.015 | 0.112 |
| Jaca Navarra | 7.46 | | 0.052 | 0.126 |
| Burguete | 16.11 | 4.62 | | 0.119 |
| Agrupación Hiperométrica del Pirineo | 210 | 1.36 | 1.99 | |

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