



ORIGINAL ARTICLE

Implementation of Optimum Contributions Selection in endangered local breeds: the case of the Menorca Horse population

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Abstract

Limiting the inbreeding rate (ΔF) while maximizing genetic gain for any trait of economic interest is especially important in small populations of local breeds, like the Menorca Horse. In this breed, dressage performance is important for the profitability of the breed and should be accounted in the selection criterion. The aim of this study was to assess if a breeding programme aiming at improved dressage performance is feasible in such a small breed. To perform the analysis, animals that were currently available for breeding (between 3 and 20 years) were used. Selection was based on the estimated breeding values for dressage obtained by BLUP. The pedigree and molecular coancestry between potential breeding horses was used (separately or in combination) to account for the restriction on ΔF . Results show that it is possible to avoid large increases in inbreeding while obtaining acceptable levels of genetic gain (i.e. a ΔF of 1% would imply a maximum loss in genetic gain of 2%). Thus, the Menorca Horse population is suitable for a management procedure which jointly optimizes the response to selection and the levels of variability and inbreeding (Optimum Contribution selection). Regarding the source of information used to calculate the relationships, molecular information would provide a greater range of solutions to increase genetic gain than using pedigree coancestry (gain was 1–4% higher for the same levels of restriction on the increase in inbreeding).

Introduction

The main aim of a commercial breeding programme is to maintain the highest rates of genetic gain for a particular trait, while restricting the loss of diversity (and the inherent increase in inbreeding). But even local breed populations under conservation programmes may increase their chance of survival if they can be associated with the expression of a particular trait. It is, therefore, necessary to carry out an evaluation of the feasibility of implementing an explicit selection

programme in the population, and to choose carefully the trait to concentrate on. For instance, performance in competitions/contests is an economically important trait in the horse industry.

In recent years, considerable work has been carried out to design strategies that optimize both tendencies, genetic diversity and response to selection, at the same time. The best management strategy (Optimum Contributions method, OC; Meuwissen 1997; Grundy *et al.* 1998) is to arrange contributions (i.e. the number of offspring left by each candidate) from one

generation to the next to yield the maximum gain, while restricting the weighted global coancestry between parents. Thus, assuming random mating, inbreeding in the next generation can be restricted to a desired level. The combined effects of selection on the gain for the target trait and inbreeding must be considered when analysing responses to selection programmes (Moreno *et al.* 2011) and when comparing the performance of different methods.

Traditionally, the management of a conservation or breeding programme is carried out using coancestry computed from genealogical information (Fernández *et al.* 2005). But, if the pedigree is absent or incomplete, it would be better to use molecular information to manage the population than to leave it unmanaged. In the context of pure conservation programmes, Fernández *et al.* (2005) and De Cara *et al.* (2011) showed that the advantage of using molecular coancestry instead of genealogical coancestry for determining minimum coancestry contributions greatly depends on the amount of markers available and, thus, on the linkage disequilibrium between those markers and the rest of the loci. When a large set of markers can be genotyped (e.g. massive SNP chips), molecular coancestry is more efficient than genealogical coancestry to maintain high levels of genetic diversity. Another advantage of molecular relationships is that they represent the genetic similarity observed between individuals whereas genealogical coancestry is a prediction for infinite unlinked loci. Therefore, molecular information can help to detect more similar pairs of individuals within homogeneous groups of pedigree-based relatives, for example full-sib families. When the costs of genotyping are not limited, this could be very helpful if large families exist in our populations or in 'shallow' pedigrees like the ones of most local breeds, where recording of genealogy began recently.

The aim of the present study was to evaluate genetic gain for different restrictions of genetic relationships based on both pedigree and molecular information in the endangered Menorca Horse population.

Materials and methods

Data sources

The Menorca Horse is an endangered local breed located on the island of Menorca (Spain). Breed definition includes coat colour considerations and only black horses are officially admitted in the breed. The main breeding goals for this population are to maintain the animals' conformation and their ability to

perform in Classic and Menorca Dressage, a special type of dressage that includes a number of typically Menorcan movements that the animals perform at the traditional festivities ('*Jaleo Menorquín*').

Genealogical information was obtained from the official studbook of the Menorca Horse, from its foundation to April 2011 (<http://men-incecca.tragsatec.es/men-incecca/caballos/fichaProducto.xhtml>), comprising a total of 3735 individuals. To carry out this study, the animals currently available for breeding (i.e. between 3 and 20 years old) were used as selection candidates in this work, comprising a total of 922 animals (388 males and 534 females).

Blood samples from the subset of selection candidates (922 animals) were obtained. Total DNA was isolated by standard procedures (Sambrook *et al.* 1989). Following previous analyses (Azor *et al.* 2007), a set of 16 microsatellites markers (AHT4, AHT5, ASB2, ASB17, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG4, HTG6, HTG7, HTG10 and VHL20) were analysed in all the sampled individuals.

The performance data were collected in the official Menorca Dressage competitions held between January 2009 and December 2010, with a total of 27 different competitions. A total of 1550 records were available for all the age groups. The entries were assigned to four levels of difficulty, based on the difficulty of the exercises included in the reprise. These levels were established according to the official rules of this discipline (<http://www.fhbalea.com>). The distribution of records between different categories is shown in Table 1.

Ten different judges evaluated the exercises, making a total of 40 combinations of judge and levels of difficulty. The number of riders was 65, with up to 22 participating with several horses. In addition, 30% of the horses participated with different riders. The final score (FS) obtained in each Menorca dressage competition was selected as a measure of performance. The FS consists on the weighted average scores (in a scale

Table 1 Mean scores obtained in the reprise, number of records (in brackets) by age groups and difficulty levels of the exercise (L) and for the global data set.

Age groups	Levels of the exercise			
	L 1	L 2	L 3	L 4
4–5 years old	6.1 (369)	6.4 (77)	6.1 (20)	–
6–7 years old	5.9 (97)	6.3 (215)	6.3 (150)	6.2 (78)
8–9 years old	6.0 (273)	6.0 (109)	6.1 (65)	6.3 (97)
	Mean	SD	Min.	Max.
Global data set	6.1 (1550)	0.5	4.0	7.5

of 0–10 points) given by the judge. The trait was assumed to be Gaussian distributed (Meyer *et al.* 2001; Albertsdóttir *et al.* 2007).

Analysis of pedigree and marker data

According to Cervantes *et al.* (2009), the following parameters were computed to determine the population structure using the subset of selection candidates: the number of founders, the mean inbreeding coefficient (F), the average relatedness coefficient (AR), the equivalent complete generations (g), the effective population size (N_e) computed by the individual increase in inbreeding (Gutiérrez *et al.* 2009), the generation interval (GI), the effective number of founders (f_e), the effective number of ancestors (f_a), the founder genome equivalents (f_g), the number of ancestors explaining 100% of the genetic variability and the number of ancestors explaining 50% of the genetic variability. Using the complete information from the studbook, the coancestry between all pairs of candidate horses was computed following the classic rules (Falconer & Mackay 1996). These parameters were computed using the ENDOG v.4.6 programme (Gutiérrez & Goyache 2005).

Based on the microsatellite data of selection candidates, the following parameters were calculated: the number of alleles per locus (n), the expected heterozygosity (H_e) and the observed heterozygosity (H_o), as well as the heterozygote deficiency within population (F_{is}) and the polymorphic informative content (PIC). Although H_e reflects the ability of the population to respond to selection in the short term, allelic diversity (i.e. the average number of alleles per locus) is sometimes more useful than heterozygosity to explain the genetic structure of the population or to compare it with others, especially when populations have gone through recent bottlenecks (Maruyama & Fuerst 1985). In addition, molecular coancestries (f_M , Caballero & Toro 2002) were obtained for the subset of candidate animals. These parameters were computed using the MOLKIN v.2.0 programme (Gutiérrez *et al.* 2005) and the GENETIX v. 4.05 programme (Belkhir *et al.* 2004).

An indication of the relationship between the two measures of identity tested (pedigree and molecular coancestry) was obtained by calculating the correlation between the corresponding matrices.

Genetic evaluation

The genetic parameters and breeding values were estimated following the univariate linear model:

$$y = Xb + Zu + Wr + Mp + e$$

with,

$$\begin{pmatrix} u \\ r \\ p \\ e \end{pmatrix} \sim N \left(\begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} G & 0 & 0 & 0 \\ 0 & R & 0 & 0 \\ 0 & 0 & P & 0 \\ 0 & 0 & 0 & S \end{pmatrix} \right)$$

where, $G = A\sigma_u^2$, $R = I_r\sigma_r^2$, $P = I_p\sigma_p^2$, $S = I_e\sigma_e^2$ and y is the final score obtained in the reprise of Menorca Dressage competitions, b represents the systematic effects of age, competition and judge combined with the level of difficulty of the exercise (3 fixed effects in total), u is the vector of direct additive genetic effect, r represents the random effect of the rider, p is the random effect of the permanent environmental animal effect and e the vector of residuals, being X , Z , W and M the incidence matrices for fixed effects, direct additive genetic effects, rider effects and permanent environmental effects respectively. A was the numerator relationship matrix, I_r the identity matrix of equal order to the number of random subclasses, I_p the identity matrix of equal order to the number of permanent environmental subclasses, I_e the identity matrix of equal order to the number of records, the additive genetic variance, the rider random-effect variance, the permanent environmental animal random-effect variance and the residual variance.

The genetic parameters were obtained using a Bayesian procedure, applying the TM programme (Legarra *et al.* 2008). A total Gibbs chain length of 1 000 000 samples for each analysis was defined, with a burn-in period of 100 000 and a thinning interval of 100. The pedigree file comprises a total of 3735 individuals, obtained from the official Menorca Horse studbook.

Optimal contributions

To study the efficiency of a method that could take into account both selection and conservation criteria, optimum contributions of the candidate horses were calculated by maximizing the expected response to selection using the following objective function

$$R = \max \frac{1}{2} \sum_{i=1}^{N_m} EBV_i \cdot x_i + \frac{1}{2} \sum_{i=1}^{N_f} EBV_i \cdot x_i$$

where R is the expected value for the performance trait in the offspring generation, N_m and N_f are the number of evaluated males and females, respectively, x_i is the contribution from individual i and EBV_i is the estimated breeding value for that individual. To account for the maintenance of diversity and the control of inbreeding, a restriction was included limiting

the allowed inbreeding rate ($\Delta F = 1, 5, 10\%$ and without restriction). From the inbreeding values in the set of candidates and the imposed ΔF , the maximum desired level of inbreeding in the next generation can be calculated. Assuming random mating, expected inbreeding in the next generation is equal to the global coancestry of the selected parents (weighted by their contributions), which is calculated using the following expression:

$$F = \frac{1}{4} \sum_{i=1}^{N_m} \sum_{j=1}^{N_m} \frac{x_i x_j f_{ij}}{N_m^2} + \frac{1}{2} \sum_{i=1}^{N_m} \sum_{j=1}^{N_f} \frac{x_i x_j f_{ij}}{N_m N_f} + \frac{1}{4} \sum_{i=1}^{N_f} \sum_{j=1}^{N_f} \frac{x_i x_j f_{ij}}{N_f^2}$$

where f_{ij} is the coancestry between individuals i and j . Several restrictions were imposed for this optimization: (i) only integer non-negative solutions were allowed; and (ii) half of the contributions arose from males and half from females. Optimizations were performed using restrictions in the inbreeding rate the genealogical coancestry (f_G), the molecular coancestry (f_M) or a mixed coancestry matrix made by adding to the genealogical coancestry the molecular value multiplied by 0.1 ($f_G + 0.1 * f_M$). Following this strategy, comparisons are primarily driven by the genealogical information, but there is still a possibility of differentiation between individuals with the same degree of pedigree relationship.

Optimal solutions for contributions were obtained via a *simulated annealing* algorithm (Kirkpatrick *et al.* 1983), as explained by Fernández & Toro (1999) for the particular implementation in OC.

Results

Analysis of pedigree and marker data

The main genealogical parameters characterizing the genetic variability in the subset of selection candidates of the Menorca Horses are shown in Table 2. A total of 281 founders were identified. The mean F , AR and g were 2.35%, 5.27% and 2.95% respectively. The N_e was 47.40, and the GI was 10.79. Regarding f_c (37), f_a (28), the number of ancestors explaining 100% (227)–50% (16) of the genetic variability and most of the evaluated parameters, these values were quite similar between the subset of selection candidates and the whole population (data not shown), which shows that the subset is representative of the whole population. However, f_g showed values of 15.44 and 23.02, for the sample and the entire pedigree respectively.

Information on the polymorphism of the genotyped markers is given in Table 3. The markers had between 5 and 11 alleles per locus. 87.5% of the markers

Table 2 Main genealogical parameters characterizing the genetic variability in the candidate group of the Menorca horse population.

Genealogical parameter	Whole population
Total number of animals	922
Number of founders	281
Mean inbreeding (F , %)	2.35
Mean average relatedness (AR , %)	5.27
Equivalent complete generations (g)	2.95
Effective Population Size (N_e)	47.40
Generation interval (GI)	10.79
Effective number of founder animals (f_c)	37
Effective number of ancestors (f_a)	28
Number of ancestors explaining 100%	227
Number of ancestors explaining 50%	16
Founder genome equivalents (f_g)	15.44

Table 3 Number of alleles per marker (k), expected heterozygosity (H_e), observed heterozygosity (H_o) and polymorphic informative content (PIC) in the data set analysed

Loci	k	H_e	H_o	F_{is}	PIC
AHT4	8	0.83	0.85	-0.02	0.81
AHT5	7	0.76	0.77	-0.01	0.73
ASB2	9	0.70	0.71	-0.01	0.65
ASB17	11	0.67	0.68	-0.01	0.64
ASB23	9	0.72	0.73	-0.01	0.67
CA425	8	0.66	0.69	-0.05	0.60
HMS1	8	0.73	0.72	0.01	0.68
HMS2	8	0.76	0.78	-0.03	0.72
HMS3	7	0.75	0.77	-0.04	0.71
HMS6	7	0.52	0.51	0.02	0.48
HMS7	7	0.80	0.80	0.00	0.77
HTG4	7	0.72	0.72	0.00	0.68
HTG6	6	0.64	0.65	-0.03	0.59
HTG7	5	0.56	0.58	-0.03	0.50
HTG10	10	0.74	0.76	-0.02	0.72
VHL20	8	0.83	0.85	-0.03	0.81
Average	7.81	0.71	0.72	-0.02	0.67

showed values above 0.6 for expected and observed heterozygosity, and 13 of the 16 markers had PIC values above 0.6. The average value for observed heterozygosity was higher than the average value for expected heterozygosity, indicating that the population had probably suffered a recent bottleneck. The average value for the parameter F_{is} , computed from microsatellite information, was -0.02. Overall, the microsatellite set typed can be considered useful to obtain reliable assessments of genetic diversity.

Selected trait and coancestry

Regarding the performance trait, Table 4 shows the mean and standard deviations of the posterior

Table 4 Mean and SD (in brackets) of the marginal posterior distribution of variance components included in the fitted univariate linear model and heritability

Performance trait	σ^2_a	σ^2_r	σ^2_p	σ^2_e	h^2
Final score	0.06 (0.026)	0.09 (0.027)	0.02 (0.020)	0.10 (0.004)	0.21 (0.090)

σ^2_a , additive genetic variance; σ^2_r , rider variance; σ^2_p , permanent animal variance; σ^2_e , residual variance and h^2 , heritability.

distributions of variance components included in the fitted univariate linear model and the heritability of FS, which was moderate (= 0.21). The EBVs for the subset of Menorca Horse selection candidates were scaled to a mean of 100 and a standard deviation of 20, following the recommendations of the Interstallion working group (Interstallion 2005), with a minimum value of 75.48 and maximum value of 115.80. The average accuracy for EBVs of candidates for the selection was 0.65.

The correlation between coancestry matrices (genealogical and molecular) was low (0.37) due to the relatively small pedigree depth. Consequently, many individuals may be loosely related in genealogical terms, but specific couples may present quite different molecular coancestries.

The average values of molecular coancestry were higher than the corresponding genealogical coancestries in all scenarios. This is expected, as molecular coancestry represents identity by state, whether due to common ancestry or not, whereas genealogical coancestry computes only the identity by descent (Toro *et al.* 2002). Obviously, intermediate values were found for the mixed matrix.

Optimum Contributions application

Figure 1 shows the balance between selection pressure (weighted mean of the EBVs of the selected individuals) and their global coancestry (expected inbreeding of offspring) when maximizing the expected response under different restrictions of ΔF and using different sources of information to obtain

the coancestry matrix (genealogy, molecular or mixed). To get an upper limit both for the expected response and inbreeding, the solution involving the use of just the best male and the best female was also included (the point on the right in each of the lines in Figure 1). These solutions are equivalent to the ones that would arise from optimizations without restriction on coancestry.

In any of the scenarios, the higher the restriction on inbreeding rate (ΔF), the lower the expected responses obtained, but with much less coancestry. For example, there is a reduction in genetic gain of 5% and 1% when using genealogical or molecular coancestries, respectively, moving from the scenario without restriction to the one restricting the inbreeding rate to the 1% (Figure 1 and Table 5). In fact, most of the reduction in coancestry is achieved with little loss in genetic gain (the slope of the graph on the right side of the figures was very steep).

In Table 5, the number of selected breeding horses, their genetic gain (average of the EBVs) and the distribution for their contribution under the different restrictions on the desired inbreeding rate are shown. When using genealogical coancestry, as the restriction on the inbreeding rate is relaxed, the number of selected horses (i.e. actually contributing) decreases. Consequently, the maximum contribution for a single selected male and female increases, as does the genetic gain. This also occurs, but less markedly, for molecular coancestry. The differences in performance could be due to the fact that the number of pedigree-based coancestry categories (levels) was few and many more individuals had to be included to substantially reduce the

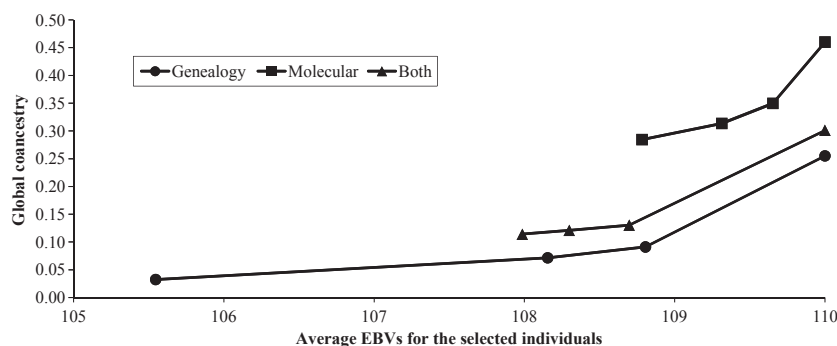


Figure 1 Relationship between the global coancestry (expected inbreeding) and the average EBVs (expected gain) of the next generation, under different restrictions of the desired inbreeding rate using genealogical information, molecular coancestry or both together. On the same line, the different points correspond to the different degrees of restriction: from left to right $\Delta F = 1, 5, 10\%$ and 'without restriction'.

Table 5 Number of selected breeding horses (NBH), genetic gain (G), number of breeding horses with a contribution over 1% (NBH >1%) and the maximum single male and female contribution (MMC and MFC respectively) under different restrictions on the desired inbreeding rate (ΔF), when genealogical and molecular (in brackets) coancestry is used in the optimization

ΔF (%)	NBH	G	NBH >1%	MMC	MFC
10	18 (13)	108.9 (109.6)	14 (9)	33.2 (33.5)	20.9 (15.3)
5	48 (18)	106.6 (108.9)	29 (18)	22.5 (24.7)	13.0 (10.4)
1	142 (20)	104.5 (108.6)	48 (19)	11.5 (22.7)	7.2 (9.7)

global coancestry. Contrarily, as molecular coancestry is based on a moderate number of markers, no horses share the same mean value and changes in global coancestry are more gradual (they involve fewer individuals for the same percentage in reduction).

When comparing the specific horses selected from genealogical information in each scenario, it is remarkable that up to eight individuals retain high optimum contributions whatever the restrictions applied (data not shown). This points to the fact that the most valuable horses (i.e. those with the highest EBVs) were not very closely related to the rest of the candidates (i.e. they did not belong to overrepresented lineages). The situation is similar when optimizing using molecular coancestry, with five individuals coinciding with those selected under the genealogical scheme.

Discussion

In breeds with an endangered status, the most urgent needs are to increase the number of breeding animals and to consider conservation parameters such as genetic diversity and inbreeding in the management techniques. However, the probability of survival of a breed of domestic animals will also depend on the economic returns that can be obtained from the population or its profitability. Therefore, the simultaneous implementation of a selection programme should be considered to make it more competitive. Selection and maintenance of diversity are opposing forces that should be carefully balanced if they are to succeed in any conservation or selection programme. In small local breed populations, the situation is particularly problematic because the low census sizes and low initial genetic diversity may impede the possibility of effectively selecting for an economically important trait. In this sense, Hasler *et al.* (2011) reported a successful case of simultaneous selection for gain in performance traits while limiting the increase in

inbreeding in the indigenous Swiss horse breed Franches-Montagnes.

The feasibility of performing artificial selection on a local breed depends on the actual census size and the levels of diversity when the programme starts (which is related to historical census size). Although pedigree analysis somehow showed reduced levels of diversity in the Menorca horse population, it was observed that most of the values were better (i.e. more diversity, higher N_e and less inbreeding and coancestry) than for other endangered Spanish breeds, such as the Mallorquí horse (Álvarez *et al.* 2010) or Asturcón pony (Royo *et al.* 2007). Similar values have been reported by Pjontek *et al.* (2012) for four endangered Slovak horse breeds, and they are within the range of those published by other authors for horse breeds not in danger of extinction (e.g. Cunningham *et al.* 2001; Zechner *et al.* 2002; Valera *et al.* 2005; Cervantes *et al.* 2008; Hasler *et al.* 2011). This latter observation shows that the Menorca horse population is in a favourable position for the implementation of selection procedures. However, compared with open horse populations (which allow the use of individuals from other breeds for reproduction, as discussed by Cervantes *et al.* 2009), the values for genealogical parameters appear to be low.

In fact, molecular data have shown high levels of allelic diversity ($k = 7.81$) and heterozygosity ($H_o = 0.72$; $H_e = 0.71$) for the Menorca horse population, which are close to the upper bounds found in the literature for other Spanish horse breeds (ranging from 6 to 9.5 for k , 0.65 to 0.76 for H_o and 0.70 to 0.77 for H_e ; Álvarez *et al.* 2010; Azor *et al.* 2007; Rendo *et al.* 2012; Royo *et al.* 2005). In addition, the negative value obtained for the parameter F_{is} , indicates that mating between relatives is avoided (Álvarez *et al.* 2010). This agrees with the assumption that the population has not been exposed to high selection pressure, as occurred in other horse populations like the Andalusian horse (Valera *et al.* 2005). Moreover, the estimate of heritability obtained for FS in Menorca dressage (0.21) agrees with that obtained in other breeds which present a range from 0.10 to 0.30 for dressage, according to Ricard *et al.* (2000).

When analysing the feasibility of implementing artificial selection for an economically important trait (such as Menorca dressage, in this case), besides the management strategies aimed at maintaining genetic diversity in small local breeds such as the Menorca Horse population, it seems that this dual objective is possible. Restrictions on ΔF of around 5% (which would not lead to a great loss of diversity) were compatible with acceptable levels of response for the trait.

This was also reflected in the fact that 80% of the individuals selected still made relevant contributions, whatever the restriction applied. The reason for such a performance may be the absence of previous selection in the population, which would have led to higher levels of relationship/coancestry between top horses.

The decision to choose one or another inbreeding rate would depend on the level of requirement in each case (e.g. changing the ΔF from 5% to 10% would imply a decrease in NBH of 62.5% and 27.8% when genealogical and molecular coancestry are used respectively). In local populations, it would be desirable to have a stricter restriction on the inbreeding rate at the beginning of the programme, to avoid endogamic matings due to the reduction in selected individuals, although the response to selection will be lower. Similar results were reported by Hasler *et al.* (2011) with Franches-Montagnes horses, where they observed a better response to selection with an increase in inbreeding rate of less than 1% per generation.

As regards the decision about using the two different types of information to perform OC management (genealogical or molecular) separately or in combination, some authors have analysed the benefits of using molecular information (Schierenbeck *et al.* 2011; Sonesson *et al.* 2012). The main result of this study is that including molecular coancestry provides a more continuous measure of the relationship between individuals, which allows for a more gradual control of inbreeding. Therefore, fewer individuals are to be included in the selected set to fit the restriction than in the case of pure genealogical coancestry, where several individuals may show the same global coancestry. This fact implies that, for the same level of restriction on ΔF , breeding values for the trait of economic interest (Menorca dressage) of the selected horses based on the pedigree coancestry are lower (EBVs is 4% less than the maximum, compared with a 1% reduction using molecular coancestry for $\Delta F = 1\%$). The combined use of genealogical and molecular information with pedigree information could be the best solution to account for the general relationship differences, as well as for the molecular information which detects the realized differences between individuals with the same degree of relationship (e.g. full-sibs).

The ability of marker information to discriminate between individuals with the same degree of genealogical coancestry has been also pointed out as an important factor for improving the efficiency of genetic evaluations by Villanueva *et al.* (2005). Obviously, the advantage of the use of molecular

information depends on the density of the markers genotyped, as accuracy of selection may further increase when the marker density is higher, up to certain degree (Sonesson & Meuwissen 2009). For pure conservation programmes, Fernández *et al.* (2005) and De Cara *et al.* (2011) showed that for a low number of markers (e.g. microsatellites) relying in pedigree information is more efficient than using molecular coancestry for maintaining genetic diversity, but this situation changes if a huge number of markers (SNP) are available.

Nowadays, a commercial SNP chip available for horses includes over 50 000 SNP (Mickelson *et al.* 2009), but the development of larger chips is expected in the near future, as up to 1 million SNP have already been detected. It is not clear if the high cost of SNP genotyping (for evaluation and coancestry estimation) still makes it unaffordable for local breeds. In any case, as shown in this study with the Menorca population, breeding programmes would benefit from the use of both sources of information (genealogical and molecular), even if only a limited number of microsatellites were genotyped. Horses are routinely genotyped for parent checking and, thus, this information can be also included in the calculation of the coancestry matrix, while giving less weight to molecular information.

Direct practical implementation of the results presented is not always straightforward. Breeder's preferences, the preferential use of certain stallions and the price for covering all play key roles in mating decisions. Horse breeding differs, for example, from cattle breeding programmes in several aspects that included the fact of far less or no A.I. practiced. Even with A.I., the number of offspring per sire remains limited compared with cattle breeding programmes (Hasler *et al.* 2011). On the other hand, in the breeding programme for the Menorca horse approved in 2007 by the Ministry of Agriculture, Food and the Environment (<http://www.magrama.es>), the selection of animals based on their performance while maintaining the levels of genetic variability is cited as a priority aim and, therefore, the results presented here will be useful for fulfilling this objective.

Conclusion

The maintenance of genetic variability within a population is important for the management of local livestock breeds, but to improve the performance of an economically relevant trait may be equally important. The optimal management tool for optimizing selection decisions, based on their breeding values for a

performance trait and inbreeding rates (OC), has proven to be applicable to the Menorca horse breed population, as inbreeding rates as low as 1% can be maintained with a reduction of less than 5% in the maximum selection response. The results also suggest that molecular information might be a powerful tool for complementing or substituting pedigree coancestry matrix. With a 1% restriction on ΔF , the loss in genetic gain would be 2% or less, if the management programme includes molecular information.

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