Assessment of population structure depending on breeding objectives in Spanish Arabian horse by genealogical and molecular information

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ABSTRACT

The Arabian Horse is one of the most valued breeds in an international and historical context and has been involved in the formation of many other horse breeds. Since 2005, the Spanish Arabian Horse Breeder Association (AECCA) has developed a breeding program aimed at improving both conformation traits and endurance performance. While this selection depends on individual breeders, a population structure might appear by preferential mating within groups of animals according to different objectives. The aims of this study were to determine the differences between Arabian horses bred for different breeding objectives: endurance competitions, morphological shows and other aptitudes and to check if this structure population can be assessed by using genealogical, molecular tools or both. Genealogical and molecular information was randomly obtained from 120 Arabian horses. The animals were classified into three groups according to the breeding goal: morphology, endurance and other aptitudes. Some initial analyses were carried out to study the structure of the sampled animals using genealogical and molecular parameters. An analysis of the genetic structure using both types of information source was performed. Both molecular and genealogical analyses were congruent, and both seemed to be valid when studying the genetic structure of this population. The correlation between coancestries using molecular and pedigree information was 0.60. The differences between the groups were minimum when compared with the genetic structure within groups. Therefore, a horse with a specific breeding objective is not genetically much different regard the rest of the objectives. However, the morphological group appeared as the most separated from the rest, both at a genealogical and molecular level. Regarding the possible impact of the subdivision in the population it can be claimed that no loss of genetic variability is expected in the short-term, because the groups were genetically connected.

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1. Introduction

The Arabian Horse is one of the most valued breeds at an international and historical level. The breed's versatility for sport performance and good conformation has resulted in an important contribution to the formation of other horse breeds. The Spanish Arabian horse is one of the main populations of this breed in Spain, with a census of 14,247 individuals (Magrama, 2011). The Arabian horse was imported to Spain in the middle of the 19th century by the Spanish Ministry of War, while private breeders started importing these horses in the 20th century. The selection

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objective of this breed is now twofold: (1) some breeders prefer an animal performing in endurance competitions within other sport disciplines, (2) while other breeders try to select animals to present in morphological shows assessed by expert judges during European Conference of Arab Horse Organization (ECAHO). The selection of the animals has been based on phenotypes and on the experience of breeders. Since 2005, the Spanish Arabian Horse Breeder Association (AECCA) has been developing a breeding program aimed at improving both conformation traits and endurance performance (Valera et al., 2009) and at selecting animals using the breeding values. While this selection depends on individual breeders, a population structure might appear by preferential mating within groups of animals according to different objectives.

The analysis of the genetic structure of a population can be carried out using genealogical or molecular information. Traditionally, the management of genetic variability was done by using genealogical information. But, if the pedigree is absent or incomplete, it would be better to use molecular information to characterize a population. Álvarez et al. (2008), using a Spanish sheep breed as a model, observed that the use of microsatellite markers could be an additional tool for herd management when pedigree is unknown or incomplete. Other authors found similar results in conservation programs (Fernández et al., 2005). Pedigree information is well completed in the Spanish Arabian population, but the parentage control has only been established since 1987 and, moreover, the molecular information provides the additional relatedness between animals appearing as founders in the pedigree. The genetic management of a population might be carried out efficiently and at low cost with pedigree data and molecular markers (such as microsatellites) that might be used to monitor pedigree errors. Nevertheless, the use of pedigree and markers together may be feasible with the development of new methods of wide scale genotyping (Kijas et al., 2009; Meuwissen, 2009) and new generation sequencing (Archibald et al., 2010).

When animals are selected for different breeding goals inside the same population, this could lead to a subdivision and consequently a loss of genetic variability within the subpopulation. Except in the case of extremely numerous livestock populations, subdividing a breed to pursue different objectives causes a substantial loss of efficiency within each sub-set of individual animals. It is preferable, first, to agree on the overall objectives across the breed and then, to try to maintain the variability in the breeding objectives in such a way that the animals are valuable for different users (Verrier, 2011).

Four ancient genetic lines were identified in the formation of the breed, but the presence of a subdivision, due to this fact, is today scarce (Cervantes et al., 2008a). Despite there not being a predefined mating system to attain animals for different performances, in recent years some Spanish Arabian horse breeders have been specializing in breeding morphological show animals ("bred for beauty") and others have specialized in breeding for sport performance ("bred for endurance") based on phenotypes. But, since the breeding program was approved for the Spanish Arabian horse the main objective has been to breed animals with functional conformation. The previous situation needs to be evaluated because the mating system developed by the breeders might have produced a strong differentiation between animals inside breeding objective.

The aims of this study were to determine the differences between Arabian horses bred for different breeding objectives: endurance competitions, morphological shows and other aptitude, to check whether this population structure can be assessed by using genealogical tools, molecular tools or both, and to study if promoting the creation of specialized lines could be the right course of action.

2. Material and methods

Genealogical and molecular information was obtained from 120 pure Spanish Arabian horses (50 females, 48 males and 22 geldings), with ages between 3 and 14 years. They were classified in three groups: 45 with morphological aptitude, 49 with endurance aptitude and 26 with other aptitudes. The sample was randomly chosen and was previously used to carry out a morphometric analysis (Cervantes et al., 2009). These animals were bred before the breeding value estimation establishment, and then only phenotypic selection was carried out on them. Classification of the animals within groups was carried out after sampling based on the aptitude in which the horses were bred for, i.e. the breeding goal. For the "morphological" aptitude classification the participating animals were evaluated for their beauty, correctness of legs, Arabic type and basic gaits in morphological shows organized by ECAHO. Participants in endurance races were classified as animals bred for "endurance" aptitude; this is a sport competition where horses have to race over long distances (even 200 km and more) on natural tracks undergoing several veterinary health checks during the race. The third level of the breeding goal was "other" aptitudes including individuals without a clear aptitude, e.g. used for recreational activities.

Some initial analyses were carried out to study the structure of the sampled animals using genealogical and molecular parameters. Finally, an analysis of genetic structure using both type of information source was performed.

2.1. Genealogical analyses

The genealogical analyses were based on available pedigree information; the genealogy was traced back to the farer known ancestors for the 120 genotyped animals with a mean of 7.7 equivalent generations known, and a maximum of 13.2. The total number of animals in the pedigree was 1326. Animals with different objectives were fully connected via genealogical information. The following parameters were computed:

Number of equivalent complete generations (t) in the pedigree was computed as the sum of $(1/2)^n$, where n is the number of generations separating the individual to each known ancestor (Boichard et al., 1997).

Effective number of founders (f_e). This parameter is the reciprocal of the probability that two genes drawn at random in the studied population originate from the same