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Demographic characterization and genetic variability of the Girgentana goat breed by the analysis of genealogical data

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ABSTRACT

The aim of this paper is to present an overview of the actual Sicilian Girgentana population structure by the analysis of genealogical data. Statistics show that in 1983 the population consisted of 30,000 Girgentana goats; ten years later almost 98% of the entire Girgentana population disappeared. The remaining population consists of 461 individuals (134 males and 327 females), with 368 living animals. The effective population size is 380 individuals. The inbreeding rate per generation was equal to 0.13%. The average estimated inbreeding level within the living male population was equal to 0.8% (0-15%); and the average inbreeding level within the living female population was equal to 0.7% (0-31%). The average relationship between males and females estimated on 27,772 possible matings was equal to 0.5% (0-8.7%). The estimated inbreeding level was not high due to the lack of pedigree information. This is resulting in a ratio between the number of founder equivalents ($f_e = 22,94$) and the number of absolute founders ($f_a = 93$) equal to 25%.

Key words: Girgentana goat, Small population, Demographic parameters, Inbreeding

RIASSUNTO

ANALISI DEI DATI GENEALOGICI PER LA DESCRIZIONE DEMOGRAFICA E DELLA VARIABILITÀ GENETICA NELLA CAPRA GIRGENTANA

La consistenza numerica della razza Girgentana, nell'ultimo ventennio ha subito una notevole contrazione, tanto da potersi annoverare tra le razze in via di estinzione. Nel 1983 la popolazione era costituita da 30.000 capi, attualmente la popolazione è costituita solamente da 461 individui (134 becchi e 327 capre). Il numero effettivo della popolazione è 380 individui. Il tasso di consanguineità per generazione è pari al 0.13%. La consanguineità media tra i maschi è stata stimata pari al 0.8% (0-15%) e la consanguineità media tra le femmine è uguale a 0.7% (0-31%). La parentela tra i maschi e le femmine stimata su 27,772 possibili accoppiamenti è stata uguale a 0.5% (0-8.7%). Contrariamente all'atteso, i livelli di consanguineità sono risultati mediamente bassi, per la scarsità di informazioni relative al pedigree. Tale affermazione è confermata dal rapporto tra il numero di fondatori effettivo ($f_e = 22,94$) e il numero di fondatori assoluto ($f_a = 93$), pari al 25%.

Parole chiave: Capra Girgentana, Piccole popolazioni, Parametri demografici, Consanguineità.

Introduction

The Girgentana goat is an indigenous breed in the area around Agrigento (Sicily). The breed, most likely, originates from Afghanistan and the Himalaya regions (Portolano, 1987). Traditionally breeding took place in urban centers where the animals were kept in the farmer's house. The profit of this breeding was based on direct retail (door to door sales) of milk used for drinking. According to the tales of older farmers born in families with a long history of breeding, the milk was primarily used for the nourishment of infants and elderly. The endangered status of the small Girgentana population is linked to the following peculiarities: statistics show that in 1983 the population consisted of 30,000 Girgentana goats (ASSONAPA, 1984), while ten years later almost 98% of the pre-existing Girgentana population disappeared (Giaccone *et al.*, 1994). In 2001, only 252 mature goats participated in the national milk recording system (AIA, 2001). Therefore, the small number of Girgentana individuals available and further the lack of exchange of individuals between farmers led to an increase of inbreeding depression and genetic drift. In order to save this breed from extinction it needs to regain its genetic, zoo-technical and economic value, and must also be protected (FAO, 1998). For this reason, since 1997 the University of Palermo has been committed to the revival of the breed; thus all available Girgentana individuals, either coming from zoos or devoted farmers, have been bought and sent to an experimental farm. The purpose of the project is to reconstitute the genetic variability of the breed, and therefore to decrease the inbreeding depression and control the loss of allelic variants due to genetic drift. So far a problem with this small population is the lack of pedigree information. The aim of this paper is to carry out the demographic characterization and to evaluate the genetic variability of the Girgentana goat breed by analyzing the available pedigree information.

Material and methods

Pedigree data used in this paper were collected at an experimental farm and updated with the

pedigree file of ASSONAPA with genealogical information corresponding to the period 1990 - 2002. The pedigree consisted of 461 individuals (134 males and 327 females), with 368 living animals (106 males and 262 females). The effective population size (N_e) of the Girgentana was calculated as proposed by Falconer and Mackay (1996) when the number of males (M) is different from the number of females (F) in the population:

$$N_e = \frac{(4MF)}{(M + F)}$$

In addition, the inbreeding rate ($\Delta F = \frac{1}{2N_e}$) per generation was estimated and subsequently the inbreeding rate per year could be derived: $\Delta F_{year} = \frac{\Delta F}{L}$ where L is the average generation interval, which for the Girgentana goat was estimated to be 2.5 years.

Several demographic parameters, including the whole population inbreeding level, the inbreeding level within the living male population, the inbreeding level within the living female population, the inbreeding level within living males and females and the coefficient of relationship between all living individuals were estimated using the software Minbreed v1.0 (Gandini and De Filippi, 1998).

Results and discussion

The updated pedigree of five generations of the Girgentana population reared at the experimental farm consists of 461 goats (134 males and 327 females). Among the 461 individuals, the living population is comprised of 368 individuals (106 males and 262 females). The effective population size was $N_e = 380$. The inbreeding rate (ΔF) was equal to 0.13%. The resulting ΔF_{year} was equal to 0.05%. These results underline an unusual situation. Nevertheless, the resulting ΔF is equal to 0.13% per generation, which is in accordance with Bijma (2000) who advises that the inbreeding level in a zootechnic population should increase at most 0.5% to 1% per generation. Furthermore the demographic parameters were estimated using the available pedigree (Table 1). The average inbreed-

ing levels correspond to those of a large population with a random mating system, instead of a small population with a fairly high chance of mating between relatives. The average inbreeding level within the living male population was 0.8% (0-15%; Table 1) and the average inbreeding level within the living female population was 0.7% (0-31%; Table 1). The average relationship between males and females estimated on 27,772 possible matings was 0.5% (0-8.7%; Table 1). This can be explained by the lack of pedigree registration (Boichard et al. 1997; Folch and Jordana, 1998). The number of founder equivalents (f_e) was equal to 22.94 and the number of absolute founders (f_a) was equal to 93. The founder equivalents (f_e) of a population are the number of equally contributing founders that would be expected to produce the same variability as in the population under study (Lacy, 1989). The inbreeding rate was estimated with f_e and with f_a instead of N_e . Subsequently the "expected heterozygosity" ($H = 1 - \Delta F$), mean proportion of founder gene diversity remaining in the descendent generation, using each of the two parameters (f_e and f_a) was calculated. This was equal to 98% when using the f_e and equal to 99%

when using f_a . However, it was considered that the total number of founders was very high, basically due to the poor quality of pedigree information. According to Boichard et al. (1997) these individuals do not represent the genetic variability which exists in the current population. Actually the ratio between effective founders ($f_e = 22.94$) and absolute founders ($f_a = 93$) was 0.25. This means that the contribution of the founders to the present population is unbalanced owing to the fact that some founders have contributed very little or in some cases not at all.

Since 1997 the University of Palermo has planned matings at the experimental farm for every mating season; so far this was the only way to control the level of inbreeding and to start a new pedigree registration process. Evidently this is not the best solution because the increase of the inbreeding level is just postponed year by year. In the long term inbreeding can be better controlled by the selection strategy than by the mating strategy. Currently selection tools are available to consider the inbreeding rate in selection strategy of small populations (Meuwissen, 2002). The use of biotechnologies, such as

Table 1. Various measures of inbreeding level and relationship in the Girgentana population.

Source	N.	Mean	Range
Inbreeding within whole population	461	0.007	0.0-0.31
Inbreeding within living male population	106	0.008	0.0-0.15
Inbreeding within living female population	262	0.007	0.0-0.31
Inbreeding within living male and female population	368	0.007	0.0-0.31
Relationship between male and female population	27,772	0.005	0.0-0.87

Table 2. Milk production traits in 302 lactations from 141 Girgentana goats.

Trait	Mean±SD	Range
Total milk yield	kg 193.55±86.65	47.21-450.16
Fat yield	" 7.94±3.47	2.03-16.17
Fat content	% 4.16±0.59	2.76-6.10
Protein yield	kg 6.70±2.91	1.77-15.26
Protein content	% 3.49±0.30	2.83-4.74
Lactation length	d 176.01±52	52-278

Artificial Insemination (AI), which is in progress, will improve the actual situation. It will be possible to optimize the management of generation intervals. Prolongation of the generation interval can be used with the aim of increasing the number of bucks and goats and thus to increase the effective population size and therefore to reduce the genetic drift. However, in order to achieve a natural and artificial selection response it is important to maintain a replacement of the animals. For these reasons a reasonable choice of generation interval must be achieved.

In the future, when the costs will be considerably reduced, semen sexing technology could be useful in a program where each potential parent has a son and a daughter. In this way it will be possible to constrain the increase in coancestry. Another future solution could be the use of techniques of DNA molecular analysis, as genetic markers can be applied to estimate coancestry between individuals in absence of a known pedigree.

Conclusions

Until now different studies aimed at safeguarding and exploitation of the breed have been carried out (Portolano *et al.*, 1998; Chianese *et al.*, 2000; Todaro *et al.*, 2000; Portolano *et al.*, 2002; Bevilacqua *et al.*, 2001). To regain its valorization and protection as suggested by FAO (1998) and in order to avoid extinction, this breed requires a revival of its economic and zoological value.

The equal contribution of the highest number of animals possible must be ensured. A minimum number of inbreeding matings should be allowed. The highest number of founder animals (ideally all of them) would then be represented in the next generation. At the same time the revival of this population should also require the spread of the breed in a considerable number of herds.

Likewise, it might be interesting to evaluate the possibility of revitalizing interest in the milk produced by the Girgentana goat to regain an important economic role in the production of quality "drinking-milk" requested for particular food products, such as milk for infants. Recently Chianese *et al.* (2000) completed a study on the

chemical composition of milk and the polymorphism at the four casein loci, and both whey protein β -Lg and α -La loci, in order to ascertain the Girgentana milk qualities in comparison with human milk characteristics. In that study the Girgentana goat milk showed that both β -Lg and α -La loci were expressed at three quantitative levels (low, medium and high), which determine a different quality of milk. This evidence is an important issue because there are many protein allergens in cow milk that cause allergic reactions in people and especially in infants (Plaza Martín *et al.*, 2001; Host, 2002; Wal, 2002).

The modern knowledge offered by molecular markers can assist in filling the gap of the missing pedigree registration. In fact, genetic markers provide a useful tool to estimate pairwise coancestry between individuals in absence of a known pedigree. Molecular markers can be used for pedigree control, especially for parentage assignment. Several estimators (Toro *et al.*, 2002) have been developed to measure pairwise coancestry using the molecular information provided by different types of markers, especially microsatellites.

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