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# Genetic improvement of small ruminant local breeds with nucleus and inbreeding control: A simulation study

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ABSTRACT

In small ruminant local breeds of Southern Europe genetic selection is often constrained by small population sizes, poor animal identification, inadequate animal performance and pedigree recording, and organizational shortcomings. Under these conditions nucleus breeding schemes can offer practical and cost effective solutions. The paper investigated genetic gain in stochastically simulated dairy small ruminant nuclei of 100, 200 and 400 females, supporting commercial populations from 500 to 5000 females. In the nucleus, a young sire selection scheme was used, with optimum contribution selection on a dairy trait, at an annual inbreeding rate of 0.3%, corresponding to a generation inbreeding rate of 0.001. Sires, both selected and not-select as sires of sires, after 1 year of use in the nucleus were utilized in the commercial population for one, or alternatively, 2 years. Annual genetic gain ranged from a minimum of 0.073 SD with 100 females nucleus supporting a commercial population of 500 females, to a maximum of 0.138 SD with a 400 females nucleus supporting a commercial population of 5000 females. Negligible differences in genetic gain were observed between nuclei and corresponding commercial populations. When sires were used for only 1 year in the commercial population, we observed 7.7 years of genetic lag with the nucleus, that increased to 8.2 years when sires were used for 2 years. Results showed that there are opportunities for selection even in populations of a few hundreds of females. Considering a specific breeds, or a specific farming area, a cost benefit analysis should be carried out to orientate the choice of nucleus size and strategy of use of sires.


## 1. Introduction

Small ruminant local breeds in Southern Europe are mainly selected for dairy traits. Selection is often hampered by small population size, incorrect animal identification, inadequate animal performance and pedigree recording, and organizational shortcomings (Serradilla and Ugarte, 2006). The use of two or more sires with natural insemination in a single flock, as often observed, does not allow to unambiguously assign paternity of newborns without the use of genetic markers. The limited use of artificial insemination often results into insufficient connections to allow for across-flock genetic evaluation (Lewis and Simm, 2000).

The introduction of exotic, more productive, breeds can result in failures because of their poor adaptability

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to the harsh conditions of the Mediterranean extensive farming environment (Kalaisakis et al., 1977; Zervas et al., 1975). Alternatively, selection within local breeds has the potential to balance genetic improvement in productive and adaptation traits accounting for the local production system (Kominakis et al., 1997), and can contribute to economic sustainability of local breeds farming (FAO, 2013).

Despite the importance of small ruminant farming in Southern Europe, the available information on genetic programs for local breeds farmed under low input and low technology production systems is scarce (Roden, 1995; Kominakis et al., 1997; Smulders et al., 2007). Some information and experience is available from tropical areas, where constraints similar to those found in Mediterranean marginal areas are observed, as reviewed by Kosgey et al. (2006) and Kosgey and Okeyo (2007).

In general, in such production systems, genetic improvement can be generated in a small fraction of the population, the nucleus, and then disseminated to the whole population. Within the nucleus, trait and pedigree recording can be carried out at limited cost and organizational effort, and breeding strategies based on sire identification, such as the use of artificial insemination or of a single sire per flock, can be implemented, allowing more reliable breeding values estimation. The nucleus population can be an institutional flock in an experimental or public station, or be constituted by two or more coordinated farmer flocks. With respect to genetic flow, the nucleus can be defined as open or closed. In open nucleus schemes there is an upward flow of animals from the commercial population to the nucleus, while in a closed nucleus there is no such migration. Advantages and disadvantages of the two systems should be considered in specific cases (Roden, 1994). In general, in an open nucleus a larger portion of the population can be used for selection and inbreeding control is expected to be easier; however, pedigree and performance recording is not limited to the nucleus. Closed nuclei require a simpler organization, but inbreeding must be carefully monitored. More generally, selection in local breeds should guarantee the maintenance of within and among-breed genetic diversity.

In the last years, different strategies have been proposed to control inbreeding in selected populations (Fernandez et al., 2011), the most efficient being selection with optimal contributions (Meuwissen, 1997; Grundy et al., 2000), which maximizes genetic gain subject to a restriction on inbreeding rate.

The aim of the present work is to investigate genetic gain in dairy small ruminant populations with a closed nucleus, where a young sire breeding scheme with inbreeding control and optimal contributions selection is applied.

## 2. Methods

A semi-stochastic computer simulation has been developed to analyze a number of breeding scenarios.

### 2.1. The breeding scheme

The whole population is divided in two tiers: the closed nucleus where recording and selection are carried out, and the commercial population that receives genetically superior sires from the nucleus. Migration from nucleus to the commercial population is restricted to males. Nuclei of various sizes, supporting populations of up to 5000 females, are stochastically simulated under different schemes of sire use.

In the nucleus, 1-year old young sires (YS), the unselected male offspring of sires of sires (SS) and dams of sires (DS), are used for a 1-year mating season on dams of dams (DD). SS are selected among YS and used on DS in the same 1-year mating season. The female offspring of SS × DS matings are kept for replacement. Should these not be sufficient, females born from YS and DD are randomly selected as replacements. YS × DD male progeny are discarded. DS are selected among all reproductive females (FFN: Fertile Females in the Nucleus). Optimum contribution selection (OCS) is applied to selection of SS and DS.

After being used within the nucleus, SS and YS are mated to females in the commercial population (FFP: Fertile Females in the commercial Population), either for 1-year mating season (scheme B1) or for two mating seasons (scheme B2). Fig. 1 illustrates the nucleus and the commercial population, and relationships between them.

### 2.2. The simulation model

#### 2.2.1. Nucleus

Age structured nuclei of 100, 200 and 400 FFN were stochastically simulated. The simulation interval was 1 year, corresponding to the parturition interval with one mating season per year, and to the interval between birth and age of reproduction. Table 1 reports the simulated demographic parameters for females and males in the nucleus.

A single trait repeatability model was used to estimate animal model BLUP EBVs, including a random genetic effect, random environmental effects and a residual effect. No fixed effects were simulated. Selection was applied for a dairy trait with heritability 0.3 and repeatability 0.5. Inbreeding and genetic level were computed each year from average values of newborn females. The founder population was assumed to be unrelated: true breeding values (TBV) were sampled from a normal distribution – N(0,1) – and genetic change was expressed in standardized genetic units.

In the selection of SS and DS, genetic gain was maximized subject to a fixed annual inbreeding rate of 0.3%, by placing a penalty on the average relationship among selected animals. The following objective function (**H**) was maximized:

$$\mathbf{H} = \mathbf{x}'\mathbf{a} - \lambda\,\mathbf{x}'\mathbf{A}\mathbf{x} \quad (1)$$

where **x** is the vector of individual candidate parents contributions, i.e. the proportion of matings; **a** is the vector of EBVs of the candidates; **A** is the matrix of pedigree relationships among candidates weighted by λ, the penalty assigned to the average relationships among candidates to control for inbreeding. Candidate contributions (vector **x**) were multiplied by 1/2 to ensure that contributions from each sex sum to 0.5 (Meuwissen, 1997). Function **H** returns the genetic level of next generation parents, minus the cost due to increased average relationships. As in Berg et al. (2007), to achieve the target annual inbreeding rate of 0.3%, λ was empirically determined through trial and error. Eq. (1) was maximized by using an annealing algorithm (Press et al., 1989). Additional details on the simulation model are described in Gandini et al. (2014).

Mating among both selected (SS × DS) and unselected animals (YS × DD) was at random, but avoiding closely inbred matings (i.e. between half and full sibs and between parents and their progeny). The number of DS was set to correspond the desired number of male progeny (YS), accounting for sex ratio at birth and random culling. The number of selected SS was obtained through the OCS algorithm, driven by the λ weight and in order to achieve the target inbreeding rate while maximizing genetic gain.

Selection in the nucleus was simulated for 25 years. During the first 5 years of simulation truncation selection was applied in order to build the pedigree used in the following 20 years of OCS. From year 15 onwards, cumulative inbreeding and genetic level both followed a monotonic and linear trend. Eight hundred iterations were used. Average annual genetic gain ($\Delta G$) and inbreeding rate ($\Delta F$) were computed at year 25 subtracting their level at year 15 and dividing by ten:

$$\Delta G = \frac{G_{25} - G_{15}}{10} \quad (2)$$

$$\Delta F = \frac{F_{25} - F_{15}}{10} \quad (3)$$

where $G_{25}$, $G_{10}$, $F_{25}$ and $F_{10}$ are the genetic and inbreeding levels at years 25 and 10, respectively.