

Empowerment of the Italian small ruminant sector: new traits and tools toward a sustainable management

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Abstract

This work summarizes the main results of the CHEESR project, a national initiative with the aim of introducing innovative tools for biodiversity conservation and genetic improvements of the Italian small ruminant populations. Pedigrees from 81 breeds and genomic data from 11 case-study breeds have been analyzed. These, together with the collection of new phenotypes, led to the development of welfare- and health-related genomic tools for the first time in Italian sheep and goats. The introduction of these new instruments, which will continue with the SHEEP&GOAT project, will contribute to devise new strategies for sustainable development of the Italian small ruminant sector.

Introduction

Livestock genetic variability has a pivotal role in the ecosystem conservation, the land management, and the mitigation of the effects of climate change (Cao et al. 2021). Thanks to its history and variety of environments, climates, and traditions, Italy is characterized by a great biodiversity of all livestock species (Cortellari et al. 2021b), with over 80 small ruminant breeds. The scientific research about the Italian biodiversity has been conducted by the *Italian Goat Consortium* for goats (Nicoloso et al. 2015; Cortellari et al. 2021a; b) and by the *Bi.Ov.Ita Consortium* for sheep (Ciani et al. 2014; Mastrangelo et al. 2018). The European Agricultural Fund for Rural Development (EAFRD) financed the Italian National Rural Development Plan (PSRN) – sub-measure 10.2 – “Conservation, Health and Efficiency Empowerment of Small Ruminant” (CHEESR project), managed by the Italian Sheep and Goat Breeders Association (Asso.Na.Pa.). This project aims to introduce in the Italian sheep and goat sector several innovative actions related to: the monitoring and conservation of the biodiversity, the improvement of the breeds with the collection of new phenotypes, and the development of new genetic and genomic breeding values.

The present work summarizes the main results of the CHEESR project, focusing on the application of innovative genomic tools in the Italian small ruminant sector to support biodiversity management and the genetic improvement of the populations under selection, eventually providing information about future developments.

Materials & Method

Genealogic data of 35 goat breeds and 46 sheep breeds were analyzed through *optiSel* R package: pedigree depth and completeness and the main genetic and demographic parameters were estimated.

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Furthermore, effective population size (N_e) was estimated using Wright's formula, based on the male (M) and female (F) ratio ($\frac{4MF}{M+F}$), calculated in 2020 for each breed.

The OvineSNP50 and GoatSNP50 bead chips were used to genotype 2,820 sheep of seven breeds (Sarda, Istriana-Carsolina, Comisana, Massese, Delle Langhe, Fabrianese, and Gentile di Puglia) and 3,320 goats of four breeds (Saanen, Camosciata delle Alpi, Garganica, and Nicastrese). Runs of homozygosity (ROH) and the related inbreeding coefficient (F_{ROH}) were analyzed using Plink software. These data were also used, together with phenotypic information collected from 3,680 goats and 766 sheep, to develop new genomic breeding values with the BLUPF90 family softwares. The Single Step Genomic Best Linear Unbiased Prediction (ssGBLUP) method was applied to estimate the variance components of the welfare score (Wel), locomotion score (Loc), body condition score (BCS), and somatic cell score (SC). Wel is composed of 2 traits (chest circumference and BCS) for goats and 4 traits (chest circumference, BCS, presence of abscesses, and *lupia*) for sheep. Loc is composed of 9 traits for goat and 8 for sheep; these morphological traits and morpho-functional defects are related to limbs, dorsal line and rump, and udder as well as hoof care.

Results

Considering the pedigrees of all the 81 Italian breeds, in median, we could trace up to 2 and 3 full generations and up to 5 and 7 maximum generations for goat and sheep, respectively. The pedigree completeness varied among breeds, with a median percentage of sheep with a complete first generation higher than goats (34% vs 14%). According to the effective population size (N_e), 18% of the breeds appear to be at risk of extinction in the short term ($N_e < 50$).

Pedigree and genomic data for the 11 genotyped breeds are reported in Table 1. The correlation between the pedigree-based (F_{PED}) and the genomic (F_{ROH}) inbreeding coefficients was significant for Sarda, Massese, Comisana, Delle Langhe, Camosciata delle Alpi and Saanen breeds. At species level, the correlation was higher in sheep ($r = 0.82$, $p < 0.0001$) than in goats ($r = 0.28$, $p < 0.0001$). Differences in the recent inbreeding, derived from long ROH, can depend on the management and structure of the populations.

Table 1. Results of the pedigree and genomic analyses for the genotyped breeds.

Breed	FullGen	MaxGen	N_e	F_{PED}	F_{ROH}	r	% F_{ROH} for ROH > 16 Mb
^S Sarda	9	40	19,169	0.093	0.134	0.80*	19%
^S Massese	8	28	1,561	0.038	0.078	0.32*	10%
^S Gentile di Puglia	4	11	1,042	0.008	0.045	0.84	22%
^S Comisana	8	20	726	0.018	0.051	0.38*	9%
^S Delle Langhe	9	33	248	0.060	0.118	0.44*	17%
^S Fabrianese	6	16	190	0.079	0.128	0.16	47%
^S Istriana-Carsolina	3	8	126	0.036	0.141	0.16	36%
^G Camosciata delle Alpi	6	22	1,891	0.016	0.065	0.26*	22%
^G Saanen	7	23	1,450	0.020	0.071	0.31*	26%
^G Garganica	3	5	793	0.021	0.077	0.02	40%
^G Nicastrese	2	4	684	0.000	0.036	0.00	24%

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^SSheep, ^GGoat, FullGen: maximum number of fully traced generations; MaxGen: maximum number of generations traced; N_e: effective population size; F_{PED}: mean pedigree-based inbreeding; F_{ROH}: mean genomic inbreeding, r: correlation coefficient between F_{PED} and F_{ROH}, *: p < 0.0001.

All the traits presented here (Wel, Loc, BCS, and SC) are not under selection and have been analyzed for the first time in the Italian populations within this project. The results of the two composed scores (Wel and Loc) are reported in Table 2. The great majority of animals do not present welfare-related problems (Wel = 0). Instead, about only one third of the sheep presents the lowest possible Loc score. The heritability of all the analysed traits was calculated. The wide highest probability density (HPD) interval of the estimated h² suggests that, increasing the sample size and selecting the most representative animals, there is room for improvement (Table 3).

Table 2. Results of Welfare and Locomotion scores.

Breed	Wel			Loc		
	0	1	2	0	1	2
^S Comisana (n. 529)	88 %	12 %	0 %	32 %	49 %	19 %
^S Massese (n. 219)	93 %	6 %	1%	31 %	51 %	18 %
^G Camosciata delle Alpi (n. 2662)	97 %	3 %	0 %	87 %	10 %	3 %

^SSheep, ^GGoat, Wel: welfare score; Loc: locomotion score; the higher scores are related to animals with more welfare-or-locomotion-related problems.

Table 3. Heritability for the analyzed traits.

Breed	Wel h ² (HPD)	Loc h ² (HPD)	BCS h ² (HPD)	SC h ² (SD)
^S Comisana	0.10 (0.006 - 0.24)	0.09 (0.001 - 0.24)	0.11 (0.02 - 0.25)	0.03 (0.01)
^S Massese	0.13 (0.004 - 0.34)	0.18 (0.005 - 0.43)	0.17 (0.004 - 0.38)	0.05 (0.02)
^G Saanen				0.09 (0.02)
^G Camosciata delle Alpi	0.30 (0.003 - 0.58)	0.13 (0.004 - 0.28)	0.26 (0.03 - 0.48)	0.10 (0.02)

^SSheep, ^GGoat, Wel: welfare score; Loc: locomotion score; BCS: body condition score; SC: somatic cell score; HPD: high probability density interval; SD: sample standard deviation; h²: heritability.

Discussion

Our findings show that the Italian small ruminant populations present a wide variety of situations in terms of pedigree management. Overall, sheep breeds are characterized by a higher pedigree depth, completeness, and effective population size than goats. These parameters are fundamental for the management of the populations, both when pursuing their conservation and genetic improvement, because they can influence the accuracy of inbreeding and parentage estimates. The integration of the genomic tools with the more traditional ones represents an important upgrade that allows to overcome unreliable or incomplete pedigree data. Moreover, the collection of new phenotypes led to the development of breeding values that meet the demands for greater guarantees in terms of animal welfare and health, paving the way for a more sustainable small ruminant sector. Our results show a low variability of Wel and wide high probability density interval (HPD) of the heritability estimates of Wel, Loc, and BCS. With the aim to develop an accurate welfare breeding evaluation we will review our results and the welfare-related traits collected and analyzed considering the difference

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between the two species and the diversified management system. All the activities undertaken within the CHEESR project, including the phenotypic and genotypic characterization for the study of biodiversity and the development of genomic breeding values, will continue with the *SHEEP&GOAT* project (supported by EAFRD for the period 2021 - 2023): through the genotyping of all the Italian small ruminant breeds present in at least three registered farms, this project will help to better portray the situation of the whole sector and will contribute to define national strategies to safeguard the Italian biodiversity.

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