

# PhD School on Agriculture, Environment and Bioenergy

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(XXXIX cycle, 2023-26)

## Project draft

### 1. Field of interest

*genetics, genomics and biodiversity in Italian small ruminant populations*

### 2. Project title

Development of new models of genomic selection and biodiversity conservation in Italian small ruminant populations

### 3. Tutor (membro del Collegio dei Docenti)

Prof.ssa Paola Crepaldi

- **Eventually: co-tutor/s**

### 4. Relevance of the topic and state of the art:

Livestock genetic variability has a pivotal role in the ecosystem conservation, the land management and mitigation of the effects of climate change (Cao et al., 2021). Thanks to its history and variety of environments, climates and tradition, Italy is characterized by great biodiversity of all species (Cortellari et al., 2021), with over 80 small ruminant breeds. These breeds are subjected to selection and conservation programs. New selection and conservation tools are needed in this sector to ensure the environmental, economic and genetic sustainability. In Italy, as in several countries all over the globe, including France (Teissier et al., 2019, 2020), Spain (Molina et al., 2018), Canada (Massender et al., 2022) and New Zeland (Scholtens et al., 2020), the collection and use of genomic data and new phenotype, have recently started in different sheep and goat populations. Moreover, the possibility to use genomic data open new possibility in conservation and selection strategies. In fact, it allows to overtake the lack of completeness and deepness of pedigree data; to check the relationship between animals and estimate the real level of inbreeding; and to define the genomic background at breed and single animal level. This advantages, together with the collection of new phenotypes and genotypes, will allow to develop new models of estimated breeding values and matings programs to improve sheep and goat production, while also ensuring animal welfare (Biffani et al., 2020), resilience, efficiency, and health (Mucha et al., 2022). Single-Step Genomic Best Linear Unbiased Predictions (ssGBLUP) represents nowadays the most used methods in genetic evaluations. It can consider simultaneously genotyped and non-genotyped animals improving the accuracy of their Estimated Breeding Values (Bermann et al., 2022). The genomic selection is gold standard in the most productive and studied dairy cattle populations, such as the Holstein and Jersey cows, but in recent years its use is starting to spread also in small ruminant breeds. Due to the different rearing system, population structure, and availability of pedigree data of the Italian sheep and goat breeds, and also the limited use of artificial insemination, it is necessary a better evaluation of the phenotypes collection, the models used to estimate breeding values, the tools used for inbreeding level estimation, and the dissemination of the results of genetic gain with the aim to improve the management of Italian sheep and goat breeds both for biodiversity conservation and selection purposes.

### 5. Layout of the project (draft)

#### 5.1. Materials & Methods:

**Phenotype Collection:** Identify and define new phenotypes relevant to small ruminant production, health, and welfare.

**Genetic Evaluation:** Develop and implement new genetic/genomic indexes for simple and complex traits using state-of-the-art methods, such as ssGBLUP, to incorporate genomic information into traditional genetic evaluations.

**Biodiversity and Inbreeding Management:** Develop and implement new systems for monitoring small ruminant biodiversity and managing inbreeding using genomic data to assess levels of inbreeding and genetic diversity within and between small ruminant populations.

## 5.2. Schedule and major steps (3 years)

Year 1 - Conduct literature review on genetic and genomic evaluation in small ruminants. Collect and analyze phenotypic and genomic data available on small ruminant populations. Estimate EBVs for single and complex traits.

Year 2- Spend 3-6 months in a foreign department to improve knowledge about EBV estimation methods. Identify and define new phenotypes relevant to small ruminant production, quality, health, and welfare to develop new EBVs.

Year 3 -Calculate pedigree and genomic information useful for monitoring genetic diversity within and between breeds, to manage inbreeding in the Italian small ruminant breeds. Disseminate project findings through scientific publications.

## 6. Available funds

PSRN 5000

## 7. Literature

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- Biffani, S., Tiezzi, F., Fresi, P., Stella, A., & Minozzi, G. (2020). Genetic parameters of weeping teats in Italian Saanen and Alpine dairy goats and their relationship with milk production and somatic cell score. *Journal of Dairy Science*, 103(10), 9167–9176. <https://doi.org/10.3168/jds.2020-18175>
- Cao, J., Baumung, R., Boettcher, P., Scherf, B., Besbes, B., & Leroy, G. (2021). Monitoring and Progress in the Implementation of the Global Plan of Action on Animal Genetic Resources. *Sustainability*, 13(2), 775.  
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- Cortellari, M., Bionda, A., Negro, A., Frattini, S., Mastrangelo, S., Somenzi, E., Lasagna, E., Sarti, F. M., Ciani, E., Ciampolini, R., Marletta, D., Liotta, L., Ajmone Marsan, P., Pilla, F., Colli, L., Talenti, A., & Crepaldi, P. (2021). Runs of homozygosity in the Italian goat breeds: impact of management practices in low-input systems. *Genetics Selection Evolution*, 53(1), 92. <https://doi.org/10.1186/S12711-021-00685-4>
- Massender, E., Brito, L. F., Maignel, L., Oliveira, H. R., Jafarikia, M., Baes, C. F., Sullivan, B., & Schenkel, F. S. (2022). Single-step genomic evaluation of milk production traits in Canadian Alpine and Saanen dairy goats. *Journal of Dairy Science*, 105(3), 2393–2407. <https://doi.org/10.3168/jds.2021-20558>
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<https://doi.org/10.1016/j.smallrumres.2017.12.010>
- Mucha, S., Tortereau, F., Doeschl-Wilson, A., Rupp, R., & Conington, J. (2022). Animal Board Invited Review: Meta-analysis of genetic parameters for resilience and efficiency traits in goats and sheep. *Animal*, 16(3), 100456.  
<https://doi.org/10.1016/j.animal.2022.100456>
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<https://doi.org/10.3390/ani11010024>

- Teissier, M., Larroque, H., Brito, L. F., Rupp, R., Schenkel, F. S., & Robert-Granié, C. (2020). Genomic predictions based on haplotypes fitted as pseudo-SNP for milk production and udder type traits and SCS in French dairy goats. *Journal of Dairy Science*, *103*(12), 11559–11573. <https://doi.org/10.3168/jds.2020-18662>
- Teissier, M., Larroque, H., & Robert-Granié, C. (2019). Accuracy of genomic evaluation with weighted single-step genomic best linear unbiased prediction for milk production traits, udder type traits, and somatic cell scores in French dairy goats. *Journal of Dairy Science*. <https://doi.org/10.3168/jds.2018-15650>