



## 14. Resilience and Efficiency in Small Ruminants

### Title presentation

Feasibility of a genomic selection approach for gastro-intestinal nematodes resistance based on a female informative population in Sarda breed sheep.

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### Abstract

Gastrointestinal nematodes (GIN) are one of the major health problems in grazing animals. GIN infections determine important yield reductions and increased production costs due to medical treatments and higher culling rates. Moreover, anti-helminthics resistance has already been reported in several countries. Fecal egg count (FEC), i.e. the number of parasite eggs per gram of faeces has been largely used as proxy trait to measure resistance to GIN. In sheep, genetic variation between individuals and breeds has been documented. However, the inclusion of GIN resistance in current breeding schemes is hampered by the difficulty to record FEC on large scale since its measure is too laborious and costly in field conditions. In Sardinia, sheep farming systems are based on grazing natural pastures and forage crops where GIN infection is unavoidable. Thus, most farmers are forced to administrate anti-helminthics often without well planned protocols in terms of individual diagnosis, doses and frequency of treatments. The aim of this work was to assess the feasibility of a genomic selection approach for GIN resistance in Sarda breed based on a female reference population bred in a nucleus flock. Since 2000, the flock has consisted of about 800 milked ewes per year with a replacement rate of 25%, generated by mating the adult ewes with rams coming from the Sarda Herd Book (HB). The flock is managed following the traditional system adopted in Sardinia that is based on grazing natural or cultivated swards. All the ewes of the experimental population born from 2000 to 2018 (n=4224) and their sires (n=181) as well as 480 sires of HB were genotyped with the Illumina Inc. OvineSNP50 Beadchip. Rectal faecal samples were collected from the ewes and FEC was determined using a copromicroscopic exam according to McMaster technique. From 2000 to 2019, 16.530 records from 4097 ewes collected on 24 dates were retained. Heritability estimates were obtained by using repeated animal models with SSGPLUP method testing different weights of the pedigree based A-matrix into the H-matrix. Cross-validation was used to assess predictive ability of different models on a validation population including the last generations of ewes. Moreover, GEBV and their expected accuracies were calculated also for rams from HB with no progeny in the female nucleus. Potential implications and selective breeding strategies will be discussed focusing on the feasibility of genomic selection of HB rams based on the phenotypes collected in the nucleus flock.