AGROECOLOGICAL BREEDING: GENOMIC EVALUATION IN AUSTRALIAN MERINO

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Introduction. An agroecological approach implies the application of ecological principles and concepts to the design and management of sustainable agroecosystems using natural processes, local resources and limiting the environmental agricultural footprint. Consequently, breeding goals should consider functional traits, in addition to production ones. Agroecological selection objectives, proposed in livestock, include robustness, reproduction, feed efficiency, product quality, behavior, and health, among other traits (1). Some of the challenges of an agroecological approach for sheep farming could be overcome by the incorporation of genomics in breeding programs, along with integrated phenotypic recording systems.

The objective of this work was to evaluate the impact of using genomics in selection decisions in the Uruguayan Merino Information Nucleus (UMIN). We focused on genetic resistance to gastrointestinal nematodes (GIN), as one of the relevant and difficult-to-measure traits for agroecological animal breeding.

Methods. A total of 26,244 animals with fecal egg count (FEC) data recorded in 13 stud-flocks, including the Agronomy Faculty Experimental Station (EEFAS) and UMIN, that are part of the Uruguayan Merino genetic evaluation. Genomic information from different panels (illumina OvineSNP50, AxiomOvine60K, illumina15K) were available for 1,800 animals and imputed to the GGP50K panel (40K SNP, postQC). Using a univariate animal model (2), breeding values (EBV) and genomic breeding values (GEBV) were estimated using BLUP and ssGBLUP, respectively, with partial (p) and complete (c) data sets. The p-dataset can be interpreted as the evaluation at the time of selection decisions, and c-dataset as *a posteriori* confirmation of the goodness of these selection decisions (3). The p-dataset was used to estimate EBV for 145 animals, as lambs, including own FEC records and GEBV adding genomic information. In the p-dataset, data of later generations was excluded. With all generations and data (c-dataset), GEBVs were estimated to the same animals as rams. Individual precisions of the (G)EBVs were calculated including inbreeding (4). Predictability was evaluated by the Pearson's correlation (R) between GEBVc and (G)EBVp.

Results and discussion. The model with the best predictive ability (Fig 1) was the one including genomic information (GEBVp), with an R value 12% higher than EBVp.

Similarly, average individual accuracies of GEBVp were higher than in EBVp (0.63 vs 0.59, respectively), confirming that the inclusion of genomic information improves the accuracy of EBVs in young rams (5). The average of individual precisions of GEBVc was 0.82.
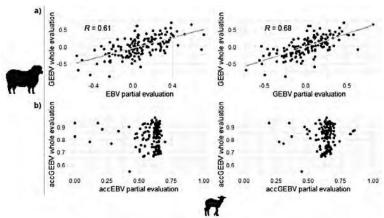

Fig 1. Comparison of GEBVs estimated using a complete dataset and (G)EBV with partial datasets (a), and their individual accuracies (b).

Conclusions. Individual accuracies of EBVs for GIN resistance can be improved when genomic information is included. It is particularly promising for the genetic improvement of difficult-to-measure traits such as resistance to GIN and can likely be extrapolated to other agroecological selection objectives.

References.
1. Phocas, F. et al. (2016). Review: Towards the Agroecological Management of Ruminants, Pigs and Poultry through the Development of Sustainable Breeding Programmes: I-Selection Goals and Criteria. Animal: An IJAB 10 (11): 1749-59.
2. Ciappesoni, G., et al. (2013). Estimates of Genetic Parameters for Worm Resistance, Wool and Growth Traits in Merino Sheep of Uruguay. LS 157 (1): 65-74.
3. Legarra, A. (2018). Semi-Parametric Estimates of Population Accuracy and Bias of Predictions of Breeding Values and Future Phenotypes Using the LR Method. GSE 50 (1): 53.
4. Aguilar, I., et al. (2020). Effects of Ignoring Inbreeding in Model-Based Accuracy for BLUP and SSGBLUP. JABG 137(4): 356-64.
5. Macedo, F. L. (2020). Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. GSE. 52(1).