SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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Second batch of practice abstracts for end-users.

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About the SMARTER research project

SMARTER developed and deployed innovative strategies to improve Resilience and Efficiency (R&E) related traits in sheep and goats. SMARTER will find these strategies by: i) generating and validating novel R&E related traits at a phenotypic and genetic level ii) improving and developing new genome-based solutions and tools relevant for the data structure and size of small ruminant populations, iii) establishing new breeding and selection strategies for various breeds and environments that consider R&E traits.

SMARTER with help from stakeholders chose several key R&E traits including feed efficiency, health (resistance to disease, survival) and welfare. Experimental populations were used to identify and dissect new predictors of these R&E traits and the trade-off between animal ability to overcome external challenges. SMARTER estimated the underlying genetic and genomic variability governing these R&E related traits. This variability is related to performance in different environments including genotype-by-environment interactions (conventional, agro-ecological and organic systems) in commercial populations. The outcome is an accurate genomic prediction for R&E traits in different environments across different breeds and populations. SMARTER also created a new cooperative European and international initiative that use genomic selection across countries. This initiative made selection for R&E traits faster and more efficient. SMARTER also characterized the phenotype and genome of traditional and underutilized breeds. Finally, SMARTER proposed new breeding strategies that utilise R&E traits and trade-offs and balance economic, social and environmental challenges.

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1. Summary

Six practice abstracts have been produced by SMARTER partners at M18 for the First batch of practice abstracts for end-users (for further details please refer to Deliverable D8.3). They have also been uploaded on the website of the new EU CAP Network website (https://ec.europa.eu/eip/agriculture/en/find-connect/projects/smarter-small-ruminants-breeding-efficiency-and.html).

This deliverable contains the second batch, made by six abstracts related to the WPs 1, 2, 3 and 6.

2. Introduction

A practice abstract is a short summary, in easily understandable language, of re-usable results. The targets are practitioners and stakeholders. It focuses on results and recommendations that can be used in practice. “A short summary” means +/- 1500 characters.

During the last ExCom meeting held on 22/5/23 in Toledo, the following practice abstracts have been identified:

- WP1 has submitted one abstract:
  - Across-country genetic selection for feed efficiency indicators in Lacaune sheep from Greece and France
- WP2 has submitted two abstracts:
  - Breeding to improve lamb survival and maternal efficiency in meat sheep
  - A low-density sheep genotype panel for SMARTER sheep breeds
- WP3 has submitted one abstract:
  - When, why & how to breed for disease resilience in livestock
- WP6 has submitted two abstracts:
  - Producing guidelines to record efficiency and resilience in small ruminants
  - Across-country genetic evaluations are feasible in small ruminants

WP4, WP5 and WP7 no practical results to present for this second batch.

As for the first batch, a specially designed template produced by EAAP was used to disseminate the second batch of practice abstracts through the SMARTER web site; the second batch will be available by mid-July.

3. Practice Abstracts

Practice Abstract n. 7 - Across-country genetic selection for feed efficiency indicators in Lacaune sheep from Greece and France

Practice Abstract n. 7

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Across-country genetic selection for feed efficiency indicators in Lacaune sheep from Greece and France

Authors: S. Vouraki[1], S. Priskas[1], J.M. Astruc[2], G. Lagriffoul[2], R. Rupp[3], G. Banos[4], G. Arsenos[1]

[1]AUTH, Greece, [2]IDELE, France, [3]INRAE, France, [4]SRUC, UK

Improving feed efficiency of small ruminants is a desirable breeding goal to maximize farm profitability, increase productivity and reduce environmental impact. Milk yield and composition could be used as proxy traits of feed efficiency. Genetic selection for these traits using data from different countries could increase progress and benefit breeding programmes particularly in small ruminant production systems that are characterised by great diversity across-countries. Therefore, a study was undertaken within the SMARTER project (www.smarterproject.eu) to investigate the feasibility of genetic evaluation and selection for feed efficiency indicators in purebred Lacaune sheep reared intensively in Greece (n=1,658) and semi-extensively in France (n=4,859). Results showed a strong genetic correlation for milk yield and protein content and a relatively high correlation for fat content between animals raised in the two countries. Consequently, there is no evidence of genotype x environment interaction across country x system. This suggests that a joint genetic evaluation of Lacaune sheep in Greece and France is feasible. However, the observed variation in fat content is most likely related mainly to the different feeding practices in the two countries and to a lesser extent in the rams used for artificial insemination. In conclusion, breeding strategies should be tailored to the needs and conditions in each country subject to accurate and systematic recording of phenotypes of individual animals to improve feed efficiency.

The SMARTER project has received funding from the European Union's Horizon 2020 Program for Research & Innovation under grant agreement n°772787.

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Practice abstract n. 8 - Breeding to improve lamb survival and maternal efficiency in meat sheep

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Breeding to improve lamb survival and maternal efficiency in meat sheep

Authors: Joanne Conington[1], Ann Mclaren[1], Maxime Ben Braeik[3], Jean-Michel Astruc[4], Noirin McHugh[2]

[1]SRUC, UK, [2]Teagasc, Ireland, [3]INRAE, France, [4]IDELE, France

It is possible to use information from adult ewes about their reproductive performance to determine the survival of their offspring. Key metrics can be used such as the number of lambs being carried (as determined by ultrasonography), number of lambs born, reared and lost to a given point in time (e.g. weaning). Typically, the non-genetic influences for these traits (e.g. feeding, management etc) largely determine their outcome as the genetic component to most of these traits is relatively low (<10%). These traits expressed by ewes are indicative of maternal efficiency affecting ewe productive longevity and flock profitability. There is also a 'direct lamb' component to lamb survival which are the lambs' own genes impacting on whether or not they survive in-utero development, the neonatal and the lamb growth periods. Also, research undertaken in the SMARTER project in the Manech Tête Rousse breed used a novel method to detect 'lethal' mutations carried by lambs affecting their survival. For example, loss-of-function in gene mutation 'CCDC65' leads to respiratory distress and lamb mortality before weaning, the MMUT gene leads to metabolic default and lamb mortality in the first 24H after birth and SLC33A1 leading to embryonic loss, also contributing to lamb mortality in the first 5 days after birth. Screening animals for these genes will lead to a reduction in lamb losses and requires validation for other breeds.

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Practice abstract n. 9 - A low density sheep genotype panel for SMARTER sheep breeds

Practice Abstract n. 9

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A low-density sheep genotype panel for SMARTER sheep breeds

Authors: A. O`Brien[1], D.P. Berry[1], J.M Astruc[2], J. Connington[3]

[1]Teagasc, Ireland, [2]INRAE and IDELE, [3]SRCU, UK

The cost of genotyping is often prohibitive to large-scale genotyping. The cost per genotype is a function of the purchase order size; hence, requesting a large order of panels could reduce the cost per genotype. The objective was to develop a low-density genotype panel for sheep that would be as informative as possible to a range of different breeds and populations represented in SMARTER.

The density of the genotype platforms developed was 384, 1,000, 2,000, 3,000, 6,000, 9,000 and 12,000 DNA markers. To develop this, a summary file of the frequency of each variant per DNA marker was available for five meat sheep breeds from Ireland (i.e., Belclare, Charollais, Suffolk, Texel and Vendeen), two meat sheep breeds from the UK (i.e., Scottish Blackface and Texel), and five French dairy sheep breeds (i.e., Basco-Béarnaise, Black-faced Manech, Corse, Lacaune, and Red-faced Manech).

A total of 38,883 DNA markers were common to all sheep populations. Each low-density genotype panel was generated separately with the genome firstly being divided into N blocks of equal size where N was the number of markers to be selected for the panel being developed.

The most informative variant per block was selected. Using the 1,000-marker panel as an example, all selected variants were informative in all populations. For the 12,000-marker panel, a total of 527 were not informative in at least 1 breed. The selected DNA markers are now publicly available.

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Practice abstract n. 10 - When, why & how to breed for disease resilience in livestock

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When, why & how to breed for disease resilience in livestock

Authors: A. Doeschl-Wilson[1], Masoud Ghaderi-Zefreh[1], Ricardo Pong-Wong[1]

[1] The Roslin Institute and R(D)SVS, University of Edinburgh

Infectious diseases are a major threat to sustainable production of high-producing animals, including sheep and goats. Breeding for increased disease resilience has been a research focus for many years, but is not yet explicitly implemented into any practical breeding program. Instead, breeders tend to indirectly select on resilience by selecting for high productivity in challenge conditions.

Within Smarter, we investigated how future breeding programs may benefit from recent research on disease resilience. Disease resilience can be estimated using reaction-norms of changes in productivity with increasing infection challenge.

We found that the genetic merit for disease resilience can be predicted far more accurately if genomic data are available, and if productivity phenotypes of related animals exist for a wide range of different challenge levels. Selecting for high productivity without explicitly estimating disease resilience may indirectly improve disease resilience, but only if the productivity measurements of animals are collected in infectious as well as disease free conditions.

We also show that breeding animals with higher disease resilience may not necessarily improve herd resilience if more resilient animals are also more infectious. Hence it is important to also measure pathogen load of individual animals. The most promising break-throughs in genetic improvement of disease resilience rely on technological innovations such as routine genotyping or automated data generation that provide accurate and frequent estimates of productivity and health.

Related papers:

Ghaderi Zefreh, M., Doeschl-Wilson, A. B., Riggio, V., Matika, O., & Pong-Wong, R. (2023). Exploring the value of genomic predictions to simultaneously improve production potential and resilience of farmed animals. Frontiers in genetics, 14, 1127530.

Knap, P. W., & Doeschl-Wilson, A. (2020). Why breed disease-resilient livestock, and how? Genetics Selection Evolution, 52, 1-18.

Doeschl-Wilson, A., Knap, P. W., Opriessnig, T., & More, S. J. (2021). Livestock disease resilience: from individual to herd level. Animal, 15, 100286.

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Practice abstract n. 11 - Producing guidelines to record efficiency and resilience in small ruminants

Practice Abstract n. 11

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Producing guidelines to record efficiency and resilience in small ruminants

Authors: J. M. Astruc - IDELE and all the SMARTER partners

One key objective of SMARTER was to promote harmonisation and international cooperation on breeding processes in small ruminant. The across country genetic evaluations implemented in SMARTER on existing traits as a proof of concept have underlined the importance of analyzing traits that have been collected and/or calculated on a same way across country. It is therefore fundamental that novel traits, such as the efficiency and resilience related traits, which are not still widely routinely recorded on-farm for selection purposes, be recorded identically in the next future, or at least in the most similar way as possible.

In this respect, one of the main practical outputs of SMARTER was the production of recommendations on recording efficiency and resilience traits in sheep and goat. The materials used to write the recommendations are mainly those produced by SMARTER, but also materials from other projects (H2020 iSAGE, POCTEFA ARDI, ERA-GAS GrassToGas). The ICAR network contributed as well.

The recommendations include seven sections: two on efficiency traits (feed efficiency and greenhouse gases emissions), four on resilience traits (health and disease, survival of fetus and young, behavior traits, lifetime resilience), one on the record of the environment (especially the meteorological data and the diet). In these guidelines, proxies of gold standard traits, that can be more easily collected on-farm, are highlighted.

The final aim is to publish these recommendations in the ICAR guidelines, to target a larger community, including academic and non-academic, as well as services organizations in selection. This will strengthen the impact of SMARTER.

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Practice Abstract n. 12 - Across-country genetic evaluations are feasible in small ruminants

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Across-country genetic evaluations are feasible in small ruminants

Authors: J.M Astruc - IDELE, D. Berry - TEAGASC and all the partners of the WP6

In sheep and goats, compared to cattle, smaller within-country populations in selection and higher relative cost of genotyping and performance recording are among the main hindrances to the development of genomic selection. International cooperation and across-country genetic evaluation might generate great benefits for stakeholders in terms of genetic progress on resilience and efficiency traits.

Across country evaluation have been implemented in three case studies: one in meat sheep (Texel and Charollais breeds across Ireland and the UK), one in dairy sheep (Manech and Latxa breeds across France and Spain), one in dairy goat (Saanen and Alpine breeds across France, Italy, Switzerland and Canada). Main results showed that genetic correlations between the same traits in different countries are in most cases above 75%, suggesting that there is an existing connectedness between the populations pooled, and consequently that across country genetic evaluations are feasible.

We assessed the potential market and feasibility of an international evaluation through a comprehensive survey towards stakeholders. It appears that the stakeholders mostly agree to share data for international evaluation, and that many breeds are potentially interested. As a practical result, we laid the foundation for an international initiative in the next future. To give a frame to this initiative, a Reference Centre for harmonisation of performance and international genetic evaluation in sheep and goat, should be beneficial. This Reference Centre might be led by a consortium gathering Interbull and ICAR.

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4. Deviations or delays

Initially, D8.5 Second batch of practice abstracts for end-users should have been submitted at M40 by the end of February 2022, but because of the COVID19 pandemic and of the prolongation of the project, the date of submission has been postponed to the end of June 2023 (M56) in order to include in the Practice Abstracts the latest results of the project.