

SMARTER

SMALL RuminanTs breeding for Efficiency and Resilience

Newsletter – Issue 8



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Final SMARTER Meeting – Toledo 2023! – by R. Rupp and R. Bica



The H2020 SMARTER project, an ambitious EU-funded endeavour, recently held the concluding meeting in Toledo, Spain on May 22-23, 2023. The meeting brought together the project's work package (WP) leaders, project partners and stakeholders to review the progress made, identify remaining tasks, and discuss the roadmap for the project's final phase leading up to its scheduled completion in June 2023. A total of 69 people

attended the conference, 59 of which were project partners coming from the institutions involved, and 10 were stakeholders. The SMARTER project, which stands for "SMALL RuminanTs breeding for Efficiency and Resilience," is a collaborative effort involving multiple European and international institutions, industry partners, and research organizations. Started in 2018, the project sought to study how genetic selection can help to increase resilience and efficiency in small ruminants (sheep and goats) in their environments and across a range of diverse environments. Each work package (WP1-8) discussed their main achievements from the start of the project until now and what the key take home points are. For WP1 (efficiency), many proxies and predictors were tested for feed efficiency. However, since feed efficiency is a complex trait, it is hard to predict with proxies without the inclusion of information on intake. A possible link between feed efficiency and milk fat in dairy breeds could be a route to take in future work, however more work needs to be done to provide any conclusive results with regards to this. With regards to WP2 (resilience), the major highlights were the first genomic breeding values obtained for footrot and mastitis in UK Texel sheep, the first genome-wide study on the genetic architecture of lifetime resilience in Chios sheep, and the discovery of several homozygous deficiency regions associated with early survival in 3 dairy sheep breeds. The third WP, which focused on the trade-offs between efficiency and resilience, showed how no major systematic antagonisms between R&E were detected (from different approaches developed in WP3, including metaanalyses and modelling) which is good news as it will allow balancing selection for both resilience and efficiency in future work in the field. The highlight of WP4 which focused on the genomic characterisation of under-utilised breeds, was the collaborative effort from the partners in the WP to produce a sizeable online data repository composed of both foreground and background data to facilitate characterisation analyses. WP5, one of the most technical WP's of the project, has produced several publications, but one in particular: [‘Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method’](#) by Andres Legarra and Antonio Reverter is set to become a benchmark paper. Other methods developed in WP5 are under consideration (metafounders, genomic inbreeding) and others have large potential to be adopted in practical breeding programmes. (e.g. detection of stress). The work done in WP6 produced the first across country evaluation methodology for small ruminants, highlighting its weaknesses and strengths and potential for future growth. This is a major achievement based on international cooperation which will improve and increase the speed at which small ruminant research can be done. On top of this, a list of common SNPs panels was identified and illustrated how it is possible compare SNPs coming from different populations. WP7 focused on balanced-breeding goals for agro-ecological resilience. Simulations were used to assess different farm scenarios under different conditions to select for R&E traits with results showing that with the SMARTER model, economic performances of farms were improved, production was increased and management by the farmer was not have to be altered. Surveys were also sent to breeders and stakeholders which furthered the understanding of their trait preferences and their view on what the optimal animal could look like. These models and surveys could really be useful to select optimal conditions/traits which can deal with the challenges of the future. And finally, WP8, the communications WP of the project, successfully achieved all of its planned activities, including the 10 round tables in 10 partner countries and the summer school, both of which had very positive feedback from those who attended, and information of which can all be found on the [SMARTER website](#). In addition to reviewing the project's progress and discussing the remaining tasks, the meeting concluded with an insightful round table discussion among the WP leaders regarding the accomplishments of the SMARTER project. They reflected on the various achievements and milestones reached throughout the project's duration, acknowledging the positive impact their collective efforts had on addressing societal challenges. The participants also explored potential opportunities beyond the project's completion, brainstorming ideas for further utilisation and expansion of the project outcomes.





Overall, the project was completed in a period of 56 months, involved 27 partners with more than 120 scientists from 13 different countries, so it really was a team effort to complete it. Especially due to the fact that the project was impacted by the covid pandemic, which significantly slowed down some practical work, as well as the death of Carole Moreno-Romieux, the person who had the idea to start SMARTER and brought it to life. The SMARTER project therefore embodies the image of Carole and shows the ability she had to bring together groups and skills to face major challenges. All of the people involved in SMARTER will continue to work on developing an eco-friendlier and environmentally respectful small ruminant production system, thus ensuring that Carole's dream is achieved. Please follow this link which will allow you to see the brilliant scientist that she was. Most collaborations developed in the project are still operational which bodes well for the continuation of the work beyond SMARTER. The impact of SMARTER is poised to resonate well beyond its completion, driving sustainable innovation and progress in the field of small ruminants in Europe and beyond.

SMARTER Training school 2023! – by R. Rupp and R. Bica

The SMARTER summer school four-day event recently took place from the March 27-30th in Toulouse, France. The primary aim of the event was to introduce early-stage researchers, technicians and post-docs to the SMARTER project and give them an overview of its various aspects, such as the most recent results obtained and the novel techniques being used inside the project. A total of 19 students from Italy, France, Spain, Greece, Nigeria, Cyprus, Switzerland and Ireland attended the event. The students were from diverse academic backgrounds and had a keen interest in animal genetics, welfare, and breeding. The event provided an excellent platform for the students to interact with each other and share their knowledge and experiences. The summer school was divided into four different modules that focused on the various work packages (WP) of the SMARTER project. The modules were led by experts in the field who are directly involved in specific WP within the project. The discussed topics included how traits for resilience and efficiency are measures, mechanistic and statistical modelling, stress detection and how an improved sociotechnical system can be used to improve selection for specific traits. Each module had practical sessions which allowed the students to undertake their own analysis and understand how data is handled and analysed within SMARTER. These modules helped the students understand the intricacies of animal breeding and genetics and how they can be used to improve animal efficiency and resilience as well as breeding practices. Two challenge sessions were conducted during the

summer school to give students a hands-on experience of the research being conducted within SMARTER, as well as allowing them to give us feedback directly on the project. The first challenge session involved data analysis to detect stress in animals, using an un-utilised SMARTER dataset. Students were provided with the dataset and were tasked with using models discussed and described within the modules to identify areas that could indicate stress in animals. The second challenge session involved undertaking a farmer-based survey to understand their perceptions and what traits they value, and would select for. This allowed us to obtain the view from a more academic audience. The students were given a questionnaire that the project usually sends directly to farmers. This challenge session gave the students an insight into the practical aspects of how farmer views are recorded and how they can be used to develop improved breeding practices that are beneficial for both farmers and animals. These challenge sessions provided the students with a chance to apply the knowledge gained during the modules and workshops and gave them a better understanding of the research being conducted in the SMARTER project. Overall, the SMARTER summer School was a success, and the students found it to be an enriching and rewarding experience. The event provided them with a unique opportunity to learn about the latest research in animal genetics and modelling and it allowed them to interact with experts in the field. The students left the event with a deeper understanding of the SMARTER project and the potential it has to improve efficiency and resilience with the ultimate goal to develop the animal of the future. The school was recorded, and all videos and presentations are available [on SMARTER website](#).



Common low density sheep genotype panel – by D. Berry and J.M. Astruc

Genotyping of animals is now commonplace in most jurisdictions. The cost of creating a bespoke genotype panel, however, is a function of the volume of the order, the larger the purchase order, the lower the cost. Rather than individual countries or breeds generating bespoke genotype panels and placing relatively small orders, the question was asked if the commonality across breeds and populations was sufficiently strong to create a single informative genotype panel that everyone could use. The approach to test this hypothesis is described [here](#) with the makeup of the genotype panel [here](#).

Genotype by environment (G×E) interactions for feed efficiency indicators in Lacaune sheep from Greece and France – by S. Vouraki

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. The objective of the study was to investigate G×E interactions and hence, the feasibility of genetic evaluation and selection for feed efficiency indicators, namely milk yield and composition, in purebred Lacaune sheep reared intensively in Greece and semi-extensively in France. A total of 1,658 Lacaune ewes from four intensive farms in Northern Greece and 4,859 Lacaune ewes from 186 semi-extensive farms in Southern France were used. Selected ewes in the two countries were daughters or granddaughters of the same rams (6 common sires and 11 common grandsires). Individual ewe milk yield was recorded monthly (5 records per animal) and milk samples (3 monthly samples per animal in early lactation) were collected to assess chemical composition. Based on these records, total milking period milk yield and the respective milk components content were calculated. Results showed a strong genetic correlation for milk yield (0.86 ± 0.13) and protein content (0.88 ± 0.12) between animals raised in the two countries suggesting no evidence of G×E interactions across country and system. In the case of fat content, a moderate to high correlation was found (0.59 ± 0.21) suggesting that some degree of sire re-ranking could be expected. This could be potentially related to the different feeding practices in the two countries. Overall, results suggest that a joint genetic evaluation of Lacaune sheep in Greece and France is feasible. 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. This study was undertaken in the framework of Smarter (WP1).

Sotiria Vouraki¹, Stergios Priskas¹, Angeliki Argyriadou¹, Vasileia Fotiadou¹, Jean-Michel Astruc², Gilles Lagriffoul², Rachel Rupp³, Georgios Banos⁴, Georgios Arsenos¹

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Lacaune sheep - © AUTH

Balancing breeding goals in Lacaune sheep – by T. Byrne

This task within WP7, describes the outcomes of a breeding program simulation in Lacaune sheep using a general selection index model framework. The objectives of this simulation are to:

- Assess the long-term impact of breeding for resilience and efficiency traits in Lacaune sheep populations.
- Test how new genomics data and tools can improve breeding programs and populations faster.
- Produce 20-year forecasts of the productivity gains that can be expected when resilience and efficiency traits are included in the breeding programme.

This simulation forms part of Task 7.4 of the H2020 Small Ruminants Breeding for Efficiency and Resilience (SMARTER) project. Adding Functional Longevity (FL) and Feed Efficiency (FE) to the breeding program results in a significant long-term (20 year) response to selection for both traits, with 0.3 more lactations and an increase of 13.2% in feed efficiency (13.2% less feed). Genomic evaluations increase these responses to 1.3 lactations and 21.3% in feed efficiency. As expected, when adding more traits to the index, the relative trait emphasis and response to selection in other traits in the index reduces, with most noticeable reductions for protein yield (PY) and fat yield (FY). The sensitivity analyses showed that outcomes were most sensitive to changes in the accuracy of genomic breeding values for FL and FE . The emphasis of FL and FE in the index increased significantly, from 11.8% to 17.7%, and 12.7% to 15.3%, respectively, when the accuracy of genomic breeding values increased from 50% to 70%. The emphasis on FL and FE in the index decreased significantly, by similar proportions, when the accuracy of genomic breeding values decreased from 50% to 30%. Adjusting these accuracies resulted in, on average, a 5.2% change in response to selection for PY and FY . For most sensitivity analyses, only slight differences were observed in responses to selection and emphasis of other traits in the breeding program. Genetic parameters like heritability, and genetic and phenotypic correlations affect responses to selection. Considering that for FE a genetic and phenotypic correlation was only estimated with MY , estimation of the correlations between FE and other index traits and re-running of simulations would provide a more complete picture of the implications of adding FE and of the sensitivity of responses to the genetic relationship between FE and other traits. Simulation outcomes from the current breeding program (base scenario) show that $LSCS$, TA , UD and TP have an unwanted long-term (20 year) response to selection; increasing $LSCS$ and TA , whilst decreasing UD and TP . By changing the FL and FE weights in the index, these unwanted responses to selection can reduce. Revisiting the weights applied to the traits in the TMI , including when traits are added to the breeding goal and carefully setting index weights for these additional traits (like FL and FE), would inform a balanced approach to selection. Furthermore, the use of economic values in the index instead of weights based on desired responses, would deliver real world value of breeders and commercial farmers. These economic values result in an index that represents the profit (or loss) to the farmer and are based on price and cost data and other sources of information.

The national roundtables in ten countries to disseminate SMARTER results towards stakeholders – by J.M. Astruc, R. Bica and C. Mosconi

The 10 roundtables planned within the SMARTER project have been organised between April 2022 and February 2023. They allowed to disseminate the main practical results of SMARTER to the stakeholders of each country,



breeders, breeding organisations, (inter)-professional organisations, researchers, agricultural education, newspapers.

The following table gives the dates and location of each roundtable.

Country	Organising partner	Date	Location
France	RDF	5-6 April 2022	Sèvremont
Uruguay	INIA_UY	21-22 April 2022	Tacuarembó
Hungary	UNIDEB	22 April 2022	Debrecen
Spain	UNILEON	8 June 2022	Valladolid (Foro Ovino)
Greece	FRIZARTA	25 June 2022	Agrinio City
Ireland	TEAGASC	12 July 2022	Thurles
Switzerland	FIBL	17 November 2022	Entlebuch
UK	SRUC	7 December 2022	Edinburgh
Italy	ARAL	9-10 February 2023	Padenghe sul Garda
Norway	NSG	17-18 February 2023	Stjørdal

All the participants had the opportunity to attend a presentation of the different achievements reached by the project and to discuss the results and give tracks for further research. The practical use of the novelties produced by SMARTER were also fully discussed. The different events highlighted the multi-actor approach of SMARTER, with academic and non academic partners working jointly to produce outcomes usable by stakeholders in actual breeding processes. All the presentations, as well as many pictures and videos are available on the SMARTER website [on the round table page](#).



Spain Roundtable © UNILEON

The following presentations will be made during the 74th EAAP annual meeting to be held in Lyon on 30th August 2023.

Improving feed efficiency in meat sheep increases CH₄ emissions measured indoor or on pasture.

F. Tortereau, J.-L. Weisbecker, C. Coffre-Thomain, Y. Legoff, D. François, Q. Le Graverand, C. Marie-Etancelin

Alpine goats divergent for functional longevity differ in metabolic profile during transition period

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The objective was to study associations among functional longevity and plasma indicators of metabolic adaption in Alpine goats during periparturient period. Two Alpine goat strains divergent for longevity (**LGV+** and **LGV-**) were produced by AI selecting for extreme functional longevity but nondifferent milk yield. A total of 174 primiparous goats were studied in 2018, 2019, 2020 and 2021. Jugular plasma collected on wk -4, -3, -2, -1 relative to expected parturition, and wk 1, 2, 4, 13, 24, 33 of lactation was analyzed for NEFA, BHB, glucose, urea and bilirubin. Data were analyzed using SAS mixed models with repeated measures, including strain, litter size (**LS**), wk, and interactions as fixed effects, and year and goat (year) as random effects. Significant wk effects were observed for all metabolites. LGV- goats had greater plasma NEFA on wk-3 (181 vs 123 μ M; strain x wk prepartum: $P = 0.05$), and greater BHB prepartum (0.45 vs 0.41 mM; strain effect: $P = 0.04$) than LGV+, which denotes greater fat mobilization and partial oxidation in late gestation in LGV-. 35% of goats carried multiple fetus (**LS2+**) and LS not differ with LGV. Prepartum plasma NEFA, BHB and bilirubin were greater for LS2+ compared to single (**LS1**; $P < 0.001$; 260 vs 174 μ M; 0.51 vs 0.39mM; 0.069 vs 0.056mg/dL, respectively), whereas glucose was lower for LS2+ ($P < 0.001$; 49.8 vs 54.7 mg/dL). Conversely, plasma NEFA was greater for LS1 during wk 1 and wk 2 postpartum ($P < 0.05$; 558 vs 442 on wk 1, and 421 vs 330 μ M on wk 2, respectively), reflecting greater availability of body reserves to support lactation in LS1. Prepartum incidence of BHB > 0.80 mM was significantly greater for LS2+ than LS1 (30 vs 3.7%), and for LGV- carrying LS2+ than LGV+ carrying LS2+ (42 vs 28%). Marked LS effects were observed in plasma metabolite profiles in primiparous goats. LGV strains differ in their metabolic adaptations peripartum.

This study has received funding from the EU H2020 research and innovation program under grant agreement No 772787 (SMARTER) and from APISGENE (ACTIVEGOAT).

Effects of sire and diet on rumen volume and relationships with feed efficiency

N.R. Lambe, A. McLaren, K.A. McLean, J. Gordon, J. Conington

Selecting feed-efficient sheep with concentrates alters their efficiency with forages and behaviour

C. Marie-Etancelin, J.L. Weisbecker, D. Marcon, L. Estivalet, Q. Le Graverand, F. Tortereau

Blending multivariate models to predict feed efficiency and explore multiple omics in meat sheep

Le Graverand, Q.¹, Tortereau, F.¹, Marie-Etancelin, C.¹, Meynadier, A.¹, Weisbecker, J.L.¹, Lê Cao, K.A.²

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Selecting sheep for feed efficiency would improve the sustainability of sheep farming by decreasing feeding needs. However, due to the costs of recording feed intake, feed efficiency is rarely selected in sheep. Identifying feed efficiency biomarkers could help resolve this issue. A total of 258 Romane male lambs were phenotyped in



the growing period for Residual Feed Intake(RFI) - in three different batches. Rumen fluid and blood were sampled as potential sources of biomarkers for feed efficiency. Multivariate analyses were performed with six distinct 'blocks' of predictors: fixed effects and covariates (FC), genotypes (SNPs), plasma NMR spectra (NMR), ruminal volatile fatty acids (VFAs), long-chain fatty acids (LFAs), bacteria and archaea abundances (16S amplicon sequencing). We modified a Partial Least Square regression approach (PLS) to account for the three batches while selecting biomarkers of feed efficiency (Rohart *et al.*, 2017). Cross-validation was repeated to fit one model per block on our training data(60% of the samples). Then, predictions for the validation set (30% of the samples) were obtained by using a weighted aggregation – based on the performance on each validation set. Testing data (10%) were independently used to assess the overall prediction accuracy based on Pearson correlations. When RFI was predicted from separate blocks, the average accuracy was low to moderate: 0.08 (standard deviation: 0.17) from VFAs to 0.44 (0.13) from SNPs. When RFI was predicted with our approach combining different omics, accuracy increased and reached an average of 0.55 (0.11). Based on weights attributed to blocks of predictors, we were able to rank the most predictive blocks to explain RFI: SNPs, FC, NMR, 16S, LFA and VFA. Furthermore, within each block we identified variables that were highly associated with feed efficiency RFI, including β -hydroxyisovaleric acid and a SNP located on the chromosome 3. To conclude, blending models is useful to integrate heterogeneous omics data: from predicting efficiency, to identifying associations between multi-omics predictors.

This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER)



Romane sheeps © INRAE

Genome-wise association study of footrot and mastitis in UK Texel sheep

K. Kaseja, S. Mucha, J. Yates, E. Smith, G. Banos, J. Conington

Genetic parameters of nematode resistance in dairy sheep

B. Bapst, K. Schwarz, S. Thüer, S. Werne

Phenotypic and genetic variability of health and welfare traits in French dairy goats

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The objective of the study was to investigate the phenotypic and genetic variability of health and welfare traits in French dairy goats. A total of 1,977 primiparous goats of Alpine and Saanen breeds, from 14 farms, were involved in the study during the years 2020-2021. Eleven indicators were assessed individually and once for each goat: abscess, arthritis, nasal discharge, ocular discharge, dirty and light *soiling hindquarters*, lameness, body condition, bag-shaped udder, dehorning issues, hair coat condition, claw issues. For the study, all the indicators were considered as binary traits (0: absence of disorder; 1: presence of disorder). The total number of disorders per animal was defined as the sum of the disorders for the eleven indicators. The disorder frequency ranged between 0.5% and 23% depending on the 11 indicators. Two groups of indicators were observed: those with a frequency lower than 5% (N=7) and those with a frequency about 20% (N=4: dehorning issues, bag-shaped udder, abscess, claw issues). The total number of disorders per goat was 0.94, on average in the total dataset, and ranged between 0 and 5. 40% of goats showed no disorder. Heritabilities were estimated using linear models for 4 traits suspected to be under genetic control and with sufficient frequency (>5%). They ranged between 4% (abscess) and 26% (bag-shaped udder). Arthritis and the total number of disorders had intermediate values (11% and 15%, respectively). These first results suggest that selection may be a potential strategy to improve health and welfare traits in dairy goats.

This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER)



Saanen goats © CAPGENES

Contrasting genetic resistance to GIN on growth performance and feed efficiency of Corriedale lambs

E.A. Navajas, G. Ciappesoni, I. De Barbieri

Australian Merino: animal welfare and resilience in extensive systems

M. Del Campo, J.L. De Araújo Pimenta, I. De Barbieri, P. Lorenze, F. Rovira, J.M. Soares De Lima

Assessment of phenotypic and genetic variability of rumen temperatures in goats

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P3R, INRAE, 2018. Small Ruminants Phenotyping Facility, doi.org/10.15454/1.5483259352597417E12, Osmoy, F-31326, France

The aim of this study was to identify the factors of variation of rumen temperatures in goats and to estimate the genetic parameters of that trait. 97 Alpine goats from an INRAE experimental farm were monitored continuously during their first lactation (267 days on average, from kidding to dry off) using Medria rumen temperature boluses (ThermoBulus San'Phone®). Temperatures were collected every 5 min (288 records per day) and have been corrected to account for drinking events. The average rumen temperature was $39.68 \pm 0.51^\circ\text{C}$ on the whole data set ($n=7,273,000$). The average temperature during the day increased from about 5.00AM to about 5.00PM and decreased afterwards: the minimum temperatures (39.28°C) were observed in early morning (between 5.00AM and 5.30AM) whereas the maximum temperatures were observed in late afternoon (39.94°C between 4.30PM and 5.00PM). In addition to the time, the phenotypic variability was also explained by the date, the birth year, the stage of lactation and the milk yield of the goat. Genetic parameters were estimated using a linear repeatability model. Data were spread into 5 periods according to their raw mean temperature and standard deviation (4.30AM-6.00AM, 6.40AM-1.20PM, 3.30PM-8.00PM, 9.00PM-3.00AM) and each one was analysed separately. Repeatability varied from 0.20 (4.30AM-6.00AM) to 0.32 (3.30PM-8.00PM), and heritability from 0.03 (4.30AM-6.00AM) to 0.12 (9.00PM-3.00AM). For this last period, breeding values ranged from -0.10 to +0.14 °C. These results suggest that body temperature measured by internal sensors has a genetic control, which is potentially linked to basal metabolism or response to various stressors (heat stress, infection).

This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER)

Heritability of novel metabolite-based resilience biomarkers in dairy goat

M. Ithurbide, T. Fossier, M. Turrett, J. Pires, T. Larsen, N.C. Friggens, R. Rupp

Genetic parameters for grazing behaviour traits of Boutsko sheep

S. Vouraki, V. Papanikolopoulou, A. Argyriadou, V. Fotiadou, V. Tsartsianidou, A. Triantafyllidis, G. Banos, G. Arsenos

Genomic signatures of adaptive response driven by transhumant pastoralism in native Boutsko sheep

V. Tsartsianidou, S. Vouraki, P. Papanikolopoulou, G. Arsenos, A. Triantafyllidis

Genetic link between fertility and resilience in sheep and goat divergent selection experiments

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The challenge for breeding is to improve resilience traits simultaneous with efficiency and reproduction. However very little information exists about possible trade-off between resilience and reproduction in small ruminants. The aim of this study was to investigate such possible trade-off in four divergent selection experiments in dairy sheep and goat. In each experiment we analyzed the success to artificial insemination (AI) using dates of AI and natural mating for return to estrus and dates of lambing/kidding. The first experiment was a divergent selection in Lacaune sheep on mastitis (SCS). The second was an experiment in Lacaune sheep selected for the SOCS2 gene associated to susceptibility to mastitis, with favorable (CC) and unfavorable (CT and TT) genotypes. The third experiment was a divergent selection in Alpine goats on mastitis (SCS). The fourth experiment was a divergent selection in Alpine goats on longevity. The data included 1254, 5375, 481, and 305 females and 3671, 5375, 788, and 617 AI events, respectively - and the fertility rate in these four experiments was 68.8, 70, 51.9, and 59.4%. We further estimated the odds ratio (OR) for success to AI using a logistic regression according to the genetic line, with year and lactation number as fixed effects. No effect on AI fertility was associated with selection on longevity in goats or mastitis (SCS) in sheep. However, an important favorable effect on AI fertility was associated: i) with divergent selection on mastitis (SCS) in goat: $OR_{SCS^- \text{ vs. } SCS^+} = 1.65$ (1.22-2.23) and ii) SOCS2 genotype in sheep: $OR_{CC \text{ vs. } Tx} = 1.36$ (1.08-1.70). The results suggest that selection for resilience in dairy sheep and goats is not associated with an adverse effect on reproduction in these species. On the contrary, selection for some resilience traits seems to drive significant beneficial effects in terms of fertility after AI.

This study has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER)



Lacaune sheeps © INRAE

Prediction of feed efficiency related traits from plasma NMR spectra.





A. Marquisseau, F. Tortereau, N. Marty-Gasset, C. Marie-Etancelin, Q. Le Graverand

Metabolism in lambs from two feed-efficiency genetic lines subjected to different early rearing practices

G. Cantalapiedra-Hijar, M.M. Milaon, S. Parisot, C. Durand, M. Vauris, F. Tortereau, C. Ginane

Coming events

List of the upcoming events with SMARTER project partners attendance.

Event 	Date 	Location 	Partners 
74th EAAP Annual Meeting	28 August – 1 st September 2023	Lyon, France	All partners



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