SMAll RuminanTs breeding for Efficiency and Resilience

WP5 Fifth and Final Annual Meeting
Toledo, 2023

Ricardo Pong-Wong and Andres Legarra

WP Objectives

1. Develop genetic models to deal with resilience and efficiency under micro- and macro- environmental challenges
2. Infer (genomic) breeding values for R&E from longitudinal data on productive traits
3. Develop and assess methods for genomic prediction particularly suited to small ruminants
4. Develop and implement new methods for selected and under-utilised populations of sheep and goats while conserving genetic variability

Objectives and Tasks

Objectives	Tasks
Develop genetic models for R&E under micro- and macro-environmental challenges	Novel genetic models for efficiency and resilience traits under challenge
Infer (genomic) breeding values for R&E from longitudinal data on productive traits	Data mining of longitudinal performance data to identify and characterise events of environmental challenges
Develop and assess methods for genomic prediction suited to S&G	Enhancing performance of genomic prediction methodology
Develop and implement new methods for selected and under-utilised populations of S&G while conserving genetic variability	Incorporating genomic information to improve management of genetic diversity and to promote expression of heterosis

Deliverables and Milestones

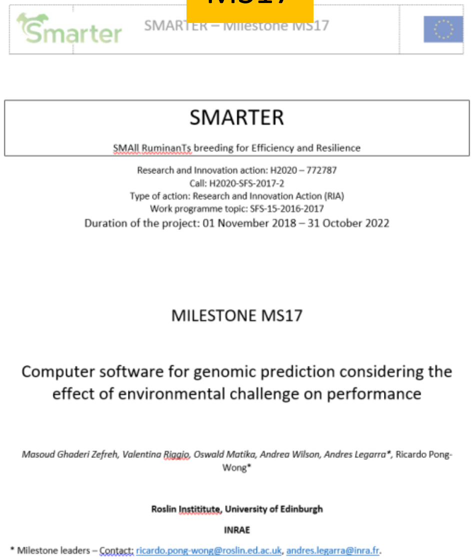
Number	Title	Lead beneficiary	Due date (M)	Due date
MS17	A computer software for genomic prediction taking into account the effect of environmental challenge on performance	UEDIN	18	30/04/2020
MS19	A computer software or method for assessing and avoiding potential bias due to design of cross-validation analysis	INRA	18	30/04/2020
MS20	A computer software to improve calculation of genomic relationship between purebred and crossbred populations	UEDIN	18	30/04/2020
D5.1	Method for identifying environmental challenge events and assessment of their value for selection for resilience	INRA	24	31/10/2020
D5.2	A report of an improved method to calculate genomic relationship across individuals of different purebred and crossbred populations	UEDIN	36	31/10/2021
MS18	A list of populationwise environmental challenges	INRA	24	31/10/2020
MS21	A computer software to optimise genetic contribution	UEDIN	24	31/10/2020
D5.3	Method for assessing potential bias due to design of crossvalidation analysis	INRA	36	31/10/2021
D5.4	A report for optimum contribution to manage diversity at critical regions and to assist mating design to maximise heterozygosity and expression of heterosis and evaluation of level inbreeding rate across genomic regions and their impact on performance	UEDIN	36	31/10/2021
D5.5	A manuscript on the development and testing of genomic evaluation tools to improve resilience and efficiency accounting for the impact of environmental challenge and using novel phenotypes	UEDIN	48	31/10/2022

M56

All Milestones and deliverables have been finished
(D5.5. needs to be submitted by June 2023)

MIlestones

MS17



SMARTER – Milestone MS17

SMARTER

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Research and Innovation action: H2020 – 772787
Call: H2020-SFS-2017-2
Type of action: Research and Innovation Action (RIA)
Work programme topic: SFS-15-2016-2017
Duration of the project: 01 November 2018 – 31 October 2022

MILESTONE MS17

Computer software for genomic prediction considering the effect of environmental challenge on performance

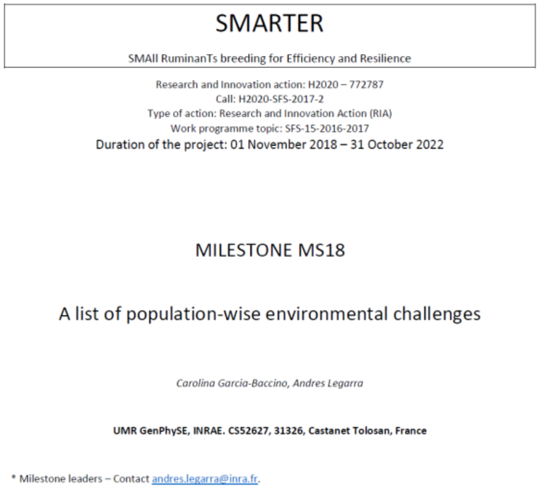
*Masoud Ghaderi Zefreh, Valentina Riggio, Oswald Matika, Andrea Wilson, Andres Legarra**, Ricardo Pong-Wong*

Roslin Instititute, University of Edinburgh

INRAE

* Milestone leaders – Contact: ricardo.pong-wong@roslin.ed.ac.uk, andres.legarra@inra.fr.

MS18



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MILESTONE MS18

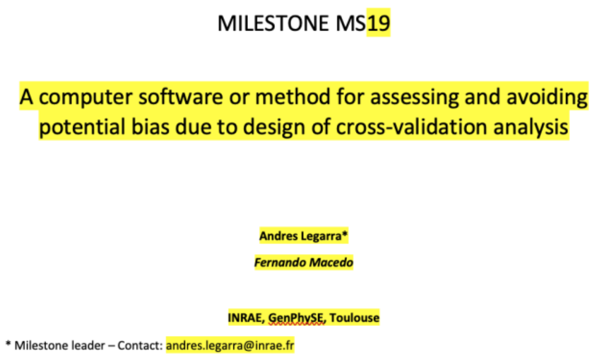
A list of population-wise environmental challenges

Carolina Garcia-Baccino, Andres Legarra

UMR GenPhySE, INRAE. CS52627, 31326, Castanet Tolosan, France

* Milestone leaders – Contact andres.legarra@inra.fr.

MS19



MILESTONE MS19

A computer software or method for assessing and avoiding potential bias due to design of cross-validation analysis

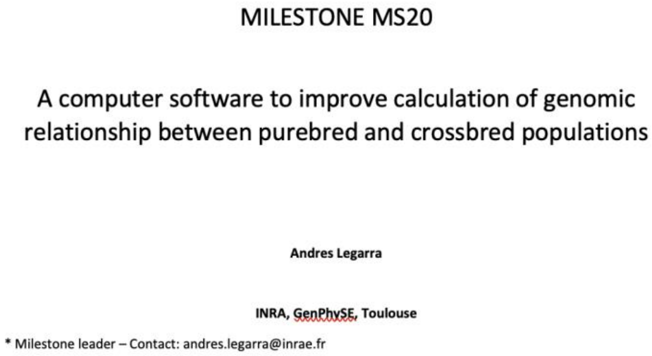
Andres Legarra*

Fernando Macedo

INRAE, GenPhySE, Toulouse

* Milestone leader – Contact: andres.legarra@inrae.fr

MS20



MILESTONE MS20

A computer software to improve calculation of genomic relationship between purebred and crossbred populations

Andres Legarra

INRA, GenPhySE, Toulouse

* Milestone leader – Contact: andres.legarra@inrae.fr

MS21

SMARTER – Milestone MS21

SMARTER

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Call: H2020-SFS-2017-2
Type of action: Research and Innovation Action (RIA)
Work programme topic: SFS-15-2016-2017
Duration of the project: 01 November 2018 – 31 October 2022

MILESTONE MS21

A computer software to optimise genetic contributions

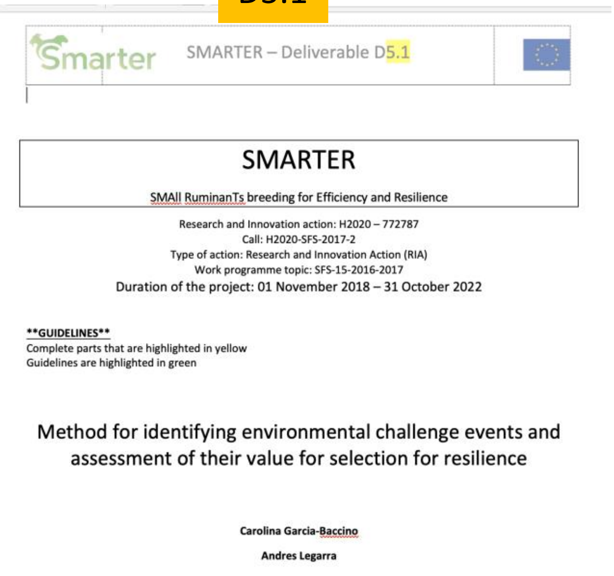
Ricardo Pong-Wong*

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

* Milestone leaders – Contact: ricardo.pong-wong@roslin.ed.ac.uk

Deliverables

D5.1



SMARTER – Deliverable D5.1

SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

Research and Innovation action: H2020 – 772787
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Duration of the project: 01 November 2018 – 31 October 2022

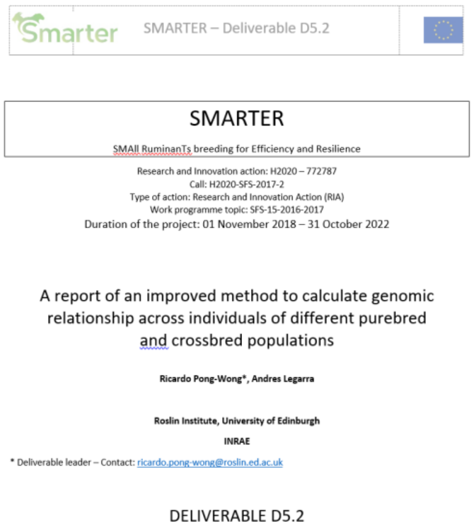
GUIDELINES
Complete parts that are highlighted in yellow
Guidelines are highlighted in green

Method for identifying environmental challenge events and assessment of their value for selection for resilience

Carolina Garcia-Baccino

Andres Legarra

D5.2



SMARTER – Deliverable D5.2

SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

Research and Innovation action: H2020 – 772787
Call: H2020-SFS-2017-2
Type of action: Research and Innovation Action (RIA)
Work programme topic: SFS-15-2016-2017
Duration of the project: 01 November 2018 – 31 October 2022

A report of an improved method to calculate genomic relationship across individuals of different purebred and crossbred populations

Ricardo Pong-Wong*, Andres Legarra

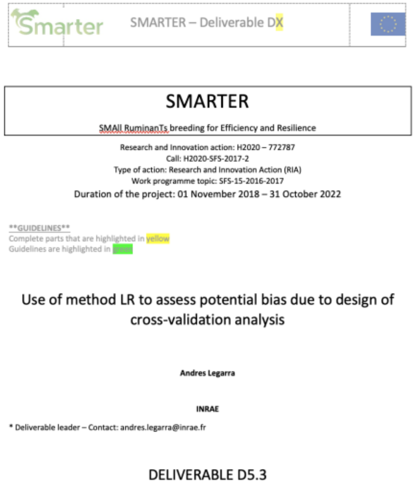
Roslin Institute, University of Edinburgh

INRAE

* Deliverable leader – Contact: ricardo.pong-wong@roslin.ed.ac.uk

DELIVERABLE D5.2

D5.3



SMARTER – Deliverable DX

SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

Research and Innovation action: H2020 – 772787
Call: H2020-SFS-2017-2
Type of action: Research and Innovation Action (RIA)
Work programme topic: SFS-15-2016-2017
Duration of the project: 01 November 2018 – 31 October 2022

GUIDELINES
Complete parts that are highlighted in yellow
Guidelines are highlighted in green

Use of method LR to assess potential bias due to design of cross-validation analysis

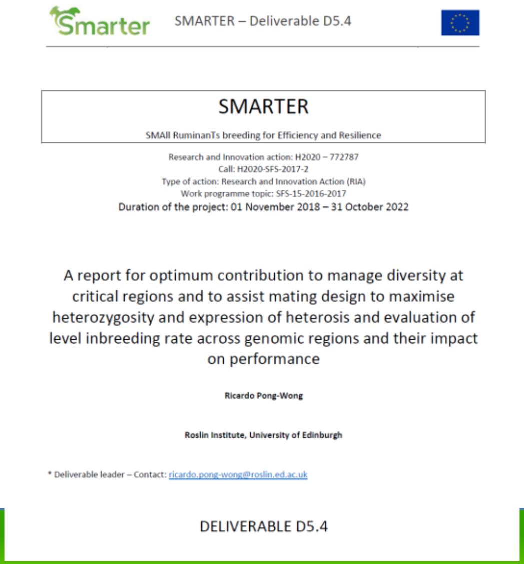
Andres Legarra

INRAE

* Deliverable leader – Contact: andres.legarra@inrae.fr

DELIVERABLE D5.3

D.5.4



SMARTER – Deliverable D5.4

SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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Call: H2020-SFS-2017-2
Type of action: Research and Innovation Action (RIA)
Work programme topic: SFS-15-2016-2017
Duration of the project: 01 November 2018 – 31 October 2022

A report for optimum contribution to manage diversity at critical regions and to assist mating design to maximise heterozygosity and expression of heterosis and evaluation of level inbreeding rate across genomic regions and their impact on performance

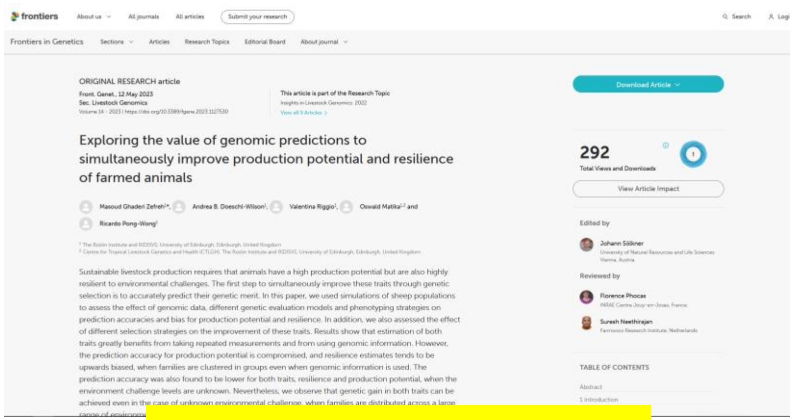
Ricardo Pong-Wong

Roslin Institute, University of Edinburgh

* Deliverable leader – Contact: ricardo.pong-wong@roslin.ed.ac.uk

DELIVERABLE D5.4

D5.5



ORIGINAL RESEARCH article
Front. Genet., 12 May 2023
Sec. Livestock Genomics
Volume 14 - 2023 | https://doi.org/10.3389/fgene.2023.1127530

This article is part of the Research Topic
Insights in Livestock Genomics: 2022
View all 9 Articles

Exploring the value of genomic predictions to simultaneously improve production potential and resilience of farmed animals

Masoud Ghaderi Zefreh[1]*, Andrea B. Doeschl-Wilson[1], Valentina Riggio[1], Oswald Matika[1,2] and Ricardo Pong-Wong[1]

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[2] Centre for Tropical Livestock Genetics and Health (CTLGH), The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom

Sustainable livestock production requires that animals have a high production potential but are also highly resilient to environmental challenges. The first step to simultaneously improve these traits through genetic selection is to accurately predict their genetic merit. In this paper, we used simulations of sheep populations to assess the effect of genomic data, different genetic evaluation models and phenotyping strategies on prediction accuracies and bias for production potential and resilience. In addition, we also assessed the effect of different selection strategies on the improvement of these traits. Results show that estimation of both traits greatly benefits from taking repeated measurements and from using genomic information. However, the prediction accuracy for production potential is compromised, and resilience estimates tends to be upwards biased, when families are clustered in groups even when genomic information is used. The prediction accuracy was also found to be lower for both traits, resilience and production potential, when the environment challenge levels are unknown. Nevertheless, we observe that genetic gain in both traits can be achieved even in the case of unknown environmental challenge, when families are distributed across a large range of environme

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Suresh Neethirajan
Farmworx Research Institute, Netherlands

TABLE OF CONTENTS
Abstract
1 Introduction

Need to be submitted by June 2023

List of publications (24 publications)

T5.1

- Ghaderi-Zefreh et al (2020) On the accuracy of estimating resilience. Proc. 71 EAAP meeting .
- Ghaderi Zefreh, et al (2022). *Selection for robustness: exploring the value of genomic prediction, reaction norm models and phenotyping strategies*. Paper presented at World Congress on Genetics Applied Livestock Production
- Ghaderi Zefreh et al (2023). Exploring the value of genomic predictions to simultaneously improve production potential and resilience of farmed animals. *Frontiers in genetics*, *14*, 1-13. [1127530].

T5.2

- Garcia-Baccino *et al.* Detection of unrecorded environmental challenges in high-frequency recorded traits, and genetic determinism of resilience to challenge, with an application on feed intake in lambs. *Genet Sel Evol* **53**, 4 (2021).

T5.3

- Aguilar et al. (2020). Effects of ignoring inbreeding in model-based accuracy for BLUP and SSGBLUP. *J Anim Breed Genet*. 2020; 137: 356– 364.
- Granado Tajada et al. (2020) Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. *J. Dairy Sci.* 103:6346–6353.
- Legarra et al (2020). The correlation of substitution effects across populations and across generations. Proc. 71 EAAP meeting.
- Legarra A, Reverter A. (2018). Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. Genet Sel Evol. 2018;50:53.
- Macedo et al (2020). Behavior of the Linear Regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. J Dairy Sci. 103:529-44.
- Macedo et al. (2022). Removing data and using metafounders alleviates biases for all traits in Lacaune dairy sheep predictions. J Dairy Sci. 2022;105:2439-52.
- Macedo et al (2020). Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. Genet Sel Evol. 52:47.

List of publications (cont)

T5.3

- Sánchez-Mayor et al (2019). Effect of genotyping strategies in the sustained genetic gain across multiple generations of selection using ssGBLUP. Proc. 37th ISAG meeting.
- Sánchez-Mayor et al (2022). Effect of the genotyping strategies on the sustained benefit of single step genomic BLUP over multiple generations. Genet Sel Evol. 54:23
- Legarra et al (2021). The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. Genetics. 219.
- Raoul J, Elsen JM. (2021). The levels of artificial insemination and missing sire information make genomic selection not always beneficial in meat sheep. animal. 15:100040.
- Bermann, M., Aguilar, I., Lourenco, D., Misztal, I., & Legarra, A. (2023). Reliabilities of estimated breeding values in models with metafounders. Genetics Selection Evolution, 55(1), 1-13.

T5.4

- Legarra et al (2020). Short communication: Methods to compute genomic inbreeding for ungenotyped individuals. J Dairy Sci. 2020;103:3363-7.
- Rodríguez-Ramilo et al (2021). Islands of runs of homozygosity indicate selection signatures in Ovis aries 6 (OAR6) of French dairy sheep. JDS Communications. 2021;2:132-6.
- Villanueva B et al (2021). The value of genomic relationship matrices to estimate levels of inbreeding. Genet Sel Evol. 53:42.
- Morales-González et al (2021). Changes in Allele Frequencies When Different Genomic Coancestry Matrices Are Used for Maintaining Genetic Diversity. Genes. 12:673.
- Macedo et al. (2021). Selection and drift reduce genetic variation for milk yield in Manech Tête Rousse dairy sheep. JDS Communications. 2:31-4.
- Antonios et al (2021). Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Béarnaise dairy sheep breed. J Dairy Sci. 2021;104:3221-30.
- Granado-Tajada et al. Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. J Dairy Sci. 2020;103:5215-26.
- Antonios et al (2023). Partition of the genetic trend of French dairy sheep in Mendelian samplings and long-term contributions. J Dairy Sci (accepted)

Over 20 citations (google scholar)

Legarra A, Reverter A. (2018) Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. Genet Sel Evol. 50:53.	168
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ALL COMMITMENTS FROM WP5 HAVE BEEN FINISHED*

(Luckily covid did not affect much this WP5 ☺)

*: need to submit D5.5 by June 2023