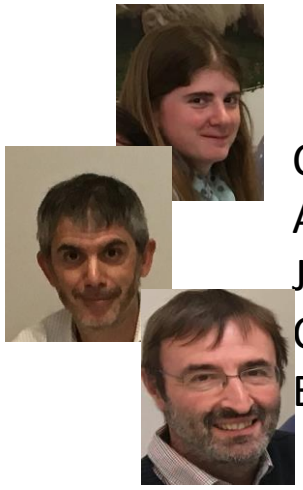
Smarter

SMAll RuminanTs breeding for Efficiency and Resilience

SMARTER WP6 - TASK 6.2
International evaluation of Dairy Sheep

22 May 2023



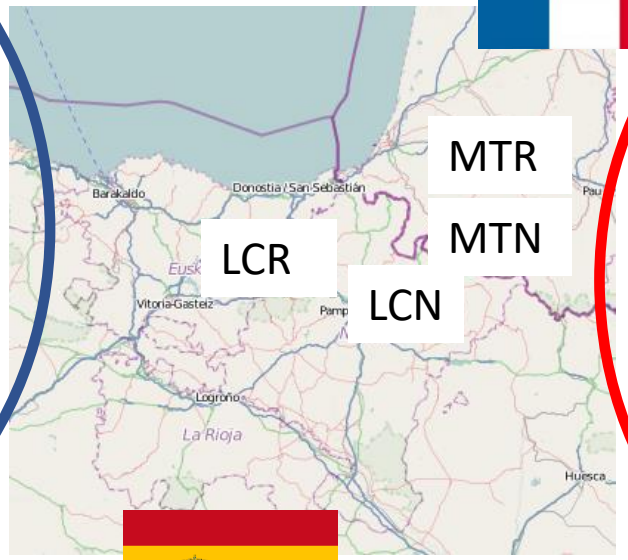
Carolina Garcia-Baccino (now in pig breeding company Nucleus, Rennes)
Andres Legarra (now in Council of Dairy Cattle Breeding)
Jean-Michel Astruc (IDELE)
Carolina Pineda-Quiroga (NEIKER)
Eva Ugarte (NEIKER)

This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Grant Agreement n°772787

BACKGROUND/PLAN

MTN = Manech Tête Noire

LCN = Latxa Cara Negra



MTR = Manech Tête Rousse

LCR = Latxa Cara Rubia

TRAIT:

milk yield

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DATA DESCRIPTION

		BLOND		BLACK	
		MTR	LCR	MTN	LCN
Pedigree (N animals)		573,501	153,765	158,055	68,830
Genotypes (N animals)		4,901	716	846	328
Phenotypes (animals with records)	Milk Yield	543,929	144,993	146,132	65,060

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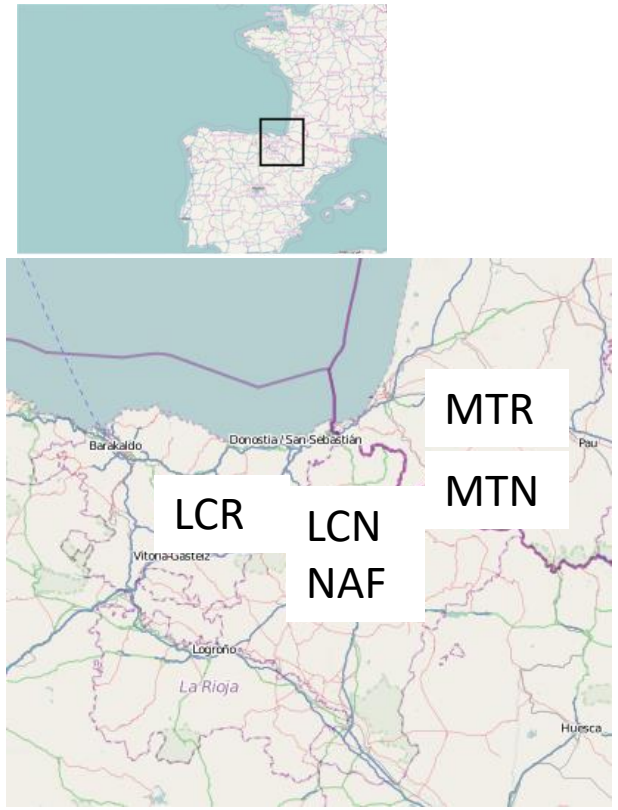
CONNECTIONS



382 MTR AI rams in LCR (most of them with >10 daughters)

73 MTN AI rams in LCN (58 with >10 daughters)

Most of these rams are genotyped

Year of birth of these exchanged rams mostly ~2000 - now

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DATA: SOME ISSUES FOUND

1) Genotypic information

Latxa uses Affymetrix 50K and Illumina 50K

Manech uses only Illumina 50K

} Different QC processes + Some edition problems found → **We used 23K SNP in common**

Fixing this kind of problems takes forever
We plan, for the future, to impute all to a common base

2) Animals' IDs format (some were not in the Interbull format used by SMARTER or had spaces in between).
3) Some genotyped animals were not in the pedigree

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MODELS

- Animal model BLUP / SSGBLUP within “color”:
  Two times two-trait analyses (“ES blond + FR blond” , “ES black + FR black”)

MYI (FR)
MYI (ES)

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Z_u u} + \boldsymbol{Z_p p} + \boldsymbol{e}$$

Permanent environmental effect

Breeding values

flock-year-parity
Age1st lambing-year-parity
Month lambing-year-parity
interv lambing 1st TD – year-parity)
Parity-year
(Manech)

Flock-year-month lambing
total born lambs
age-numberofbirth
Interval lambing 1st TD
(Latxa)

$$Var(\boldsymbol{u}) = \boldsymbol{G}_0 \otimes \boldsymbol{A}^{\Gamma}$$
$$Var(\boldsymbol{u}) = \boldsymbol{G}_0 \otimes \boldsymbol{H}^{\Gamma}$$

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Metafounders

- To account for missing pedigree, we use metafounders, which take into account relationships of missing parents within and across breeds
- They reduce the problem of double counting and incompatibilities of genomic and pedigree relationships
- We used 10 metafounders per breed
- Estimating $\boldsymbol{\Gamma}$ is tricky and is based on a “inbreeding trend” thing and heuristics ☺
- Some results are sensitive to $\boldsymbol{\Gamma}$!!!
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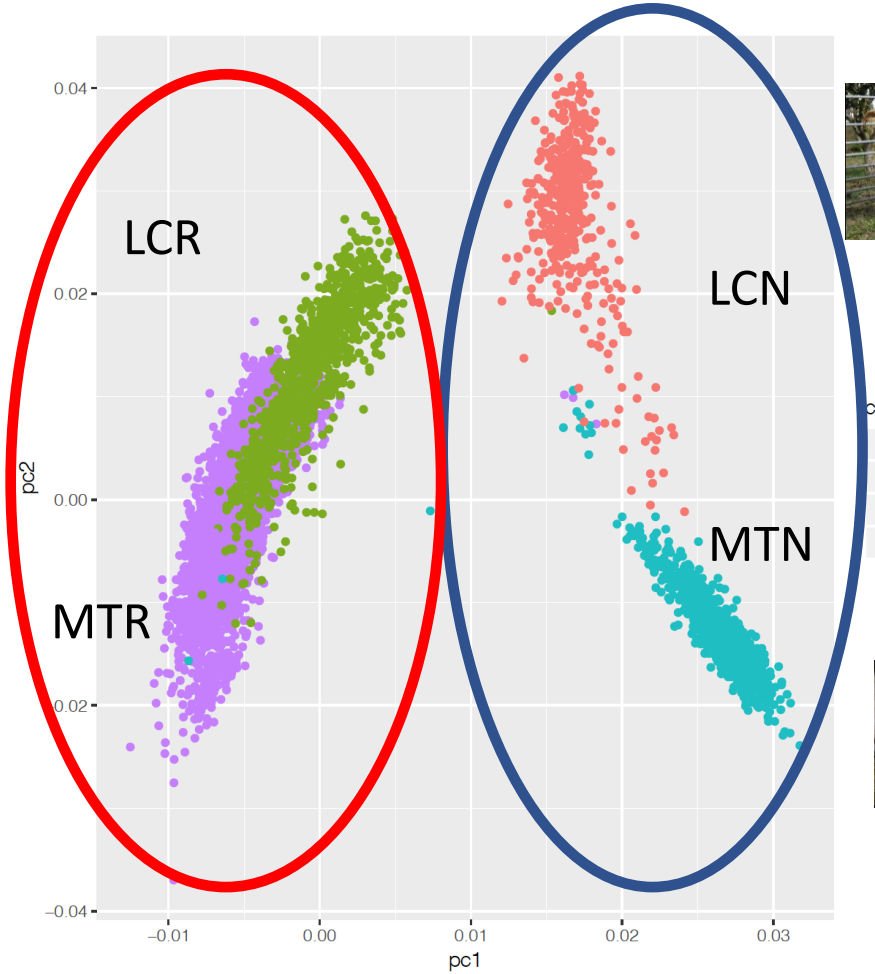
SOME RESULTS : PCA across breeds



- As expected. “blond” animals are closer than “black”

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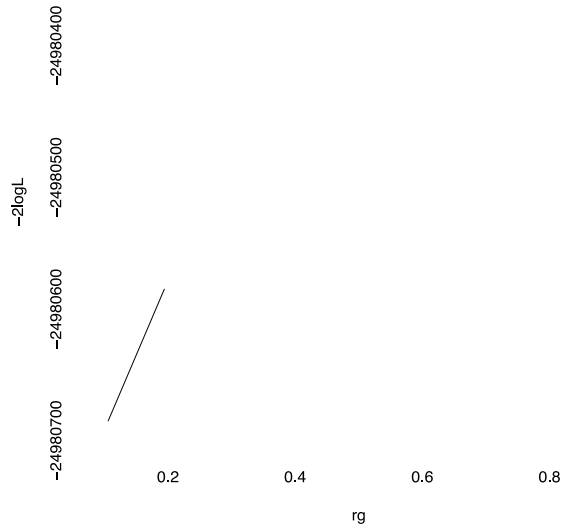
SOME RESULTS: genetic correlation

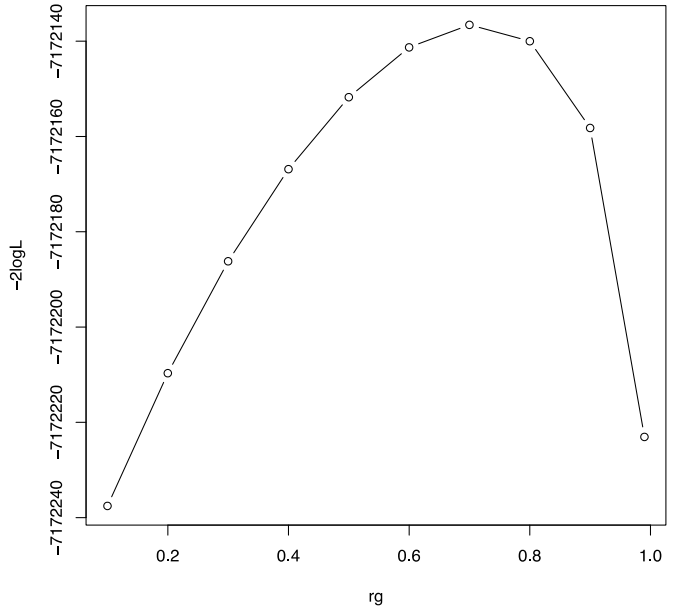
We ran a REML grid search for genetic correlations r_g, fixing other variances to single-breed estimates.

- Genetic correlation MTR-LCR: ~0.7
- Genetic correlation MTN-LCN: ~0.7

this is good because it means that improvement in one breed translates into the other breed



MTR/LCR (SSGREML)



MTN/LCN (SSGREML)

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LCR/MTR

- Genetic trends for any breed are identical in BLUP or ssGBLUP and with the breed analysed separately (single-breed) or jointly (two-breed, each breed a trait)

- However the trend of a breed, in the scale of the other breed, is not correctly estimated
- This means that a MTR breeder that would look at the EBV of LCR rams in the MTR scale, would see that EBVs of all LCR rams look terrible - and much worse than reality

- I show the example of LCR/MTR but similar behaviour exists for MTN/LCN
- The phenomenon is not fully symmetric because exchanges are one-way only

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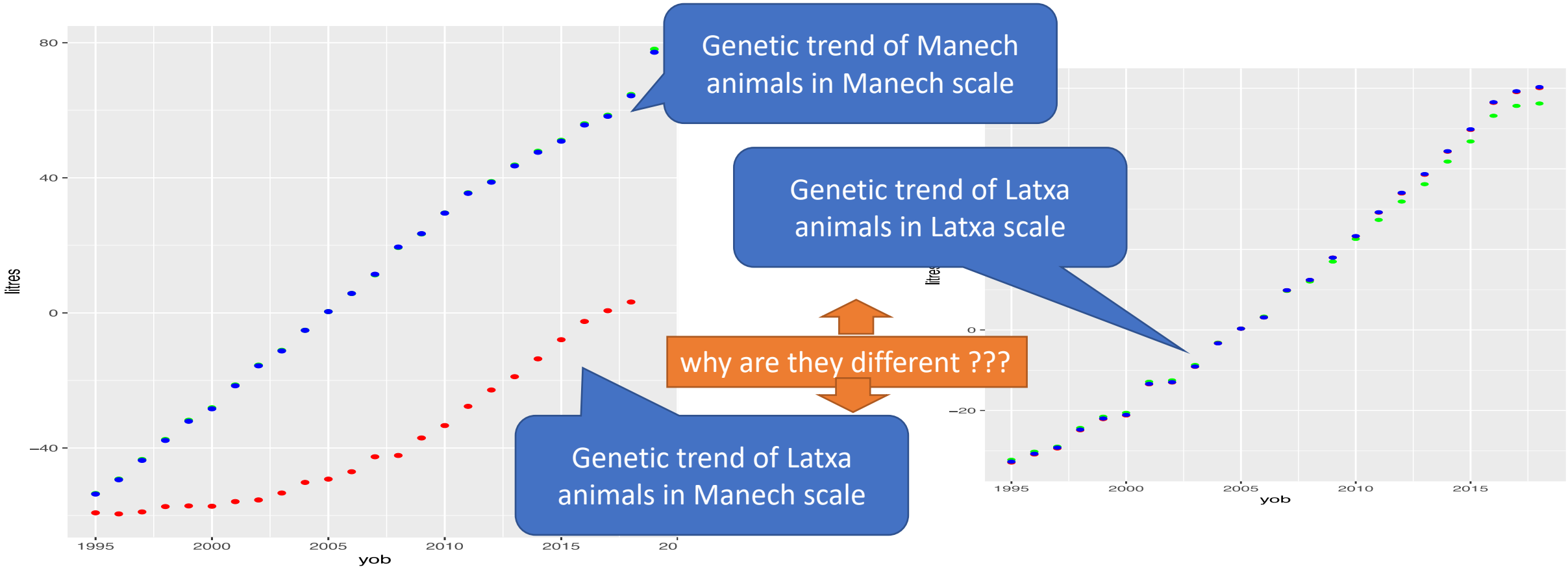
- SOME RESULTS
- GENETIC TRENDS

LCR/MTR



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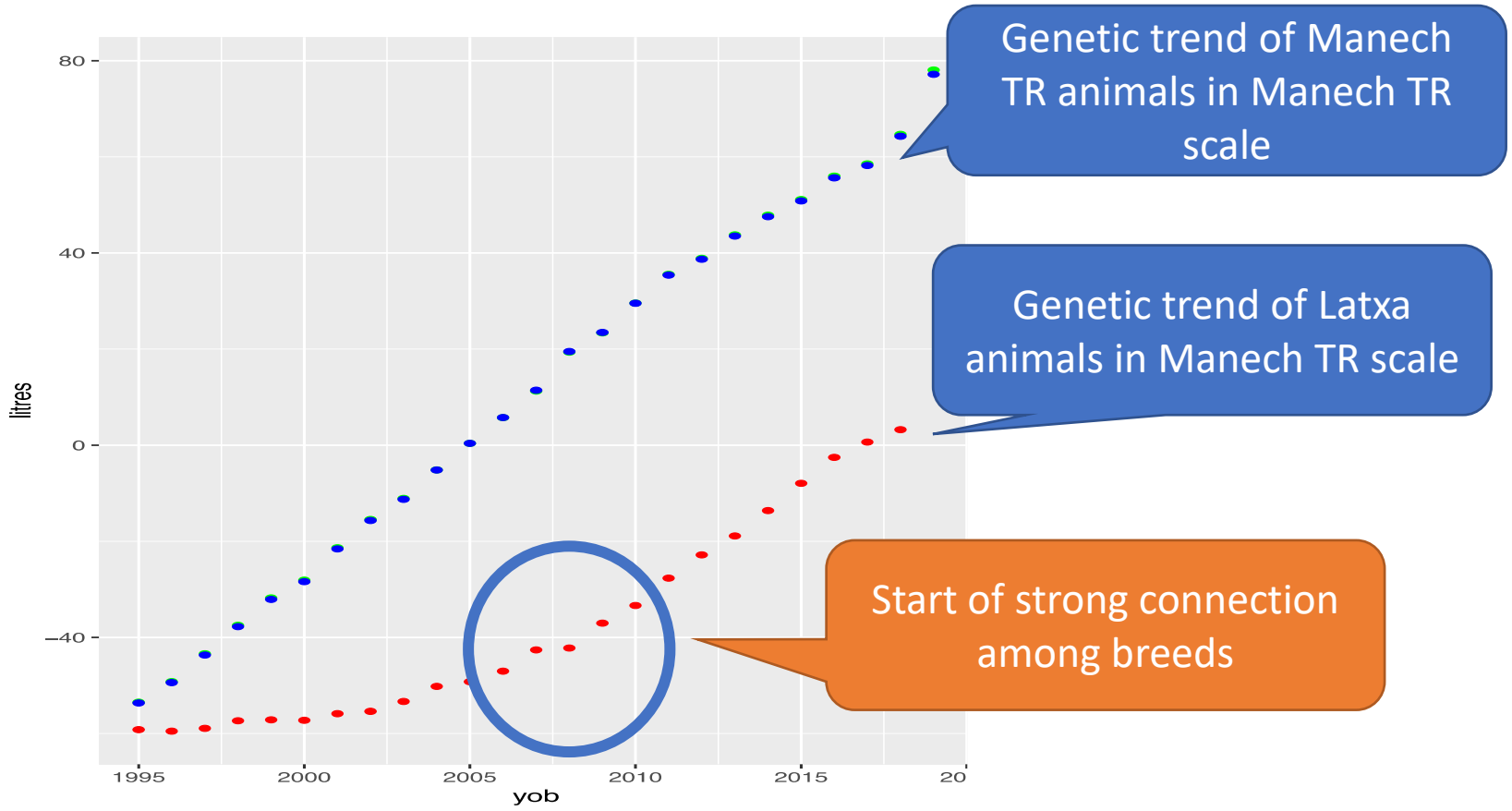
- SOME RESULTS
- GENETIC TRENDS

LCR/MTR



- Because exchanges are one-way (MTR => LCR) and mostly recent, trends “in the other scale” are biased
- e.g. at the beginning, LCR has no genetic trend in the MTR scale (and it should have !!) because the data has no information on that
- as a result, differences across breeds are unfairly high (or unstable) and not acording to actual records
- We can’t give this to breeders

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LCR/MTR

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- However the trend of a breed in the scale of the other breed is not correctly estimated

- In spite of all our sophisticated BLUP machinery and fancy SNP chips, we need to inseminate females of one side with rams from the other side
- We can't go back to the past and inseminate
- The most sensible solution is to truncate data and keep the last 15 years which are well connected
- We MAY do this some day in future projects (ARDI2 which has just been sent to Poctefa financing)

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Computing time, memory, perspectives

- All computations were ran in cluster Genotoul Bioinfo,
- SSGBLUP or BLUP run easily (hours). A REML grid search took ~1 day
- Memory needs were not large
- What is really limiting is pooling data, data edition and catching errors, in particular because it is the 1st time and it is across 2 countries, 3 institutions and 3 languages
- The joint evaluation is technically doable. With a well done pipeline and exchange protocol, and some experience in all parties, it should also be smooth.

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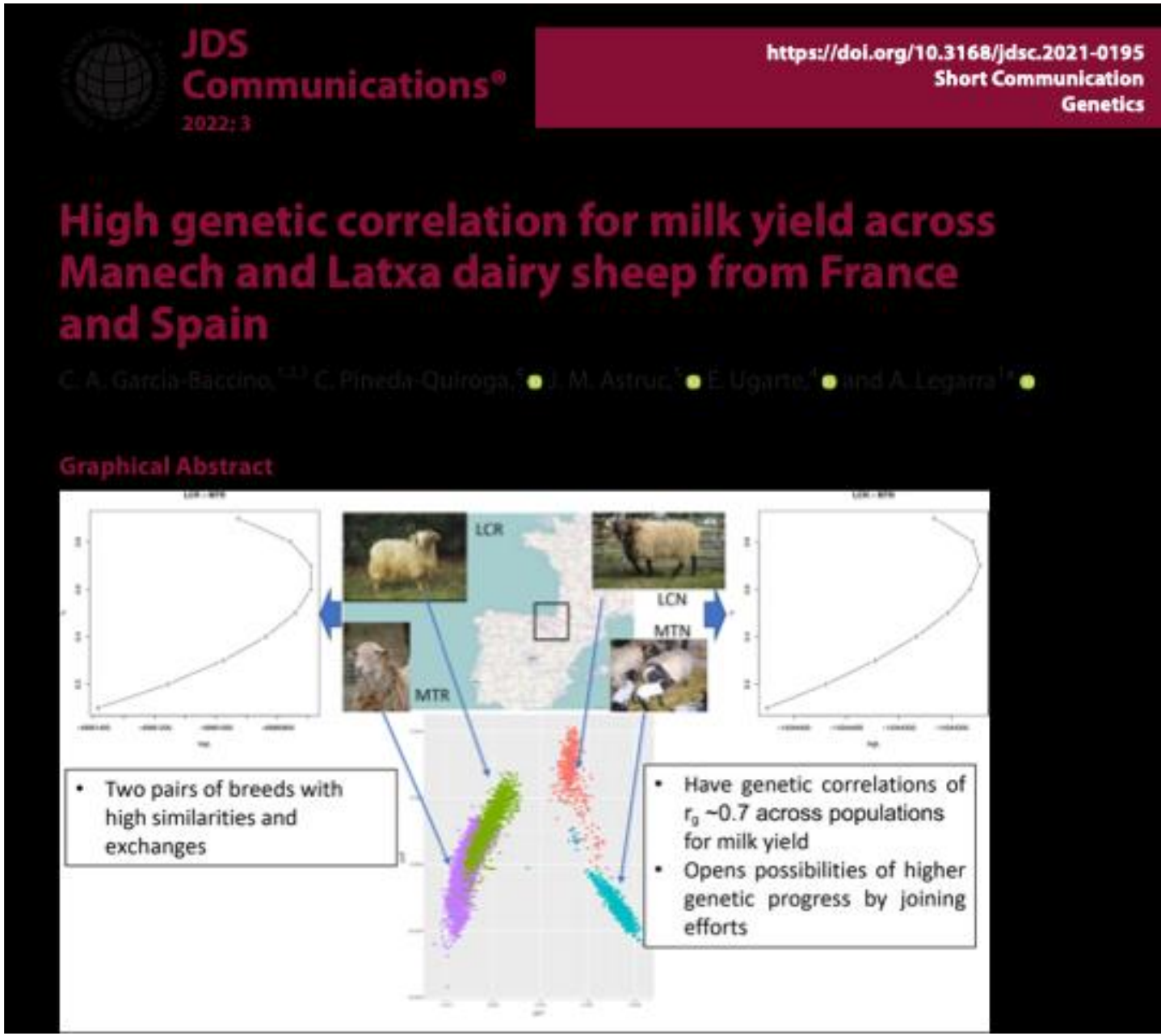
JDS Communications
2022; 3
https://doi.org/10.3168/jdsc.2021-0195
Short Communication
Genetics
High genetic correlation for milk yield across Manech and Latxa dairy sheep from France and Spain
Graphical Abstract
LCR
LCN
MTN
MTR
• Two pairs of breeds with high similarities and exchanges
• Have genetic correlations of r_g ~0.7 across populations for milk yield
• Opens possibilities of higher genetic progress by joining efforts

SMARTER PARTNERS

Thank you for your attention

www.smarterproject.eu

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