Agroecological Breeding of sheep in Uruguay: genetic and genomic tools

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INTA Buenos Aires Argentina
From the Neolithic to the biotechnological era: old and new development scenarios for sheep farming, an economic resource and a common cultural heritage

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INIA URUGUAY

Content

1. **Agroecological focus:** Role of Genetics
2. **Genetic and genomic tools**
3. **Implementation in Wool systems**

Agroecological focus

Agroecological focus: Role of Genetics

NATIVA PRECIOUS FIBER

RWS RESPONSIBLE WOOL STANDARD CERTIFIED

Animal Welfare

Quantity & Quality

Evaluaciones Genéticas Ovinas

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SUL SECRETARIADO URUGUAYO DE LA LANA

URUGUAY BEEF & LAMB

Uruguay Wools

RUMIAR

Smarter

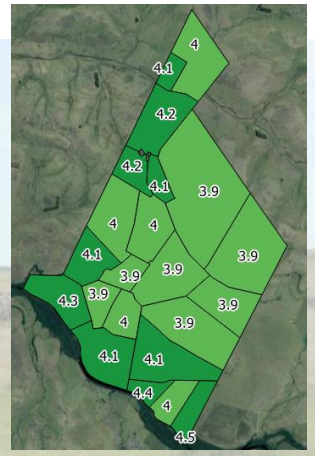
GrassToGas

Life Cycle Assessment & Carbon Stock

Social aspects

Environmental impact

Biodiversity

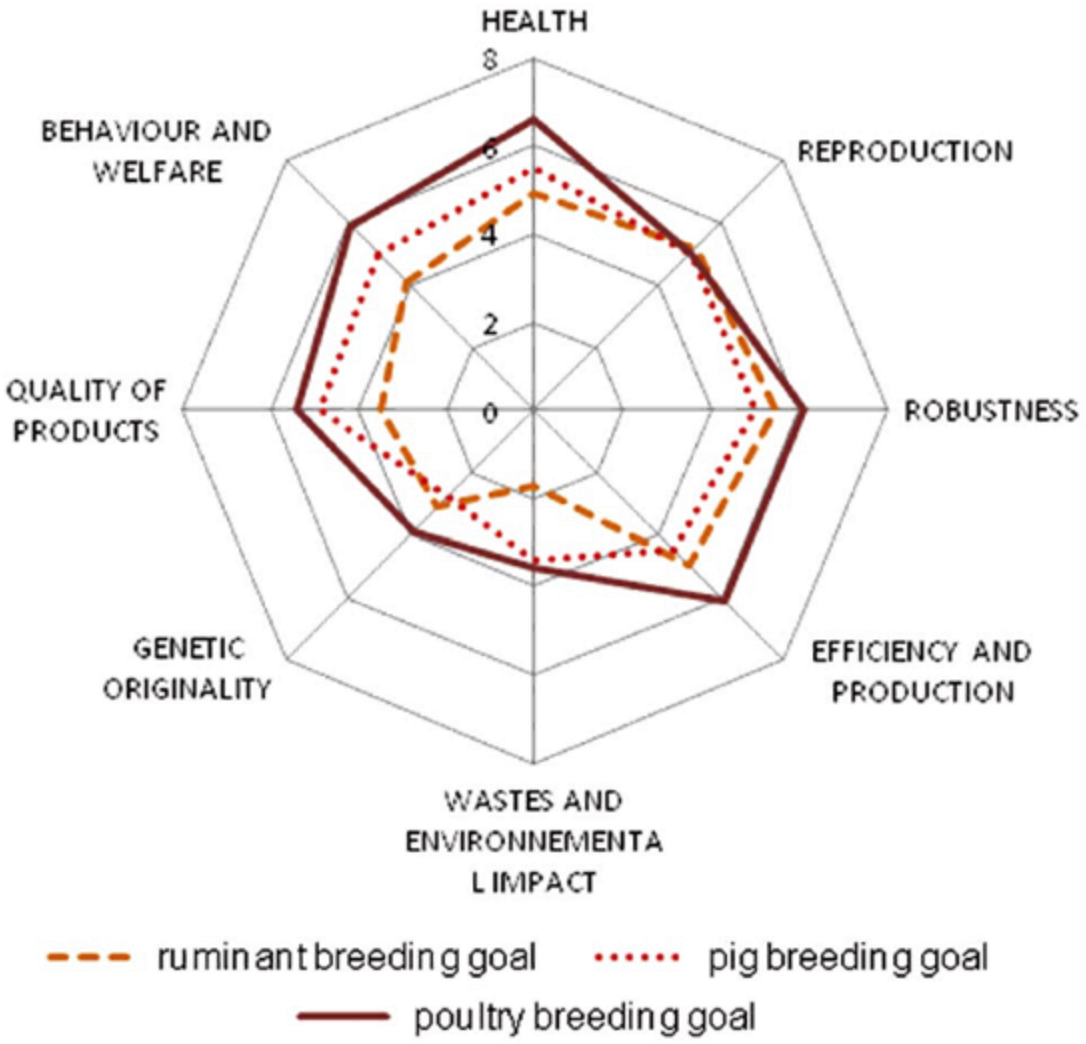


Ecosystem Integrity Index

Blumetto et al. 2019

INIA

Agroecological breeding goals for livestock

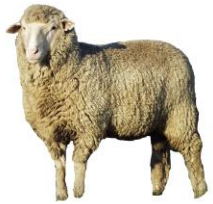


Phocas et al. 2016

Sociedad Criadores Merino Australiano del Uruguay

S.C.C.U. - desde 1945
CORRIEDALE
Moneda fuerte de la majada nacional

MERINO DOHNE URUGUAY



TEXEL URUGUAY

Health

FEC

FAMACHA

Foot rot

Temperament

Behaviour & Welfare

Resilience

BCS

Lamb survival

Twinning rate

Fertility

Wool traits: FD, yield, SL, colour

Quality of products

Reproduction

Scrotal circ

Maternal ability

Genetic originality

Efficiency & Production

BW

REA - BF

RFI

Feed intake

Environmental impact

Methane

Smarter
SMAll RuminanTs breeding for Efficiency and Resilience

GrassToGas

RUMIAR

Number of animals recorded per trait and breed

Traits	Merino	Dohne	Corriedale	Texel	Total (end 2022)
Individual intake (kg/a/d) Wool data (5 traits) Rib eye area + Backfat Condition score FEC DNA	981 +390*	357 +120*	368	129	2.345
Methane (g/a/d)	981	230	298	129	2.275
Genotype (50 K)	x		x	x	1.868

** In 2022*

Genetic and genomic tools

Genetic and genomic tools

- **New** (old) **traits:** Efficiency, Residual feed intake, Methane emissions

  Correlations with other traits (trade off) – FEC

- **Genomic tools:**

  1. Accuracy increase (?)

  2. ¿Can we evaluate something we didn´t measure?

  3. GWAS

¿What do we know? - GIN resistance

Correlations

↑ Wool, BW → ↓ FEC 👍

↓ FD → ↑ FEC 👎

rg	FEC	
GFW	-0.15	+
CFW	-0.08	+
FD	-0.16	!
SW	-0.35	+

Heritability

0.15±0.01 Merino

0.21±0.02 Corriedale

How to measure (protocol)

Cardellino el al. 1994; Castells 2009, Bell et al. 2020

FEC in lambs vs FEC in periparturient ewes (periparturient rise)

rg=0.81±0.11

More efficient to use lamb FEC for selection

Merino (Ciappesoni et al., 2013) (Goldberg et al., 2012)

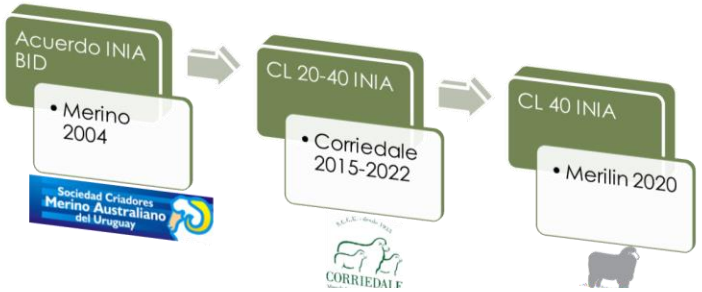
FEC in low or high worm burden challenge: **rg=0.87±0.04**

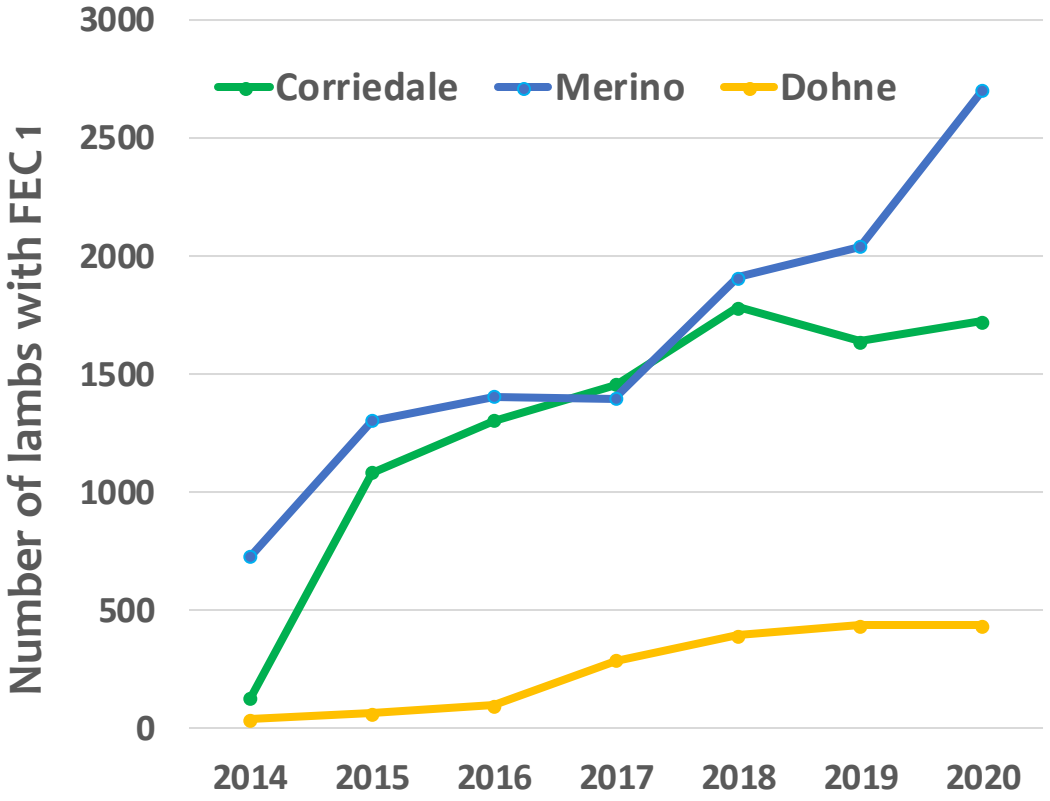
FEC correlation with **FAMACHA:** **rg= 0.55 ±0.12**

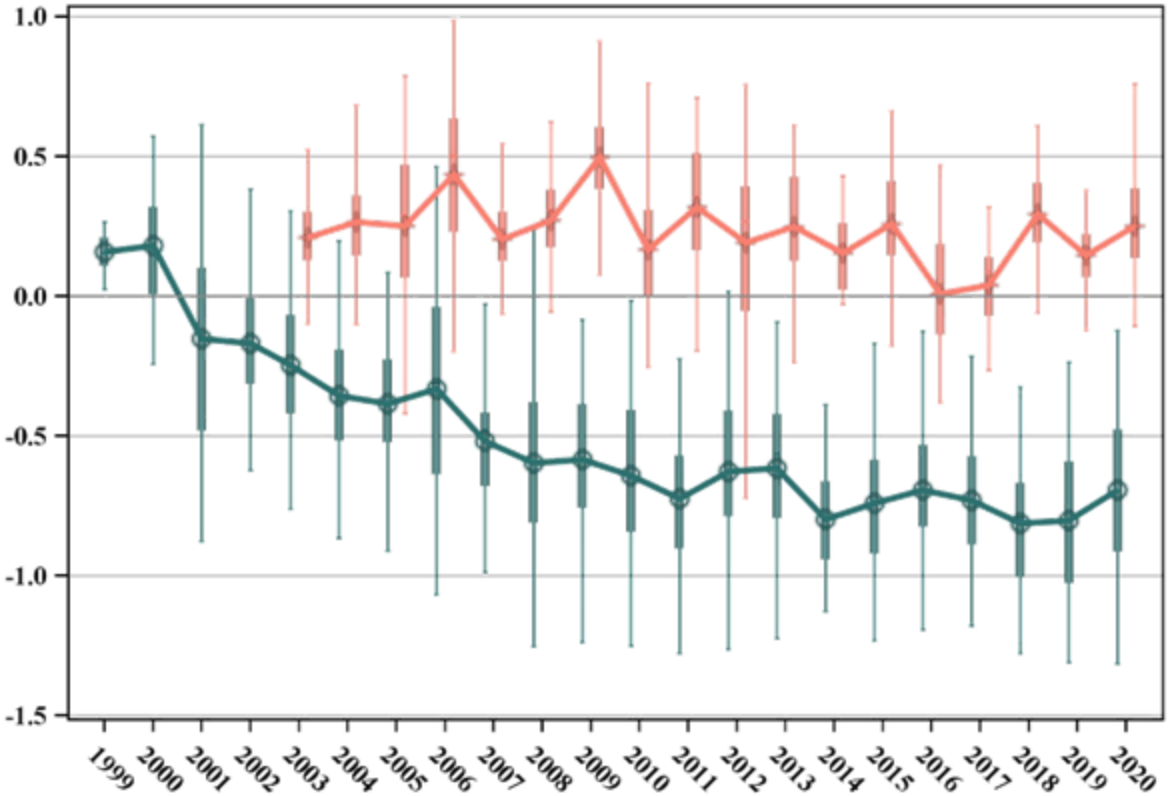
FEC correlation with **BCS** **rg= -0.35 ±0.10**

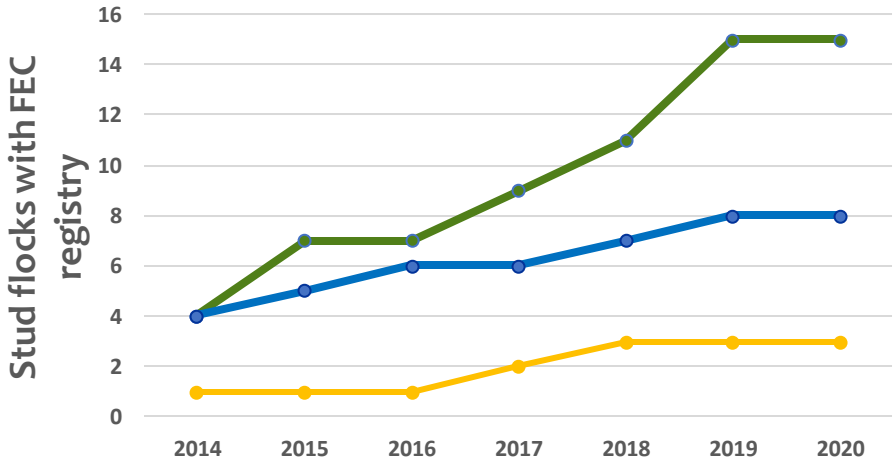
Corriedale (Castells, 2009) (Balconi et al., 2020)

¿What do we know?









PhD Camila Balconi Marques

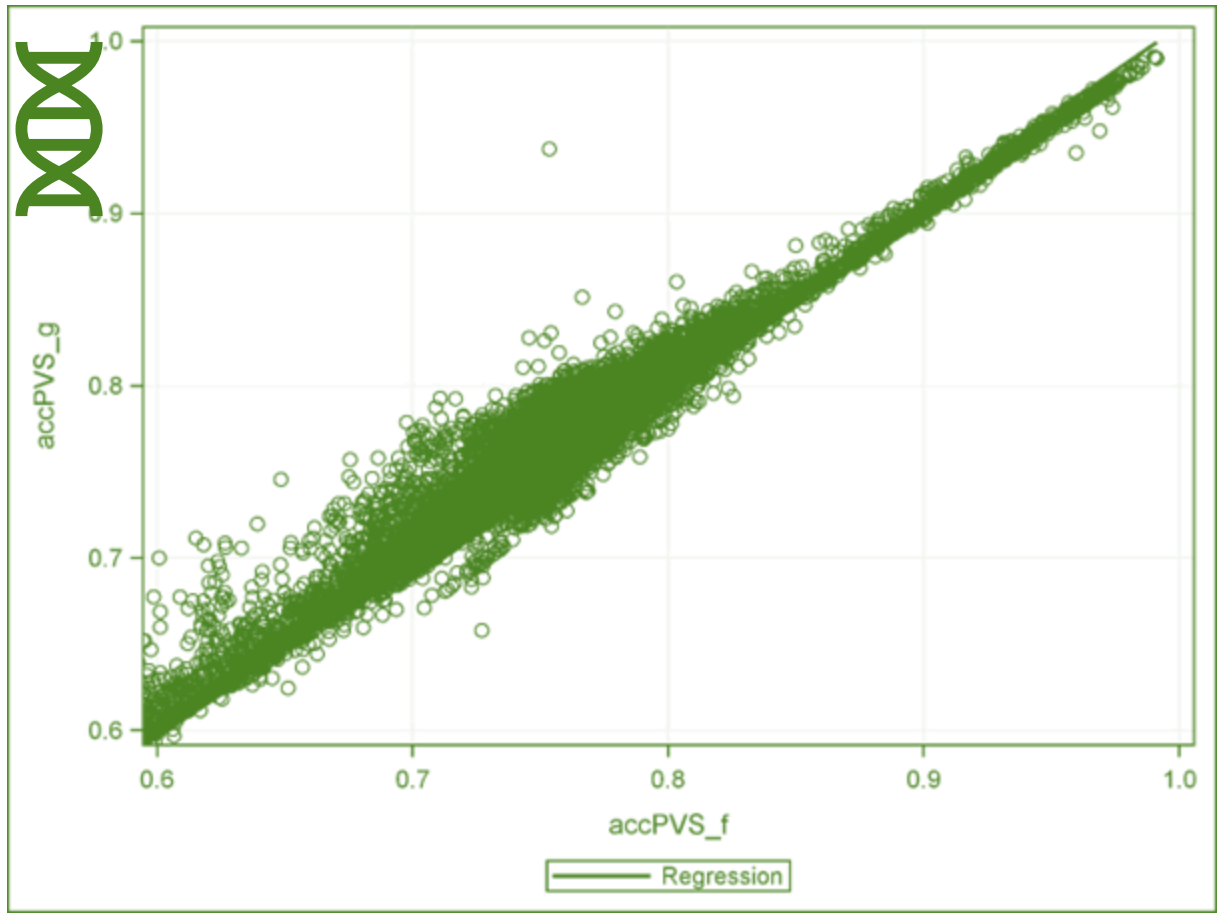
New traits

	RFI	Feed intake	O_2	CH_4	CO_2	GFW
RFI	0.27					
Feed intake		0.38				
O_2			0.26			
CH_4				0.23		
CO_2					0.27	
GFW						0.41

Genomic tools : accuracy increase

PhD Brenda Vera

First genomic evaluation in sheep in America



>63.582 **Australian Merino** phenotypic records

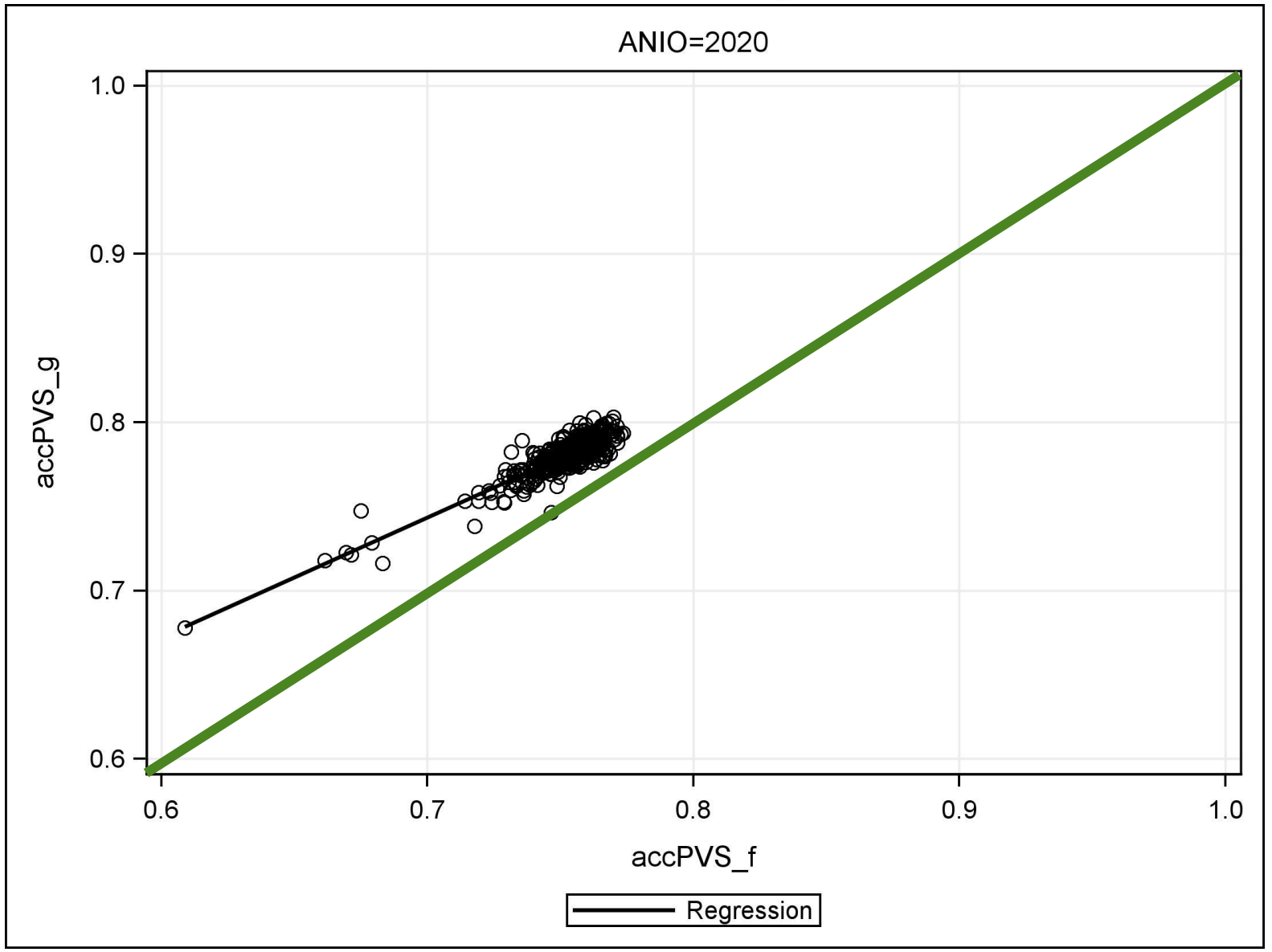
>83.000 animals in the pedigree

2.230 genotyped animals (imputed to 40K GGP)

Genotypes	N	%
only lamb	159	0.2
Lamb and Dam	63	0.07
Lamb and Sire	675	0.8
Trio (L+S+D)	1,301	1.5
only Dam	395	0.5
only Sire	16,759	19.2
Nothing	67,839	77.8

Genomic tools : accuracy increase

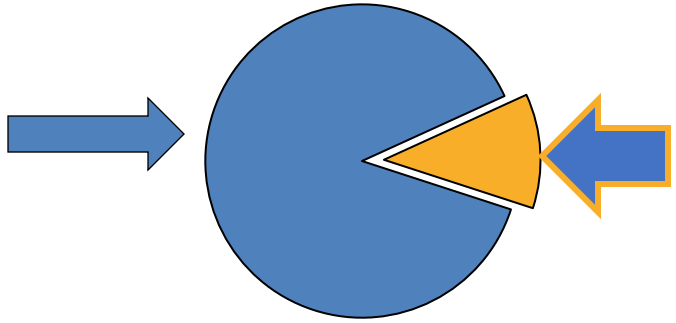
PhD Brenda Vera



With genomics: can I evaluate something I didn´t measure?

PhD Brenda Vera

Stud flocks with FEC
Glencoe´s Nucleus with FEC and Genomic information

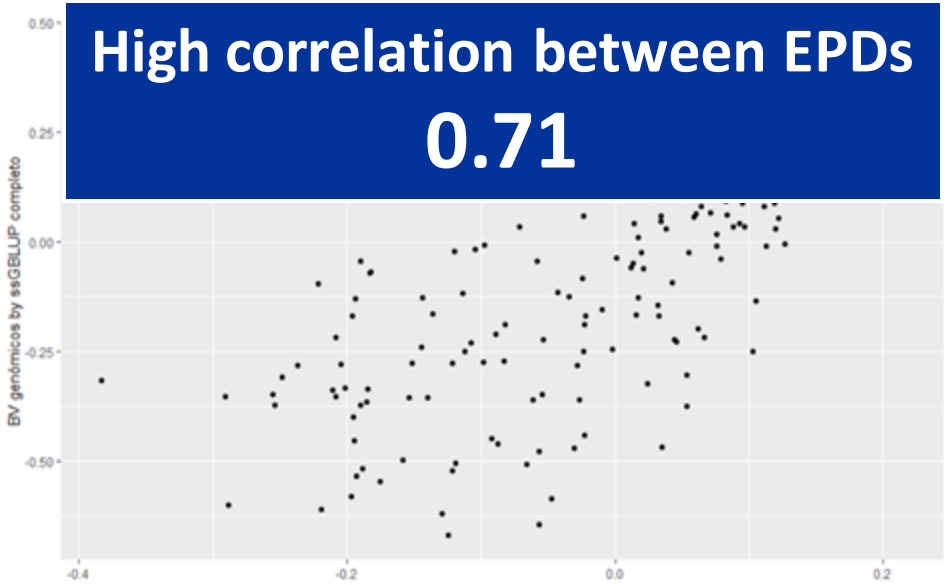


- FEC records from one stud flock are “erased”
- 156 animals with genomic information
- EPDs are estimated only with genomics

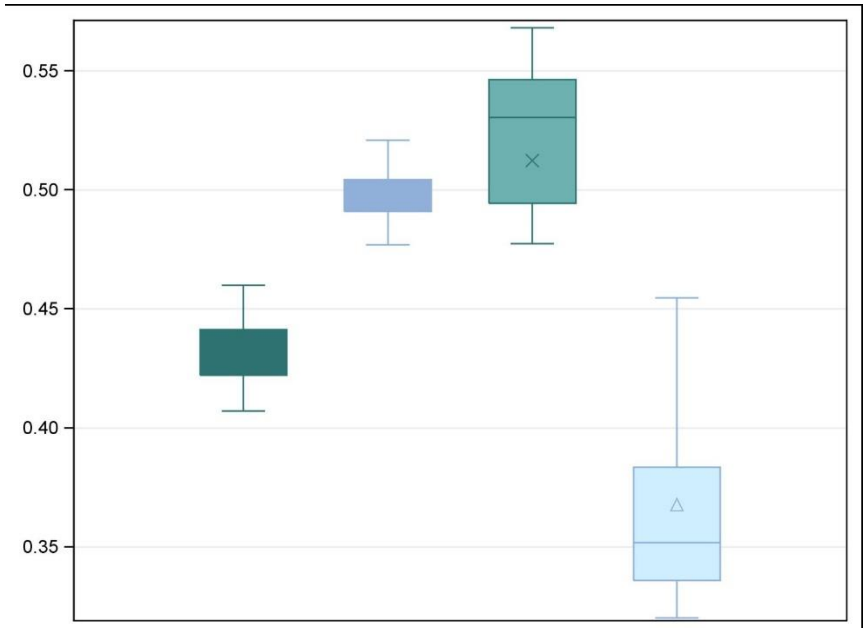
EPD with **data and genomics**

High correlation between EPDs

0.71



EPD only with genomics



FEC mean accuracy per Sire group

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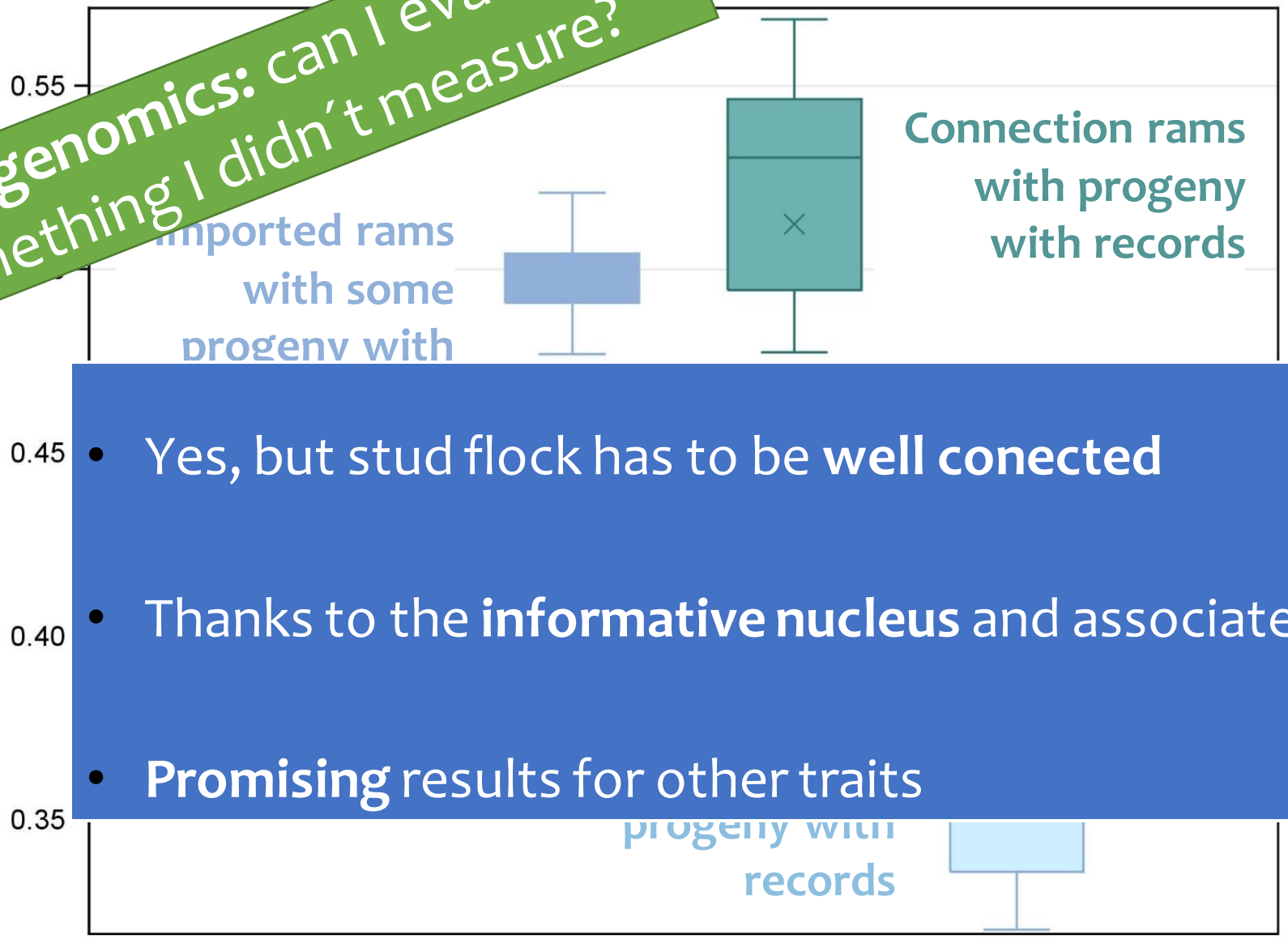
With genomics: can I evaluate something I didn´t measure?

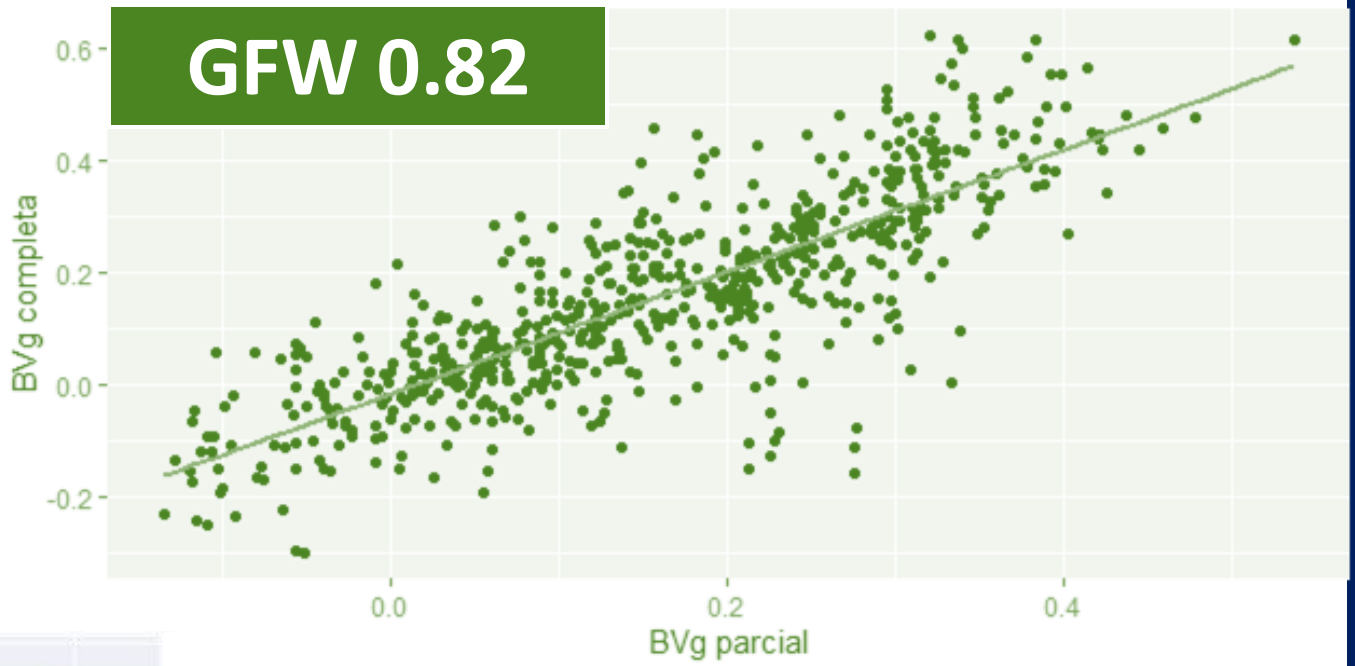


- Yes, but stud flock has to be **well conected**
- Thanks to the **informative nucleus** and associated **stud flocks**
- **Promising** results for other traits

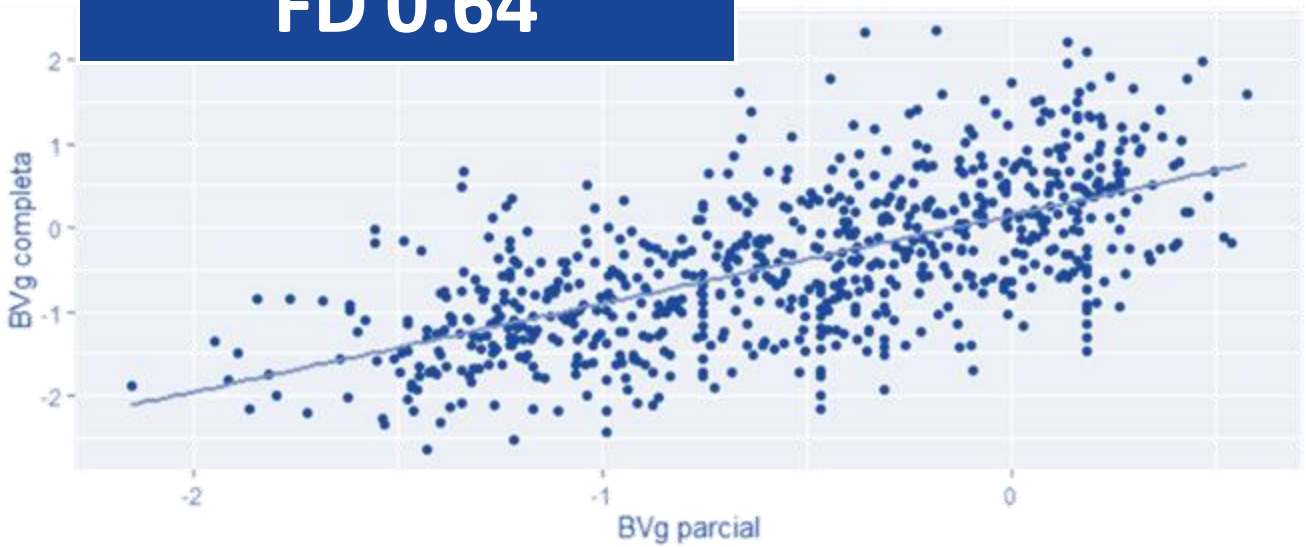
With genomics: can I evaluate something I didn´t measure?

Total records	63.582
EEFAS records	724
Genotyped animals	239
Effective SNPs (post QC)	37,802
Total genotyped animals	2,230

GFW 0.82



FD 0.64



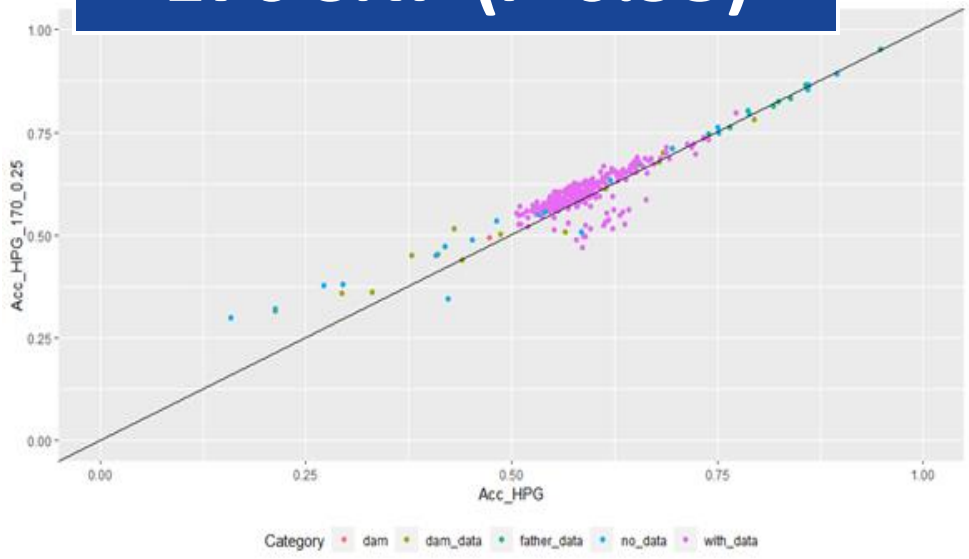
Brenda Vera, unpublished

MSc Beatriz Carracelas

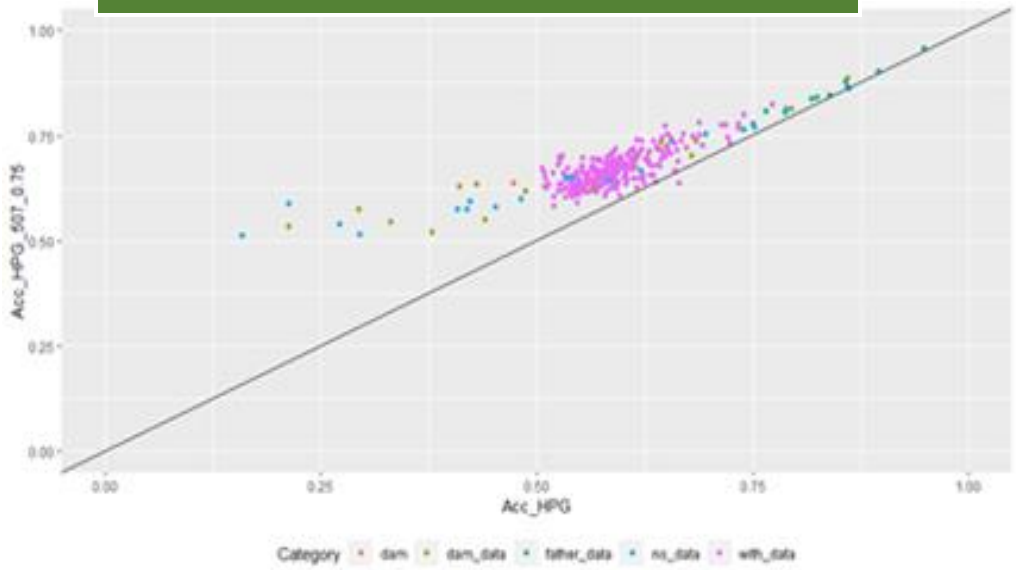
Genomic tools : accuracy increase

- 19,547 **Corriedale** phenotypic records
- 40,056 animals in the pedigree
- 305 animals genotyped with both 170 and 507 SNPs

170 SNP (r=0.93)



507 SNP (r=0.88)



Genomic tools : GWAS

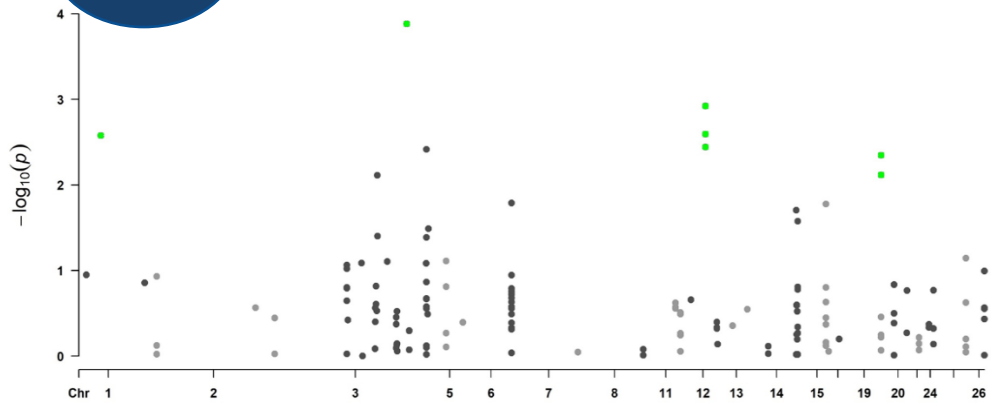
Corriedale

FEC

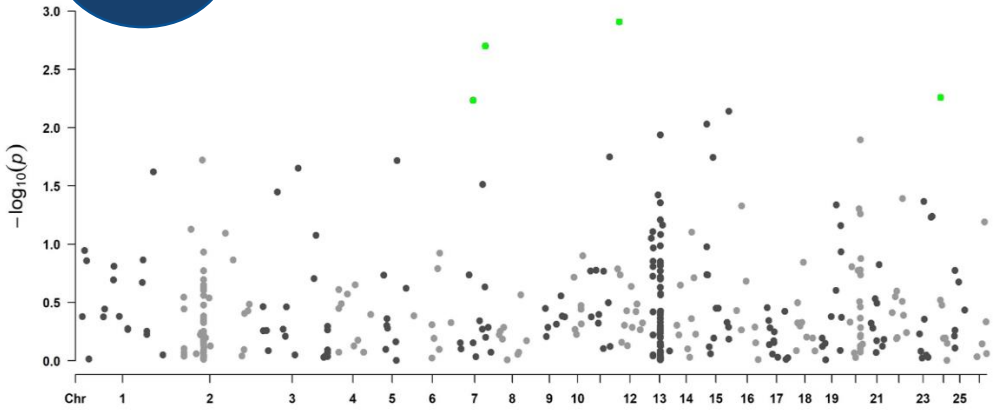
MSc Beatriz Carracelas

Density	SNP	Animals
170	148	454
507	373	702
50K	29,832	375

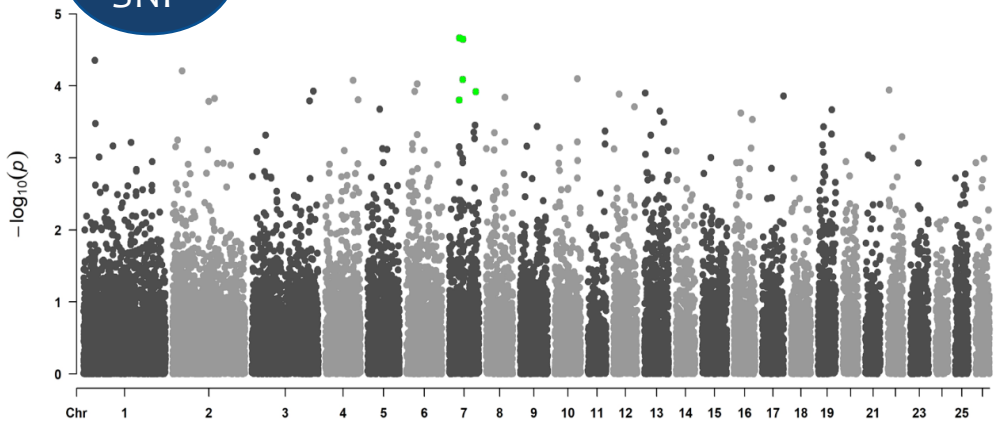
170 SNP



507 SNP



50K SNP



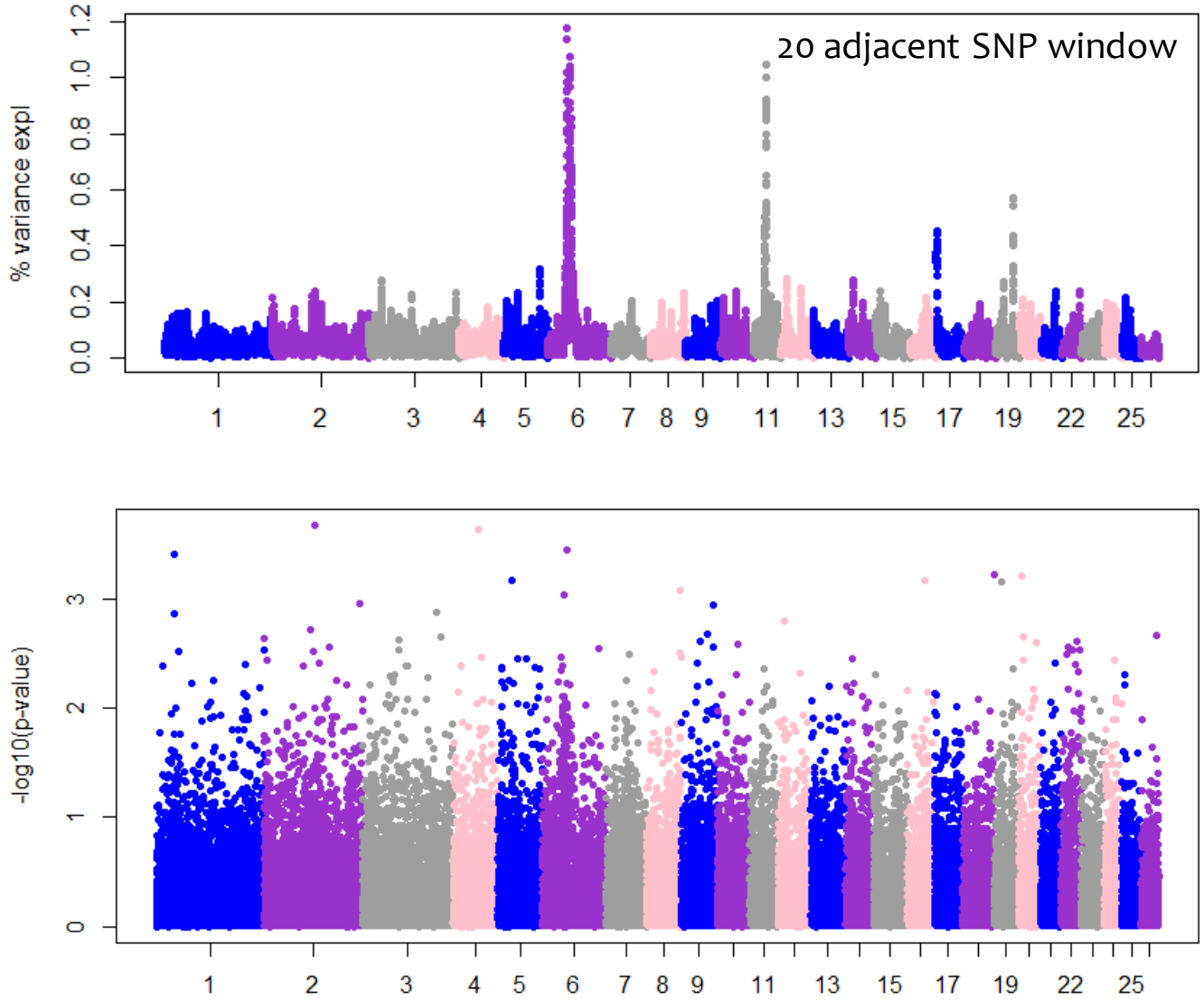
- TIMP3, TLR5, LEPR and TLR9 (170 SNP)
- SYNDIG1L and MGRN1 (507 SNP)
- INO80, TLN2, TSHR and EIF2AK4 (50K SNP)

Genomic tools : GWAS

PhD Brenda Vera

Australian Merino

FEC



SENP3, CD68, MPDU1, PFAS, PELP1, DLG4, ACADVL, DVL2, ACAP1, DCAF16, NCAPG, LAP3, DNAH2, IBSP, FAM13A, ASGR1, LCORL, LOC101121185, MINK1, FAM184B, HERC3, ABLIM2, CHRNE, PLD2

Density	SNP	Animals
40K	37,802	2,230

LAP3, FAM184B

Agroecology: Implementation in sheep systems

Agroecology: Implementation in sheep systems

The new breeding pyramid

Informative Nucleus

Research platform: generation of knowledge, training courses for technicians and filed days for farmers

Stud Flocks

Applied Research platform: stud flocks with specific traits (e.g. FEC, Methane), reference farmers, pilot plan for design of agroecological transitions, field days

Commercial farmers

Validation & Development Platform: Initial picture (environment & genetics), define agro[illegible]ological transition (co-innovation) linked to the value of the system (e.g. wool fr[illegible]enerative a[illegible]ure)

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Thank you for your attention

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Thank you for your attention