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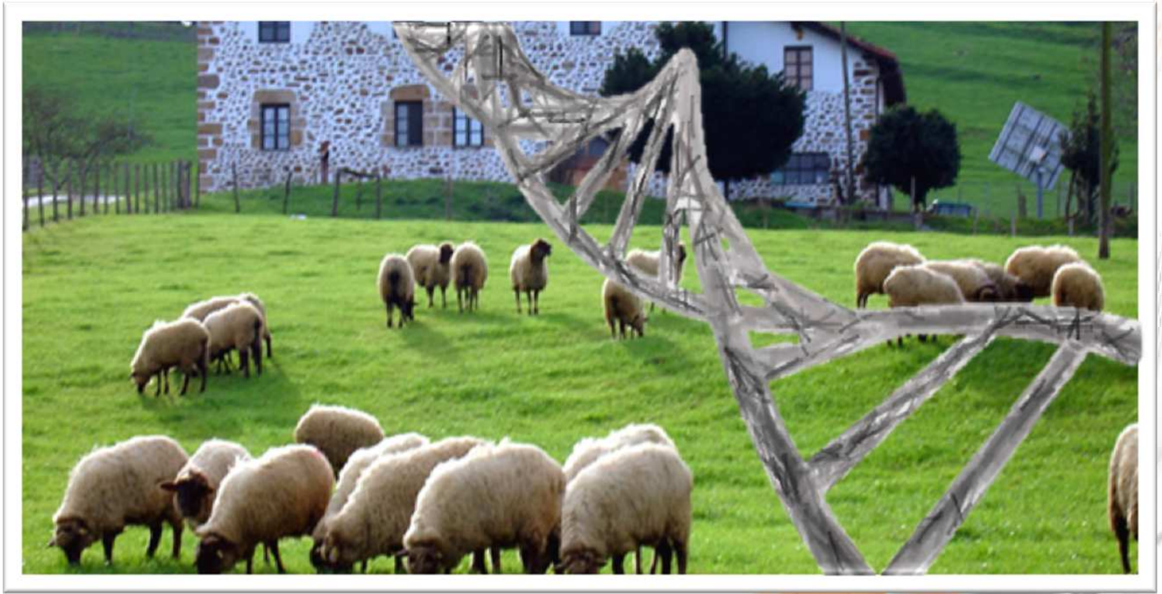
Session 26 Genetics & Genomics

Connectedness and application of breeding schemes for sheep & goats

Genomic selection on Latxa dairy sheep

Itsasne Granado-Tajada & Eva Ugarte



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Research, Development and Innovation in sheep

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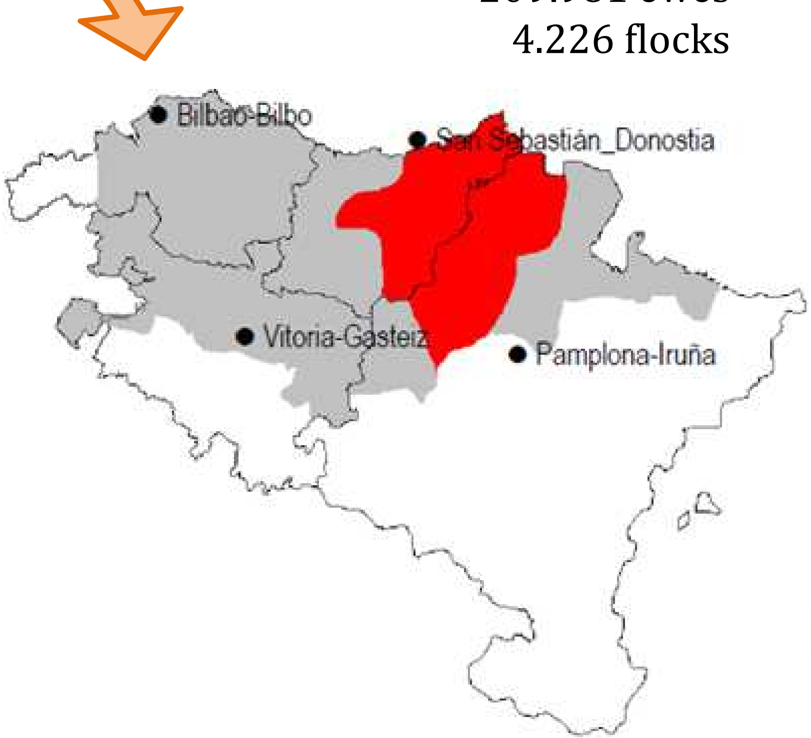
DEPARTAMENTO DE DESARROLLO ECONÓMICO Y COMPETITIVIDAD

Breeding program of Latxa breed (1984)

- Dairy sheep breed native from Basque Country and Navarre (Spain)



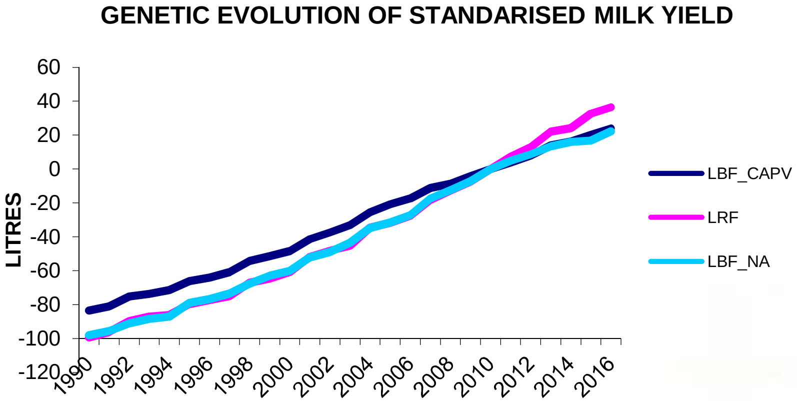
LATXA RED FACED
209.981 ewes
4.226 flocks

LATXA BLACK FACED
from BC
120.792 ewes
3.742 flocks

LATXA BLACK FACED
from Navarre
100.088 ewes
985 flocks

Breeding program of Latxa breed (1984)

- Dairy sheep breed native from Basque Country and Navarre (Spain)
- Selection based on pure breed
- Breeding goals:
    - Milk yield
    - Milk composition: fat and protein content
    - Udder morphology
- Annual genetic improvement of 3.5-4% in milk yield (Ugarte, 2017)



GS in dairy sheep

Lacaune (Baloche et al., 2014; Barillet et al., 2014)

- Accuracy gain of GS over parent average
  - Milk yield: 0.15
  - Other characters: 0.10-0.20
- Reduction of AI rams by 20-40 %

Lacaune: GS was implemented in 2015

Manech and Basco-Béarnaise (Legarra et al., 2014)

- Increase in accuracy in single-breed predictions
  - MTN: 0.11 MTR: 0.16 BB: 0.06
- Multiple-breed pooled predictions
  - No increase in accuracy of genomic evaluations

Manech and Basco-Béarnaise: GS was implemented in 2017

Objective

Latxa (Legarra et al., 2014)

- Hardly understandable results → No conclusive
  - Negative accuracy for CS
  - Contradictory results between breeds
- Probably due to the data structure
  - Weak relationship between training and validation group
  - Reduced number of genotyped rams

Latxa: Further studies are required

→ **Ascertain the benefit of including molecular information into genetic evaluations of the Latxa sheep**

Materials & Methods

Latxa Red Faced

illumina
OvineSNP50
Genotyping BeadChip

Data 1984-2017	
Genealogical	150.164
Phenotipical	392.295
Nº ♀ in data	133.230
Nº flocks	325
Nº ♂ in data	1835
Genotyped	429
SNPs	39.593

Materials & Methods

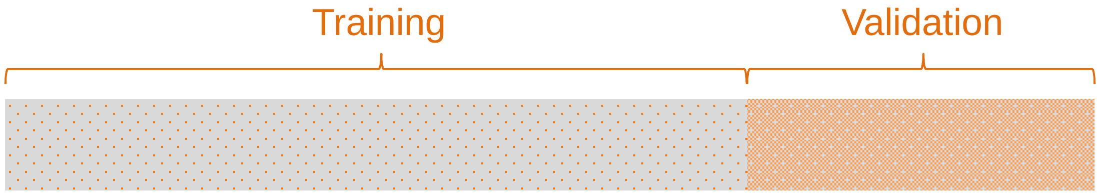
Criterion:
Accuracy difference

$$R_{validation}=\frac{cov(EBV,TEBV)}{V_{EBV}\ VTEBV}$$

$$R^2_{validation} = R^2(EBV, TEBV)\frac{1+k}{\overline{\overline{EDC}}} \qquad k = \frac{4-h^2}{h^2}$$

(Mäntysaari el at., 2010)

Data



→ BLUP genetic evaluation

Rams in training group				**Rams in validation group**		
Nº genotyped	Nº nongenotyped	Birth years	Average EDC	Nº genotyped	Birth years	Average EDC
184	1158	1984-2011	79.76	93	2012-2014	40.26

Validation group

Results

Model	Bias	Slope	R
CS	32.64±2.13	0.60±0.11	0.41±0.06
GS	14.09±4.33	0.52±0.08	0.44±0.05
GS - CS	-18.55±3.07	-0.08±0.06	0.03±0.03

R(CI,GI): 0.89

R(CS,GS): 0.97

7.6%

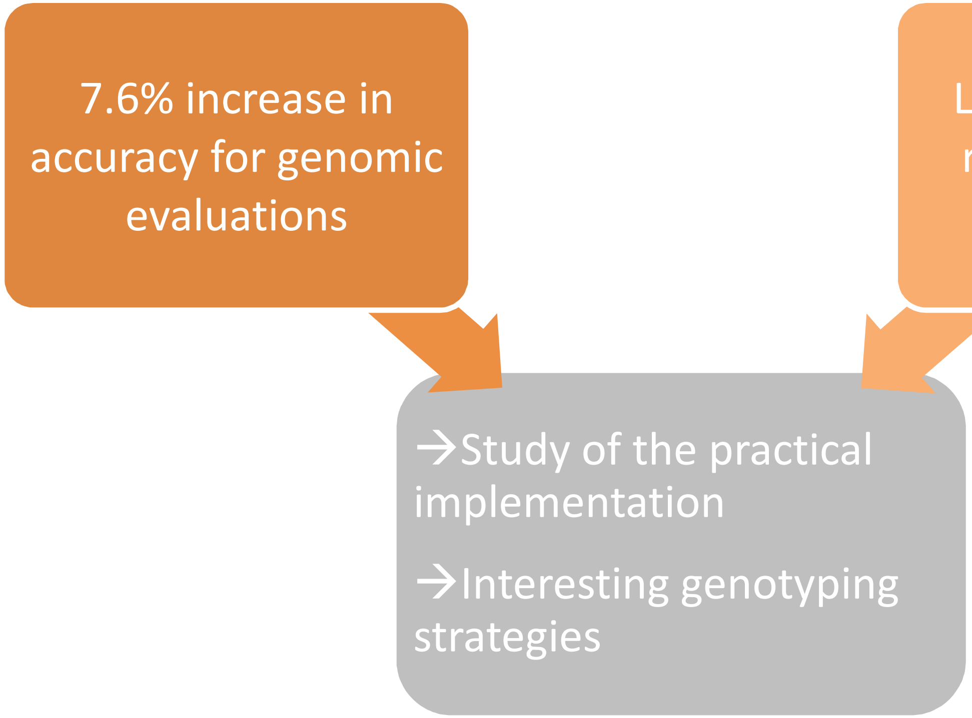
Previous results (Legarra et al., 2014)

Model	Bias	Slope	R
CS	145.81±51.72	-0.08±0.39	-0.05±0.26
GS	91.05±36.72	0.33±0.27	0.26±0.20
GS - CS	-50.34±29.12	0.37±0.22	**0.30±0.13**

Families

Model	Nº father	Nº new families	50 lambs selected
CS	42	3	44
GS	46	7	

Conclusions



7.6% increase in accuracy for genomic evaluations

Lower than values reported in other breeds

→Study of the practical implementation

→Interesting genotyping strategies

ESKERRIK ASKO
MUCHAS GRACIAS
THANK YOU
MERCI BEAUCOUP
HVALA

igranado@neiker.eus

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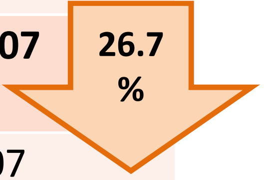
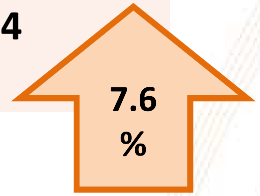
2018 results

Breed	Model	Bias	Slope	Accuracy
LBF	Pedigree	8.02±22.97	0.96±0.17	0.59±0.08
	Genomic	104.84±8.17	0.62±0.17	0.43±0.09
	Genomic-pedigree	96.82±18.05	-0.34±0.13	**-0.15±0.07**
LRF	Pedigree	32.64±2.13	0.60±0.11	0.47±0.07
	Genomic	14.09±4.33	0.52±0.08	0.50±0.06
	Genomic-pedigree	-18.55±3.07	-0.08±0.06	**0.03±0.04**


26.7 %


7.6 %

Previous results (Legarra et al., 2014)

Breed	Model	Bias	Slope	Accuracy
LBF	Pedigree	57.47±27.94	0.33±0.28	0.34±0.28
	Genomic	70.54±32.02	0.19±0.32	0.19±0.31
	Genomic-pedigree	14.77±15.38	-0.15±0.16	**-0.18±0.13**
LRF	Pedigree	145.81±51.72	-0.08±0.39	-0.05±0.26
	Genomic	91.05±36.72	0.33±0.27	0,26±0.20
	Genomic-pedigree	-50.34±29.12	0.37±0.22	**0.30±0.13**

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