



**ICAR** 2023  
TOLEDO **SPAIN**

# Genomic selection in spanish dairy sheep: current state and futur perspective

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# Genomic selection nowadays: Spanish breeds

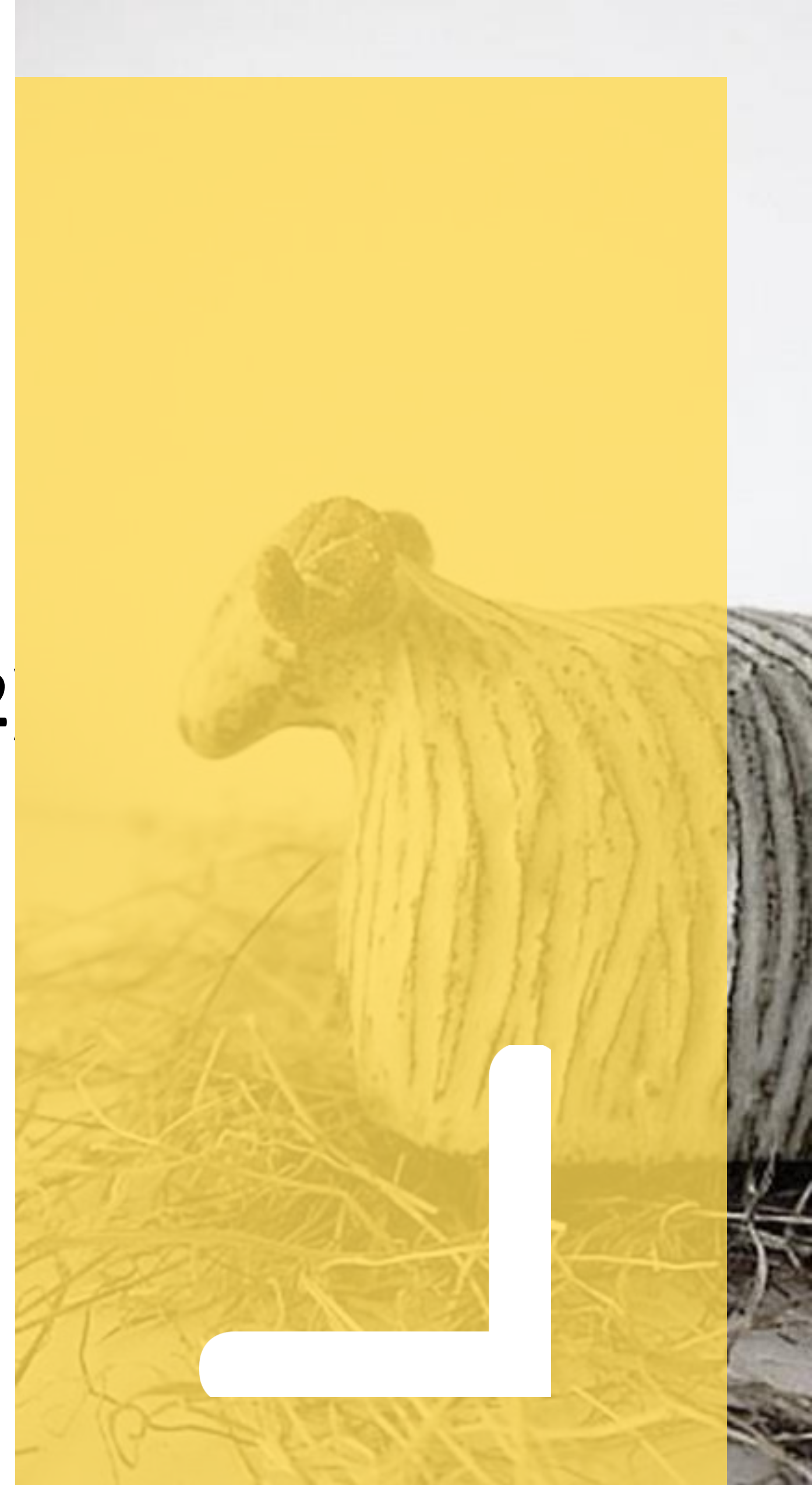




# Genomic selection

## Genomic selection: Current situation

- **Project financed by the Ministry of Agriculture (2018-2022)**
- **Regional projects**
- **Individual initiatives of breeder's associations**



# Genomic selection nowadays: Genotyped animals



Affimetrix 50K

AxiomTM 50K



Asociación Nacional de Criadores de Ganado ovino Selecto de Raza Manchega



**ANCHE**  
ASOCIACIÓN NACIONAL DE CRIADORES DE GANADO OVINO SELECTO DE RAZA CHURRA

Affimetrix 50K

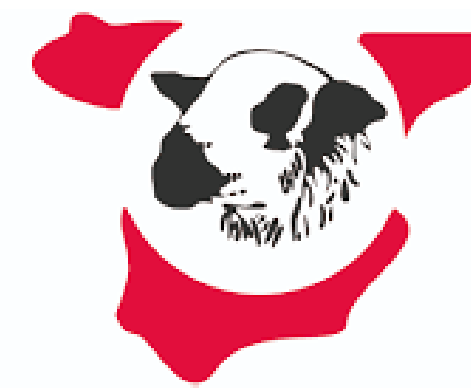
AxiomTM 50K

OvineSNP50 BeadChip



	Assaf	Churra	Latxa	Manchega
Rams with progeny	3.034	272	1.593	1.902
Ewes with lactations	3.640	2.960	1.483	988
<b>Young rams</b>	<b>4.749</b>	<b>95</b>	<b>592</b>	<b>3.093</b>
Young ewes	927	37	46	57
<b>TOTAL</b>	<b>12.350</b>	<b>3.154</b>	<b>3.714</b>	<b>6.040</b>

# Genomic evaluation: Evaluated characters



	Assaf	Churra	Latxa	Manchega*
Milk yield	✓		✓	✓
Fat	✓	No	✓	
Protein	✓	Implemented	✓	
Udder morphology	✓		✓	✓
Cell score	✓			

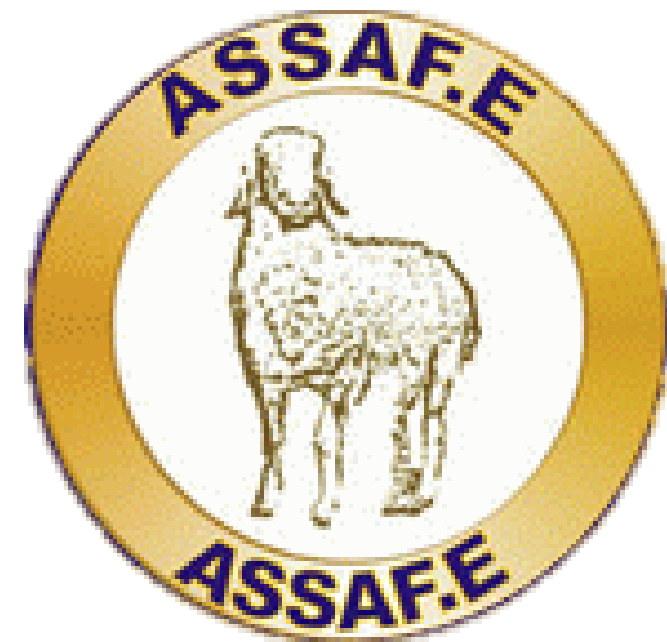
## ssGBLUP

# Genomic selection: Benefits



**ASSAF**

Increase of prediction accuracy of milk yield genomic values



Methodology N= 1.024	Bias	Slope	Accuracy
Pedigree (P)	3,99	0,899	0,769
Genomic (G)	7,17	0,855	0,787
Difference (G-P)			<b>0,018 (2,34%)</b>

# Genomic selection: Benefits



LATXA

Increase of prediction accuracy of milk yield genomic values



Breed	Methodology	Bias	Slope	Accuracy
LCNEUS 1571	Pedigree	4.20 ± 7.75	0.88 ± 0.16	0.57 ± 0.08
	Genomic	7.86 ± 5.43	0.79 ± 0.11	0.65 ± 0.07
	<b>G-P</b>	<b>3.66 ± 4.91</b>	<b>-0.09 ± 0.11</b>	<b>0.08 ± 0.05 (14 %)</b>
LCR 1695	Pedigree	21.85 ± 9.12	0.59 ± 0.13	0.48 ± 0.09
	Genomic	23.37 ± 6.43	0.56 ± 0.08	0.55 ± 0.07
	<b>G-P</b>	<b>1.51 ± 5.77</b>	<b>-0.03 ± 0.09</b>	<b>0.07 ± 0.05 (14 %)</b>
LCNNAF 645	Pedigree	7.76 ± 6.59	1.02 ± 0.18	0.63 ± 0.12
	Genomic	8.97 ± 8.10	1.00 ± 0.20	0.66 ± 0.12
	<b>G-P</b>	<b>1.21 ± 6.98</b>	<b>-0.02 ± 0.17</b>	<b>0.03 ± 0.08 (5 %)</b>



# Genomic selection: Benefits



**MANCHEGA**

Increase of prediction accuracy of milk yield genomic values



Breed	Methodology	Accuracy
Manchega 5256	Pedigree	0.54
	Genomic	0.59
	<b>G-P</b>	<b>0.05 (9 %)</b>



Increase of prediction reliability of milk yield genomic values

	Assaf		Latxa*		Manchega*	
	BLUP	ssGBLUP	BLUP	ssGBLUP	BLUP	ssGBLUP
Rams with progeny	56	56	63	64	70	70
Rams with progeny + geno	62	<b>70</b>	77	<b>79</b>	87	<b>89</b>
Ewes with lactations	43	43	63	63	60	60
Ewes with lactations + geno	50	<b>61</b>	72	<b>75</b>	63	<b>66</b>
Young rams	30	30	27	41	30	30
Young rams + geno	30	<b>48</b>	52	<b>60</b>	35	<b>48</b>
Young ewes	30	30	23	35	30	30
Young ewes + geno	30	<b>49</b>	53	<b>58</b>	30	<b>40</b>

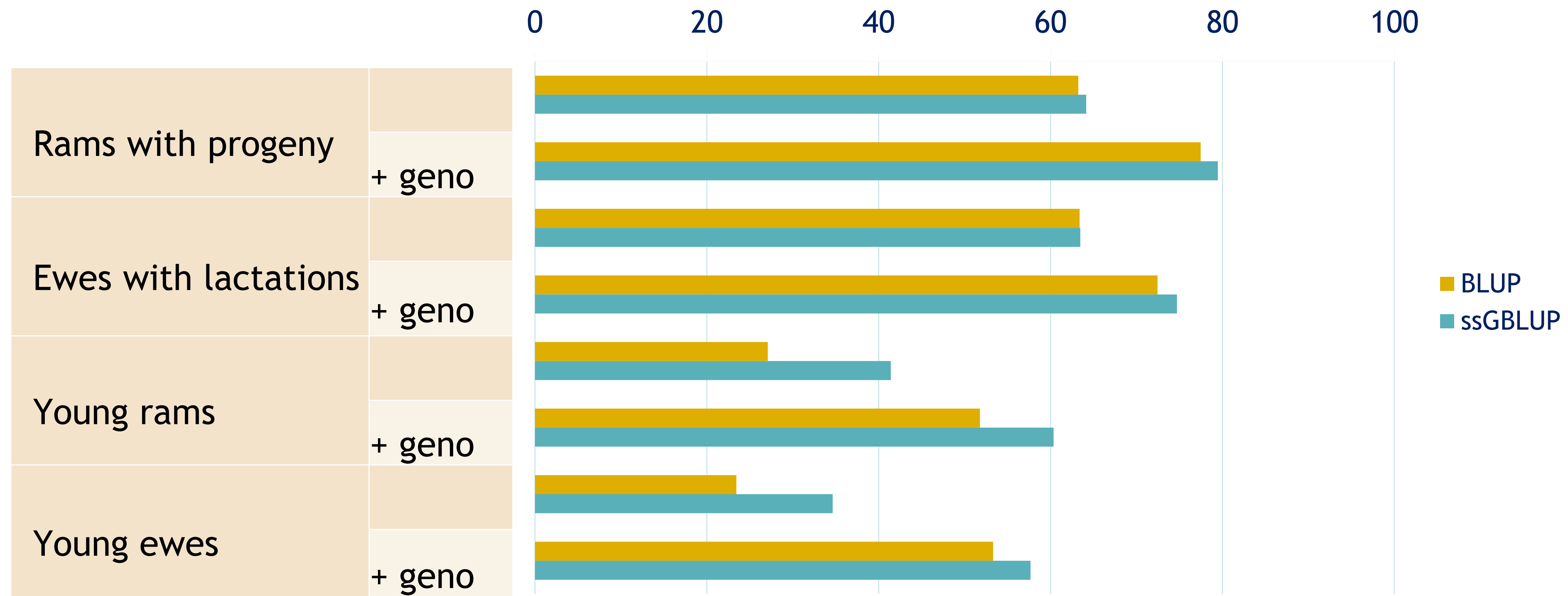
\* Mean results for Latxa Cara Negra from Euskadi and Latxa Cara Rubia

\* For Manchega breed test-day methodology is used

# Gebomic selection : Benefits



Increase of prediction reliability of milk yield genomic values





Evaluations with higher reliability are obtained for:

- Rams with a lower number of progeny
- Ewes with less lactations

Selection decisions are taken earlier → decrease of generation interval

## Classic BLUP evaluation, 60 % of reliability:

- Rams with 14 progeny data
- Ewes with 5-6 lactations

## Genomic BLUP evaluation, 60 % of reliability:

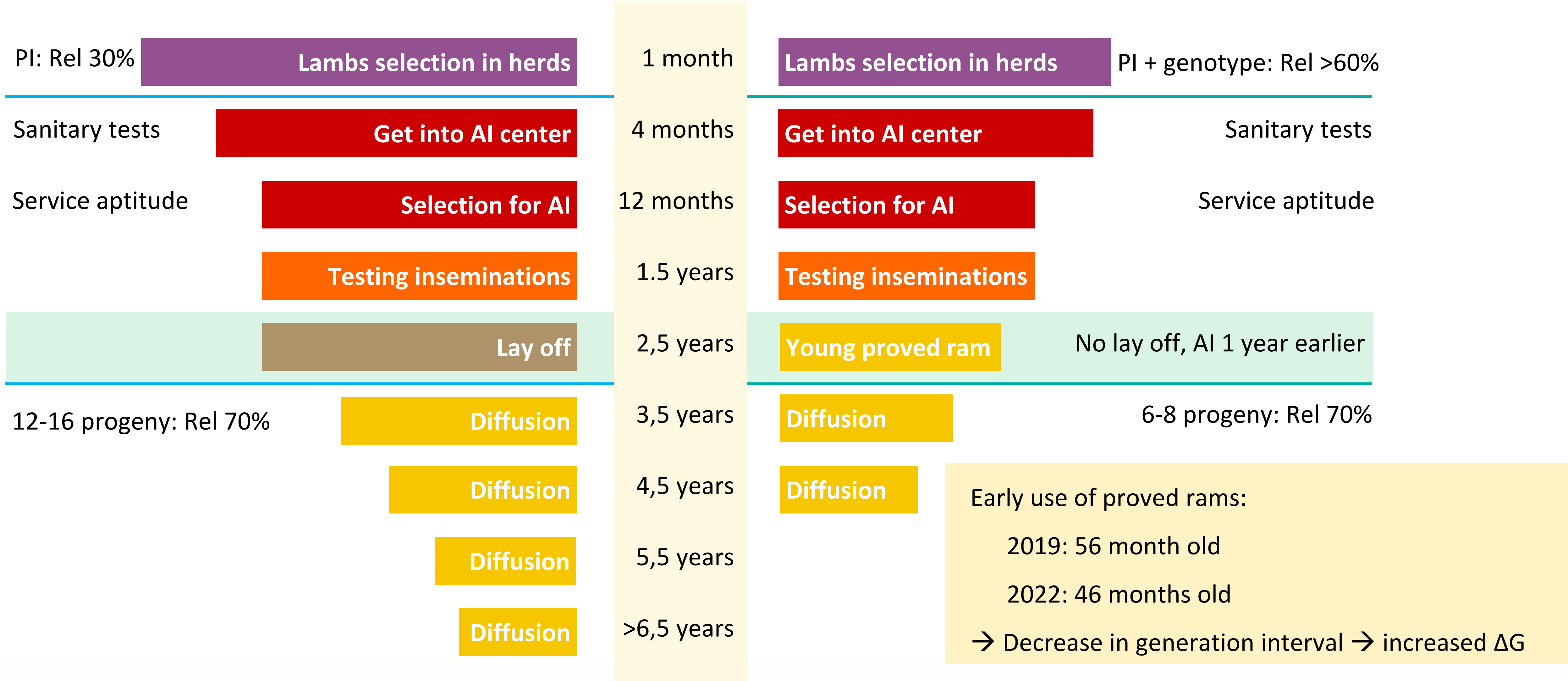
- Rams with 5 progeny data
- Ewes with 2-3 lactations

# Genomic selection: Benefits



## GENETIC EVALUATION

## GENOMIC EVALUATION



# Genomic selection: Benefits



It is possible to **distinguish full sibs** with the same pedigree index by BLUP evaluation, when their **genomic information** is added (mendelian deviation is considered) and thus better breeding decisions could be taken

Individual	Sire	Dam	Year of birth	Sex	Herd	BLUP	Reliability	ssGBLUP	Reliability
CHR210013	CHR190692	CHR190440	2021	M	CHR	86.004	19	<b>116.538</b>	42
CHR210014	CHR190692	CHR190440	2021	M	CHR	86.004	19	94.522	42
STG210174	STG190103	STG170004	2021	M	STG	82.109	21	<b>128.597</b>	42
STG210169	STG190103	STG170004	2021	M	STG	82.109	21	84.729	42
STG210170	STG190103	STG170004	2021	M	STG	82.109	21	99.071	42
SJT213099	DGM140956	SJT160049	2021	M	SJT	97.416	37	<b>171.222</b>	51
SJT213089	DGM140956	SJT160049	2021	M	SJT	97.416	37	108.703	51
JMR210050	TRR172095	JMR200027	2021	H	JMR	75.371	28	<b>124.687</b>	48
JMR210016	TRR172095	JMR200007	2021	H	JMR	75.371	28	106.181	48



# Future perspectives and challenges

## Future perspectives: Profitability

- The cost of genotyping platforms could be profitable?
- Do the increase in genetic gain make up for the genotyping cost?
- Low density platforms are more economical
- Genotyping platforms that allow **unifying several analysis** like filiation, scrapie and genomic evaluation
- Incorporation of **new characters** (fertility, illness resistance, longevity, rusticity, adaptation to global warming...) which improvement could make profitable the cost of genotyping platform



## Implementation challenges: Methodological

- **Mistakes in genealogy**

Based on genotypic information (SNPs) pedigree mistakes from microsatellites analysis could be revealed

**which should be the inconsistency threshold allowed?**

- **Unknown parent groups**

To model missing pedigree they work well on classic BLUP evaluations, but they are

**more problematic in genomic BLUP evaluations**

- **Direct genomic value**

Based on the pedigree index and the estimated SNP effects from genomic evaluations

**how reliable are this values?**

## Implementation challenges: Methodological

- **Inflation of genomic values**

it is found especially in selection candidates. The cause is not known, and currently it is being managed by the scaling of G and A matrixes

*Proc. Assoc. Advmt. Anim. Breed. Genet. 19:359-362*

### CHOICE OF PARAMETERS FOR REMOVAL OF INFLATION IN GENOMIC BREEDING VALUES FOR DAIRY CATTLE

Choice of parameters for single-step genomic evaluation for type.

A. Legarra<sup>3</sup>, and T. J. Lawlor<sup>4</sup>. <sup>1</sup>University of Georgia, Athens, GA; <sup>2</sup>INIA, Las Brujas, Uruguay; <sup>3</sup>INRA, 32326 Castanet-Tolosan, France; <sup>4</sup>Holstein Association, Brattleboro, VT 05302.

Martini et al. Genet Sel Evol (2018) 50:16  
<https://doi.org/10.1186/s12711-018-0386-x>

GSE Genetics Selection Evolution

SHORT COMMUNICATION

Open Access



The effect of the  $\mathbf{H}^{-1}$  scaling factors  $\tau$  and  $\omega$  on the structure of  $\mathbf{H}$  in the single-step procedure

Johannes W. R. Martini<sup>1\*</sup>, Matias F. Schrauf<sup>2†</sup>, Carolina A. Garcia-Baccino<sup>2†</sup>, Eduardo C. G. Pimentel<sup>3</sup>, Sebastian Munilla<sup>2,4</sup>, Andres Rogberg-Muñoz<sup>2,5</sup>, Rodolfo J. C. Cantet<sup>2,6</sup>, Christian Reimer<sup>7</sup>, Ning Gao<sup>7,8</sup>, Valentin Wimmer<sup>1</sup> and Henner Simianer<sup>7</sup>

- **Imputation from low density platforms to medium and high density**

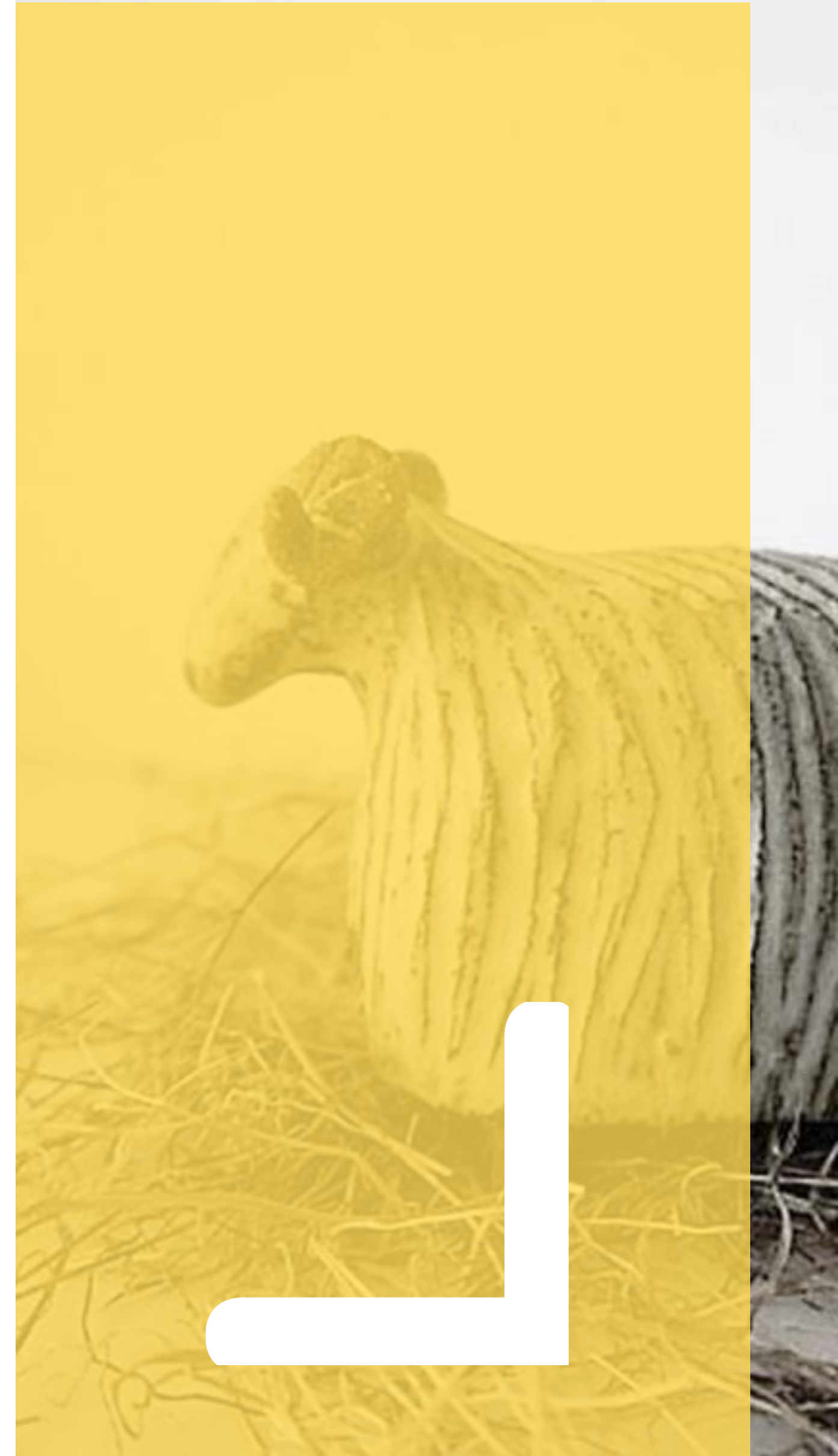
It is based on the existence of linkage disequilibrium (LD) between SNPs. In sheep breed the LD is very low, thus

**the imputation is highly inefficient**

## Implementation challenges: Organizational



- **Reference population: number and type of genotyped animals**
- **Changes on selection scheme**
  - Selection of animals to enter to IA centre (genotype more animals, ¿how many?)
  - Combine genotype for the program/genotype for de farmer
  - Time, chronology and speed in obtaining genotyping
  - .....
  - **Advice to technicians and farmers**



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M<sup>a</sup> Ángeles Jiménez  
Malena Serrano



ASOCIACIÓN NACIONAL DE CRIADORES DE  
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DE RAZA CHURRA

Roberto Gallego  
Manuel Ramón



Asociación Nacional de Criadores de  
Ganado ovino Selecto de Raza Manchega

Lourdes Mintegui  
Itsasne Granado  
Eva Ugarte



CONFEDERACIÓN DE ASOCIACIONES DE CRIADORES  
DE OVINO DE RAZAS LATXA Y CARRANZANA.



Thank you

