

# MARKER ASSISTED SELECTION FOR MILK PRODUCTION AND QUALITY TRAITS IN CHURRA DAIRY SHEEP

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# SELECTION OF CHURRA SHEEP

## AI-Driven Selection Schema.

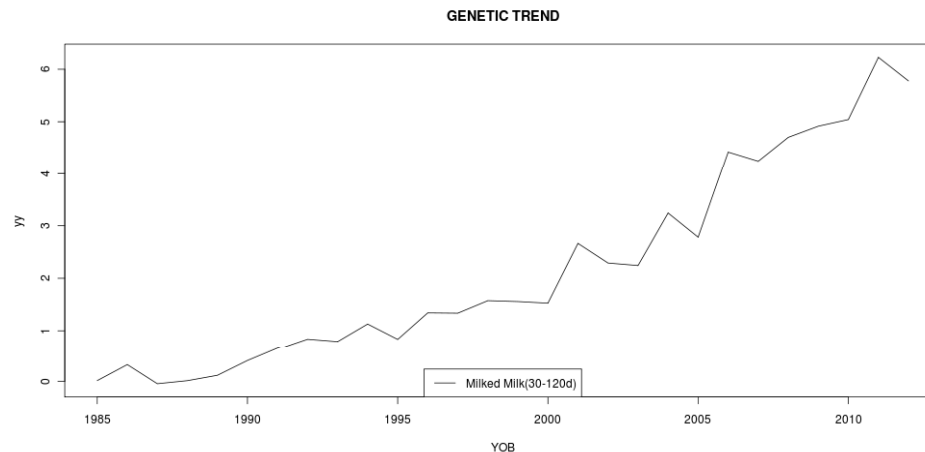
### 2011 Evaluation

77 herds

60,816 Animals with genetic index

553 AI rams (90 born after 2009 (40-33-17))

$$I=0.5*MY+0.2*PP+0.05*NBA+0.25*Morf$$



Milk Trend 1990-2010  
~ 300 ml/year  
Average (133 L.)

MY Average ACC of rams  
to be tested: ~ 0.25

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# Genomic Selection / MAS

1.- Increase rate of genetic progress

2.- New traits as selection criteria

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## OBJECTIVE

**Could the current available information in Churra sheep be used for implementing a successful selection procedure considering molecular information?**

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## January 2011 MT Genetic Evaluation

	Ave.	S.D.	N	h <sup>2</sup>	r <sup>2</sup>
<b>MY</b>	1,017.8	538.1	1,125,728	0.09	0.27
<b>PP</b>	5.7	0.8	435,255	0.17	0.26
<b>FP</b>	6.7	1.9	435,255	0.05	0.11
<b>PY</b>	59.7	27.0	435,255	0.09	0.26
<b>FY</b>	68.8	33.7	435,255	0.07	0.20
<b>SCS</b>	5.4	0.7	381,554	0.06	0.25

$$YD = Z'(y - X\hat{\beta} - Z\hat{p})(Z'Z)^{-1}$$

$$W_i = \frac{(1 - h^2) * n_i}{((1 + (n_i - 1)) * r^2) - h^2}$$

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## Genotypes

### *Illumina Ovine SNP50 BeadChip*

AROS Applied Biotechnology AS (Aarhus, Denmark)

LABOGENA (Jouy-en-Josas, France)

52,510 autosomic SNPs

1,650 animals

### *Quality Control*

Intra-locus verifications according to pedigree and gene frequency computation.

Not considered SNPs

- 1.- Missing in more than 5% of the individuals.
- 2.- MAF < 0.05
- 3.- Lack of H-W equilibrium (p-value<0.00001)

Retained: 43,779 SNPs

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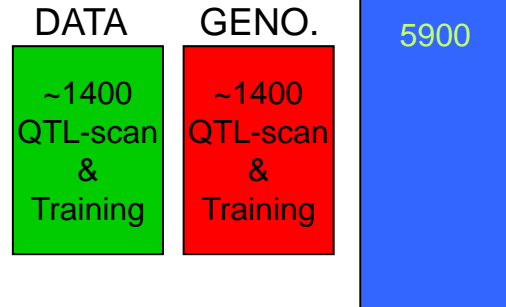
## MAS

(Boichard et al., 2012)

### 1.- QTL detection in each position

$$YD = 1\beta + Z_i u + Z_{qtl} q + e$$

$$Var(YD) = Z_i G Z_i' + Z_{qtl} Q Z_{qtl}' + D$$



$Z_{qtl}$  → 0, 1 or 2. Indicating, for each YD, the QTL alleles carried by the animal

$Q$  → IBD Probability between each pair of QTL alleles.

LDLA (Druet et al., 2008; Meuwissen and Goddard, 2001)

LD (No pedigree information was considered)

LA (0 generations since the mutation appears)

LRT → Type I error 0.05

The strongest associated within a window of 4 Mbp

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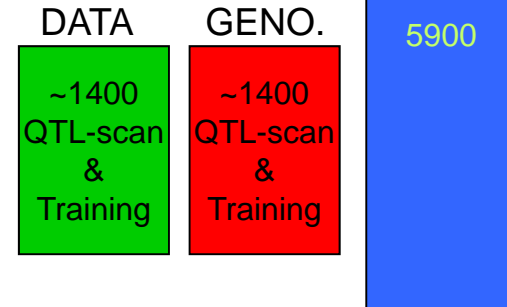
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# MAS (Boichard et al., 2012)

## 2.- TRAINING

$$YD = 1\beta + Z_i u + \sum_{j=1}^{N_{qtl}} Z_{qtl,j} q_j + e$$

$$Var(YD) = Z_i G Z_i' + \sum_{j=1}^{N_{qtl}} Z_{qtl,j} I_j Z_{qtl,j}' + D$$



Sum over all QTL-declared positions

Length of  $q_j$  number of distinct 6-SNPs IBS haplotypes around each QTL-declared position.

$I_j$  Identity matrix of dimension equal to the length of  $q_j$



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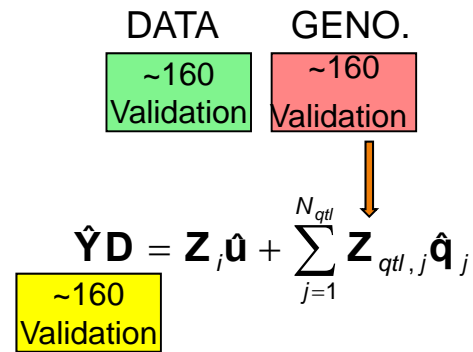
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# MAS

(Boichard et al. 2012)

## 3.- VALIDATION



## WEIGHTED CORRELATION

OBSERVED DATA

~160  
Validation

PREDICTED DATA

~160  
Validation

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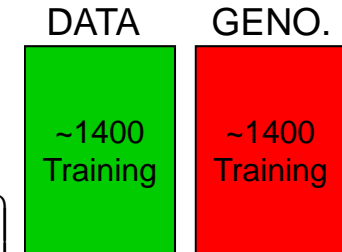
# EN (Elastic Net) (Friedman et al., 2010)

## 1.- TRAINING

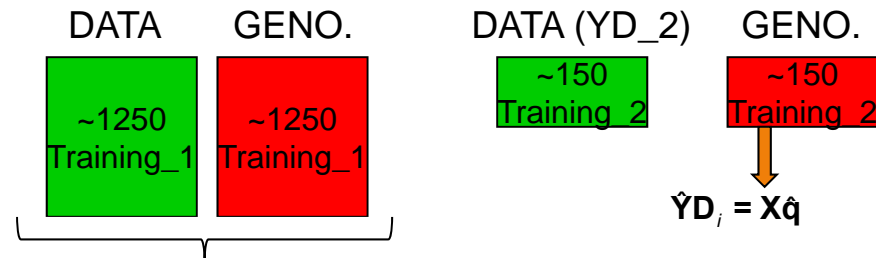
$$YD = Xq + e$$

$$q = \operatorname{argmin} \left\{ \sum_{i=1}^N (YD_i - \mathbf{x}'_i \mathbf{q}) + \lambda \left( (1 - \alpha) \sum_{j=1}^{N_{snp}} \frac{q_j^2}{2} + \alpha \sum_{j=1}^{N_{snp}} |q_j| \right) \right\}$$

$$\alpha = 0.9$$



Training Data was split to identify the optimal value for  $\lambda$



$$\lambda_1 \rightarrow \mathbf{q}_1 \rightarrow \rightarrow \rightarrow \rho_1$$

$$\lambda_2 \rightarrow \mathbf{q}_2 \rightarrow \rightarrow \rightarrow \rho_2$$

.

.

$$\lambda_z \rightarrow \mathbf{q}_z \rightarrow \rightarrow \rightarrow \rho_z$$

$\rho_i$  correlation between  $\hat{YD}_i$  and YD\_2

Selected  $\mathbf{q}_i$  will be that maximizing  $\rho$

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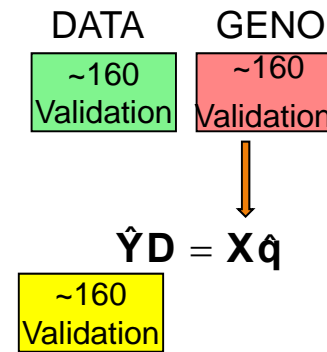
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EN

(Friedman et al.,2010)

## 2.- VALIDATION



## WEIGHTED CORRELATION

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# ONE-Step (Aguilar et al., 2010)

## 1.- TRAINING – PREDICTION

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \alpha H^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

$$H = A + A_J$$

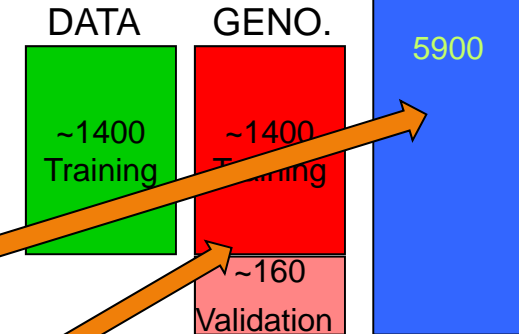
$A$  - conventional numerator relationship matrix

$A_J$  - matrix modified to account for genomic relationships

$$A = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{bmatrix} \quad H = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & G \end{bmatrix}$$

$$A_{\Delta} = \begin{bmatrix} 0 & 0 \\ 0 & G - A_{22} \end{bmatrix}$$

1 - ungenotyped    2 - genotyped



## 2.- VALIDATION

### WEIGHTED CORRELATION

OBSERVED DATA

~160  
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PREDICTED DATA

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Validation

$$\hat{Y}D = \hat{u}$$

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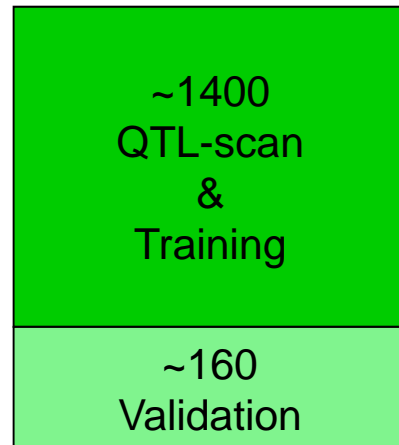
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# 10-Fold Cross Validation

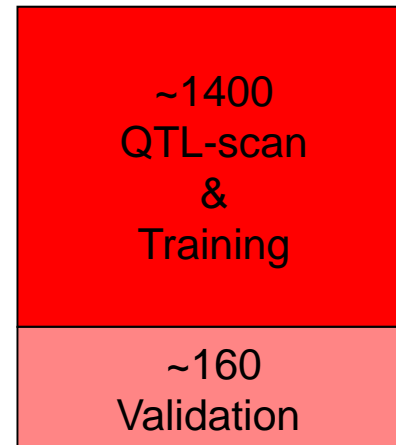
1 fold...

PEDI.

DATA



GENO.



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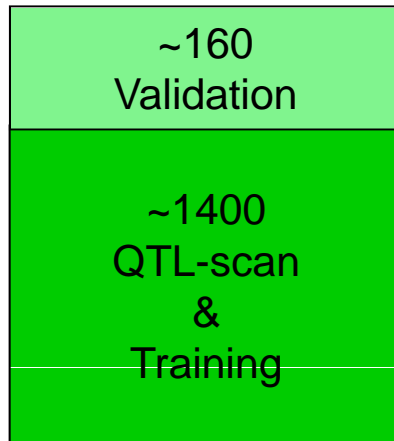
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# 10-Fold Cross Validation

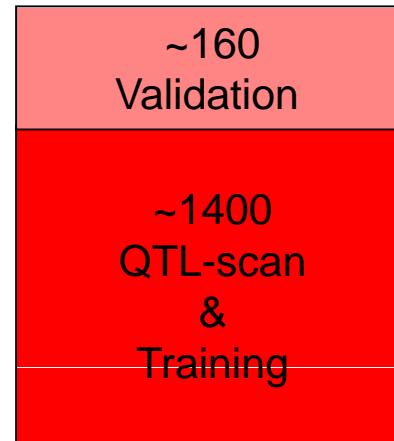
2 fold...

PEDI.

DATA



GENO.



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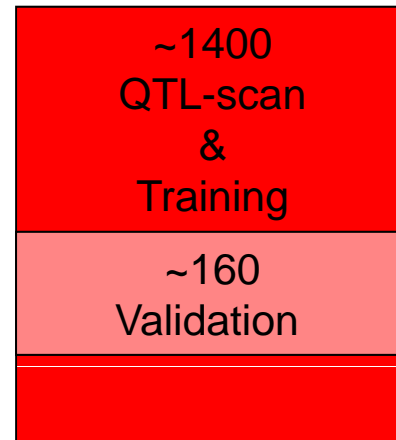
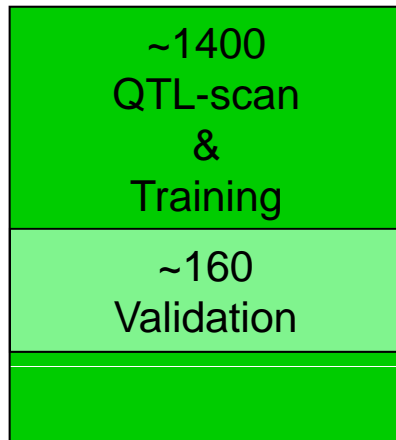
# 10-Fold Cross Validation

10 fold...

PEDI.

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GENO.



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# ACCURACY

## Weighted correlation $YD_{pre} - YD_{obs}$

T	PED	ONE-Step	EN	LDLA	LD	LA
MY	* 0.34(0.03)	<b>0.37(0.05)</b>	0.30(0.05)	0.27(0.04)	0.27(0.04)	0.28(0.07)
PP	0.46(0.06)	<b>0.53(0.06)</b>	<b>0.51(0.07)</b>	<b>0.49(0.06)</b>	<b>0.49(0.05)</b>	0.4(0.04)
FP	0.33(0.05)	<b>0.38(0.04)</b>	0.32(0.07)	0.29(0.06)	0.31(0.05)	0.28(0.05)
PY	0.21(0.07)	<b>0.26(0.09)</b>	0.17(0.07)	<b>0.24(0.06)</b>	<b>0.24(0.06)</b>	0.18(0.08)
FY	0.27(0.08)	<b>0.32(0.07)</b>	0.25(0.1)	0.23(0.1)	0.22(0.08)	0.18(0.09)
SCS	0.42(0.08)	<b>0.46(0.08)</b>	<b>0.43(0.08)</b>	0.37(0.06)	0.38(0.07)	0.37(0.08)

\* Average(SD)



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## PERCENTAGE OF GAIN IN ACCURACY WITH RESPECT TO PED

T	ONE-Step	EN	LDLA	LD	LA
MY	*7.6(15.27)-7	-12.2(17.6)-2	-21.3(8.54)-0	-22.7(7.41)-0	-20.4(16.75)-1
PP	14.4(6.4)-10	10.2(8.18)-8	6.3(15.09)-6	7.2(13.1)-7	-12.6(8.14)-1
FP	16.3(14.75)-9	-2.9(20.53)-5	-9.3(18.29)-3	-5.6(18.75)-3	-13.2(15.52)-2
PY	33.4(50.54)-8	-11.2(39.9)-3	32(70.03)-4	31.7(78.26)-5	-1(57.78)-3
FY	24.6(32.44)-9	-1.7(42.67)-4	-11.2(42)-4	-11.5(39.15)-4	-33.3(28.23)-2
SCS	9.8(6.68)-9	1.4(7.85)-5	-11.5(10.87)-2	-10.6(10.66)-3	-12.6(12.74)-2

\* Average(SD) - # of times being positive

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# NUMBER OF POSITIONS SYSTEMATICALLY DECLARED AS QTL

## average(across-replicates) effect

	LDLA		LD		LA	
Trait	M_10	effect	M_10	effect	M_10	effect
MY	3	7.5	2	4.5	0	0
PP	9	31.8	8	29.6	0	0
FP	4	9.1	5	11.7	0	0
PY	8	22.7	8	22.9	1	15.1
FY	6	18.6	6	20.2	1	12.2
SCS	3	8.4	5	14.5	1	18.1

OAR2 (2204, 3548)  
 OAR3 (1669, 2593, 2606, 2802)  
 OAR6 (1584, 1585)  
 OAR14 (220)

OAR2 (754)  
 OAR3 (159)  
 OAR4 (1293, 1298)  
 OAR5 (1526)  
 OAR14 (893)  
 OAR18 (311)  
 OAR19 (949)

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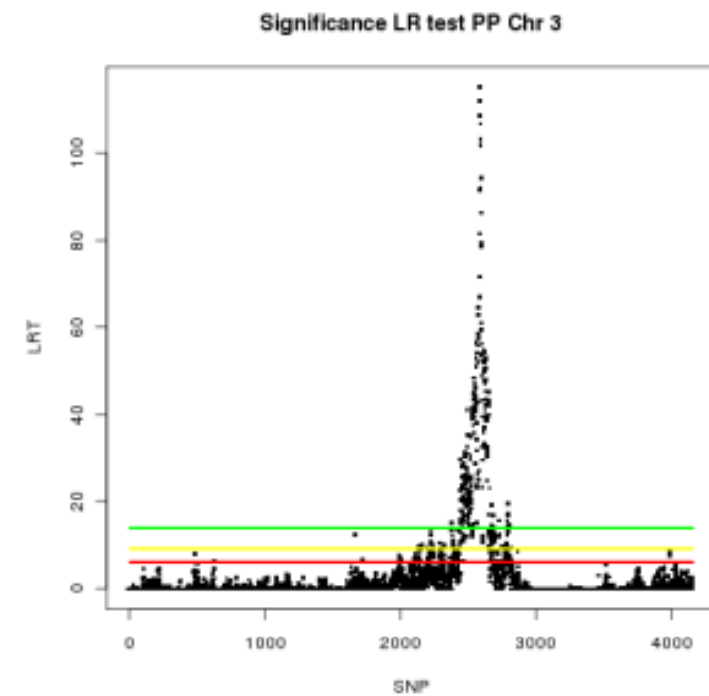
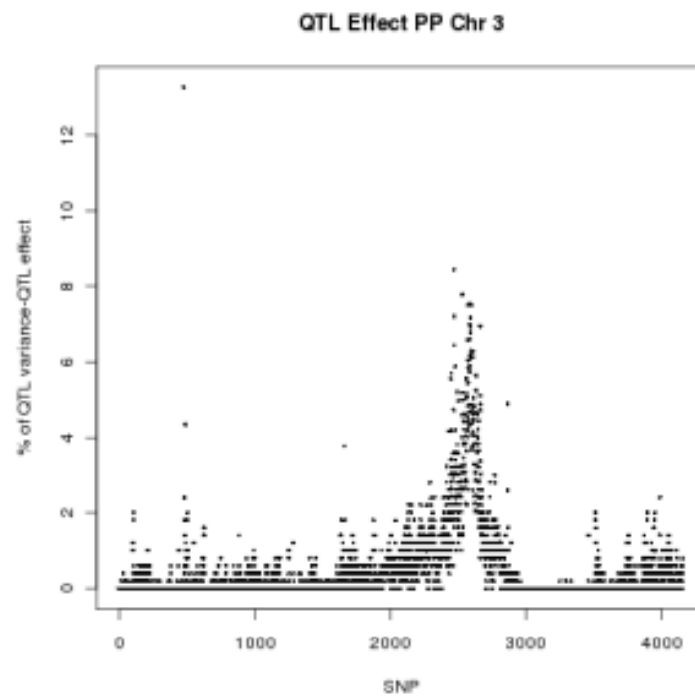
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# LDLA LRT profile CHROMOSOME 3 - PP



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**1.- Relevant gains in accuracy can be achieved for some traits when considering molecular information.**

**2.- ONE-step method provided positive results independently of trait.**

**3.- MAS only showed positive results for traits controlled by QTLs which were properly detected. This only can be done when considering LD information during the analysis.**

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