

QTL detection for traits of interest for the dairy goat industry

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Sustainable Solutions for Small Ruminants

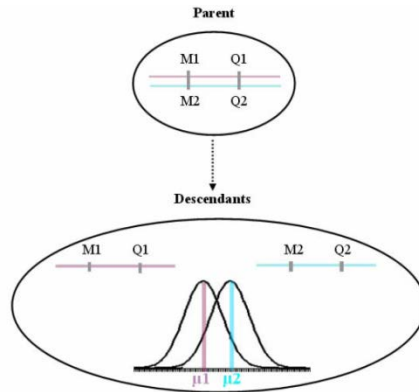
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PhénoFinlait

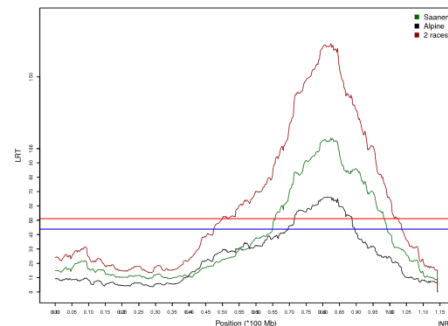
This presentation focuses on the first QTL detection in dairy goats with the recent released international 50k goat chip



QTL design and international goat chip



QTL detection methods

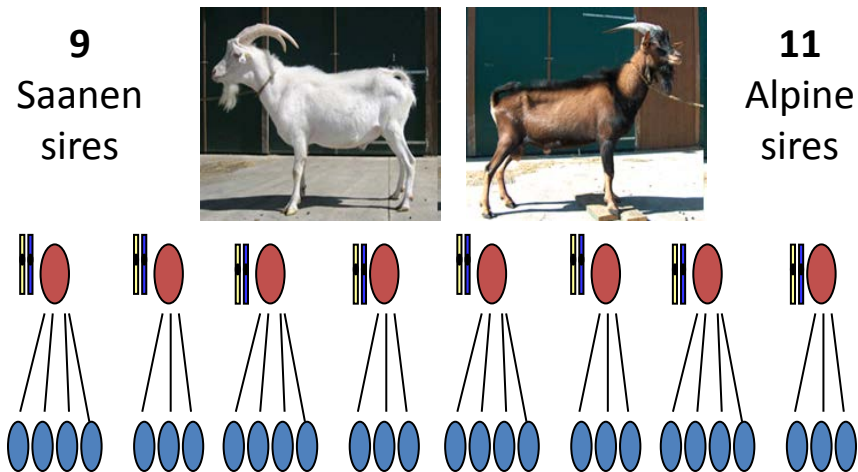


Some important QTL results

The EU “3SR” and French “PhénoFinLait” programs permit the development of a large French QTL design

Daughter QTL design

- ✓ 2 breeds ; 170 herds
- ✓ ≈ 115 daughters/sire
- ✓ 2 246 phenotyped and genotyped females



Traits

- ✓ **Production** (Milk, PC, PY, FC, FY, LSCS)
- ✓ **Morphology** (11 traits)
- ✓ **Fatty acids**: 20 individuals or groups in 2 units (/100g milk fat; /100g milk)

BLUP
genetic evaluation



Yield deviations
performances adjusted for fixed effects

49 663 SNP of the Illumina goat beadchip validated by the marker quality control

Marker quality control

- ✓ Illumina goat chip : **53 347** SNPs
- ✓ Mapped on **29** chromosomes

	53 347 SNP
Call frequency (< 0.99)	1 964
Hardy Weinberg (5%)	532
Minor allele frequency (<1%)	1 337

➔ **49 663 SNP** (*3 684 SNP removed*)

Linkage analyses and linkage disequilibrium were applied on yield deviations of 57 traits

Linkage Analysis (LA)

- ✓ interval mapping
- ✓ within-sire linear regression (Elsen et al., 1999)

Linkage Disequilibrium (LD)

- ✓ haplotypes of 4 consecutive SNP
- ✓ regression analysis of the phenotypes on founders' haplotypes (Legarra et Fernando 2009)

- ✓ **Likelihood Ratio Test : $LRT=2[\log(L1)-\log(L0)]$**

L1= likelihood under H1 (QTL effect)

L0= likelihood under H0 (no QTL effect)

→ Chromosome- and genome-wise significance thresholds

Permutation tests

Simulation tests

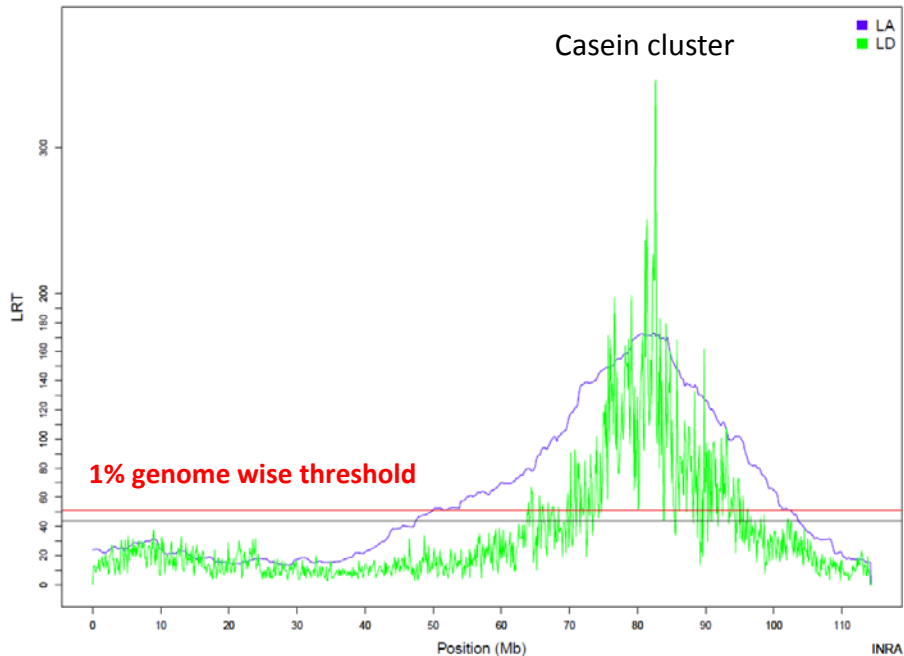
- ✓ **Bonferroni correction : $p_{exp}=1-(1-p_{value})^n$**

*n=(18 independent traits*29 chromosomes)*

QTLmap software

2 QTL of major effect were found in regions of Caseins and DGAT1

QTL for Protein Content on CHI 6

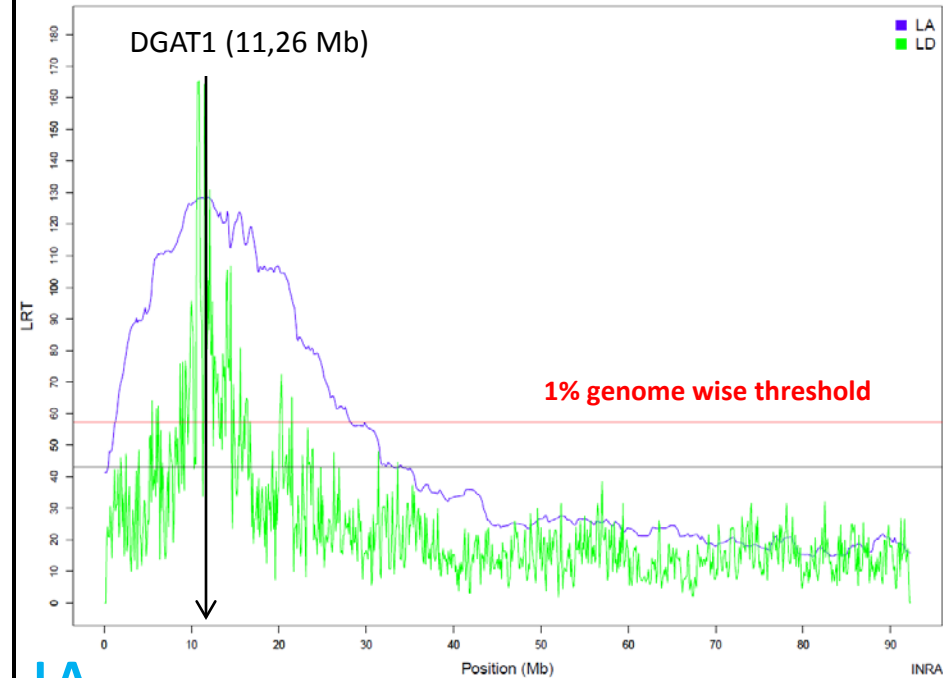


LA

- ✓ QTL substitution effect from 0.58 to 0.67
- ✓ Confidence interval of 5.5 Mb
- ✓ 2/3 significant families

LD ✓ Confidence interval of 200Kb

QTL for Fat Content on CHI 14



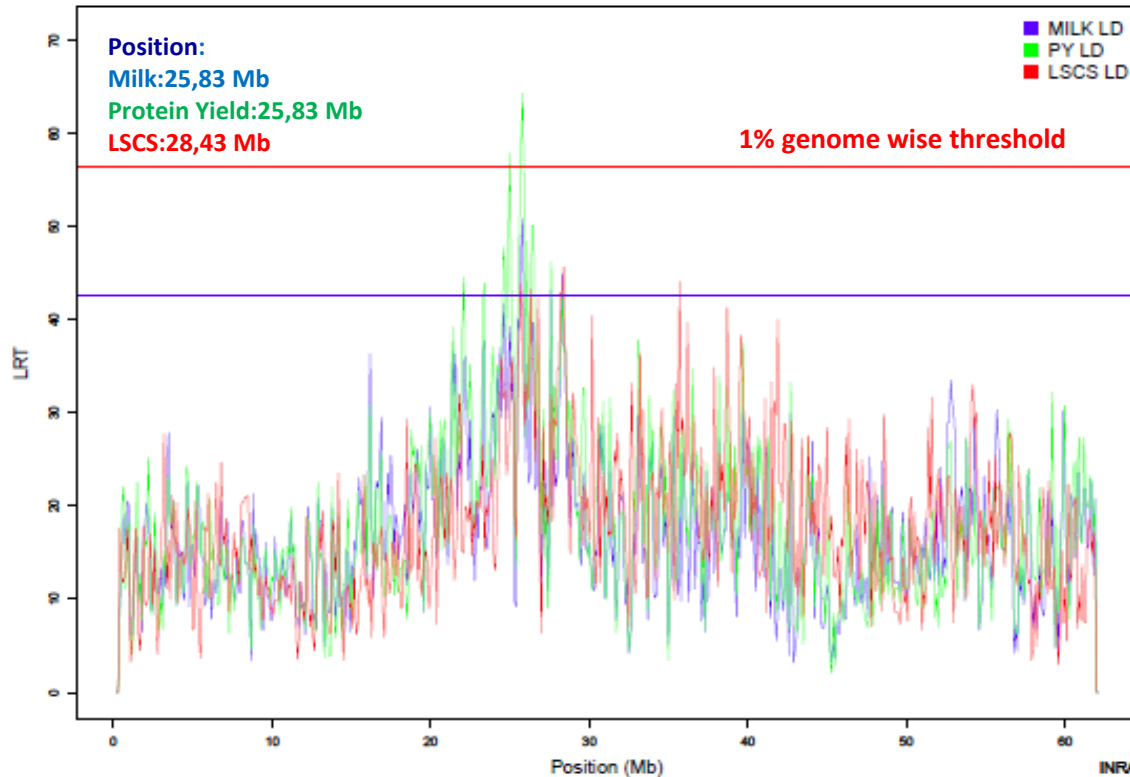
LA

- ✓ QTL substitution effect from 0.48 to 0.58
- ✓ Confidence interval of 5.2 Mb
- ✓ 2/3 significant families

+FA QTLs in Alpine breed (C6:0-C16:0)

Important QTL cluster of 15Mb for different production and morphology traits on CHI19

LD LRT profil for LSCS, milk and protein yield

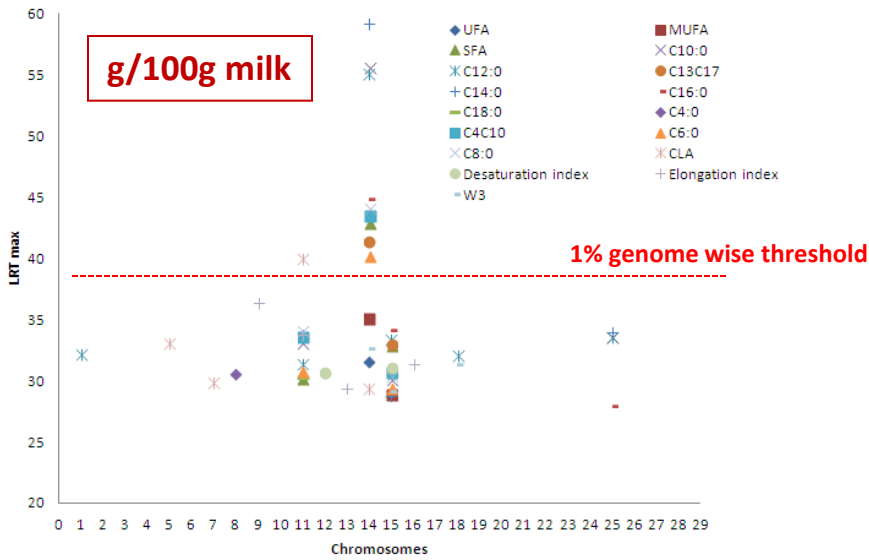


LA

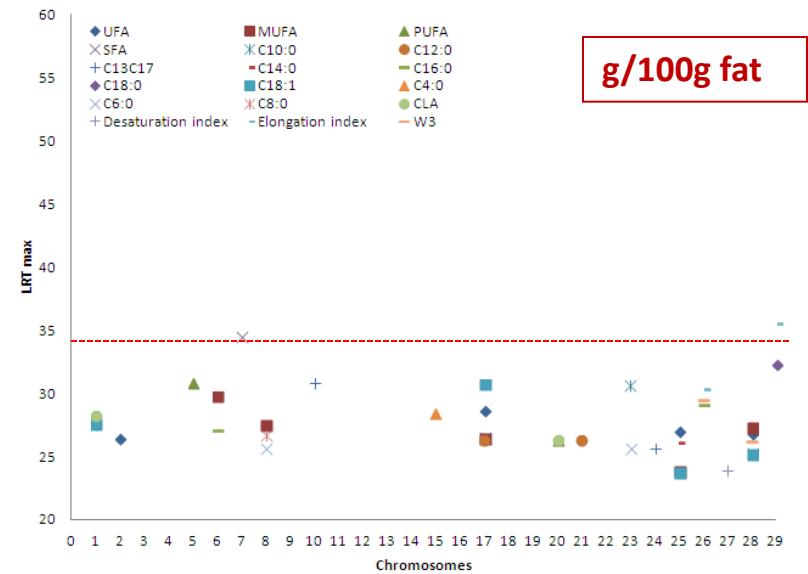
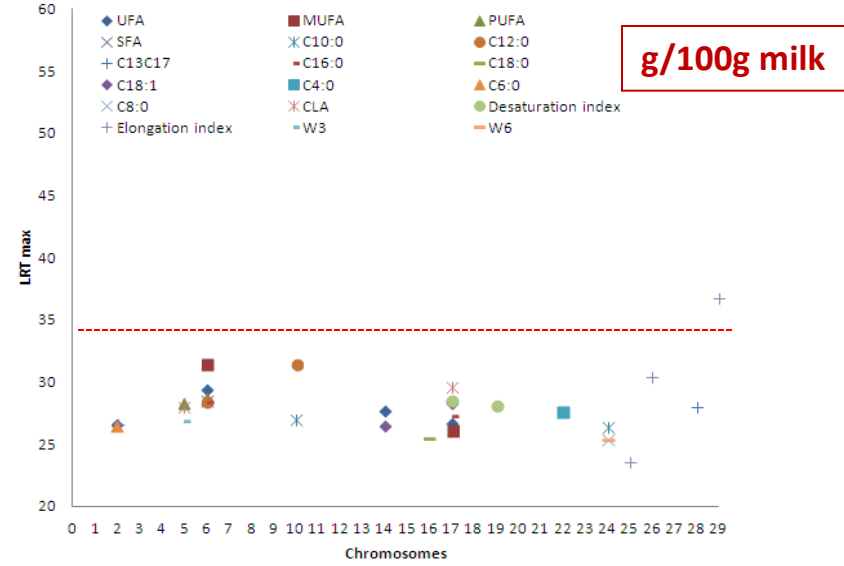
- ✓ Traits : heart girth, FY, PY, udder floor position, MY, Rear udder attachment, Udder profil, Teat length, LSCS
 - ✓ QTL substitution effect from 0.36 to 0.53
 - ✓ 2/3 significant families
- Orthology with LSCS QTL on OAR11 in ovine

FA QTLs seemed to be breed-specific in both units

LA results in Alpine



LA results in Saanen



In summary, many regions of the genome controlling traits of interest in dairy goat were detected with some evidence of major genes for protein and fat yield

- ✓ 1st QTL results in dairy goats with the 50K SNP beadchip
- ✓ Lots of QTL detected
- ✓ Known region and new regions of interest
- ✓ Apparent breed specificities

On going researches: -Fine mapping and characterisation of DGAT1



Sustainable Solutions for Small Ruminants

PhénoFinlait

Thank you for your attention



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*avec la contribution financière du
compte d'affectation spéciale
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International Goat Genome Consortium



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