Fine Mapping of Quantitative Trait Loci for Pig Meat Quality Traits

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FOOD & NUTRITION
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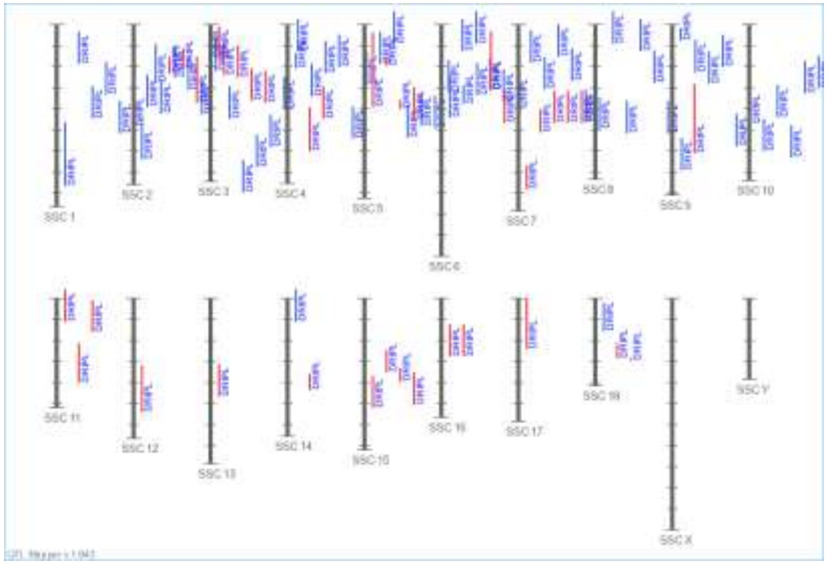
Background

- 6344 QTL are reported for all traits in pig
- 4434 QTL for meat quality traits
- 945 (!) for drip loss



(PigQTLdb, August 2011)

QTL and selection

- Very few QTL used in breeding schemes
  - Limited precision for location ?
  - Economic importance ?

- Need to refine QTL location
  - characterizing SNPs associated with quality traits using 60K chip

Experimental design

56 French Large White boars

x

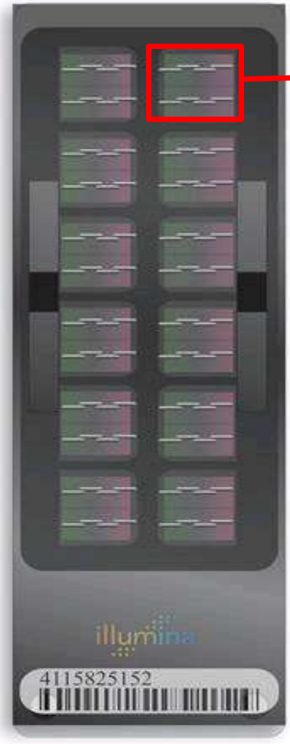
98 French Large White sows

580 entire male piglets reared in INRA experimental farm till 110 kg

Phenotypes and Genotypes

15 traits:

- ADG
- Backfat Thickness
- Lean Meat Content
- Dressing %
- Water Holding Capacity
- 6 color measures
- 4 ultimate pH measures



64000 SNPs for
1 animal

(1 chip = 12 animals)

428 piglets and sires were genotyped.

Statistical analyses

- Phenotypes were corrected for
  - fixed effect of slaughter date,
  - random effect of dam,
  - weight at slaughter as covariate.

- Genome-wide Association Study (GWAS)
  - To identify genomic polymorphisms associated with trait variation

Quality control

- SNPs were excluded in analysis for:
  - Genotype call rate below 95%
  - Individual call rate below 90%
  - Failing Hardy-Weinberg Equilibrium test (p <= 1e-05)
  - Minor Allele Frequency (MAF) < 0.05
- 42580 SNPs passed these filters

Genome-wide Association Study

- GRAMMAR-GC procedures in GenABEL

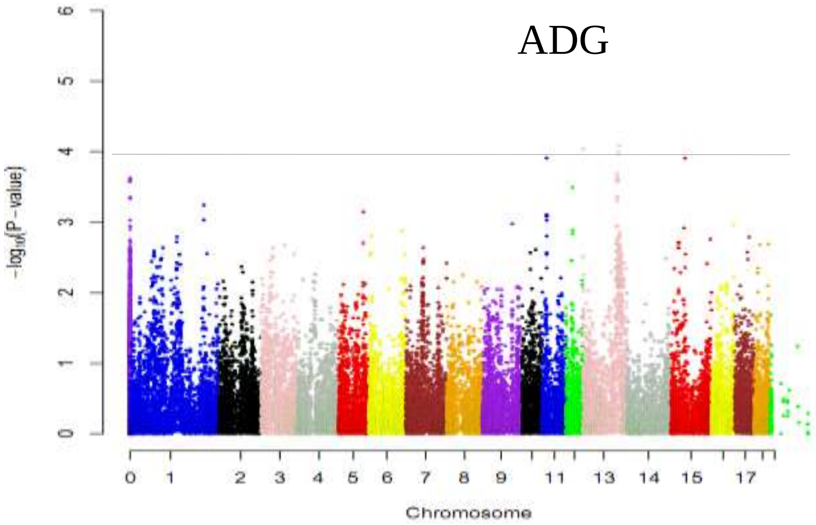
  Fast and powerful method for the analysis of pedigree-based quantitative traits.

1st step: individual environmental residuals are estimated, using a Mixed Model.

2nd step: markers are tested for association with these familial correlation-free residuals with a rapid score method.

3rd step: Genomic Control is applied to correct the test statistics.

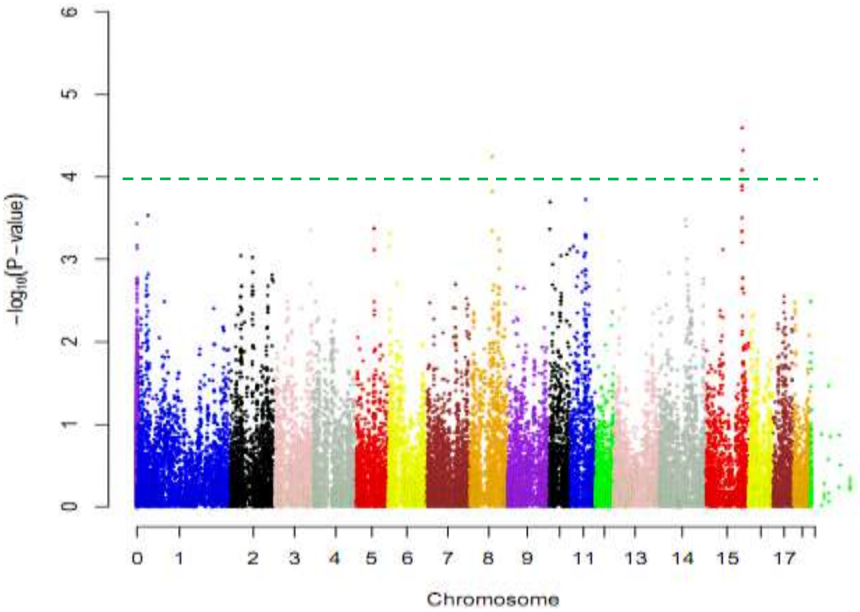
Results: growth and carcass



- ADG: 4 QTL
  - Most convincing = SSC13
- BT: 5 QTL
  - ?
- LMC: 2 QTL
  - Most convincing = SSC11
- Dressing %: 2 QTL
  - Most convincing = SSC12

Results: WHC

- 2 QTL, 1 on SSC15



Trait	SSC	SNP	Position (Mbp)
WHC	15	DRGA0015508	113.726097
	15	ALGA0087340	116.735371
	8	ASGA0039159	71.443924
	15	ALGA0087116	113.451557
	15	ALGA0087118	113.464523

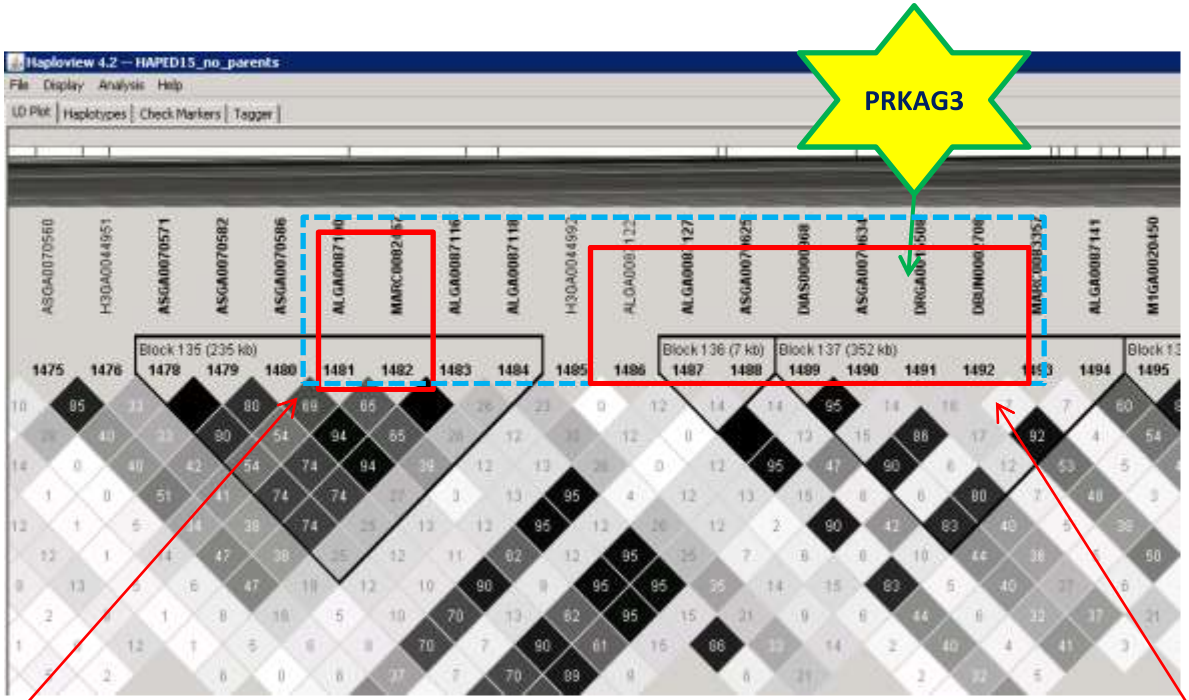
Results: color and pH

- 20 SNPs significantly affected 6 color and 18 SNPs affected pH measures.

- SSC15 contained the largest number of SNPs affecting both groups of traits in general.

Distal part of SSC15

7 SNPs affected WHC, b* and pH24



WHC & b*

WHC, b* and pH24

Conclusion

- GWAS proved to be a quick method to detect all associated markers but the correct threshold for livestock data remains a challenge.
- Many pork quality QTL still segregate throughout the genome of French Large White pigs.
- SSC15 is important for WHC, colour and pH24 measures.

- Further analyses :
  - LDLA is believed to improve QTL estimates
  - Haplotypes effects

Aknowledgements

- CNG
- UE (SABRE, Q-Porkchains)