

Mapping of QTL for feed intake traits in a back-cross between Large White and Piétrain pig breeds

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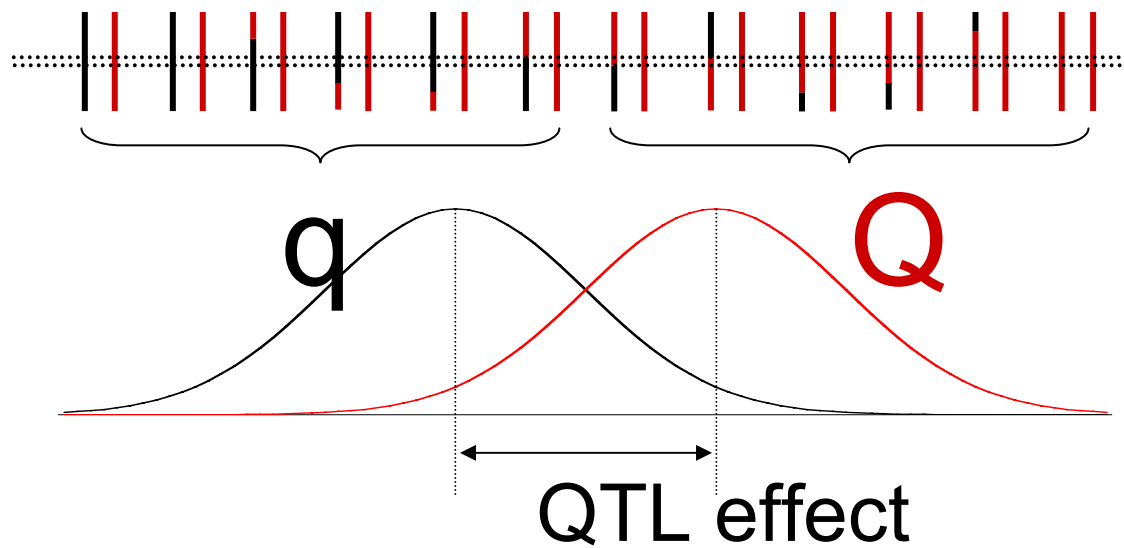


Rationale

Pietrain breeds show differences in voluntary feed intake (around 20 %) and, to a much lesser extent, in feed efficiency (Labroue et al. 1999)

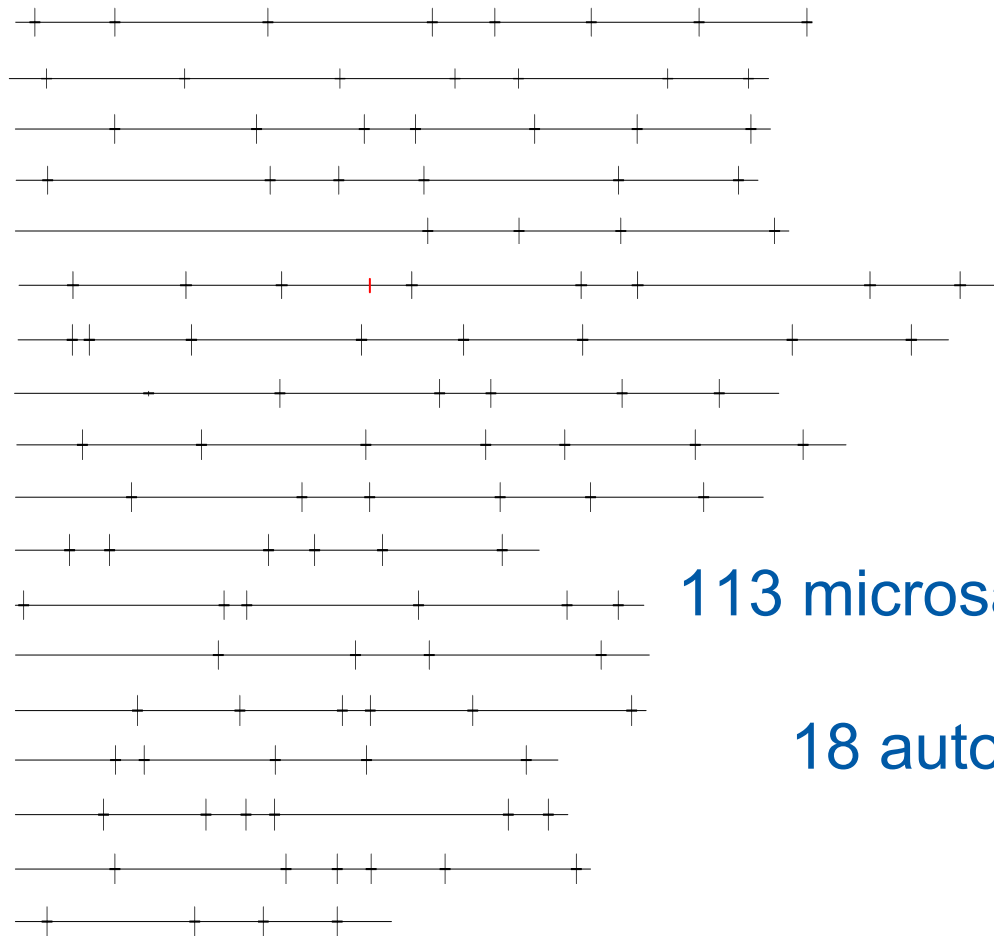
→ mapping loci involved in feed intake and feed efficiency

BC population



(GEPA, ROUILLE)

Genetic map & genotyping



113 microsatellites + HAL (SSC6, 79cM)

18 autosomes (SSC1 to SSC18)

1860 cM

Traits

Growth, feed intake and feed efficiency (9 weeks of age to slaughter - 108kg on average)

Individual feed intake recorded (electronic feeders ACEMA 64)

→ Daily feed intake }
→ Total feed intake } Feed intake

→ Food conversion ratio FCR }
→ Residual feed intake RFI } Feed efficiency

$FCR = (\text{Total feed intake}) / (\text{weight gain})$

$RFI = \text{Daily feed intake} - [a * \text{metabolic weight} + b * \text{average daily gain} - c * \text{lean meat content}]$

Carcass composition , Meat quality

Analysis

Fixed effects corrected (SAS, GLM)

Growth and feed intake: sex, contemporary group, group size

Carcass composition : sex, contemporary group, carcass weight
(covar)

Meat quality : sex, slaughter day

+ HAL genotype (NN / Nn) for 652 BC



QTL detection (QTLMAP, Le Roy et al 1998)

Interval mapping,
likelihood ratio test,
sire family analysis

Thresholds : simulations under H_0

Results on feed intake, without HAL correction

SSC	TRAIT	p value	cM
2	Total Feed Intake	*	77
6	Daily Feed Intake	*	72
	Food Conversion Rate	**	105
7	Daily Feed Intake	**	71
	Food Conversion Rate	***	90
9	Residual Feed Intake	*	104
	Daily Feed Intake	*	104
16	Residual Feed Intake	*	86

← HAL

*: 5% chromosome **: 1% chromosome ***: 5% genome

Carcass composition and meat quality: effect of HAL correction

		no correction		correction	
SSC	TRAIT	LRT	cM	LRT	cM
6	Water Holding Capacity	***	74		
	Meat Quality Index	***	75		
	Ham weight	***	79		
	Loin weight	***	51		
	Dressing percentage	***	54		
	Lean Meat Content	***	74		

only QTL with $p < 5\%$ genome

→ HAL : no interaction with QTL detected on other chromosomes

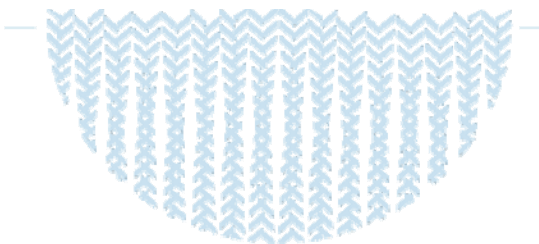
Major conclusions

QTL for feed intake and feed efficiency = low significance, effects $\sim 0.25\sigma_p$

→ SSC16 and SSC9 (Geldermann et al 2003)

→ SSC6 : HAL effect on daily feed intake
+ 1 QTL on food conversion ratio

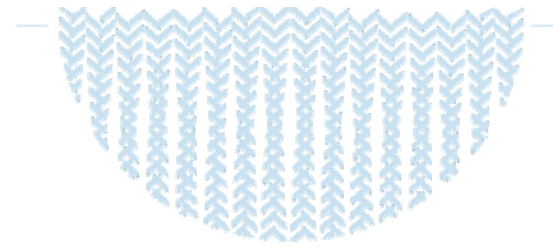
No marked interactions with HAL



SABRE

CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING





Thank you