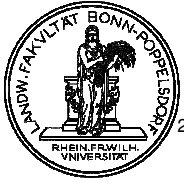


Detection of epistatic QTL for meat quality and carcass composition in a porcine Duroc × Pietrain population



Christine Große-Brinkhaus¹, Chirawath Phatsara¹, Elisabeth Jonas^{1,2}, Dawit Tesfaye¹,
Heinz Jüngst¹, Ernst Tholen¹ & Karl Schellander¹

¹ Institute of Animal Science, Group of Animal Breeding and Genetic, University of Bonn, Endenicher Allee 15, 53115 Bonn, Germany

² ReproGen-Centre for Advanced Technologies in Animal Genetics and Reproduction, Faculty of Veterinary Science University of Sydney
cgro@itw.uni-bonn.de



Introduction

Many QTL analysis in pig revealed numerous of individual QTL affecting performance traits (Rothschild et al. 2007). Standard models used for single QTL analysis include additive and dominant effects. However, to explain the variance of complex traits epistasis may play an important role (Carlborg and Haley 2004). The aim of this study was to identify epistatic QTL pairs for meat quality and carcass compositions traits and to compare these to single QTL.

Material & Methods

- ▶ 330 F2 animal, a reciprocal cross of breeds from Duroc and Pietrain (DuPi)
- ▶ Phenotype: 13 meat quality and 12 carcass composition traits
- ▶ Genotype: 122 microsatellites and 10 SNP on 18 autosomes
- ▶ Statistical analysis:
 - QTL pair detection* follows a concept of Estelle et al. (2008)
 - Statistical models:

$$\begin{aligned}\text{General:} & y = \mu + F + e & [0] \\ \text{Main effect - 1 QTL:} & y = \mu + F + c_1a + c_2d + e & [1] \\ \text{Main effect - 2 QTL:} & y = \mu + F + (c_1a_p + c_2d_p) + (c_3a_q + c_4d_q) + e & [2] \\ \text{Epistatic:} & y = \mu + F + (c_5l_{axa} + c_6l_{axd} + c_7l_{dxa} + c_8l_{dxd}) + e & [3] \\ \text{Full:} & y = \mu + F + (c_1a_p + c_2d_p) + (c_3a_q + c_4d_q) \\ & + (c_5l_{axa} + c_6l_{axd} + c_7l_{dxa} + c_8l_{dxd}) + e & [4]\end{aligned}$$

μ : mean, F : fix effects (gender, season, slaughter weight, age), c : regression coefficient, a/d : additive/dominant effects, l : Interaction, p , q : locations of individual QTL, e : residual error

- Models were tested against each other by **Likelihood Ratio Test**
- Calculation of the variance based on the differences residual variance between the compared models

* The analysis were performed with Qxpak 4.0 (Perez-Enciso and Misztal 2004)



Step 1: Single QTL-Scan
LRT: Model [1] vs Model [0] (P-value ≤ 0.01)

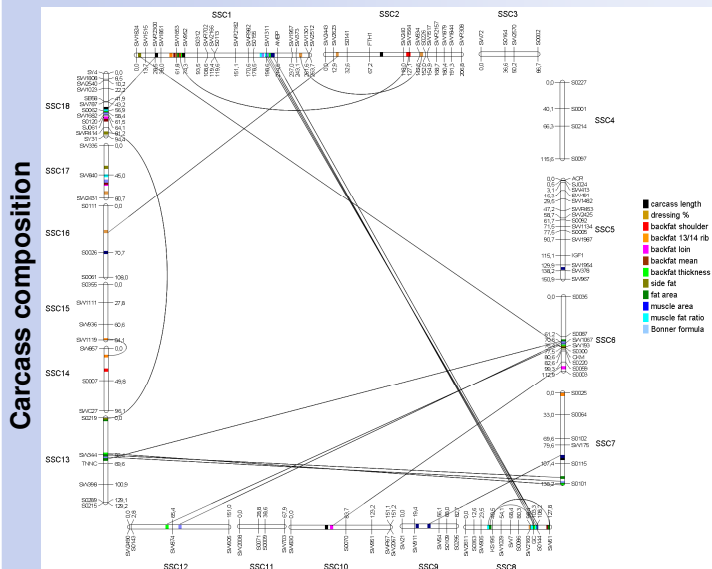
a Interchromosomal epistasis:
- Combinations of all chromosomal pairs

Step 2: b Intrachromosomal epistasis:
- chromosome splitted into two equal long parts
- 20 cM distance or one marker between two interacting QTL

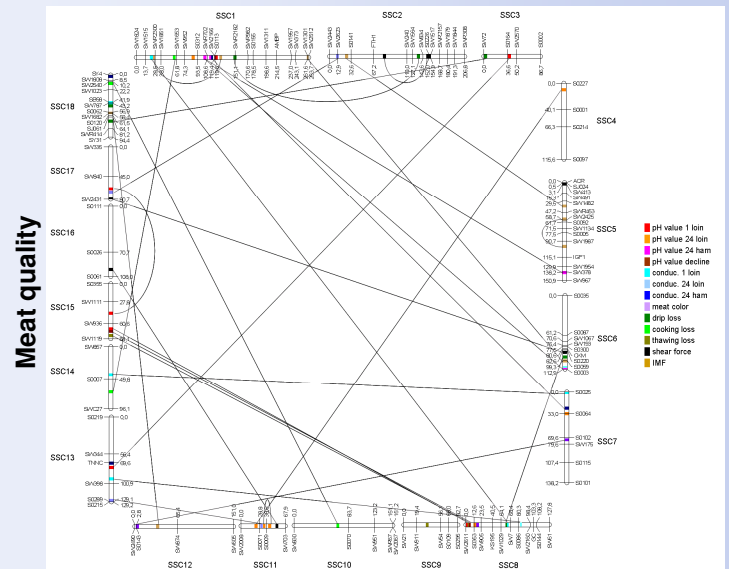
c Segmentation of chromosomes in 5 cM intervals
LRT: Model [3] vs [0] (P-value ≤ 0.0001)

Step 3: Analyze detected QTL pairs with a full model,
within a 20 cM interval
LRT: Model [4] vs Model [2] (P-value ≤ 0.001)

Results



Trait	Explained variance (Number of QTL)	
	single QTL	epistatic QTL
backfat thickness	12.05% (2)	23.92% (3)
fat area	15.89% (2)	21.48% (3)
muscle area	18.90% (4)	11.78% (2)
muscle fat ratio	18.60% (3)	10.97% (2)



Trait	Explained variance (Number of QTL)	
	single QTL	epistatic QTL
pH value loin 24 h	17.91% (3)	13.73% (2)
meat color	5.24% (1)	6.10% (1)
drip loss	8.34% (1)	17.79% (3)
shear force	11.00% (3)	20.43% (3)

Conclusion

Beside single QTL many interacting QTL pairs for several traits were identified in this study. Epistatic QTL explained a considerable proportion of the variance of these traits. In the next steps this results will be compared with additional studies e.g. related to gene expression, to explain the biological interaction.