

# Genetic analysis of fertility and growth traits in a Duroc x Pietrain Resource Population

Sarah Bergfelder, Christine Große-Brinkhaus, Christian Looft, Mehmet Ulas Cinar, Heinz Jünger, Karl Schellander & Ernst Tholen



Institute of Animal Science, Group of Animal Breeding and Genetic, University of Bonn, Endericher Allee 15, 53115 Bonn, Germany; e-mail: sber@itw.uni-bonn.de



## Introduction

Intensive selection for increased litter size and number of piglets born alive has negative impact on piglet survival. According to this trait, a) direct selection might be inefficient because of low heritability, b) mammary gland and number of teats have a major influence and c) individual birth weight is the most important risk factor. Because of high  $h^2$  and genetic relationship with piglet mortality, selection on birth weight might have a favourable influence on piglet survival. Moreover, birth weight has a positive influence on daily gain in fattening period. **The aim of this study:** Detection of QTL affecting birth and weaning weight, daily gain and number of teats.

## Materials & Methods

- 8278 animals of a Duroc x Pietrain Resource Population
- QTL Analysis was performed using 914 F<sub>2</sub> animals
- Phenotype: Individual birth weight (IBW), average daily gain during suckling period (ADG), weaning weight (WW) and number of teats (Teats)
- Genotype: 113 genetic markers equally spaced across the porcine autosomes



### ➤ QTL Analysis:

#### ➤ Models

➤ Single QTL:  $y = \mu + F + \beta\text{cov} + c_{ai}a + c_{di}d + u + e$  [1]

➤ Single QTL with imprinting:  
 $y = +F + \beta\text{cov} + c_{ai}a + c_{di}d + c_{ij}i + u + e$  [2]

➤ Two QTL:  
 $y = \mu + F + \beta\text{cov} + c_{ai1}a_1 + c_{di1}d_1 + c_{ai2}a_2 + c_{di2}d_2 + u + e$  [3]

$\mu$  = mean;  $F$  = fix effects (breed, month of birth, sex, parity);  
 $c$  = regression coefficient;  $\beta\text{cov}$  = covariates (age of sow);  
 $a/d/i$  = additive/dominant/imprinting effects;  $u$  = random effects (dam\*litter);  $e$  = residual error

#### ➤ Software:

- GridQTL (Seaton et al., 2006)

## Results

- **Descriptive statistics:** IBW of  $1.4 \pm 0.4$  kg, WW of  $8.0 \pm 2.3$  kg and ADG of  $215.2 \pm 65.3$  g/d, Teats of  $13.8 \pm 0.99$
- **Heritability (polygenetic model):**
  - IBW = 0.15, ADG = 0.4, WW = 0.3, Teats = 0.4
- **Correlation:** Significant negative phenotypic correlations obtained
  - between litter size and IBW, WW and ADG ( $r = -0.5, -0.03$  and  $-0.05$ , respectively)
  - between IBW and piglet mortality ( $r = -0.04$ )

### ➤ QTL-Analysis:

- 8 QTL on 6 different chromosomes (Tab. 1 & 2)
- 3 imprinted QTL (Tab. 2)
- Paternally imprinted QTL on SSC 15
- Maternally imprinted QTL on SSC 4 and SSC 12
- On SSC3 and SSC7 evidence for 2-QTL affecting Teats were found (Model [3])

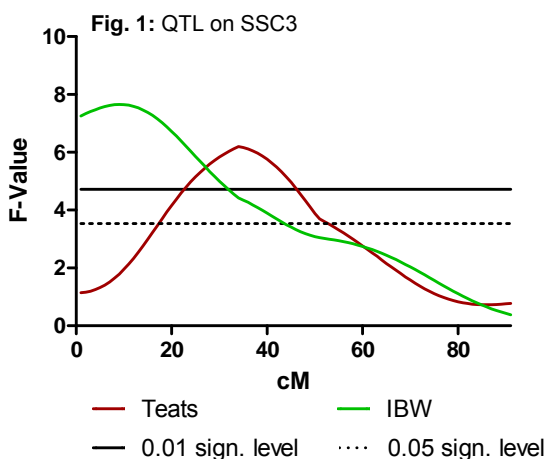
Tab. 1: Results for QTL Analysis with Model [1]

| SSC | Trait | F-Value | Position | Var% | Add±SE     | Dom±SE     |
|-----|-------|---------|----------|------|------------|------------|
| 3   | IBW   | 9.49**  | 2 cM     | 1.76 | -0.03±0.01 | 0.06 ±0.02 |
| 3   | Teats | 6.19**  | 33 cM    | 1.12 | -0.15±0.04 | 0.01±0.06  |
| 4   | Teats | 6.57*   | 124 cM   | 1.21 | -0.20±0.05 | -0.10±0.09 |
| 7   | Teats | 10.40** | 125 cM   | 2.02 | 0.21±0.05  | -0.07±0.07 |
| 14  | ADG   | 5.48*   | 35 cM    | 1.00 | 8.40±2.61  | -2.86±4.67 |

Tab. 2: Results for imprinted QTL Analysis with Model [2]

| SSC | Trait | F-Value | Position | Var% | Add±SE     | Dom±SE     | Imp±SE     |
|-----|-------|---------|----------|------|------------|------------|------------|
| 4   | ADG   | 3.97*   | 27 cM    | 1.00 | -3.16±2.82 | 13.47±5.36 | -6.61±3.1  |
| 12  | IBW   | 3.84*   | 139 cM   | 1.00 | -0.04±0.02 | 0.04 ±0.06 | -0.03±0.02 |
| 15  | WW    | 4.46*   | 70 cM    | 1.12 | 0.04±0.07  | -0.31±0.12 | 0.20±0.07  |

F-Value = Significance of the QTL; \* = 5 % suggestive chromosomeswide significant level; \*\* = 1 % suggestive chromosomeswide significant level; Var% = phenotypic variance explained by a QTL; Add ± SE, Dom ± SE = Additive or Dominance effect with standard error; Impr ± SE = Estimated Imprinting effect, computed as the effect of paternal – maternal alleles



## Conclusion

As expected, individual birth weight and weaning weight showed an antagonistic relationship to number of piglet born alive. This result indicates that selection for increased litter size has a strong indirect negative impact on economical important traits like piglet survival and fattening performance. Overall 8 suggestive QTL for birth weight, average daily gain during suckling period, weaning weight and number of teats were mapped. When imprinting effects were included in the Model [3], 3 QTL with a parent-of-origin effect were detected. Further analysis will be performed to identify QTL for piglet survival.