Linkage and QTL mapping for Sus scrofa chromosome 17

By M. Pierzchala, D. Cieslak, G. Reiner, H. Bartenschlager, G. Moser and H. Geldermann

Summary
Linkage and QTL maps of Sus scrofa chromosome 17 (SSC17) were analysed with five markers and in three F2 families based on Wild Boar (W), Meishan (M) and Pietrain (P) crosses. The maps were similar across the three families and agree well with published maps. In the M·P family, new quantitative trait loci (QTLs) for growth and fat deposition were located in the vicinity of GHRH, whereas in the W·P family one minor QTLs for daily gain was detected. No QTL was found in the W·M family.

Introduction
Linkage maps of Sus scrofa chromosome 17 (SSC17) (http://www.thearkdb.org) span between 97.0 cM (18 loci; USDA-MARC.2, Rohrer et al. 1996) and 113.5 cM (six loci; Nordic.2, Marklund et al. 1996). The length of the USDA-MARC.2 map to locus S0014 is 88.7 cM whereas the corresponding position of the Nordic.2 map spans 113.5 cM and thus is about 28% longer. Malek et al. (2001) described quantitative trait loci (QTLs) for loin light reflectance and colour score on SSC17 near S0332 in a Berkshire·Yorkshire cross. The Berkshire QTL alleles were associated with superior reflectance and colour scores in comparison with Yorkshire alleles. A QTL mapped in the interval SW840–S0339 for post-stress ACTH level in a Large White·Meishan cross explained about 12% of the phenotypic variance and was negatively influenced by Meishan QTL alleles, with evidence of imprinting effects (Déasautès et al. 2002).

Materials and methods
F2 pigs – based on Meishan (M), European Wild Boar (W) and Pietrain (P) crosses – were used. Family structure, housing, selection of quantitative traits and marker loci as well as statistical analysis are described elsewhere (Geldermann et al. 2003). SSC17 has been genotyped for four microsatellites and one restriction fragment length polymorphism in all three families (Table 1).
Results and discussion

Marker characterization and linkage maps

Table 2a lists 31 different alleles that were found at the five loci in the founder groups. Twenty-one of the alleles were unique to a single founder group, and only three alleles were observed in all three groups (Table 2a). In the F1 generation (Table 2b), the
heterozygosity per family ranged between 0.68 in the W × M family and 0.96 in the M × P family. An average of 535 informative meioses was observed per family. Figure 1 plots the information contents which generally exceeded 0.6 in the M × P and W × P families, except the interval GHRH–SW2427 where the distance between loci was large and the cumulative information content dropped down to about 0.3.

The sex-averaged linkage maps for the M × P, W × P and W × M families were similar in length and had identical order of loci (Fig. 2). The average distances between the markers for these families were 24.5, 22.7 and 24.4 cM, respectively. GHRH mapped close to SW1920, but had an average distance of 48 cM to the distal locus SW2427. In the USDA-MARC.2 map (Rohrer et al. 1996), our most proximal marker, SW1921, was at 17.3 cM on SSC17 and our terminal marker, SW2427, mapped at the distal end. Thus our maps covered about 82% of the chromosome. The order of markers agrees with the USDA-MARC.2 map; however, the length of the comparable region was about 15 cM longer in

**Fig. 1.** Information content for SSC17. For individual marker loci, the polymorphism information content (PIC) values are shown as crosses. The cumulative information content across the chromosome is indicated by the solid line. Distances between loci are given in sex-averaged cM
our maps. In all three families, maternal maps were substantially longer than the paternal ones (p < 0.001). Ratios of the lengths of maternal and paternal maps were 2.04, 1.61 and 1.61 cM in the M·P, W·P and W·M families, respectively.

Map positions and effects of QTLs

Genome-wide significant QTLs were found for carcass length and live weight at slaughter in the M × P family (Table 3a). The Meishan QTL alleles increased the values of growth and fat deposition, whereas Pietrain alleles were associated with higher daily gain compared with the Wild Boar alleles. Most of the QTL alleles showed considerable dominance effects. Test statistic profiles in the M × P family (Fig. 3a) show QTLs for

Table 3. Significant QTL effects on SSC17

<table>
<thead>
<tr>
<th>Trait</th>
<th>M × P family</th>
<th>W × P family</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass length (cm)</td>
<td>8.3**</td>
<td>5.5*</td>
</tr>
<tr>
<td>Live weight at slaughter (kg)</td>
<td>8.1**</td>
<td>10.70 ± 7.48</td>
</tr>
<tr>
<td>Shoulder external fat weight (kg)</td>
<td>7.6*</td>
<td>28.53 ± 9.51</td>
</tr>
<tr>
<td>Fat area on M.l.d. at 13th/14th rib (cm²)</td>
<td>6.8*</td>
<td>5.0 ± 10.70</td>
</tr>
<tr>
<td>Ham external fat weight (kg)</td>
<td>6.2*</td>
<td>28.53 ± 9.51</td>
</tr>
<tr>
<td>Back fat depth on M.l.d. at 13th/14th rib (mm)</td>
<td>5.6*</td>
<td>28.53 ± 9.51</td>
</tr>
<tr>
<td>Fat-to-meat ratio</td>
<td>5.4*</td>
<td>5.0 ± 10.70</td>
</tr>
<tr>
<td>Daily gain (g/day)</td>
<td>5.5*</td>
<td>5.0 ± 10.70</td>
</tr>
</tbody>
</table>

Significant at **p < 0.05 genome-wide threshold and *p < 0.05 chromosome-wide threshold. QTL, quantitative trait locus; SSC17, Sus scrofa chromosome 17; a, additive effect (positive/negative signs indicate the superior/inferior trait values inherited from the paternal resource group); d, dominance effect (positive for higher values of heterozygous individuals than the mean of homozygotes; negative for lower values); VF² (%), percentage of F² phenotypic variance explained by the QTL; M.l.d., Musculus longissimus dorsi.
carcass traits in an interval of about 40–80 cM. In a corresponding interval Désautés et al. (2002) described QTL effects on stress reaction. This interval includes the locus GHRH, and the highest F values for carcass length and live weight QTLs were found here. GHRH encodes the growth hormone releasing hormone, a member of the somatotropin axis, which has been characterized for effects on adipose tissue and growth (Etherton et al. 1986). However, QTL profiles were too broad to target underlying single-gene effects. In the W × P family, a single QTL for daily gain was found, and no QTL was observed in the W × M family. The QTLs for meat quality traits near SW2427 described by Malek et al. (2001) could not be confirmed from our data. Thus altogether, the SSC17 QTLs point to large differences between families.

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References

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