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Linkage mapping of five genes on SSC12 in a Berkshire × Yorkshire cross (Brief report)

(Kartierung von fünf Genen auf SSC12 in einer Berkshire × Yorkshire Kreuzung)

Background: A three-generation family of pig was generated by an intercross between animals of two Berkshire grand sires and nine Yorkshire grand dams (BY), and a total of 525 F_2 offspring were produced. The initial genome scan analysis identified suggestive quantitative trait loci (QTL) for fat traits on chromosome 12 (SSC12) (MALEK et al., 2001). Animals that were homozygous for Berkshire alleles had relatively less back fat than those with Yorkshire alleles, and heterozygotes were fattest for these QTL. The objective of this study was to further characterize these SSC12 QTL by mapping five additional genes (*PSME3*, *GRB7*, *MAC30*, *RPS6KB1* and *TAX1BP3*) in the BY family and see if they were associated with fatness traits.

Procedures:
Primer sequences:
PSME3-F: 5'-ATT GGA AAT GGG AGA GGA AG-3'
PSME3-R: 5'-CCA AGC AGC CCT ACC TAG AA-3'
GRB7-F: 5'-GGA AAC TTC GAG AGG AGG AG-3'
GRB7-R: 5'-AGG ATG GGG GTC TGT GAA-3'
RPS6KB1-F: 5'-TGT GTG AGC ATC CTG CAA-3'
RPS6KB1-R: 5'-GGT TGA GAA GAT GTC GCT AGG-3'
MAC30-F: 5'-CCC TGC AAT CAT CTA CTC-3'
MAC30-R: 5'-AGG GGA TGT AAA CGG ACA-3'
TAX1BP3-F: 5'-CTT TCC TGT GTG TGG TGG CG-3'
TAX1BP3-R: 5'-CAG CCA TCA GAA GCC AGG AC-3'

Porcine genomic fragments of the 5 genes (*PSME3*, *GRB7*, *MAC30*, *TAX1BP3* and *RPS6KB1*) were isolated for single nucleotide polymorphism (SNP) identification. For each gene, only the SNP showing the largest differences in allele frequency between the founders of the BY family was selected for linkage mapping by using CRIMAP (GREEN et al., 1990). Gene names, accession numbers with the SNP positions, SNP types, PCR product sizes, restriction enzymes used and alleles for each SNP are given in Table 1. The statistical models used in the QTL and association analyses in this study have previously been described (MALEK et al., 2001).

Results: Linkage mapping analysis allowed us to map the 5 genes to the SSC12 linkage map in the BY family. The best sex-averaged map order (in cM) is: S0229(0.0) -*PSME3*(25.6)-*GRB7*(32.7)-SW874(35.8)-*RPS6KB1*(44.0)-S0090(50.1)-S0147(65.7)-*MAC30*(85.5)-SWC23(87.8)-*TAX1BP3*(94.4)-SW2180(103.0). Compared with the

previous reports (MALEK et al., 2001), linkage mapping of these five additional genes on SSC12 altered the location of three suggestive QTL peaks for tenth rib back fat, last rib back fat and average back fat, to the same position (33 cM away from the first marker of *S*0229), although they still were not significant. The *GRB7 Sac* II marker position which is located only 0.3 cM away from the QTL peak for fatness traits is suggestive of its involvement in those traits. As expected, association analysis revealed that the *GRB7 Sac* II marker was significantly associated with last rib back fat, average back fat and marbling ($P<0.05$). In addition, the effect of the marker approached a significant level for tenth rib back fat ($P<0.1$). Among the 11 F_0 animals, both the two Berkshire grandsires were homozygous for allele *C* and the frequency of allele *T* for *GRB7 Sac* II in the nine Yorkshire granddams was 0.83.The *CC* genotype tended to have the lower back fat compared with the *TT* genotype, and the heterozygote was significantly associated with increased back fat. Our results are in agreement with the QTL effects on SSC12 for fatness found in the BY population (MALEK et al., 2001) There have been several reports that suggested a role for *GRB7*, one of the GRB7 family proteins, in mitogenic signaling and interaction with the insulin receptor, implying the importance of *GRB7* in development and growth (KASUS-JACOBI et al., 2000). It may explain, in part, the association of the *GRB7* polymorphism with carcass traits in pigs and will allow further study.

Table 1 Primers, SNP locations, restriction enzymes and alleles for SNP genotyping used in this study

Gene Symbol	Gene name	Access. No (position) [a]	SNP type (Restriction enzyme)	PCR size in bp	Size (bp) of two alleles
PSME3[b]	Proteasome (prosome, macropain) activator subunit 3 (PA28γ; Ki)	AY134853 (1425)	A/G (*Alu*I)	215	215 (*A*) 175+39 (*G*)
GRB7	Growth factor receptor-bound protein 7	AY350907 (242)	C/T (Leu/Pro) (*Sa* II)	97	97 (*C*) 73+24 (*T*)
RPS6KB1	Ribosomal protein S6 kinase, polypeptide 1	DQ376533 (597)	T/G (*Bsm*AI)	208	208 (*T*) 158+51 (*G*)
MAC30	Hypothetical protein MAC30	DQ376144 (865)	C/T (*Taq*I)	155	155 (*C*) 89+66 (*T*)
TAX1BP3	Tax1 (human T-cell leukemia virus type I) binding protein 3	DQ376143 (998)	G/T (*Pvu*II)	369	369 (*G*) 280+89 (*T*)

[a] Accession number of the source sequences and the position of SNP in each sequence
[b] The SNP for *PSME3* gene has previously been reported by YU et al. (2004)

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