Plant & Animal Genomes XI Conference

January 11-15, 2003
Town & Country Convention Center
San Diego, CA

Poster: Swine

P629

DEVELOPMENT OF A HIGH-DENSITY SNP MAP OF A QTL REGION FOR BACKFAT THICKNESS ON PORCINE CHROMOSOME 2

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A maternally imprinted quantative trait locus (QTL) for backfat thickness was identified on the p-arm of porcine chromosome 2 (SSC2) (Rattink *et al.*, 2000).
For further investigation of this region, single nucleotide polymorphism (SNP) markers are developed by locus specific amplification and comparative sequencing of PCR products from 8 individuals each from a different breed. Primers are designed from:

- sequences of genes mapped to SSC2,
- sequences of subclones from BAC clones containing loci mapped to SSC2,
- BAC-end sequences of clones containing loci mapped to SSC2,
- porcine cDNA sequences orthologuous to human chromosomes 11 or 19.

To date, more than 50 STSs with a total length of 32 kb are sequenced. The STSs represent loci covering 80 cM of SSC2, including the complete p-arm. More than 200 SNPs have been identified, yielding a SNP density of 1 SNP per ~160 bp. Normalized for sample size (16 chromosomes), SNP density is 1 SNP per ~500 bp.
Currently (October 2002), SNP markers are used for detailed haplotyping of 40 unrelated animals. Based on these haplotypes the size of Linkage Disequilibrium (LD) blocks will be estimated. The size of the LD blocks holds consequence for both the number of markers required for screening of the chromosomal region and for the maximum resolution of future fine-mapping of the QTL.

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