

**E040****Mapping of QTLs for conformation, fertility, health and production traits in the Danish-Swedish Holstein Friesian Cattle population**

VIVI NIELSEN, BERNT GULDBRANDTSEN, MOGENS S. LUND, PETER H. NISSEN, JUST JENSEN, DANIEL A. SORENSEN, CHRISTIAN BENDIXEN  
*Danish Institute of Agricultural Sciences, Tjele, Denmark*

A QTL-study is performed in the Danish-Swedish Holstein-Friesian Cattle population using a granddaughter design with 23 grand-sires and 1718 sires. In total, 71 traits related to milk production, disease resistance, fertility, calving ease, conformation, and temperament are analysed. At present, 19 chromosomes have been scanned with 144 microsatellites with an average distance of 10-20 cM. Analyses of marker data are conducted using all markers simultaneously for each chromosome position in a marker-interval based least squares regression analysis. The results presented confirm the presence of QTLs for milk protein percent on chromosome 6 and for milk yield on chromosome 14, previously reported in other studies.

**E041****Association of GH and IGF-1 polymorphisms to growth traits in a synthetic beef cattle breed**

ANDRÉA P. PEREIRA<sup>1</sup>, MAURÍCIO M. ALENCAR<sup>2</sup>, HENRIQUE N. OLIVEIRA<sup>3</sup>, LUCIANA C.A. REGITANO<sup>2</sup>

<sup>1</sup>Federal University of São Carlos, Genetics and Evolution Department, São Carlos, Brazil; <sup>2</sup>Embrapa Southeast Cattle Research Center, São Carlos, Brazil; <sup>3</sup>São Paulo State University, Animal Breeding and Nutrition Department, Botucatu, Brazil. This work was supported by FAPESP and CNPq

The Canchim beef cattle (5/8 Charolais + 3/8 Zebu), has been selected for meat production in Brazil since 1953. In the present work the effect of candidate genes polymorphisms was investigated in 688 animals born between 1998 and 2000. From these 307 belonged to the original Canchim population (GG1) that was formed in 1953 and the remaining belong to a

Canchim population formed by recent crosses (GG2). DNA extracted from blood samples using a salting out procedure was amplified for a 223 bp fragment, spanning intron IV and exon V of the growth hormone (*GH*) gene, and for type 1 insuline like growth factor (*IGF1*) microsatellite in 25 µl reactions. *GH* products were digested with *AhaI* and fragments were resolved in 3% agarosis electrophoresis. *IGF1* products were separated by electrophoresis in 8 % non denaturing polyacrylamide gels and silver stained to identify the alleles. Genotype effects on breeding values for birth weight (BW), weaning weight (WW) and yearling weight (YW) were investigated by the SAS GLM procedure. The statistical model included the effects of genetic group and *GH* and *IGF-1* genotypes. Significant effects were found for *GH* genotype on YW ( $P \leq 0.05$ ), with positive effects associated to the V allele, and for *IGF1* on BW ( $P \leq 0.01$ ) and YW ( $P \leq 0.01$ ).

**E042****Combined approaches at INRA to fine map QTL influencing growth, fatness and carcass composition traits in pig.**

JULIETTE RIQUET<sup>1</sup>, MARIE-PIERRE SANCHEZ<sup>2</sup>, OLIVIER DEMEURE<sup>1</sup>, NATHALIE IANNUCELLI<sup>1</sup>, KATIA FEVE<sup>1</sup>, HÉLÈNE GILBERT<sup>2</sup>, CARINE GENÊT<sup>1</sup>, MICHÈLE BONNET<sup>1</sup>, CHRISTOPHE PÉRY<sup>2</sup>, YVON BILLON<sup>2</sup>, JEAN GOGUÉ<sup>2</sup>, JEAN-CLAUDE CARITEZ<sup>2</sup>, PASCALE LE ROY<sup>2</sup>, CHRISTINE RENARD<sup>3</sup>, JEAN-PIERRE BIDANEL<sup>2</sup>, DENIS MILAN<sup>1</sup>

INRA, France: <sup>1</sup>Laboratoire de Génétique Cellulaire, Castanet-Tolosan; <sup>2</sup>Station de Génétique Quantitative et Appliquée, Jouy-en-Josas; <sup>3</sup>Laboratoire de Radiobiologie et d'Etude du Génome, Jouy-en-Josas

A whole genome QTL analysis of growth, fatness and carcass composition data from a F2 experimental cross between 6 Meishan (MS) sows and 6 Large White (LW) males has been performed at INRA. Highly significant QTL effects were detected in several chromosomal regions: the telomeric regions of SSC 1q (growth, fatness, lean cuts weights) and SSC 2p (lean and fat cuts weights), SSC 4 (growth, fatness) and SSC 7 (growth, fatness, lean and fat cuts weights) were selected for further analyses. Unlike other studies, our analysis did not reveal any imprinting effect for the SSC2