reaching 55.76% for QTLFCA of .95 $\sigma_a{}^2$, while the accuracy increased from .513 and .543 to .981 and .955, respectively for sires and dams. Response to MAS, with QTLFCA effect corresponding to .1, .3 and .5 $\sigma_a{}^2$, at embryo level and different pre-selection rates was evaluated resulting in lower genetic gains when compared to MAS with one-stage selection due to the lower intensity at 2 years old (when more information is available: own performance for cows, full and half sibs) resulting in smaller total accuracy. Therefore, it is possible to obtain responses larger than 98% of the total response using embryo selection rates of .6, .3 and .2 for QTLFCA substitution effects of .1, .3 and .5 respectively. The production of 3 times more embryos allow to increase the genetic gain approximately 23%, due to the increase in selection intensity. When 13 of the 40 embryos were transferred, even markers with small effect (.02, .05 $\sigma_a{}^2$) could be used in MAS resulting in satisfactory response: 9.0% and 12.6%, respectively. Considering that most of the total cost in a MOET nucleus breeding program is due to maintenance of recipients and feeding growing animals until selection age the MAS utilization on embryo pre-selection can lead to a substantial improvement in the genetic response, even with markers with small substitution effect, without relevant increase in costs.

Key Words: Marker assisted selection, Embryo pre-selection, Beef cattle

1409 A heterogeneity model for estimating the number of QTL alleles in a segregating population.

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A frequently observed phenomenon in data analysis for the detection of a quantitative trait locus in a segregating population is the genetic heterogeneity of a quantitative trait among different families. This heterogeneity could be due to the following situations: 1) some families do not have segregating alleles so that marker effects tend to be zero for those families, 2) families with segregating QTL alleles in fact have multiple QTL alleles, 3) different families have the same QTL effect but different marker-QTL recombination frequencies, and 4) different families have multiple QTL alleles and different marker-QTL recombination frequencies. Assuming situation 2), families with similar QTL effects can be placed in the same group using a cluster analysis and a heterogeneity model can be used to estimate the QTL effects of different family groups. Then, the number of QTL alleles can be estimated under the assumption of equal difference between two adjacent QTL alleles when QTL alleles are ordered according to the sizes of their effects. Let k = the number of QTL alleles, α_m = the average of QTL effects of different family groups, and α_d = the largest QTL distance obtained as the difference between the largest and smallest QTL effects. Then, the number of QTL alleles can be estimated as $k = [2 + (3\alpha_m/\alpha_d - 1)]/(3\alpha_m/\alpha_d - 1)$.

Key Words: Heterogeneity model, QTL alleles, segregating populaton

1410 Evidence of paternally imprinted QTL around *IGF2* in a Berkshire-Yorkshire cross.

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A paternally imprinted QTL with major effect on muscle mass and fat deposition near *IGF2* on SSC2 has been reported for crosses of the Large White with Pietrain and Wild Boar breeds. Our objective was to confirm the presence of an imprinted QTL on SSC2 in an F2 cross between the Berkshire and Yorkshire breeds. Data on average backfat (ABF) and loineye area (LEA) from 512 F2 animals and genotypic data for eight markers on SSC2 were used. Breed cross regression interval mapping was implemented using the following QTL models: Mendelian (additive and dominance effects), full imprinting (allowing for different maternal and paternal allele effects plus dominance), paternal imprinting (only paternal expression), and maternal imprinting (only maternal expression). Tests of each model against the no-QTL model and tests of full imprinting against the Mendelian, paternal and maternal imprinting models were used in a decision tree to determine presence and mode of inheritance of QTL. Chromosome-wise significance thresholds were determined by permutation. Tests of the Mendelian against the no-QTL model showed no evidence of QTL for ABF and LEA (P>0.05) but tests of the full imprinting against the no-QTL model detected a QTL for both traits at the same position on the distal end of SSC2p (P<.01 for LEA and P<.02 for ABF), near *IGF2*. Further testing for mode of inheritance showed that the full imprinting model was not significant over paternal imprinting (P>.10) but highly significant over maternal imprinting (P<.01), indicating evidence for exclusive paternal expression. The final analysis of paternal imprinting against the no QTL model was highly significant (P<.01). Favorable alleles originated from the Yorkshire and, when transmitted through the sire, reduced average backfat by .1 cm and increased LEA by 1.0 cm2, compared to Berkshire alleles. Evidence of these QTL, which were not detected based on a Mendelian model, confirms that the *IGF2* region is imprinted in pigs and harbors important QTL for muscularity and fat deposition. Supported by USDA CSREES # 00-52100-9610

Key Words: QTL detection, Imprinting, *IGF2*

1411 Combined interval mapping of QTL using mixed models in reference families with complex pedigrees and its application to chromosome 13 of swine.

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A method for mapping quantitative trait loci (QTL) was introduced incorporating information from various types of progeny and from multiple generations. Effects and positions of QTL were obtained by a joint estimation using the joint QTL-marker distribution of mixed populations or by a weighted least square method. Interval mapping was used to illustrate the theory based on a mixed model. Analysis of variance using multi-point analysis suggested that a Danish pig family carried a QTL on chromosome 13 which significantly affected slaughter weight (SWT) and average daily gain to slaughter (ADSG) (P<0.05), but QTL effect on backfat depth (BFDP) was inconsistently observed. This QTL was located between loci SW1898 and SW398 (ρ = 0.520.36). This was a region which flanked the PIT1 gene, an essential transcriptional regulatory factor of growth hormone, prolactin and thyrotropin β subunit. This result agreed with previous results that suggested a QTL for other growth traits at the estimated PIT1 position. Variance contributed by this QTL was 9.37% for SWT and 9.45 % for ADSG.

Key Words: Linkage Maps, Segregation Families, QTL

1412 PIT-1, a candidate gene for mass assisted selection in dairy bulls.

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Pit-1 is a protein important for pituitary cell differentiation and proliferation. It acts as a transactivator that regulates growth hormone and prolactin, TSH-b genes. In a previous study (Renaville et al. 1997, J. Dairy Sci. 80, 3431-3438), we have reported that the polymorphism associated to a transition A to G in the exon 6 of the gene could be associated to milk performances. The aim of this study was to search for eventual associations between Pit-1 polymorphism and dairy production traits by using a representative population of dairy sires. DNA was extracted from 1100 A.I. Holstein bulls using in A.I. scheme by Semex-Alliance (Guelph, Canada). A primer-specific PCR test has been developed to reveal the two alleles of Pit-1 gene which are called A and B. A mixed linear animal model including milk data of 2,400,000 lactations from 1,100,000 daughters of tested bulls was developed. The allelic frequencies were 53% and 47% for A and B respectively. Allelic frequencies were introduced as regression into the mixed linear animal model. The results showed an a value of +46,3 kg, + 1,9 kg and + 1,5 kg for milk, protein and fat yield, respectively. This a value represents the effect, on the trait, of the substitution of a B allele by a A allele. In conclusion, this study showed an significant relationship between the A allele of Pit-1 and dairy production traits of Holstein bulls. This gene could be considered as an interesting tools for marker assisted selection of dairy bulls. (Supported by the Belgian Ministry of Small Enterprises, Traders and Agriculture (grant 5983S), Semex-Alliance (Guelph, Canada) and Tomen Corp. (Tokyo, Japan))

Key Words: Pit-1, Marker, Lactation