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ABSTRACTS

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A quantitative trait locus for body conformation maps to bovine chromosome one in Japanese Black cattle 6.C.0973

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Chromosomal regions of bovine chromosome one were scanned for the detection and mapping of segregating QTL influencing preweaning withers height, hip height, hip width, body length, chest width, chest depth, shoulder width, lumbar width, thurl width, pin bone width, rump length, cannon circumference, heart girth, abdominal width and abdominal girth. QTL analysis was performed by genotyping 132 half-sib progeny of 5 Japanese Black sires using 108 microsatellite DNA markers. Genotyped data on progeny and their sires were combined in a multi-point approach to calculate Identity-By-Descent (IBD) probability coefficients of inheriting allele 1 or 2 from the sire at specific chromosomal locations. The phenotypic data on progeny were regressed on these IBD coefficients in a within-common-parent regression analysis. A linear model containing the fixed effects of sex, parity and season of birth as well as age as a covariate, was fitted to the IBD coefficients and phenotypic data. Data were analyzed using QTL Express by generating an F-statistic through permutation tests at chromosome-wide significance thresholds over 1,000 iterations at 1cM intervals. A significant QTL for chest width was detected at 91cM in Sire 3. Suggestive QTL for thurl width, hip height, chest depth and abdominal girth were all located at 18cM in Sire 2. Other suggestive QTL detected were withers height (58cM) in Sire 5 and rump length (11cM), withers height (77cM) and chest depth (81cM) in Sire 1. The detection of these QTL boosts the prospect of implementing marker-assisted selection for body conformation traits in Japanese Black beef cattle.

SELECTIVE DNA POOLING AS A TOOL FOR DETERMINING MARKER ALLELE FREQUENCY DIFFERENCES BETWEEN TWO GROUPS: IMPROVING SENSITIVITY AND ASSESSING ITS LIMITATIONS. 6.C.0974

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DNA pooling is a strategy where individual DNA samples from each of two test groups are pooled and amplified in a PCR reaction. This enables rapid screening of a large number of markers for linkage with polygenic traits. The technique is combined with selective genotyping, whereby subjects will only be added to the pool if their scores for the trait under study fall at the extremes of the phenotypic distribution. DNA from the "high" and "low" groups respectively can then be pooled separately. We have utilized such a method to identify genes affecting milk yield and composition in Australian dairy cattle using a genome wide scan. This poster focuses on techniques to make selective DNA pooling reproducible and sensitive to small changes in allele frequency differences between groups. Of critical importance is the accurate quantification of DNA. It is proposed that quantitative competitive PCR (QC-PCR) offers the best prospects in this regard. By using a suitable correction procedure, we have also shown that accurate estimates of allele frequencies can be obtained from a pool. We also assess the importance of errors from several sources to determine the power of pooled genotyping to detect QTLs and the optimal design.

GESTATION LENGTH VARIATION: CAUSES AND EFFECTS 6.C.0975

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Gestation length is determined mainly by the genotype of the foetus, with a heritability of about 0.51, but the maternal genotype has a relatively small contribution, with a maternal heritability of 0.05. The calving records of 66,302 Australian Holstein cows, with traits of calf size, mortality rate, cow gestation length and presence or absence of dystocia was used in an analysis to determine relationships between these calving traits. The genetic standard deviation of gestation length was 3.7 days for primiparous cows and 3.3 days for multiparous cows. All calf had know sires and grandsires, so maternal effect could be clearly demonstrated. Gestation length varied by one day due to month of calving, and was longest in August; cow age caused a variation of two days, and was shortest for primiparous cows. Male calves had gestation lengths one day longer than female calves. Longer gestation lengths were associated with larger calves, higher mortality rates and increased rates of dystocia.

USE OF LINKAGE AND LINKAGE DISEQUILIBRIUM ANALYSIS TO MAP QUANTITATIVE TRAIT LOCI (QTL) FOR PROTEIN % IN MILK OF DAIRY COWS 6.C.0976

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Linkage disequilibrium (LD) can be used to map QTL more precisely than linkage mapping. By using a variance component method, information from both linkage and LD can be combined. The method uses a linear model which includes a random effect of the QTL. The covariance between these random effects is proportional to the probability that two QTL alleles are identical by descent (IBD) and this is estimated from the markers. This method has been applied to data on the protein % in the milk of cows that have been typed for 20 microsatellite markers on chromosome 20. There is evidence for at least one and probably two QTL associated with protein percentage on chromosome 20.

CHARACTERIZATION OF THE TWO COMMON CARP (CYPRINUS CARPIO L.) GROWTH HORMONE GENES 6.C.0977

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A lot of studies on different classes of vertebrates have shown that polymorphisms at the growth hormone (GH) gene in promoter or introns could lead to growth differences. Therefore, these polymorphisms could be of interest in marker assisted selection to obtain fast growing animals. We have studied the common carp because of its economical importance for world aquaculture and its phylogenetically tetraploid origin. We could show by sequence analyses that common carp possesses two GH genes and that both are still expressed. However, the two gene products are different. A single replacement is found in the signal peptide and six replacements occur in the mature protein. One of the two proteins (encoded by the GH-1 locus) shows atypical amino acid substitutions compared to other vertebrate species what could result in a suboptimal function as somatotropin. We could also show that the two GH genes differ from each other in introns. These differences could play an important role in GH expression (developmental stage at which the genes are expressed as well as strength of their expression). Moreover, both GH genes were found to be polymorphic. Whereas most of the allelic variants of both genes differed only by substitutions, length polymorphisms were detected in the third intron of both genes (340 bp difference at GH-1 and 17 bp difference at GH-2). The characterization of the two GH genes will be completed by a comparative analysis of consensus sequences what also could predict differences in their expression.

TRANSGENIC LIVESTOCK FOR HUMAN HEALTH: CHANGING THE COMPOSITION OF MILK 6.C.0978

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Genetic engineering of livestock for use in agriculture has held great promise since the creation of the first transgenic mice more than 20 years ago. However, this promise has not yet been realized. Transgenic plants have entered production but have met resistance in some parts of the world, in part due to the perception that the new varieties, while assisting the producer, have no direct benefit for the consumer. As a model, we have genetically engineered dairy goats in order to improve the nutritional and health benefits of milk for consumers. Transgenes designed to express lysozyme or desaturase in lactating mammary gland epithelial cells were transferred into goats by pronuclear microinjection. Preliminary results from tests with three species of bacteria showed that expression of the lysozyme transgene in milk confers additional anti-bacterial properties on the milk. Milk with increased anti-bacterial activity may decrease the growth of bacterial contaminants