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micro-calpain, involved in meat post-mortem tenderiza-  
tion, and variants of the CAPN1 gene are known to have  
a major effect on beef tenderness. However, studies with  
Limousin-Jersey backcross progeny herein showed that  
shear force is not only affected by 2 variants of CAPN1  
(SNP316 and SNP530), but there are also significant  
epistatic interactions between CAPN1 and 5 other genes  
(SNIP1, FST, FSTL1, LOXL1 and IGF1). In many cases,  
the size of the effect of the interaction was larger (eg  
CAPN1-SNP316 and SNIP1-SNP3) than the effects of  
the individual CAPN1 variants. These epistatic effects  
of CAPN1 alleles were not necessarily additive. For in-  
stance, the CAPN1-SNP316/GG genotype in combina-  
tion with the SNIP1-SNP3/TT genotype showed much  
higher shear force values than all other combinations of  
genotypes. The results were also not consistent across  
muscles. For example, the CAPN1-SNP316 had the op-  
posite effect on muscles in that the G allele was domi-  
nant for the M. longissimus dorsi but recessive for the  
M. semitendinosus. Thus, epistasis and muscle-specific  
effects may lead to unintended consequences in breed-  
ing programs using marker-assisted selection of the  
CAPN1 variants for tenderness.

**Key Words:** cattle, epistasis, meat quality

**P4007 Verification of gene variants associated with residual feed intake in cattle.** F. E. Bowley\*<sup>1,2</sup>, C. D. K. Bottema<sup>1</sup>, and W. S. Pitchford<sup>1</sup>, <sup>1</sup>Cooperative Research Centre for Beef Genetic Technologies, School of Animal and Veterinary Sciences, Roseworthy, SA, Australia, <sup>2</sup>AbacusBio Limited, Dunedin, Otago, New Zealand.

Feed is the single largest input cost in beef produc-  
tion systems, and so making improvements in the ef-  
ficiency with which cattle utilize feed is a prime target  
for increasing profitability. Residual feed intake (RFI)  
is a common measure of feed efficiency, but is expen-  
sive to measure. This study involved analyzing data  
from Beef CRC1 cattle to verify 12 single nucleotide  
polymorphisms (SNPs) found to be associated with RFI  
in the Davies Gene Mapping Herd. Four of these SNPs  
accounted for a total of 18% of the additive genetic vari-  
ance in RFI, and more than half of this was attributed  
to a single SNP that was significant ( $P < 0.05$ ). Based  
on the mean reduction in RFI for the favorable allele  
from each of these 4 SNPs, selection for all 8 favorable  
alleles would reduce RFI by 0.76 kg per day per animal.  
However, epistasis, variation in SNP effects between  
breeds, potential correlated effects on carcass traits and  
evidence of overdominance mean further valida-  
tion studies are required before implementation of these  
SNPs in genomic selection of RFI.

**Key Words:** cattle, feed efficiency, variant

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**P4008 Identification of genetic markers associated with behavioral traits in cattle.** J. Friedrich<sup>1</sup>, B. Brand\*<sup>1</sup>, K. L. Graunke<sup>2</sup>, J. Langbein<sup>2</sup>, B. Brandt<sup>1</sup>, S. Ponsuksili<sup>1</sup>, and M. Schwerin<sup>1</sup>, <sup>1</sup>Research Group Functional Genome Analysis, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, <sup>2</sup>Research Unit Behavioural Physiology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.

The ability of cattle to cope with environmental stimuli is important for animal welfare. Animals with sufficient coping abilities are assumed to be less prone to stress and more adaptable to new management systems. Behavioral traits can be described as consistent action and reaction pattern to environmental stimuli. Stable behavioral traits like calmness, boldness, aggressiveness or fearfulness also influence ease of handling, productivity and health. Today little is known about the genetic background of behavior in cattle, and besides milking temperament there is a lack of phenotypes routinely monitored to be considered for sire evaluations. The objective of this study is to identify molecular markers that might help to discriminate behavioral traits on the molecular level and to gain further insights into the genetic background of cattle behavior. Therefore, female calves of a Charolais x German Holstein F2 resource population were genotyped (Illumina BovineSNP50 BeadChip) and subjected to 3 behavioral tests (open field, novel object and novel human test) at 90 d post natum. Latency, frequency and duration of behaviors like activity, exploration and grooming were monitored during each test. First results of a whole genome scan using these measurements as phenotype indicate that there are genomic regions affecting the predisposition to certain behavioral traits in cattle.

**Key Words:** cattle, behavior

**P4009 Genomic selection for tick resistance in Braford and Hereford cattle using single-step methodology.** F. F. Cardoso\*<sup>1,2</sup>, C. C. G. Gomes<sup>1</sup>, M. M. Oliveira<sup>1,3</sup>, V. M. Roso<sup>4</sup>, M. L. Piccoli<sup>4</sup>, F. V. Brito<sup>4</sup>, R. H. Higa<sup>5</sup>, S. R. Paiva<sup>2,6</sup>, M. V. G. B. Silva<sup>2,7</sup>, L. C. A. Regitano<sup>2,8</sup>, M. J. Yokoo<sup>1</sup>, A. R. Caetano<sup>2,6</sup>, I. Misztal<sup>9</sup>, and I. Aguilar<sup>10</sup>, <sup>1</sup>Embrapa Southern Region Animal Husbandry, Bage, RS, Brazil, <sup>2</sup>National Counsel of Technological and Scientific Development (CNPq), Brasilia, DF, Brazil, <sup>3</sup>Coordination for the Improvement of Higher Level Personnel (CAPES/PNPD), Brasilia, DF, Brazil, <sup>4</sup>Gensys Associated Consultants, Porto Alegre, RS, Brazil, <sup>5</sup>Embrapa Agriculture Informatics, Campinas, SP, Brazil, <sup>6</sup>Embrapa Genetic Resources & Biotechnology, Brasilia, DF, Brazil, <sup>7</sup>Embrapa Dairy Cattle, Juiz de Fora, MG, Brazil, <sup>8</sup>Embrapa Southeastern Region Animal Husbandry, Sao Carlos, SP, Brazil, <sup>9</sup>University of Georgia, Athens, GA, USA, <sup>10</sup>National Agricultural Research Institute, Canelones, Uruguay.

The *Rhipicephalus microplus* tick is one of the main sources of losses in tropical cattle production, causing decreased performance, hide devaluation, and increased costs with treatments and transmission of infectious agents. The aim of this work was to evaluate the utility of genomic evaluation of Braford and Hereford cattle for genetic resistance to ticks. Repeated tick counts were obtained in 2010 and 2011 from 3,114 Braford and Hereford cattle from 7 herds of the "Delta G Connection" breeding program, totalizing 8,004 records. A sample of 1898 Braford and 262 Hereford animals was genotyped using Illumina BovineSNP50 Beadchip. Averaged and log-transformed records were combined with pedigree and genotypes to carry out single step genomic evaluation using BLUPF90 programs. Heritability of tick counts was estimated to be  $0.42 \pm 0.05$ , with a 75% increase compared with the estimate based on traditional pedigree evaluation ( $0.24 \pm 0.06$ ). Finally, data was split into 8 subsets (7 Braford and 1 Hereford) for a cross-validation study. Correlation between genomic predictions from the cross-validation and from full data analyses were  $0.61 \pm 0.13$  and  $0.47 \pm 0.05$ , respectively for Braford and Hereford animals. These results indicate that genomic selection could be used as a reliable tool to improve genetic progress for resistance to ticks in these breeds and to obtain resistant lines of cattle raised at South America.

**Key Words:** beef cattle, BovineSNP50 Beadchip, *Rhipicephalus microplus*

**P4010 Genes involved in muscle lipid composition in 15 European *Bos taurus* breeds.** S. Dunner<sup>\*1</sup>, N. Sevane<sup>1</sup>, D. García<sup>1</sup>, H. Levéziel<sup>2,3</sup>, J. L. Williams<sup>4</sup>, B. Mangin<sup>5</sup>, and A. Valentini<sup>6</sup>, <sup>1</sup>Dpto Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid, Madrid, Spain, <sup>2</sup>INRA Université de Limoges, Limoges, France, <sup>3</sup>Université de Limoges, Limoges, France, <sup>4</sup>Parco Tecnologico Padano, Polo Universitario, Lodi, Italy, <sup>5</sup>INRA Chemin de Borde-Rouge-Auzeville, Castanet-Tolosan, France, <sup>6</sup>Department for Innovation in Biological, Agro-Food and Forest Systems, Università della Tuscia, Viterbo, Italy.

Consumers demand healthy and palatable meat, both factors being affected by the fat composition. It has been shown that polyunsaturated fatty acids (PUFA) have beneficial health effects; however red meat, especially beef, has relatively high concentration of saturated fatty acids (SFA) and low concentration of PUFA. Modifying the fat composition of meat may be achieved by changing the diets of the cattle or selecting animals predisposed to synthesizing particular fat types. In this paper an association study has been performed in which a large panel of candidate genes involved in adipogenesis, lipid metabolism and energy homeostasis has been tested for effects on fat composition in 15 European cattle

breeds. Sixteen genes were found to have significant effects on different lipid traits, and among these CFL1 and MYOZ1 were found to have large effects on the ratio of 18:2/18:3, CRI1 on the amount of neutral adrenic acid (22:4 n-6), MMP1 on docosahexaenoic acid (22:6 n-3), and PLTP on the ratio of n-6:n-3. Several genes were also found to be associated with both lipid and organoleptic traits although with smaller effect. These included ALDH2, CHRNE, CRHR2, NEB, SOCS2, SUSP1, TCF12 and FOXO1. The results presented here help to understand the genetic and biochemical background underlying variations in fatty acid composition and flavor in beef.

**Key Words:** beef cattle, lipid, candidate genes

**P4011 Genetic variation in porcine Zip4-like zinc transporter.** G. Erhardt,<sup>\*</sup> F. Siebert, and G. Lühken, Department of Animal Breeding and Genetics, Justus-Liebig-University, Giessen, Hessen, Germany.

Zinc (Zn) is an essential trace element which is involved in several metabolic pathways. On the other hand, Zn can cause environmental problems if its emission via manure is too high. The Zn transporter Zip4 gene is known to play a major role in intestinal Zn absorption. The aim of this study was to analyze in a first step the sequence variability of the porcine Zip4-like zinc transporter gene. For this purpose, cDNA samples were generated from intestinal mucosal tissue and used to amplify and sequence 4 fragments covering the complete coding region of the gene. The sequence analysis revealed the presence of 7 nucleotide substitutions. Six of the nucleotide substitutions were synonymous whereas a substitution of A with C in exon IX caused an amino acid exchange from glutamic acid to alanine. Genotyping results including DNA samples from Pietrain, Deutsche Landrasse, Deutsches Edelschwein, commercial crossings and wild boars suggest a breed-specific presence of the A allele in Pietrain for this amino acid substitution while wild boars were homozygous CC. Alignment of exon IX sequences of other species revealed that most species have alanine in this position of the Zip4 peptide chain. Association studies of identified sequence variants with apparent zinc absorption are in progress.

**Key Words:** zinc, transporter, absorption

**P4012 Genomic selection and scan for major genes for a new lamb survival trait for the New Zealand sheep industry.** B. Auvray<sup>1</sup>, S. Vanderick<sup>2</sup>, S.-A. Newman<sup>1</sup>, and J. Everett-Hincks<sup>\*1</sup>, <sup>1</sup>AgResearch Ltd, Mosgiel, Otago, New Zealand, <sup>2</sup>Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium.

Lambing percentage is one of the most significant factors affecting profitability on New Zealand sheep farms. Since the early 1990s, lambing percentage has increased at about 1% per year from a relatively stable level of approximately 100%, and top performing sheep

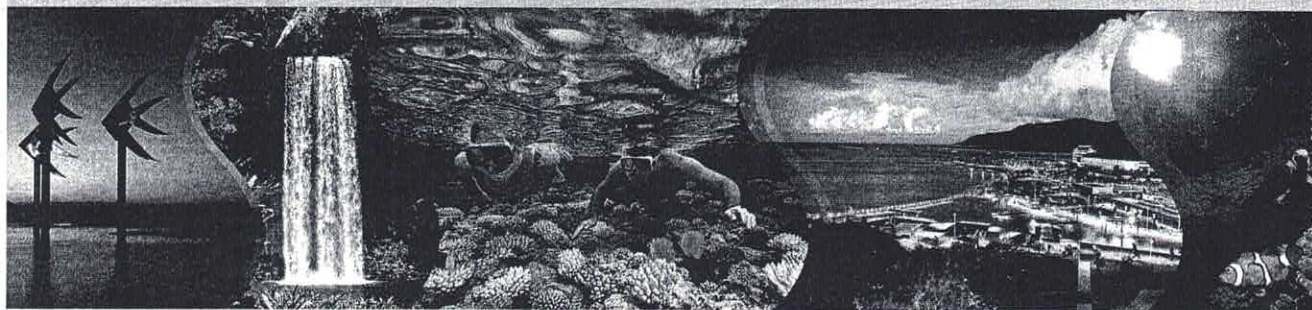


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