

of lactose intolerance, preventing intestinal diseases, and even reducing the risk of colon cancer. After gaining much popularity in other parts of the world, several probiotic dairy products are now on the market within the United States. Leading this campaign is Dannon which manufactures DanActive, a probiotic fermented milk product. Additionally, Dannon has recently released Activia, the first probiotic yogurt available in the United States. To assist consumers in identifying products which contain probiotics, the National Yogurt Association has established the Live and Active Cultures seal that manufacturers can place on their products that contain at least 100 million bacterial cultures per gram. As Americans become more and more concerned about the health benefits of their foods, products such as probiotic yogurts and fermented milk drinks will gain public interest and appeal.

Key Words: Probiotic, Yogurt, Cultured dairy products

230 The rippling effects of processor expansion: A Texas sized example. S. Brauning*, *Virginia Polytechnic Institute and State University, Blacksburg.*

Cheese consumption across America has been on the rise for many years in the United States. The demand and market for cheese products are continuing to increase both a domestically and internationally. Hilmar Cheese Company, located in the Central Valley, of California is

currently the largest single site producer of wholesale cheddar cheese and whey products in the United States. The company was founded in 1984 by twelve Jersey dairy farmers who wanted to capitalize on the value of their high-component milk. Today Hilmar Cheese Company processes the world's largest volume of Jersey milk, over 11 million pounds per day, with over 600 employees. The company prides itself in maintaining "mutually beneficial relationships between company owners, employees, milk producers, customers and the local community." To keep abreast the growing demand for their product, they have broken ground in Dalhart, Texas to install a second processing plant. Dalhart is located in the northwest panhandle of Texas, with a population of 7500 people; the local economy flourishes off agriculture. The Dalhart expansion of Hilmar is to be made in two phases. It is anticipated that the plant will originally have the capacity to process about 5 million pounds of milk per day with room for future expansion. The company expects to hire approximately 120 local residents, and hopes to contract their milk supply exclusively from Jersey herds. With such an expansion upon Texas's Dairy Industry one must consider the impacts the expansion could have. One may expect changes to be seen in areas such as cattle numbers, milk supply, milk prices, dairy cattle replacement availability and replacement pricing. The installation of the new plant can be expected to have local, regional and national effects on the economy in various facets.

Key Words: Cheese plant

Sheep Species: Application of Genomics to Sheep Production

231 Resources available for sheep genomics research. N. E. Cockett*, T. S. Hadfield, C. H. Wu, and K. Nomura, *Utah State University, Logan.*

Animal geneticists have been searching for the molecular basis of production traits in livestock species, including sheep, for over 40 years. Phenotypes of interest in sheep include fertility, reproduction, growth rate and efficiency, milk production, carcass quality and composition, wool characteristics, and disease resistance. The development of an ovine genome map containing molecular markers and genes has greatly advanced the identification of genetic regions containing quantitative trait loci (QTL) in sheep. Other genomic resources available for researchers investigating traits in sheep include an ovine radiation hybrid panel, large insert genomic libraries, and large-scale sequencing projects. These resources will greatly facilitate current positional cloning efforts to identify causal mutations that underlie economic trait loci. Scientists involved in sheep molecular genetics will be better able to exploit comparative information from the fully sequenced, information-rich genomes (human, mouse, and rat). These resources will also provide the scaffold for sequencing the ovine genome, a project that the sheep community is working towards for the future. In order to continue the identification of genes controlling important phenotypes in sheep, development of ovine genomic resources should continue.

Key Words: Ovine, Genomics, Resources

232 Molecular tools for sheep breeding: DNA-based markers for monogenic traits and QTL. J. E. Beever* and A. D. Markey, *University of Illinois, Urbana.*

Advances in sheep genomics during the past decade have led to the identification of molecular variation influencing a number of

phenotypic characteristics. As a result, DNA-based genetic tests are becoming common in selection programs and thus, are destined to impact breeding management. A review of current DNA-based diagnostic tests for monogenic traits, as well as the potential use of marker-assisted selection for QTL will be discussed.

Key Words: Sheep, DNA, QTL

233 How genomics will continue to improve productivity for the New Zealand sheep sector. T. Wilson*, *AgResearch, University of Otago, Dunedin, New Zealand.*

The New Zealand sheep industry has been very successful over the past 15 years in increasing production of lambs and increasing the meat produced per lamb for the export market. This is due to many factors such as better fertilisers, and improved plant cultivars and farming systems. Alongside this, significantly more attention has focused on detailed phenotyping and selection of rams for key traits which has maintained this growth in an upward direction. Genomics has already started to deliver benefits with the discoveries of the causative gene mutations for reproduction genes (Inverdale and Booroola) now having commercial application in certain farming systems. Several other research programmes are close to finding the gene mutations, with many traits fine mapped to regions where commercial strategies can be employed. For the next five to ten years, outcomes from genomic research programmes will be needed to maintain the growth in on-farm productivity within the New Zealand sheep industry. Strategies combining bioinformatics, expression profiling and high density SNP chips soon to be available will offer unprecedented opportunities for the sheep sector.

Key Words: Genomics, Productivity, DNA technologies

234 SheepGenomics – An integrated gene discovery program.

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SheepGenomics (the Program) is a functional genomics program designed to discover genes and their functions and deliver products based on new genetic technologies for the benefit of the Australian sheep industry. There are four industry subprograms contained within the program, including wool biology, muscle growth and development, host resistance to internal parasites and reproductive efficiency. The research strategy of each of these industry subprograms uses positional and functional candidates for gene mapping with a view to identifying precise QTL regions for use in selection and then identification of candidate gene targets for therapeutic intervention of these traits. The most immediate outcome from the program is a series of DNA marker tests for muscle quality and quantity, parasite resistance and wool quality. Work is currently underway to validate existing marker tests and integrate allele effects into routine breeding value calculations so as to facilitate optimal use of genomic information in breeding decisions. SheepGenomics has placed particular emphasis on developing the tools needed to conduct genomic research in sheep including evaluation of bovine micro arrays, development of gene screening assays as well as building large well characterised sheep flocks to enable powerful gene mapping studies. A number of public domain outcomes arise from the Program, which are the result of significant international collaboration. They include development of a virtual sheep genome based on alignment of the end-sequences of BAC clones spanning the entire sheep genome with existing bovine sequence. Current research also involves development of a 1.5x ovine sequence, discovery of tens of thousands of new SNP and microsatellite markers as well as timely integration of this information into an informative sheep genome map. The scope for delivery of long-term benefits to the Australian sheep industry is enormous. Furthermore, each of the publicly available resources will be extremely beneficial to worldwide sheep genome related research efforts.

Key Words: Genomics, Sheep, DNA markers

235 Genomic regions associated with sheep muscle and carcass traits.

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Linkage maps for the sheep genome have been developed but to date no complete genome scan for muscle, adipose or carcass traits are in the public record. Genome scans of selected chromosomes have identified four regions affecting carcass traits in Suffolk and Texel breeds. Chromosomes 2 and 3 were reported to have quantitative trait loci for fat depth and chromosomes 1 and 18 had quantitative trait loci for muscle depth. Several loci affecting muscle growth traits have been identified in sheep. These include callipyge and rib-eye muscling (Carwell) on chromosome 18. The muscle hypertrophy locus in Texels maps near the myostatin locus on chromosome 2. The rib-eye muscling locus lies close to the callipyge region on chromosome 18 but the specific mutation is not known. The callipyge mutation has been identified as a single nucleotide polymorphism in an intragenic region of an imprinted gene cluster. The mutation has altered the expression of at least 5 genes surrounding the mutation. Two of the genes, DLK1 and PEG11 that have paternal allele-specific expression, are candidates for causing muscle hypertrophy in callipyge lambs. With the completion of whole genome sequences in several species including human, rodents, chickens and cattle, the role of noncoding RNA and micro RNA in regulating gene expression has become better understood. The imprinted gene cluster surrounding the callipyge mutation expresses several noncoding RNA and micro RNA that are likely to be involved in polar overdominant inheritance of the phenotype. Recently, a micro RNA that is normally expressed in sheep skeletal muscle has been reported to down-regulate a mutant myostatin allele in Belgian Texels resulting in the muscle hypertrophy phenotype. The callipyge allele and Belgian Texel myostatin allele provide examples of how single nucleotide mutations can have substantial phenotypic effects on muscle and carcass traits through genomic regulatory mechanisms.

Key Words: Sheep, Genomics, Muscle

ADSA – SAD Undergraduate Competition: Original Research

236 Probiotic ice cream manufactured with a weight loss ingredient. M. Brown* and K. J. Aryana, *Louisiana State University, Baton Rouge.*

Obesity is directly related to about 300,000 deaths per year in the United States. The Surgeon General estimated obesity to cost \$117 billion a year. A novel ingredient, namely “Super Citrimax”, is being marketed as a weight loss ingredient (WLI). *Lactobacillus acidophilus* is one of the most effective forms of probiotic (good, helpful) bacteria discovered. The objective was to determine the effect of various amounts of the WLI on the physico-chemical, microbiological and sensory characteristics of probiotic ice cream. The WLI “Super Citrimax” was incorporated at the rate of 0, 1.5, 3.0 and 4.5g per 473 ml (pint) of ice cream. *L. acidophilus* was incorporated into all the pasteurized, homogenized and cooled ice cream mixes at the rate of 0.7% w/v mix. Product manufacture was replicated three times. The meltdown time for the first 15 ml of the ice creams with 3.0 and 4.5g WLI was significantly lower compared to the control. The meltdown volume of the control after one hour was significantly lower compared

to the ice creams with WLI at all concentrations. There were no significant ($p < 0.05$) differences between the control and all treatments for standard plate counts. Control had significantly the highest lactobacilli counts followed by the ice creams with 1.5 g WLI. The ice creams with 3.0 and 4.5g WLI had significantly the lowest lactobacilli counts. The flavor scores for the ice creams with 0, 1.5, and 3.0g WLI were not different from each other but were higher than the ice cream with 4.5 g. Similar results were obtained for the flavor scores of the heat shocked ice creams. There were no differences in body and texture scores of any of the ice creams. The body and texture scores of the heat shocked ice creams with 0, 1.5, 3.0g WLI were not significantly different from each other, but scores for the ice creams with 4.5g were significantly lower than the ice creams with 0 and 1.5g. Incorporation of WLI up to 3 g per 473 ml of ice cream did not influence its flavor. The use of WLI decreased meltdown time, increased meltdown volume, did not alter the standard plate counts, lowered the lactobacilli counts and did not influence sensory body and texture.

Key Words: Probiotic, Obesity, Dairy