

20, 19 turned out to be false positives and one dexamethasone-induced gene was identified; its full-length cDNA was cloned from a library and sequenced. The cDNA is a novel member of the Ras-superfamily and was named Dexras1 due to its ability to be induced by dexamethasone. Experiments are in progress to characterize the role of Dexras1 in the pituitary and in other steroid-responsive tissues. Overall, differential display was extremely useful in identification of a novel gene, however, it may require considerable effort in terms of testing various PCR primer combinations and the technique may be expected to generate a significant number of false positives.

**Key Words:** Differential , Display, Dexamethasone

**594 Genes, Chips and Animal Biology.** Nagappan Mathialagan\*<sup>1</sup>, Charles Bolten<sup>1</sup>, Steven Wagner<sup>1</sup>, John Byatt<sup>1</sup>, and Frances Buonomo<sup>1</sup>, <sup>1</sup>Monsanto Animal Agricultural Group.

Genomic technologies have transformed the animal biology research into a new era of discoveries in a similar fashion as the introduction of radioimmunoassay techniques. Genomics has resulted in the identification of thousands of new gene sequences in farm animal species with no real link to functional association. Comparative genomic analysis with completed genomes such as human has been used to discover orthologous genes. However, this approach still leaves out the annotation of genes which are novel to the animal species. Gene expression technologies like Microarrays and Serial Analysis of Gene Expression (SAGE) are used to determine the expression of thousands of genes simultaneously. Species-specific microarrays need to be used to associate a function to these new genes. However, cross-species microarrays may be used in instances where there are no species-specific arrays. We have used Incyte human microarrays for transcript profiling of bovine mammary gland to identify regulated genes associated with milk production. A set of human gene homologues were identified that are regulated during lactation and involution. Genes up-regulated during lactation, identified by heterologous profiling, were selected for confirmation by other methods such as Northern blot analysis, quantitative RT-PCR, subtractive cDNA libraries and nylon arrays. One example of a regulated gene we selected for confirmation was Stearoyl-CoA-Desaturase (SCD), an enzyme involved in the synthesis of conjugated linoleic acid. An increased expression was associated with lactation while a sharp decline in the expression was observed with involution. In addition, our experience with

## Preharvest and Postharvest Approaches to Modification of Milkfat

**596 The milk fat globule membrane of buttermilk: a unique ingredient.** M. Corredig\*, *Department of Food Science and Technology, University of Georgia.*

The presence of material derived from the milk fat globule membrane (MFGM) makes buttermilk (the byproduct of buttermaking) distinct from any other dairy product. Studies of MFGM have revealed strong associations of the membrane lipids with various membrane proteins (butyrophilin, xanthine oxidase and some minor proteins). When membrane material is isolated from buttermilk a high ratio of polar lipids is found, in particular phosphatidyl ethanolamine, phosphatidyl choline and sphingomyelin. Phospholipids play an important role in many metabolic processes, and phospholipid-enriched fractions are today marketed as important ingredients in a variety of dietary products. Furthermore, evidence is emerging that sphingomyelin from milk may have anti-cancer properties and other health-related benefits. In addition to

## Role of Extracellular Matrix (ECM) in Growth and Development

**597 The role of the extracellular matrix in growth and development: An introduction.** M.W. Orth\*, *Michigan State University.*

Besides providing structural support, the extracellular matrix (ECM) has recently been shown to play a significant role in the regulation of tissue growth and development. As an example, certain ECM molecules can sequester growth factors and release them during tissue remodeling. Also, proteolytic products of ECM molecules can have a unique biological activity via interactions with cell surface receptors. The focus of this symposium will be to examine the role and regulation of the ECM in four tissues of particular interest to the animal scientist. Dr. Sandy

heterologous arrays showed that genes can be erroneously identified due to sequence identity of bovine genes to unrelated genes in human. This observation emphasizes the preference to use species-specific arrays for gene expression studies.

**Key Words:** Transcript Profiling, Microarrays, Genomics

**595 Proteomics in the animal sciences.** Lawrence Dangott\*, *Texas A&M University, College Station, TX.*

One of the goals of biologists in the post-genome era will be to characterize all the proteins within an organism, tissue or organelle, in order to describe the pathways and protein interactions that mediate cellular function. Proteomics is the term given to the large-scale analysis of proteins using biochemical, biophysical and chemical techniques of analysis. Although traditionally associated with the two-dimensional display of large numbers of proteins, in the post-genomic era, proteomics is dividing into three main areas; 1) protein identification and micro-characterization; 2) differential expression analysis of proteins in normal and altered tissues; and 3) studying protein-protein interactions. Approaches to achieve these goals require the combination of traditional molecular biological, biochemical and biophysical techniques with the expanding capabilities of high-throughput robotics and high-sensitivity, high-resolution mass spectrometry as well as the development of new technologies. These kinds of approaches are being used in our laboratory and others to explore and explain the functions, interactions and regulation of proteins in animal reproductive biology and environmental toxicology. Proteins involved in embryo implantation are being identified in ovine uteri using 'knock-out' ewes, two-dimensional gels and in gel digestion techniques coupled to automated protein micro-sequencing and MALDI-TOF (matrix-assisted laser desorption ionization time-of-flight) mass spectrometry. Similarly, proteins involved in horse sperm differentiation are being identified by applying these techniques to proteins isolated from in vitro cultures of equine seminal tubules. In related experiments, post-translational modifications are being mapped by ion-trap electrospray mass spectrometry and multi-dimensional chromatography coupled with mass spectrometry is being used to identify components of protein complexes.

**Key Words:** Proteomics, Mass spectrometry

the nutritional quality of MFGM, a more detailed analysis of the composition of buttermilk has suggested the utilization of buttermilk as an ingredient in the manufacture of foods, for example low fat cheese and yogurt. The behavior of buttermilk as a functional ingredient can be attributed to the presence of skim milk proteins and the MFGM, however the role played by the various components and their interactions is not understood. Processing history and compositional differences also seem to affect the functionality of MFGM. Understanding the various components and the functional properties of buttermilk will allow this byproduct to become a source of new and unique ingredients. Our discussion will review the current literature in this area and present some thoughts on the further development of commercial products derived from the MFGM.

**Key Words:** phospholipids, MFGM, buttermilk

Velleman will describe the architecture of the ECM in skeletal muscle tissue with an emphasis on the function of the proteoglycan component. The predominant focus on myofibrillar proteins traditionally has overshadowed this exciting area of research. Dr. Tom Schmid will discuss the role of the ECM during endochondral bone formation, with an emphasis on ECM proteins found in unique regions of growth plate and articular cartilage that were discovered in his laboratory. He will also discuss the potential of using ECM molecules as biological markers in physiological fluids to monitor the development and health of the skeleton. Dr. Russ Hovey will discuss the development of the mammary gland and its complex architectural structure. Specifically his research interest focuses on understanding the contribution of the mammary stroma dur-