28 Exploiting the public genome databases for equine science. L. C. Skow*, *Texas A&M University*, *College Station*.

Improved technologies developed during and consequent to the human genome project have resulted in the complete genome sequences of more than a thousand species of microbes and eucaryotes, including 25 species of mammals and 10 non-mammalian vertebrate species. These vast sources of publicly available data represent invaluable potential information for inquiry at all levels of biological processes. This presentation will provide an introductory overview to on-line genome databases, gene mining tools and genome annotation resources as a prelude to the following speakers who will speak to specific genome resources and tools recently developed for equine science based on the horse genome sequence. Emphasis will be on functional genomics applications.

Key Words: Equine, Genome Tools, Functional Genomics

29 Identification of genes for health and performance traits in horses through whole genome analysis. J. Mickelson*, *University of Minnesota*, *St Paul*.

An extraordinary and sustained effort by the equine genome research community, and the excellent downstream potential of the horse as a biomedical model, played a significant role in the selection of the horse for full genome sequencing and genome structure analysis by the National Human Genome Research Institute. As a result, we are now extremely well-positioned to address our long-term research goals, which can briefly be summarized as identifying genes and pathways associated with normal health, disease, performance, growth, development, fertility, and disease resistance in horses. With focused research investments we can now expect advances in our understanding of equine biology, improvement in health, performance and well being, as well as the development of equine models of significant human health concerns.
The equine research community now has the technology to rapidly genotype tens of thousands of single nucleotide polymorphism (SNP) DNA markers on a single horse for less than $300. These whole genome SNP chips can, in principle, allow the identification of genes having a major influence on traits of interest provided that a sufficient population of well phenotyped horses can be acquired. In this presentation the principles, practice, and limitations to such whole genome scans to identify the chromosomal location of genes contributing to a trait, and the means to find the specific genes and alleles that may be responsible, will be presented.

Key Words: Equine Genetics, Equine Genome, SNP Marker

30 Transcriptional profiling for gene expression analyses of equine samples. J. N. MacLeod*, *University of Kentucky*, *Lexington*.

Analyses of gene expression are widely performed in experimental biology to investigate cell and tissue function, cellular differentiation, disease pathogenesis, and the molecular mechanisms of different therapies. The basic premise is that valuable insight about a tissue or cell type can be obtained from studying qualitative and quantitative changes in the patterns of gene expression. Several laboratory techniques are used routinely to evaluate gene expression on a transcriptional level. Selection of a specific procedure is usually dependent on the experimental objectives, amount of sample available for analysis, investigator preferences and resources, and cost considerations. One challenge in quantitative analyses of gene expression can be trying to select the individual genes that will be most interesting and biologically relevant to study. Transcriptional profiling enables scientists to initially make a broad assessment of the approximately 22,000 genes in the mammalian genome. Using cDNA and oligonucleotide microarrays, expression across large subsets of genes and even the entire genome can be evaluated in a single experiment. These screening procedures often enable a more informed decision to be made on which individual genes, or groups of functionally related genes, should be most interesting to focus on at greater detail in subsequent experiments. Essentially, the scientist can evaluate the "forest" before making a decision on which individual "trees" should be investigated further. This presentation will overview transcriptional profiling concepts and microarray platforms, concentrating on procedures that are currently being used to profile gene expression in equine RNA samples. Emergent technologies based on "next generation sequencing" and mRNA resequencing will be discussed.

Key Words: Equine, Transcriptional Profiling, Microarray

31 Let the genome give your project a leg-up: Real-time qPCR strategies in equine research. S. Brooks*, *Cornell University*, *Ithaca, NY*.

Sequencing of the equine genome has opened-up a multitude of possibilities in research techniques for equine scientists. During the last 100 years great discoveries have been made using antibodies, histochemistry, biochemistry and population or quantitative statistics. Unfortunately, reagents needed for traditional assay methods, like antibodies, are not as readily available in the horse as they are in other species. Furthermore, the methods often require special expertise. In some cases, Real-Time qPCR can offer a convenient alternative. With a genome sequence literally at our fingertips we can now design primers and probes for virtually any target in record speed. As the complexity of gene regulation is unraveled, use of gene expression studies has likewise expanded. Real-Time qPCR, using mRNA as a template, can measure changes in gene expression for proteins of interest faster and more accurately than ELISA or western plot can for the protein itself. Additionally, purified nucleic acids and more easily aquired and stored than fresh tissue or protein. In addition to gene expression Real-Time platforms are currently being used for genotyping, quantification of copy-number variants, mutation scanning, mirco and siRNA detection, DNA-methylation analysis and finally, coming full circle, in immuno-qPCR, which can improve sensitivity up to 1000-fold over traditional ELISA.

Key Words: Horse, Genome, Real Time qPCR