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MEF2A expressions, and a decrease of Akt1, CDK2, MEF2C, and Myf5. On the contrary, overexpression of myostatin contributed to an increase of Akt1, CDK2, Myf5, and PPARγ, and a decrease of p21, C/EBPα and leptin expressions at the transcript level. These results suggested that myostatin positively regulated Akt1, CDK2, Myf5, leptin and C/EBPα, but negatively regulated p21 mRNA expression in adult fibroblasts. This research would provide a reference for utilizing the lentiviral system inactivated myostatin gene in fibroblasts to generate transgenic sheep and ameliorate muscle fibrosis and atrophy by gene therapy in the future.

Key Words: myostatin, sheep, lentiviral vector

P2015 Resources of pig expressed genes: Full-length-enriched cDNA libraries and large-scale sequencing based on the libraries. Hirohide Uenishi¹, Takeya Morozumi², Daisuke Toki², Tomoko Eguchi-Ogawa*¹, Lauretta A. Rund³, and Lawrence B. Schook³, ¹National Institute of Agrobiological Sciences, Tsukuba, Ibaraki 305-8602, Japan, ²Institute of Japan Association for Techno-innovation of Agriculture, Forestry and Fisheries, Tsukuba, Ibaraki 305-0854, Japan, ³University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA.

Collection of the nucleotide sequences of genes expressed in various porcine tissues and determination of entire cDNA sequences are necessary for investigations of gene function in pigs. The cDNA sequences are also valuable for annotation of the pig genome, the draft sequencing of which was completed by the international consortium. Here we present a summary of sequencing analysis by using 32 full-length-enriched cDNA libraries derived from 28 kinds of porcine tissues and cells, including tissues derived from pigs that were cloned from a sow subjected to the genome sequencing. We conducted a large-scale expressed sequence tag (EST) analysis in pigs with the libraries and obtained more than 330,000 EST reads from the 5'-ends of the cDNA clones, corresponding to more than 15,000 genes. In parallel with the EST analysis we conducted sequencing of the entire inserts of the representative cDNA clones in the libraries. We have finished sequencing more than 31,000 clones corresponding to at least 12,000 genes. Mapping of the sequences of these cDNA clones on the latest draft sequence of the pig genome indicated that the clones originate from about 15,000 independent loci on the pig genome. The porcine ESTs and cDNA sequences presented here are not only useful for the genome annotation, but also valuable for molecular biology-based analyses in pigs.

P2016 Genetic effects on expression of *IGF2R* and *AIRN* in bovine fetal tissues. M. Ghanipoor*¹, A. Javadmanesh¹, D. Thomsen¹, G. Nattrass², K. Kind¹, and

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The insulin-like growth factor 2 receptor gene (IGF2R) encodes a transmembrane receptor that binds and regulates bioavailability of insulin-like growth factor 2, a potent growth promoting hormone. Mouse gene knockout experiments have demonstrated the essential role of IGF2R in prenatal growth and development. The gene is subject to genomic imprinting and expressed from the maternal allele in mouse and bovine, but is not imprinted in human. Imprinted IGF2R expression is regulated by expression of a partially overlapping, reciprocally imprinted noncoding antisense RNA, AIRN. We analyzed expression of IGF2R and AIRN in brain, cotyledon, heart kidney, liver, lung and skeletal muscle of bovine Day153 fetuses with Bos taurus (Angus), Bos indicus (Brahman) and B. taurus × B. indicus reciprocal cross genetics (n = 74) by real time quantitative PCR to determine effects of fetal genetics and sex. Statistical analysis of qPCR data in general linear models (PASW Statistics 19) showed that AIRN expression in brain, and IGF2R expression in cotyledon, was affected by fetal genetics (ANOVA, both P < 0.001). Expression of both genes was significantly higher in Brahman (sire) × Angus (dam) fetuses compared with all 3 other groups of fetuses (t-tests P < 0.01). In addition, expression of IGF2R in skeletal muscle was affected by an interaction between fetal sex and genetics (P < 0.05) where female fetuses with Brahman maternal genetics showed significantly higher transcript levels than all other groups. These findings suggest a complex tissue-specific pattern of expression for IGF2R and AIRN which is controlled by the interplay between genetics, epigenetics and fetal sex.

Key Words: bovine, IGF2R, AIRN

P2017 MiRNAs in host-virus interaction: The Pseudorabies Virus (PrV) model. Nada Mahjoub¹, Barbara Klupp², Walter Fuchs², Marie-Laure Endale Ahanda¹, Sophie Dhorne-Pollet¹, Francois Lefevre³, Thomas C. Mettenleiter², and Elisabetta Giuffra*¹, ¹National Institute for Agronomical Research (INRA), Animal Genetics and Integrative Biology Unit, GIS Team, Jouy-en-Josas, France, ²Friedrich-Loeffler-Institut (FLI), Institute of Molecular Biology, Greifswald-Insel Riems, Germany, ³National Institute for Agronomical Research (INRA), Virology and Molecular Immunology Unit, Jouy-en-Josas, France.

MicroRNAs (miRNAs) are micromanagers of gene expression. Due to their non immunogenic nature, viral miRNAs represent an efficient tool to control the cellular environment. Most herpesviruses encode miRNAs to manipulate the post-transcriptional regulation of their