

experiment on two samples, which allowed us also to optimize the whole process of: RNA extraction, RNA sequencing by Illumina technology, and implementation of the bioinformatic pipeline for sequence data analyses. This first assay allowed the identification of more than 350 miRNA expressed in adipose tissue, some of them till now unknown in pigs. We observed that all mitochondrial genes are expressed in adipose tissue and, as far as nuclear genes are concerned, it was possible to identify more than 16,000 genes expressed. We computed that around 400 genes, approximately the 2% of those annotated in the pig genome, are responsible for half of the overall transcripts expression in fat tissue and could. The proteins coded by these genes could have the highest functional relevance on fat metabolism in pigs. In order to elucidate their role a functional classification of these genes is under way.

#### *Acknowledgments*

This research was supported by Progetto AGER, grant n°2011-0279.

## C-060

### **Combined genomics and metabolomics approaches to identify markers associated with production traits in pigs**

Luca Fontanesi<sup>1</sup>, Stefania Dall'Olio<sup>1</sup>, Flaminia Fanelli<sup>2</sup>, Emilio Scotti<sup>1</sup>, Giuseppina Schiavo<sup>1</sup>, Francesca Bertolini<sup>1</sup>, Francesco Tassone<sup>1</sup>, Antonia Bianca Samoré<sup>1</sup>, Samuele Bovo<sup>1</sup>, Gian Luca Mazzoni<sup>1</sup>, Maurizio Gallo<sup>3</sup>, Luca Buttazoni<sup>4</sup>, Giuliano Galimberti<sup>5</sup>, Daniela Giovanna Calò<sup>5</sup>, Pier Luigi Martelli<sup>6</sup>, Rita Casadio<sup>6</sup>, Uberto Pagotto<sup>2</sup>, Vincenzo Russo<sup>1</sup>

<sup>1</sup>*Dipartimento di Scienze e Tecnologie Agro-alimentari, Università di Bologna, Italy*

<sup>2</sup>*Dipartimento di Scienze Mediche e Chirurgiche, Università di Bologna, Italy*

<sup>3</sup>*Associazione Nazionale Allevatori Suini, Roma, Italy*

<sup>4</sup>*Consiglio per la Ricerca e la Sperimentazione in Agricoltura - Centro di Ricerca per la Produzione delle Carni e il Miglioramento Genetico, Monterotondo Scalo (RM), Italy*

<sup>5</sup>*Dipartimento di Scienze Statistiche Paolo Fortunati, Università di Bologna, Italy*

<sup>6</sup>*Biocomputing Group, Università di Bologna, Italy*

*Corresponding author: luca.fontanesi@unibo.it*

The development of high throughput genomics (next generation sequencing and high throughput genotyping) and metabolomics platforms has opened new perspectives for the identification of the genetics factors affecting traits of biological relevance in all species, including production traits in farm animals. In pigs, benefits derived from the recent sequencing of the pig genome can be fully exploited by combining advanced genomics and metabolomics approaches. In this work we integrated several resources, experiments and data with the final aim to identify markers (DNA polymorphisms and metabolites) associated with

production traits in Italian Large White pigs. High throughput genotyping was carried out using the Illumina Porcine60SNP BeadChip array and customized Golden Gate system on extreme and divergent pigs for back fat thickness (BFT) estimated breeding values (EBVs) (300-560 animals) and average daily gain (ADG) EBVs (360 pigs), chosen among a population of about 12,000 performance tested pigs. Next generation sequencing was carried out using the Ion Torrent PGM machine to identify single nucleotide polymorphisms (SNPs) from two reduced representation libraries developed from pooled genomic DNA constructed from 50 pigs with most positive and 50 pigs with most negative BFT EBVs, respectively. A total of 7,510,918 reads were produced and 447,031 SNPs were called, using stringent criteria. Genome wide association studies made it possible to identify a quite large number of significant SNPs affecting BFT, ADG and correlated traits. In addition, several genome regions containing significant SNPs for BFT were enriched of SNPs identified from the Next Generation Sequencing experiment. Metabolomics information was obtained from 800 performance tested pigs using a mass spectrometry (MS/MS) analytical pipeline to measure 180 blood plasma metabolites. Estimated heritability and correlation among all these parameters and production traits indicated that a few metabolites could be useful predictors of EBVs for production traits. All these data will be used to develop a first systems biology platform to understand the fine biological mechanisms affecting production traits in pigs.

## C-061

### **Proteomics for milk proteins characterization in Girgentana goat breed**

Giuseppina Monteleone, Salvatore Mastrangelo, Maria Teresa Sardina, Giuseppe Gallo

*Dipartimento di Scienze Agrarie e Forestali, Università di Palermo, Italy*

*Corresponding author: giuseppina.monteleone@unipa.it*

Proteomics has been widely used to characterize milk protein content in livestock species and unravel protein biological functions. The aim of this work was to characterize the Girgentana goat breed whole milk and milk fraction proteins by two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) and mass spectrometry. Bulk milk samples from two farms locate in Palermo and Agrigento (Sicily) areas were collected during the early stage of lactation. Initially, 2D-PAGE and protein detection protocols were set-up. In particular, 2D-PAGE analyses were carried out on whole milk using 18-cm IPG strips ranging from pH 3-10 and 4-7 and 12.5% polyacrylamide gel for first and second dimension separation, respectively. Then, staining methods (silver-, colloidal Coomassie Blue G-250- and fluorescent dye-based method) were tested to reveal protein spots in 2D-gels. In silico 2D-gel image analysis, performed using Image Master 2D Platinum software, revealed that silver and fluorescent (based on SyproTM Ruby) staining methods showed similar results in terms of sensitivity/resolution. Then, centrifuge-based protocols were set-up to obtain milk protein fractions. The protein profiles