linkage disequilibrium (LD) with SNPs in the promoter region of the nearby gene *ELOVL elongase 6* (*ELOVL6*), located on SSC8 at 120 Mb. In the analysed ILW population we confirmed the presence of LD between H3GA0025321, SIRI0000509 and INRA0030422 and *ELOVL6* promoter variants. These results seem to indicate the presence of a mutation influencing BF FA composition in the promoter sequence of *ELOVL6* gene. Furthermore, in addition to the GWA study evidencing the role of *ELOVL6* gene on BF FA quality, we performed for this gene an expression study in porcine BF tissue. Sixty samples chosen out of the 800 ILW for their extreme and divergent BF FA composition (high and low level of long chain FA) were analysed. qRT-PCR was performed using *YWHAZ* and *HPRT1* as normalising genes. *ELOVL6* showed different expression levels between samples divergent for the length of FA chain but no difference was found between different genotypes for the three considered markers. These findings suggest that *ELOVL6* has a strong role in determining BF FA profile and the identification of variants of this gene may provide markers for genetic selection addressed towards the improvement of pork FA composition.

O140

Genome wide association studies for haematological and clinical-biochemical parameters in Italian Large White pigs

Samuele Bovo[1,2], Gianluca Mazzoni[1,3], Giuseppina Schiavo[1], Francesca Bertolini[1,4], Giuliano Galimberti[5], Antonia B. Samorè[1], Stefania Dall'Olio[1], Luca Fontanesi[1]

[1]*Dipartimento di Scienze e Tecnologie Agroalimentari, Alma Mater Studiorum University of Bologna, Italy*
[2]*Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Alma Mater Studiorum University of Bologna, Italy*
[3]*Department of Veterinary Clinical and Animal Sciences, University of Copenhagen, Denmark*
[4]*Department of Animal Science, Iowa State University, United States of America*
[5]*Dipartimento di Scienze Statistiche "Paolo Fortunati", Alma Mater Studiorum University of Bologna, Italy*
Contact: luca.fontanesi@unibo.it

Diseases are the most important causes of economic losses in all livestock species. Genetic improvement for disease resistance and resilience is becoming an essential issue in pig breeding programmes. Haematological and clinical-biochemical parameters reflect, at least in part, the immune capacity and the basic physiological states of the animals that can be considered as potential indicators of the capacity of the animals to cope with infections. We recently demonstrated that several of these parameters are highly heritable in pigs and that, for this reason, it could be possible to use them as proxies of disease resistance-related traits in breeding programmes. With the aim to identify genetic factors that might indirectly explain part of the genetic variability of these traits, we carried out genome wide association studies for 15 haematological and 15 clinical-biochemical parameters measured in about 900 performance tested Italian Large White pigs. All animals were genotyped with the Illumina PorcineSNP60 BeadChip genotyping tool. Association analysis was carried out using GEMMA. The most significant QTLs were identified for the number of basophils on porcine chromosome (SSC) 14, the number of eosinophils on SSC3, SSC7 and SSC10, the number of monocytes on SSC15, the levels of total cholesterol and LDL-cholesterol on SSC3, mean corpuscular hemoglobin level on SSC14, alanine aminotransferase activity on SSC7 and hemoglobin level and hematocrit on SSC18. These results will be useful for the identification of the causative mutations of these phenotypes that could be important to dissect disease resistance and resilience related traits in pigs.

O141

Estimation of genetic parameters for honey production in the honeybee – Preliminary results

Elena Facchini, Rita Rizzi, Giulio Pagnacco, Giulietta Minozzi

Dipartimento di Medicina Veterinaria, University of Milano, Italy
Contact: elena.facchini@unimi.it

The estimation of breeding values in genetic selection programs is a tool of paramount importance, as it allows to identify genetically superior individuals that can then become parents of the next generation, improving traits of economic interest. Honeybees represent an important productive livestock species due to hive products such as honey, bees wax, pollen and to its invaluable role as pollinators of agricultural crops and wild plant species. Genetic evaluation in the honeybee is considerably difficult due to their peculiar mode of reproduction. Phenotypes are measured on the colony, which consists of one queen and her daughters, *i.e.* thousands of

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workers. The queen is the only fertile female of the colony that mates with 10 to 20 drones just once, and stores a life lasting reserve of sperm cells in her spermatheca. Drones are haploid and their gametes are clones of their genotype. Furthermore, drones die right after mating, which means they mate just once in their lifetime.

Restricted Maximum Likelihood (REML) and Best Linear Unbiased Prediction (BLUP) are important methodologies in livestock breeding for estimating variance components and predicting breeding values, respectively. These methods require information on the genetic relationship among tested individuals in order to estimate the individual additive genetic merit for a phenotypic trait. Ordinary rules for the estimation of genetic relationship are not applicable to honeybees due to queen's multiple mating and haploid males. The aim of the work was to develop a numerator relationship matrix adapted to honeybee peculiarities, in order to estimate breeding value, variance components and genetic parameters for honey yield. Tested colonies ($n = 120$) derived from 8 parental lines have been distributed in 4 apiaries nearby Lodi (Lombardy). Honey was harvested twice during spring 2016. A modified R function was used to compute the inverse of numerator relationship matrix, which is required for the estimation of variance components and the prediction of breeding values. The fitted mixed model included fixed effects of apiary, strength of the colony and production, and both genetic additive and permanent environment random effects. Preliminary results show heritability and repeatability of honey production of 0.33 and 0.54, respectively. These results are in agreement with parameters estimated through different methods reported in literature.

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Genomic landscape and biodiversity of Italian dogs

Andrea Talenti[1], Dayna L. Dreger[2], Stefano Frattini[1], Beatrice Coizet[1], Federica Danelli[1], Stefano P. Marelli[1], Amedeo Picchi[1], Jacopo Riva[3], Enrico Moretti[3], Raffaella Cocco[4], Daniele Bigi[5], Luigi Liotta[6], Michele Polli[1], Gustavo Gandini[1], Giulio Pagnacco[1], Elaine A. Ostrander[2], Paola Crepaldi[1]

[1]*Dipartimento di Medicina Veterinaria, University of Milano, Italy*
[2]*National Human Genome Research Institutes, National Institute of Health, Bethesda, MD*
[3]*Vetogene - Spinoff, University of Milano, Italy*
[4]*Dipartimento di Medicina Veterinaria, University of Sassari, Italy*
[5]*Dipartimento di Scienza e Tecnologie Agro-Alimentari, Alma Mater Studiorum University of Bologna, Italy*
[6]*Dipartimento di Scienze Veterinarie, University of Messina, Italy*
Contact: andrea.talenti@unimi.it

The availability of genomic tools, such as SNP chip and whole genome sequencing technologies, have given researchers the opportunity to understand the relationships between, and genetic background of, dog populations. However, such international studies have included few Italian populations. This project aims to highlight the uniqueness of Italian dog populations and deepen our understanding of the genetic relationships that exists between them.

Almost 300 dogs from 18 important Italian breeds and ecotypes (17 ± 4 average number $\pm$ SD of animals per breed, breeds list: http://www.enci.it/libro-genealogico/razze-italiane) were considered for this study. Within each population, dogs were selected for analysis if they were unrelated at the second generation. Biological samples were collected according to the European regulations on animal welfare. All samples were genotyped with the Illumina 170K HD SNP chip. Data were checked for missing genotypes, minor allele frequencies, cryptic relatedness and duplicate individuals. Genotype phasing used individual pairwise identity by descend estimations. Distances were estimated as shared alleles identity by state between individuals, whereas populations distances were estimated as Reynolds distances. Both distances were then used to assemble a Neighbor-joining phylogenetic tree using the PHYLIP software. Finally, the genetic background of populations was defined using ADMIXTURE software. Those results provide the first deep insight into the genomic landscape of Italian dog breeds and ecotypes, highlighting their phylogenetic relationships. Our findings confirm most of the known history of the breed analyzed, grouping by their working ability and show an average inbreeding ($\pm$ SD) of 0.15 ($\pm$ 0.11).

Genomic data analysis has proven to be an important tool for revealing relationships within and across populations. These data can be used to define individual relationships, such as parentage and inbreeding, or those between populations, estimating genetic distances and phylogenetic relatedness. These studies will provide the Italian Kennel Club (ENCI) with new tools that, together with classic management instruments, can improve genealogical registration quality, selection strategies for breeding, as well as understanding of genetic makeup and breed composition, all leading to improved health and welfare for Italian breeds.