[b]Dipartimento di Scienze Mediche e Chirurgiche, University of Bologna, Bologna, Italy
[c]Associazione Nazionale Allevatori Suini, Roma, Italy
[d]Dipartimento di Scienze Statistiche 'Paolo Fortunati', University of Bologna, Bologna, Italy
[e]Dipartimento di Farmacia e Biotecnologie, University of Bologna, Bologna, Italy

Pig production and reproduction traits are complex phenotypes demanding novel strategies for their genetic improvement. Complexity arises from the interplay within and between different biological layers encompassing the genome, proteome and metabolome spaces. Metabolites are simple and intermediate phenotypes that upon genetic regulation, establish molecular routes resulting in the expression of complexity. As such, the deconstruction of complex phenotypes in their single biological components may be useful to describe the genetic factors affecting economically relevant traits. Here, we obtained the metabolomics profile of about 1300 heavy pigs, including 900 Italian Large White and 400 Italian Duroc pigs. Targeted and untargeted metabolomics was applied to plasma samples to recover abundance levels of about 1000 metabolites. Pigs were also genotyped with the Illumina PorcineSNP60 BeadChip. Metabolomics profiles were initially used to study the metabolite-metabolite relationships and to reconstruct metabolic routes. A Gaussian Graphical Model approach was used for this purpose. Metabolomics profiles were then coupled with genotype data to study the effect of genome variability over the metabolome via genome-wide association studies (GWAS). Association of both single metabolite abundances and metabolites ratios were tested. For each trait, genomic heritability was also estimated. Whole genome sequencing data from hundred animals were than used to identify putative causative mutations. Reconstructed metabolic networks resulted quite similar though differences emerged, pointing out putative breed specific metabolic routes. Networks were characterized by poorly interconnected modules representing the specific metabolism of the different metabolite classes. Several associations were recovered from GWAS; as expected, most significant associations were between an enzyme-encoding gene and a metabolite constituting its specific substrate or final product. Overall, we obtained a first catalogue of genes and variants affecting the pig metabolism and that represent a novel source of information for explaining, indirectly, complex traits. This information gives the possibility to include metabolites and novel genetic markers for fine tune breeding and selection programs, to improve sustainability of the pig production sector.

O41

Effect of morphological characteristics and productive traits on the survival of dual-purpose Simmental cows

Giovanni Buonaiuto[a], Nicolas Lopez-villalobos[b], Angela Costa[a], Andrea Formigoni[a] and Giulio Visentin[a]

[a]Department of Veterinary Medical Sciences, Alma Mater Studiorum, University of Bologna, Ozzano dell'Emilia, Italy
[b]School of Agriculture and Environment, Massey University, Palmerston North, New Zealand

In recent years, dairy farmers have observed a substantial decrease in cow survival, with a direct negative consequence on the profitability. Shorter lifespan raises questions about animal welfare and farming conditions at which cows are exposed to. Traditionally, the cows' productive life length is affected by voluntary and involuntary culling, e.g. sale, slaughter, salvage, or death. Culling risks are affected by animal-related features such as calving events, lactation stage, energy balance, reproduction, and aging, but also external factors, namely management and season. The present study aimed to investigate the morphological and productive traits affecting the survival of Italian Simmental dual-purpose cattle. Data available belonged to 2656 Italian Simmental dairy cows from 324 dairy herds (Emilia Romagna region, Italy). Cows involved in the study were linear classified once, as primiparous, between the 2002/2003 to 2019/2020 dairy seasons. Kaplan-Meier survival analyses were performed with the LIFETEST procedure of SAS software v 9.4 using milk yield, muscularity, and body condition score (in classes) as independent variable and survival at the subsequent lactation up to the 6th as dependent variable. As expected, the culling risk increased with parity, i.e. as the age of cows progressed. In general, animals with a low production level and medium body conditions have the highest probability of survival compared to high-producing cows. This trend was more evident in later parities: in fact, cows in parity 5 with low milk production and medium muscularity were more likely (+20.11% of probability) to survive at the subsequent lactation compared to others (13.99 vs 10.49, for medium and high production levels, respectively). Moreover, high-producing cows with medium body conditions were those with the lowest probability to survive at the subsequent lactation. The reasons that could explain these findings may be linked to the metabolic stress experienced by the cows during lactation. Indeed, especially during the peripartum period, lactating cows undergo a state of negative energy balance and a reduction of immune competence. Results from this study indicated that other than productivity level, morphological traits are important for making culling decisions in the Italian Simmental cattle.

Taylor & Francis
Taylor & Francis Group