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Camille Juigné, Emmanuelle Becker, Florence Gondret. Combined transcriptomics and metabolomics in the whole blood to depict feed efficiency in pigs. 74. Annual meeting of the european federation of animal science (EAAP), EAAP, Aug 2023, Lyon, France. pp.516. hal-04103974

HAL Id: hal-04103974

<https://hal.science/hal-04103974>

Submitted on 23 May 2023

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Combined transcriptomics and metabolomics in the whole blood to depict feed efficiency in pigs

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Abstract:

Feed efficiency is a research priority to support a sustainable meat production, but it is also recognized as a complex trait that integrates multiple biological pathways orchestrated in and by various tissues. This study aims to determine the relationships between biological entities underlying the inter-individual variation of feed efficiency in growing pigs. The feed conversion ratio (FCR) was calculated from a total of 47 Large White pigs from a divergent selection for residual feed intake and fed high starch or high-fat high fiber diets during 58 days. We considered transcriptomics (60 k porcine microarray) and metabolomics (1H-NMR analysis and target gas chromatography) datasets obtained in the whole blood of pigs at the end of the trial. We studied whether connecting these two levels of biological organization will help for a better understanding of the key biological processes driving the phenotypic difference in feed efficiency. We identified 33 weighted gene co-expression networks (WGCNA) in the whole blood (13 to 2,491 unique genes). The eigengenes of six modules were correlated to FCR ($P < 0.05$). Most of these modules were enriched in genes participating in immune and defense-related processes. Profiles in circulating metabolites and fatty acids were summarized by weighed linear combinations from principal component analyses, and correlated to the eigengenes of the co-expressed genes modules. A significant association was found between a module of co-expressed genes participating to T cell receptor signaling and cell development process and related to FCR, and the circulating concentrations of omega-3 fatty acids. Finally, we provided a new method to integrate those experimental data and the public knowledge from metabolic pathway networks databases, to show where and how these molecules at different levels of biological organization participate and interact with each other. Databases of biological pathways in BioPAX format, represented by graphs, were queried to identify participants of interest in interactions. Altogether, these different approaches will help to depict biological systems and understand complex traits such as feed efficiency.

Preferred session:

42: Open the black box: using omics to better understand biological interpretation of complex traits