

Invitation to the “PaP” PhD Seminar

We would like to kindly invite you to the presentation of **Paolo Trevisi**,
Department of Agricultural and Food Science, Bologna University, Italy

Date: 07 December 2017, Thursday

Time: 5:00 p.m. (s.t.)

Room: lecture hall E

Title: “New frontiers to disclose the ways to manage/understand the nutrient requirement in pigs: special focus on Tryptophan and Threonine”

The identification of genetic mutations that showed the relevance of individual variability in the interaction with microorganisms and, consequently, in the magnitude of activation of the immune system was a key milestone. These aspects, involving the different quanti-qualitative production of immune proteins are strictly connected with the nutrient requirements of the host to satisfy the requirement in not optimal rearing conditions. Indeed Melchior *et al.* (2003) observed an increase in tryptophan (Trp) catabolism in pigs suffering of chronic lung inflammation. A certain degree of variation is observable between the studies designed to determine the amino acid requirements in pig feeding, supporting the hypothesis that factors other than the environment can affect them. To support this thesis, a series of trials has been set up to study the variation in Trp and threonine requirements in pigs genetically or phenotypically characterized for the susceptibility against *Escherichia coli* F4ac (ETEC). The results confirmed a high demand for these two amino acids, stimulated by ETEC in susceptible pigs, but not in resistant (Trevisi *et al.*, 2009; 2015). Moreover, in pigs genetically predisposed to ETEC infection, but not stimulated with this pathogen, the Trp requirement remains higher than in not susceptible animals, suggesting a possible stimulation of the immune system in this type of pigs, even in absence of specific challenge (Trevisi *et al.*, 2010).

In the last years, the connection between genetic and nutrition strengthened, thanks to the progresses on the “omic” sciences. The progress in targeted metabolomic approach, to deeply describe the organisms and dissecting raw phenotypes (Bovo *et al.*, 2016), is of growing importance for animal scientists. This stimulates the new approaches based on genome/metabolome wide association study, based on properly designed bioinformatics tools, that allows to identify specific genetic mutations (Single Nucleotide Polymorphism – SNP), associated with different concentrations of metabolites in biological body fluid. Based on this assumption, a large study on pigs was conducted by our group, and several associations between SNPs, and key nutrients were disclosed. Until today, the effect of a

polymorphism for the porcine kynurenine 3-monooxygenase (KMO) gene on metabolites of the kynurenine pathway after tryptophan supplementation was confirmed by a properly designed in vivo trial; this definitively confirms the importance to consider the genetic background of the animals to precisely define the nutrient requirements for a specific group of animals.

In conclusion, the recent findings highlighted that deepening the integration between disciplines of animal science is mandatory to speed on the progress in livestock production field, especially for topics as the “efficient use of diets” that is strictly connected with the economic and environmental sustainability of the production of protein of animal origin.

We are looking forward to seeing you there!