

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

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The adaptive capacity of the organism in response to specific environmental conditions (e.g. diet, heat stress, pathogens) is mediated by the complex interaction between biological signals that at different levels can modulate the behavior and wellbeing of the animals. Moreover, the improvement of the efficiency of the livestock production systems is the one-way strategy to increase the production of protein of animal origin without worsening or, reducing the environmental impact.

For the livestock, it is a common opinion that an effective strategy to exploit the productive efficiency permitted by the rapid progress in the genetic selection for productive traits, requires keeping the animals in healthy conditions and, eventually, make them able to express a rapid activation against infections to limit growth losses. Under this vision, all the management factors - including welfare, biosecurity, nutrition - play a key role in exploiting the genetic potential of the animal. Anyway, as highlighted in experimental conditions, as well as in field conditions, the variability of the animal response to the improvement of specific factors is quite high, even when the animals are reared in similar farm situations. This observation led the scientists to believe that a deep synergy between the genetic approach and the animal management methods is mandatory, to continue to improve the efficiency of the animals. An improvement of animal efficiency could also come from applications derived from a deeper understanding of the interplay between the animal host, the environment and hosted bacteria (including pathogens), but for this achievement, the knowledge of the genetic background of the animals is essential. As an example, notwithstanding that the immune system activation in response to pathogen infection was known since longer time, it was the discovery of the Toll Like Receptors (TLRs) that gave the evidence of the continuous dialogue between the host and the microbiota. Moreover, 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 in 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.

## References

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