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Proceedings of the 9th European Symposium on Poultry Genetics

June 16-18, 2015, Tuusula, Finland

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16.-18. June 2015
Tuusula, Finland

Edited by

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http://www.epgs2015.com

2015
WPSA Finnish branch

Genomics of microbiota and gut health

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Human as well as livestock animals are made up of much more bacteria from the gut microbiota than host cells. Recent studies relying on high-throughput sequencing of host microbiota genomes (or metagenome) show that gut microbiota is essential not only for digestion and defense against enteric pathogens, but also for immunity, metabolism and even psychology. This is why it is sometimes viewed as a new organ or as a symbiont forming with its host a supra-organism [1]. Several metabolic and/ or inflammatory diseases, digestive disorders or cancers are associated with changes in gut microbiota composition in human, although in most cases the causality relationship is not known. The study of gut microbiota is currently offering new therapeutic tools in medical research: modifying the gut microbiota by nutrition or substitution could reduce the symptoms or cure the disease. Besides, describing the gut microbiota could assist the diagnostic of complex, multifactorial health disorders. At least, it could be relevant to take into account individual microbiota compositions for personalised medicine.

In livestock species, this new player should be taken into account to understand how it modulates the expression of phenotypes of interest. In chicken, its study has been renewed by the possibility to use high-throughput sequencing technologies to determine its bacterial composition by sequencing the gene coding for the 16S ribosomal subunit. The role of gut microbiota in digestion and its "barrier" effect toward enteric pathogens, preventing intestinal colonisation, have been studied for decades. It is also known that gut microbiota composition in chicken vary according to time, position along the digestive tract, feed or ingestion of pre-/pro-biotics and antibiotics. Besides, host genetics controls part of gut microbiota composition in chicken, as attested by a few pioneer studies comparing different chicken lines ([2-7]; Mignon-Grasteau et al, this proceedings). The full sequencing of bacterial genomes, by giving access to all the genes and not only to the 16S rRNA coding gene, has the potential to lead to a more in-depth understanding of the mechanisms at stake in these variations by deciphering the complex cross-talk occurring between gut microbes and host, but it requires a gene catalog of the chicken microbiota which remains to be produced. One of the most relevant challenges in chicken production will be to relate gut microbiota composition with variations of traits of interest, especially health and productivity related traits ([8]). This could lead to the development of nutrition or breeding strategies to influence the microbiota in a favourable way, or to diagnostic tools. Since gut microbiota variations potentially impact so many traits, it is essential to take many traits into account in multidisciplinary,

integrative studies.

We are currently investigating the role of genetics on gut microbiota composition and its relations with digestive efficiency and immune status by studying the divergent lines D+/D– (Mignon-Grasteau et al., same proceedings). Our aims are to: (i) identify host genetic components influencing gut microbiota composition, (ii) investigate their impact on the animal's immune status and (iii) identify operational taxonomic units (OTUs) predicting the level of digestibility in the animals under study. We thus hope to determine how genetic selection on digestive efficiency led to modifications of gut microbiota composition, and whether these modifications had an impact on the animal's immune status. Preliminary results have shown that these lines display different microbiota composition [9]. By sequencing the 16 S rRNA gene in gut microbiota samples, we first showed that gut microbiota communities differ primarily according to the position along the intestinal tract. We could then identify OTUs with abundances significantly differing according to the digestibility level of the animal, in each of the three intestinal segments studied, thereby confirming previous results. Further analyses will be led to confirm the QTLs for microbiota composition previously identified and refine both their position and their specificity.

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