

Special issue on livestock metagenomics

The Journal of Animal Breeding and Genetics is pleased to present this special issue on microbiome analysis in the context of animal genetics. This is a hot research topic, as evidenced by the numerous manuscripts that were received. This issue contains the final nine papers that were selected. Microbiomes and their effects on host phenotypes have emerged as major factors to be considered in animal science. Current generation-sequencing technologies have made it affordable to analyse a large number of microbiota samples with a price typically lower than that of a SNP genotyping chip (for the 16S gene re-sequencing approach). The effect of microbiota on feed efficiency, host health, methane emissions and many other traits is beyond discussion. What is less clear, though, is how microbiome data can be incorporated into current genetic evaluations. The term “microbiability” has been coined as the proportion of phenotypic variance explained by the microbiome, although its real usefulness and biological interpretation has been disputed. It is also possible to perform metagenome-wide association studies to link microbiota with host phenotypes. Certainly, the microbiome can also be analysed as an ordinary phenotype in evaluating the effect of host genetics on microbiota composition. It is, for example, possible to compare different breeds with a shared environment in terms of their microbiota to assess the impact of environmental changes on microbiome for a fixed genotype. Further, metagenomic studies can be performed on different animal receptacles (rumen, gut, respiratory system, etc.) and at different time points, adding an extra layer of complexity. The papers in this issue address these and other challenges. Maltecca et al. deal with the important interaction between feed efficiency and microbiome in pigs. They suggest that understanding the role of microbiota—and being able to modify it—can be critical to enhance feed efficiency and therefore contribute to a more sustainable agriculture. Weishaar et al. delve on feed efficiency and propose a new index to utilize the “hologenome,” that is, the combined genomes of host and microbes. Verschuren et al., in a different but related aim, focus on predicting nutrient digestibility based on faecal microbiome. Saborio-Montero et al. and Ramayo-Caldas et al. deal with the highly relevant topic of methane emission in cattle, although from completely different perspectives and well illustrate the richness of the microbiome research area. While Saborio-Montero proposes microbiome modelling recursively, Ramayo-Caldas harness on multivariate analysis to identify a series of taxons associated with methane emission. Importantly, both papers do suggest a partial genetic control by both microbiome and the host of this phenotype. The metagenome is also relevant for disease, and this is discussed by Massacci et al. (a) (diarrhoea in pigs) and Esteban-Blanco et al. (mastitis in sheep), while Sanglard et al. investigate the relationship between vaginal microbiota and immune response in pigs. Although we focused on farm animals, the microbiome is being investigated in basically all domestic species. A good example is Massacci et al. (b), which studies longitudinal differences in the microbiota among six horse breeds. This issue will continue alive online, and new relevant papers on the topic will be added to the collection. We thank the authors for their effort and hope you enjoy reading.

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