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The potential impact of the microbiome in future agriculture

General aim: Most microbial communities are living in symbiosis with the host (plant, animals) so that improvement of their interactions, e.g. by genetics, nutrition, is expected to result in an increase in performance, health, efficiency and less environmental impact of production. For enhancement of plant performances many microbial products (bio-fertility and biocontrol) are developed which valued USD 1 billion in 2012 and expected to exceed USD 7 billion in 2019. For animal breeding, our own results indicate that there is a host genetic effect on the composition of the microbial community. Animal breeding is known to be very cost-effective because the genetic improvement is cumulative, persistent and can potentially be disseminated worldwide. The purpose of this study is to give a general overview of the impact of the microbiome on plant and animal production and to provide strategies to use microbial information in breeding, nutritional intervention, etc.

Methodology & Theoretical Orientation: Metagenomic whole genome sequencing of the microbial community is very informative to provide the composition of microbial community and the microbial gene abundances, which were related to traits.

Findings: The relative abundances of the microbial community and the microbial genes are closely related to feed conversion efficiency (FCE) and methane emissions (CH4) in bovine explaining 86% and 81% of the variation of these traits, respectively. Additionally, most microbial genes identified could be associated with biological mechanisms of those traits.

Conclusion & Significance: The relative abundance of the significant microbial genes is recommended to be used to predict the traits of interest, which can be used for their improvement using genetic selection, nutritional intervention, etc. (Fig. 1). In cases, in which performance testing is very costly (as for FCE and CH4); this methodology is substantially more cost-effective and will improve symbiotic effects between microbiome and host.

Biography

Rainer Roehe is Professor of Animal Genetics and Microbiome at SRUC. He has a long-term carrier in animal breeding and genomics using trials and cutting-edge Bioinformatics to understand the genomic architecture of complex traits in farmed animals. His current research is focusing on host genetic interactions with the microbiome in ruminants and monogastrics to genetically improve important animal trait such as growth, feed conversion efficiency, meat quality, animal stress susceptibility, health, methane emissions, etc. He is using whole genome metagenomic sequencing of samples from the rumen and the intestinal tract to simultaneously identify the relative abundance of the microbial community and the microbial genes. Relating this information to important traits, he developed a new microbiome strategy for improvement of complex traits. The strategy can be used more generally for soil microbial improvement, plant and animal breeding, nutrition and even to identify the impact of the microbiome on human health.

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