



Thesis  
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## Systemic understanding of microbial interactions and ruminal fermentation

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The rumen microbiota plays an essential role in ruminant nutrition by breaking down and fermenting feedstuffs, transforming them into a source of energy and protein for the host. In order to optimise these functions, it is necessary to know the mechanisms involved and to be able to effectively predict the effects of biotic and abiotic factors on the structure and activity of this complex ecosystem. The development of omics approaches has allowed a description of the composition of the ruminal microbiota, its genomic potential, and its activity with regard to some targeted functions. However, science still does not know how to precisely describe the functioning of the ecosystem at the level of the microbiota, to optimise its long-term functioning and to predict its evolution following different disturbances. In this respect, mathematical modelling offers a powerful approach to better understand the functioning of the ruminal ecosystem.

The thesis project aims to improve our understanding of rumen functioning at the systemic scale, by developing a multidisciplinary approach integrating characterisation of microbial metabolism using omics approaches, and the development of genomic-scale models of rumen microbes. Microbial interactions will be studied in vitro using a synthetic ecology approach of the "bottom-up" type with the help of mini-consortia composed of key rumen microorganisms representing the main functions of this ecosystem (cellulolysis, amylolysis, proteolysis, methanogenesis) and whose genome is known.

The mini-consortia tested will be of increasing complexity and will be supplemented by the yeast *Saccharomyces cerevisiae*, in order to model the effect of this probiotic, used as an additive in animal nutrition, on microbial activities.

