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## **MicroNor: Studying the microbiota of Normandy cows to improve production, disease resilience and longevity.**

The intestinal microbiota is considered as the second mammalian genome. It contains as many bacteria as there are cells in the body. These bacteria contain 100 times more genes than the host genome. Discoveries about the role of the microbiota on its host are constantly increasing: absorption and synthesis of nutrients, development of the intestine, intestinal function, protection against pathogens, bone homeostasis, synthesis of neurotransmitters, impact on behaviour and pain perception, etc.

In dairy cows, it has been shown that there is a link between ruminal and intestinal microbiota. They appear to influence animal performance, health and longevity. The heritable bacteria in the rumen of cattle are correlated with the cow's ability to obtain energy from its feed. It is possible to prolong the productive life of cows and improve milk production performance in dairy cows by influencing the gut microbiota.

A proof of concept has been produced on the possibility of modulating the genetic potential of bulls according to the performance of the cows and their environment, analysed through their intestinal microbiota (GHP Prim'Holstein: Gènes Diffusion).

The MicroNor project aims to develop a methodology that will enable the Normande breed to characterise the breeding environment through its gut microbiota, with a view to selecting the most suitable animals and practices for improving the performance, resilience and environmental impact of farms.

This project, led by Littoral Normand and co-financed by the European Union and the Normandy Region, involves the partners Origen Normande, Gènes Diffusion and Seenovia.

2600 dairy cows from 40 farms will highlight :

- Interactions between genotype and microbiota to select the best adapted animals for the breeding environment.
- Interactions between microbiota and performance, to identify the most favourable microbiota.
- Interactions between practices and microbiota to identify the practices that are best suited to the development of favourable microbiota.