Athletes and Probiotics: A case for precision bioengineering?

Brunette Katsandegwaza[1], Irma Gonza[1], Céline Antoine[1], Cindy Staerck[2], Martine Schroyen[3], Patrice Filee[2], **Véronique Delcenserie[1].**

[1] Laboratory of Food Quality Management, Department of Food Sciences, FARAH - Veterinary Public Health, University of Liège, 4000 Liège, Belgium.
[2] CER Groupe, Belgium.
[3] Animal Sciences, TERRA Teaching and Research Centre, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium

The complex interaction between the gut microbiome and the host is significant to gut health research. The gut microbiome is not only demonstrated to play a big role in modulating gut health but is also indicated pivotal to systemic conditions that include dermatitis, vaginosis, mental health and respiratory conditions. A better understanding of how the gut microbiome directly, or indirectly, impacts different conditions is of major interest to parties from different aspects of research. Equally important is elucidating how internal and external factors shape the microbiome itself, knowledge that could ultimately enable the manipulation of the gut microbiome for therapeutic or preventive purposes.

Although studies demonstrate significant differences in the gut microbiome of individuals clustering along lifestyle, diets, genetic background, health conditions and extent of physical activity, studies into how these different clusters respond to an identical microbial modulating treatment are becoming of great interest in the microbiome field. Through use of a human gut simulation model, we recently demonstrated a differential response to a probiotic, *Lactiplantibacillus plantarum,* from 3 donors meeting a 'healthy' donor criterion. Donor 2 presented with a significantly different microbial profile compared to Donor 1 and Donor 3 at baseline. Furthermore, samples from Donor 2, who comes from an athletic background, clustered separately from the other 2 donors after probiotic treatment. The same donor exhibited increased propionic and lactic acid production before and after probiotic treatment, with a significantly truncated butyrate acid signature. Interestingly, fermentation of Donor 2 fecal material after probiotic treatment in the SHIME system resulted in statistically reduced colony forming units on MRS agar, suggesting that the metabolic profile of Donor 2 resident microbes did not support the growth and colonization of *Lactiplantibacillus plantarum*, as well as other microbes capable of growing on MRS agar. In conclusion, although probiotics are designed and optimized to effect a standard beneficial impact on a wide range of individuals and gut microbiomes, certain specific clusters that include high intensity athletes will benefit from precisely designed probiotics, given their highly modified gut microbiome that has evolved to support intense physical activity.