



## Bacterial imbalance – the reason for many clinical symptoms

It is becoming more and more apparent that the composition of the gut microbiota affects human health. Bacterial imbalance is associated with different conditions including inflammatory bowel diseases (IBD's), metabolic syndrome and obesity.

Besides a variety of different species of bacteria, 90 % of the normal human gut flora is populated by two phylogenetic groups which exist in a symbiotic balance: *Bacteroides* and *Firmicutes*. *Clostridium* Cluster XIVa are a class of firmicutes to which, besides others, *Eubacterium* spp. and *Roseburia* spp. belong.

External influences such as stress and diet can influence this balance of gut bacteria and decreased presence of *Bacteroides* with increased presence of *Firmicutes* is often described in obese patients.<sup>1,2,3,4</sup>

*Akkermansia muciniphila* represents 3 - 5 % of the microbial community in a healthy subject.

*A. muciniphila* is present in distinct parts of the human mucosa and is detected in fecal samples of infants from the age of 1 month on and rapidly increases with increasing age. In the elderly however, presence of *A. muciniphila* numbers are significantly decreased.<sup>5</sup> Low *A. muciniphila* numbers are associated with diabetes, obesity and IBD's.

*Faecalibacterium prausnitzii* is one of the most abundant bacteria of the healthy gut where it accounts for 5 % of the total fecal microbiota. *F. prausnitzii* is not detected in fecal samples of infants less than 6 months of age and increases rapidly after that. It is accepted that diet can influence the abundance of *F. prausnitzii* and that overall the presence of *F. prausnitzii* in the gut is seen as good intestinal health indicator. Hereby, *F. prausnitzii* shows anti-inflammatory effects and reduced *F. prausnitzii* numbers are described in Coeliac disease patients.<sup>6</sup> In contrast to that, high numbers of *F. prausnitzii* were associated with obesity compared to healthy subjects.

With the RIDA®GENE assays for Gut Balance, *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* differential analysis of the gut microbiome can be performed in less than two hours.

## RIDA® GENE real-time PCR assays for gut microbiome analysis

**RIDA® GENE Gut Balance** Art. No. PG0105



**RIDA® GENE Akkermansia muciniphila** Art. No. PG0145




**RIDA® GENE Faecalibacterium prausnitzii** Art. No. PG0155



- Real-time multiplex PCR
- All assays are quantitative – DNA standards included
- RIDA® GENE Gut Balance: Detection and differentiation of *Bacteroides* und *Clostridium* Cluster XIVa in human stool samples
- RIDA® GENE Akkermansia muciniphila: Detection of *Akkermansia muciniphila* in human stool samples
- RIDA® GENE Faecalibacterium prausnitzii: Detection of *Faecalibacterium prausnitzii* in human stool samples
- **Flexible** – The assays can be run on the commonly used real-time PCR instruments, such as the Mx3005P, LightCycler® 480II, SmartCycler®, ABI 7500, m2000rt, CFX96 or Rotor-Gene Q
- **Reliable** – An included extraction control (Internal control DNA, ICD) detects PCR inhibition, monitors reagent integrity and confirms that nucleic acid extraction was sufficient

## Ordering information

Product	Description	Tests	Matrix	Art. No.
<b>Bacteria</b>	<b>Real-time PCR</b>			
RIDA® GENE Gut Balance	Real-time multiplex PCR for the direct qualitative or quantitative detection and differentiation of <i>Bacteroides</i> and <i>Clostridium</i> Cluster XIVa in human stool samples	100	Stool	PG0105
RIDA® GENE Akkermansia muciniphila	Real-time multiplex PCR for the direct qualitative or quantitative detection of <i>Akkermansia muciniphila</i> in human stool samples	100	Stool	PG0145
RIDA® GENE Faecalibacterium prausnitzii	Real-time multiplex PCR for the direct qualitative or quantitative detection of <i>Faecalibacterium prausnitzii</i> in human stool samples	100	Stool	PG0155

<sup>1</sup> Max Rubner Institut: Nationale Verzehrs-Studie II.

<sup>2</sup> Ley, RE et al. Microbial ecology: human gut microbes associated with obesity. Nature 2006, 444(7122): 1022 - 1030.

<sup>3</sup> Turnbaugh P et al. A core gut microbiome in obese and lean twins. Nature 2009, 457(7228): 480 - 484.

<sup>4</sup> Vaarala O. Gut Microbiota and Type 1 Diabetes. Rev. Diab. Stud. 2013, 9(4): 251 - 259.

<sup>5</sup> Carmen Collado M. et al. Intestinal integrity and Akkermansia muciniphila, a mucin-degrading member of the intestinal microbiota present in infants, adults, and the elderly. Appl. Envir. Microbiol. 2007, 73: 7767 - 7770.

<sup>6</sup> Miquel S. et al. Faecalibacterium prausnitzii and human intestinal health. Current Opi. Microbiol. 2013, 16: 1 - 7.