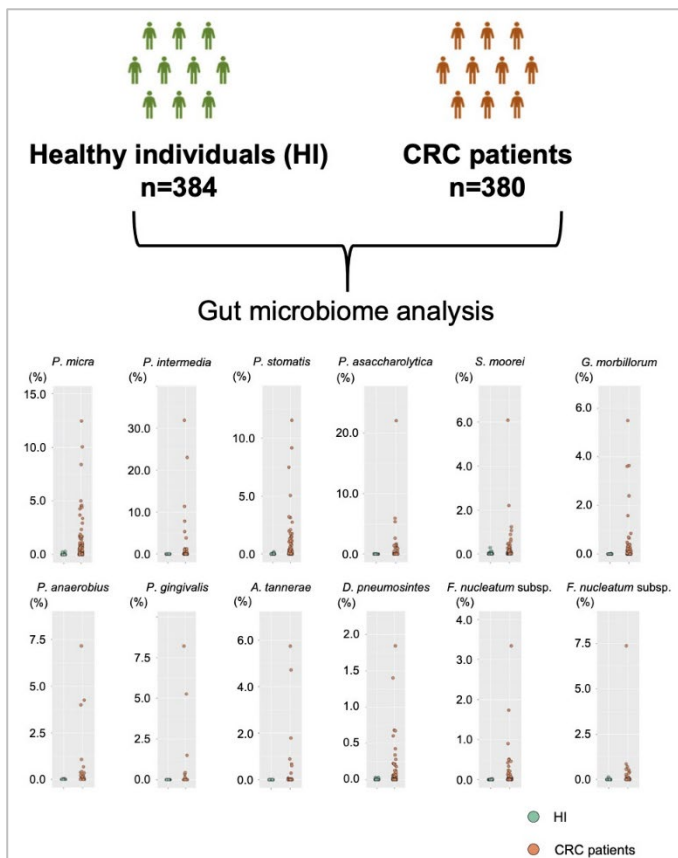


Gut bacteria identified in colorectal cancer patients promote tumourigenesis via butyrate secretion

Emerging evidence is revealing that alterations in gut microbiota are associated with colorectal cancer (CRC). However, very little is currently known about whether and how gut microbiota alterations are causally associated with CRC development. The research group of Eiji Hara (Aging Biology, IFRc/RIMD Osaka University) showed that 12 faecal bacterial taxa are enriched in CRC patients in two independent cohort studies. Among them, 2 *Porphyromonas* species are capable of inducing cellular senescence, an oncogenic stress response, through the secretion of the bacterial metabolite, butyrate. Notably, the invasion of these bacteria is observed in the CRC tissues, coinciding with the elevation of butyrate levels and signs of senescence-associated inflammatory phenotypes. Moreover, although the administration of these bacteria into *Apc*^{-14/+} mice accelerate the onset of colorectal tumours, this is not the case when bacterial butyrate-synthesis genes are disrupted. These results suggest a causal relationship between *Porphyromonas* species overgrowth and colorectal tumourigenesis which may be due to butyrate-induced senescence.

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Figure: Gut microbiome analysis.

Twelve bacterial taxa that were abundant in CRC patients and rarely present in healthy individuals were identified.