**Key Messages**

- Saccharolytic fermentation metabolites (SCFA) may have varying effects on colonic health, host physiology, lipoprotein metabolism and appetite.
- Protein fermentation metabolites (phenol, p-cresol, indole, ammonia) occur at non-toxic concentration ranges in the colon.
- There is insufficient data to support the use of any individual bacterial metabolite as faecal biomarker of gut health.

**Background**

Colonic microbial fermentation is a key function of the microbiota that might contribute to gastrointestinal health as well as overall health. As products (not necessarily end products) of intestinal metabolic activity some metabolites are generally accepted as beneficial to the host, whereas others are considered as potentially toxic and involved in chronic human disease both within the gut as well as systemically.

**Objectives and Methods**

A literature search was performed to address:
- Available evidence for the beneficial or harmful effects of known microbial metabolites including short chain fatty acids and protein fermentation products;
- The potential for functional analysis of faecal water;
- The applicability of metabolome signatures and systems biology.

**Results**

1. Available evidence for beneficial or harmful effects of known microbial metabolites
   - Targeted analysis of individual microbial metabolites provides an information ‘snapshot’.
   - Several metabolites are considered as potentially toxic. However, there is no convincing evidence of harmful effects in healthy humans.
   - SCFAs are important mediators of human physiologically activities but the correlation between their faecal concentration and physiological effects is not well substantiated.
   - Normal ranges might contribute to providing ‘the biological bandwidth’ of the metabolites and to ‘define health’

2. Functional analysis of faecal water
   - It provides an integrated measure of the overall contribution of the compounds present to a defined biological endpoint.
   - It provides no information on the biological functional effects of compounds.

3. Applicability of systems biology
   - Metabolome signatures are provided by targeted or untargeted analysis of non-invasive samples.
   - Type of biofluid and analytical technique influences the nature of the metabolome.
   - Metabolome signatures can be correlated to:
     - microbiota composition or activity datasets,
     - individual metadata of the subjects
     - specific responses to dietary interventions
   - Metabolome signatures are analysed in the context of overall biochemistry of the tissue or sample
     - “biochemical connectivity”
   - Enables analysis of the overall impact of the microbiota on host-biochemistry and function.

**Conclusions**

No formal systematic reviews evaluating the physiological or toxicological properties of bacterial fermentation metabolites were found. We were suggesting the evaluating impact of microbiota on gut function and host health by profiling metabolites in the context of overall tissue biochemistry and by correlating (multivariate) metabolome signatures with microbial, dietary and physiological data. Furthermore, study should focus on measuring metabolite fluxes to provide an accurate picture of colonic metabolite nutraceutics. An optimised implementation of bioinformatics with the aim of interpreting such data would be promising.


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