

The important role of gut microbiota for the therapeutic activity of herbal extracts

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Gut bacteria are processing food, but also herbal medicinal products, and produce signalling molecules that regulate appetite, satiety, and digestion, but also other body functions. Dysbiosis of gut microbiota can contribute to systemic inflammation, it can lead to obesity, asthma, diabetes, autoimmune diseases, and even to certain forms of cancer. Therefore, herbal extracts certainly modulate our health by influencing the gut ecosystem [1,2].

In our research platform, predigestion is conducted in a static *in-vitro* model, according to the InfoGest consensus method. Subsequently extracts are incubated with human fecal suspension under anaerobic physiological conditions. Samples are taken at time points 0.5 h, 4 h, and 24 h. Changes in the composition of plant extracts are monitored by LC-HRMS. Microbiome shifts are tracked by 16S RNA sequencing.

Microbial degradation of many classes of compounds has been observed during incubation of various herbal extracts with human fecal suspension. Flavonoid glycosides and aglycones, procyanidins, salicylic alcohol derivatives, caffeic acid derivatives, and triterpene glycosides, are rapidly and intensively metabolized. Numerous newly formed compounds could be assigned to putative microbial metabolites [3].

In conclusion, the combined LC-HRMS and next-generation sequencing approach allows straightforward detection of relevant microbiome shifts and metabolites. The role of the metabolites as active principles urgently needs to be investigated.

References

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- [2] David LA et al. *Nature* 2014; 505:559-63.
- [3] Pferschy-Wenzig EM et al. *Front Pharmacol.* 2017; 8:893.