

## Simulator of Human Intestinal Microbial Ecosystem

**Commonly used acronym:** SHIME

Created on: 24-07-2024 - Last modified on: 26-07-2024

### Organisation

**Name of the organisation** ProDigest

**Department** Gastrointestinal Expertise

**Country** Belgium

**Geographical Area** Flemish Region

## SCOPE OF THE METHOD

<b>The Method relates to</b>	Animal health, Human health
<b>The Method is situated in</b>	Basic Research, Translational - Applied Research
<b>Type of method</b>	In vitro - Ex vivo

## DESCRIPTION

### Method keywords

gut health  
gut microbiota  
colonic metabolism  
dose response  
metabolomics  
metagenomics  
long-term effects  
repeated dosing  
in vivo-like models  
predictivity  
humans  
companion animals  
farm animals  
Compartmentalized

### Scientific area keywords

fibre  
prebiotics  
probiotics  
postbiotics  
synbiotics  
proteins

carbohydrates  
nutraceuticals  
plant extracts  
drugs  
api  
formulations  
polyphenols  
minerals  
HMO  
vitamins  
digestion  
host-microbiome interaction  
pathogen  
Fermentation (kinetics)  
kinetics

## Method description

The SHIME® (Simulator of Human Intestinal Microbial Ecosystem) model is currently the most representative *in vitro* technology for the combined simulation of the physiological, chemical and microbiological properties of the gastrointestinal tract. The model enables study of the impact of long-term repeated dosing and of the modulation of the microbiota in function of the gut location. The SHIME® can be seen as a clinical trial *in vitro*, which can provide the spatiotemporal insight into the mechanism of action of a specific treatment, therefore providing complementary data to *in vivo* studies. The SHIME® simulates all the compartments of the GI tract, starting with the stomach followed by the small intestine, the proximal and the distal colon (with an option to include the mouth and a specific ileal compartment with ileal microbial community). To be as close as possible to the *in vivo* situation, the SHIME® model reproduces multiple physiological and microbial *in vivo* parameters, including body temperature, intestinal volumes, enzyme concentrations, feeding cycles, pH, microbial diversity across anatomical compartments... Due to its flexibility, interindividual variability as well as various specific population groups (babies, children, elderly, healthy and diseased humans, or adjusted to the research question) and even animal models (cats, dogs and pigs) can easily be studied.

## Method status

History of use  
Internally validated  
Published in peer reviewed journal

## PROS, CONS & FUTURE POTENTIAL

### Advantages

- Closest to the *in vivo* context
- Validated with *in vivo* data (IVIVC)
- Most accurate reproduction of the gut microbiota (composition and functionality) over a longer period of time
- Provides insights into the impact of repeated dosing and into the long-term effects
- Facilitates the understanding of the mechanism of action (MoA)
- Takes into account interindividual variability
- Predicts the impact of a product on the top of a normal diet

- Able to recreate the specific composition and functionalities of the microbiome in the specific parts of the gut.
- In its most extensive configuration: the microbiome in the ileum, the ascending, transverse and descending colon can be simulated.
- Enables the simulation of the ileal microbiome
- Representative of the microbiome of a specific donor.
- Complementary representation of the Luminal and Mucosal gut microbiota (M-SHIME)
- Adaptations of the conditions to mimic those of a specific population group: for example baby SHIME
- Incorporation of multiple treatment in a sequential manner, e.g., antibiotic treatment.
- Wash-out phase extension, to evaluate the long-term effects of a test product after stopping its administration, to establish the engraftment of probiotics, etc.
- Possibility to establish a dose-response relationship.

## Modifications

- Dysbiotic SHIME: allows the representative simulation of a dysbiotic microbial community, e.g., IBD, IBS, etc.
- Screening SHIME: allows the screening of multiple colonic vessels in parallel (multiple test products/microbiomes)
- M-SHIME: allows the simulation of the mucosa-associated microbial community
- Upper GIT model: focuses on the single passage of a test product through the stomach and small intestine (duodenum, jejunum, ileum). The inclusion of a dialysis module enables the simulation of intestinal absorption.

## REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION

### References

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