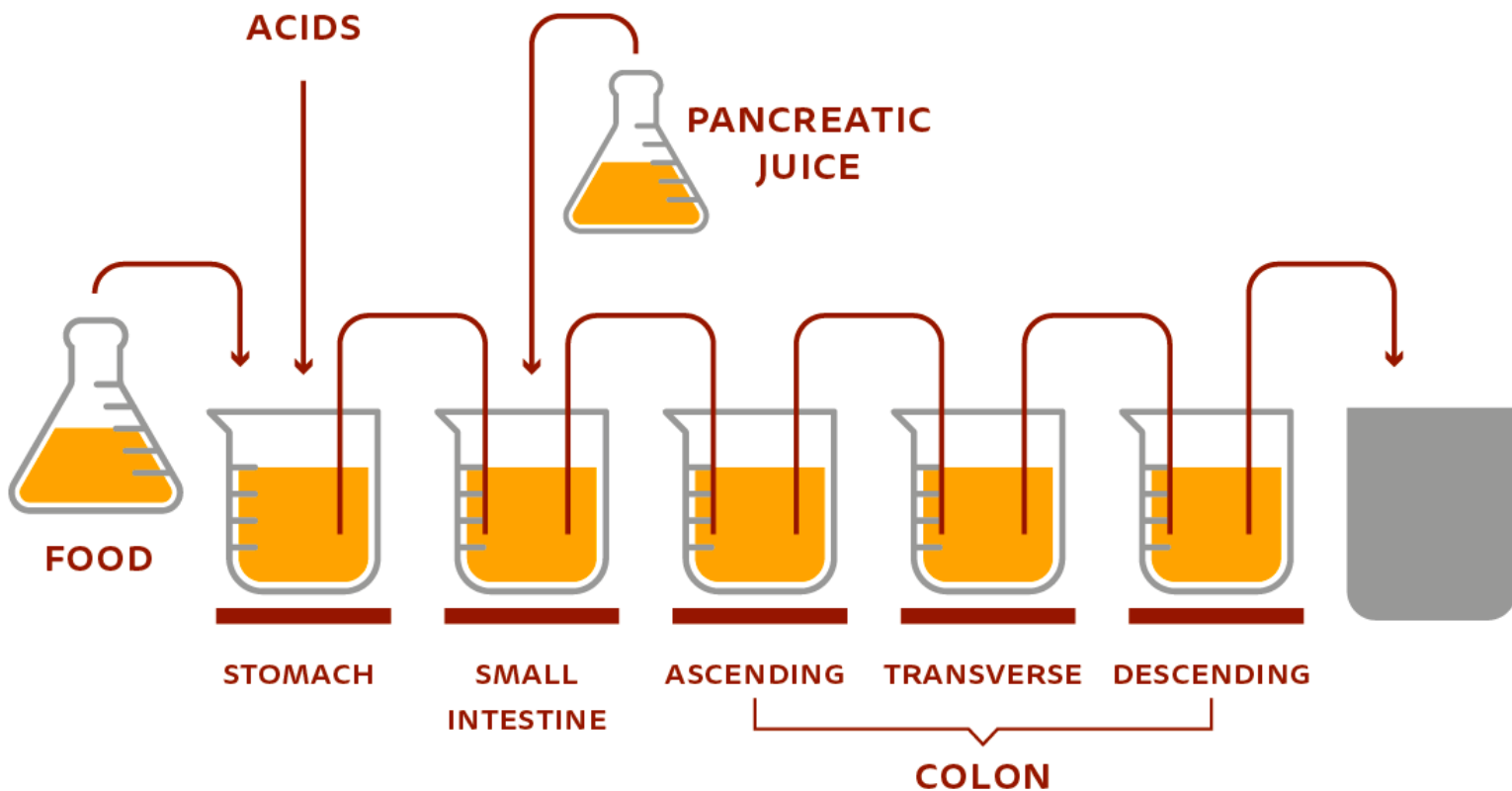


AT A GLANCE

MEGASPOREBIOTIC™ + MEGAPRE™ SYNBIOTIC STUDY

A SYMBIOTIC CONCEPT CONTAINING SPORE-FORMING BACILLUS STRAINS
AND A PREBIOTIC FIBER BLEND CONSISTENTLY ENHANCED METABOLIC
ACTIVITY BY MODULATION OF THE GUT MICROBIOME *IN VITRO*

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RESEARCH SUMMARY

Symbiotic supplementation of prebiotics and probiotics has been linked with several human health benefits. Using an in vitro SHIME model study design, investigators were able to evaluate how the addition of MegaSporebiotic plus MegaPrebiotic impacts short-chain fatty acid production and alters microbial populations. The use of MegaSporebiotic with MegaPrebiotic resulted in significant increases in SCFA production and microbial diversity for keystone health promoting bacteria. There was also a decrease in bacteria associated with higher LPS production. Combining prebiotic fibers, like those found in MegaPrebiotic, are a useful strategy in modulating the microbial community, as they selectively stimulate different microbial groups.

GOALS

Evaluate the symbiotic effect of MegaSporebiotic and MegaPrebiotic in order to elucidate potential synergistic effects on microbial metabolic activity and community composition.

KEY TERMINOLOGY

- Prebiotics are considered non-digestible substrates that are selectively used by the gut microbial community, thereby conferring a health benefit to the host.
- Probiotics are considered the administration of live microorganisms that when administered in adequate amounts, confer a health benefit to the host.
- Mucosal Simulator of the Human Intestinal Microbial Ecosystem (M-SHIME) in vitro model similar to a human GI tract. The SHIME model allows researchers to analyze the intestinal microbial community that is fully stable so that treatment effects are not obscured by natural variation in gut microbiome composition and functionality. In the current study, investigators were able to evaluate the symbiotic effect of the test in three consecutive colon regions, both consisting of a luminal and mucosal environment.

SUBJECTS

3 fecal samples were obtained from different human adults.



SUBJECT 1
Male
35-year-old



SUBJECT 2
Female
29-year-old



SUBJECT 3
Male
34-year-old

MATERIALS AND METHODS

STEPS TO SIMULATE A HUMAN GI TRACT:

1. Two-week initiation period to establish a stable microbial community
2. Two -week control period for baseline measurements
3. Four-week treatment period during which the symbiotic test product was administered once daily with a nutritional medium.

SAMPLES WERE COLLECTED THREE TIMES PER WEEK TO MEASURE:

- SCFA: Acetate, propionate, butyrate, isobutyrate, isovalerate, and isocaproate
- Lactate concentrations
- Ammonium

STOOL SAMPLES WERE EXTRACTED, AND MICROBIAL COMMUNITY PROFILING WAS CONDUCTED AND TESTED FOR:

- *Lactobacillus* spp.
- *Bifidobacterium* spp.
- *Akkermansia muciniphila*
- *Faecalibacterium prausnitzii*

RESULTS

CONTROL PERIOD WITHOUT MSB AND MPB:

No significant differences in SCFA between the three models

Microbial populations between donors showed some significant differences

Lactate levels remained low during entire study period

Ammonium levels changed appropriately within different segments of the colon

MEGASPORE VERSUS MEGASPORE PLUS MEGAPREBIOTIC

The combination of MSB plus MPB increased SCFA production by (80-140%) versus MegaSpore alone (24-70%).

EXPERIMENTAL PHASE ADDING MSB AND MPB:

Short Chain Fatty Acid Production

- Acetate concentrations significantly increased in the distal colon
- Propionate concentrations significantly increased in the transverse and distal colon
- Butyrate concentrations significantly increased in all three sections of the colon
- Non-significant increases in branch short chain fatty acids

Microbial Composition:

- Microbial diversity significantly increased in transverse and distal colon
- *Bacillus* bacterial strains increased in all colon areas
- *Bifidobacteria* significantly increased in the ascending colon
- *Lactobacillus* trended toward increased abundance in ascending colon
- *Prevotella* significantly increased in the transverse and distal colon
- *Faecalibacterium prausnitzii* significantly increased
- Several proteobacteria species significantly decreased
 - *Burkholderia*, *desulfovibrio*, *enterobacteria*, *pseudomonas*

CONCLUSIONS

- The symbiotic use of MSB and MPB in the current study resulted in a consistently stronger increase in acetate, propionate, and butyrate in the colon. This result was mainly attributed to the significant increases in *Faecalibacterium prausnitzii*.
- An increase in microbial diversity was observed in the distal colon. Specifically, increases in keystone health-promoting bacteria and decreases in pathogenic species.