*Supplementary Material*

# The Effect of Psyllium Husk on Intestinal Microbiota in Constipated Patients and Healthy Controls

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**Table S1.** Differences in the amount of short-chain fatty acids (SCFAs) during the intervention in both healthy and constipated. Significant difference against the baseline level (t-test, p < .05) indicated with an asterisk, standard deviation in brackets.

| | | Acetate (μM/g wet faeces) | Propanoate (μM/g wet faeces) | Butyrate (μM/g wet faeces) |
|---|---|---|---|---|
| Healthy controls | Baseline | 6.90 (3.72) | 5.49 (2.71) | 5.88 (3.75) |
| | Psyllium 10.5g | 8.68 (2.80) | 7.16 (3.68) | 6.17 (2.83) |
| | Psyllium 21g | 8.86 (2.08) | 7.12 (3.98) | 5.58 (1.49) |
| | Placebo | 11.56 (6.23) | 8.42 (8.10) | 8.36 (5.12) |
| Constipated | Baseline | 21.65 (3.64) | 4.70 (3.44) | 5.32 (4.78) |
| | Psyllium 21g | **24.03* (2.75)** | **7.26* (3.47)** | 6.87 (3.85) |
| | Maltodextrin | 21.11 (3.44) | 5.25 (4.15) | 6.03 (4.99) |
| | Wash-out | 21.74 (4.53) | 5.09 (4.17) | 5.54 (3.72) |

**Table S2.** Associations between the intestinal microbiota composition and whole gut transit time (Weighted Average Position Score after 24 h (WAPS-24) and 48 h (WAPS-48)), relative stool water content and SCFAs, introduced by psyllium consumption in constipated patients. Each cell contains information of the direction of the association ( +/- ) and the FDR corrected p-value for this association. If the cell is empty, no significant association was found.

| taxon | WAPS-48 | WAPS-24 | Water content | Propionate | Butyrate | Acetate |
|---|---|---|---|---|---|---|
| Actinobacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Actinomyces | | + , q=0.08 | - , q=0.01 | | | |
| Actinobacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium | | | - , q=0.03 | | | |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Asaccharobacter | | | - , q=0.02 | | | |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Eggerthella | | + , q=0.005 | | | | - , q=0.05 |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; Slackia | | - , q=0.05 | | | | |
| Actinobacteria; Coriobacteriia; Coriobacteriales; Coriobacteriaceae; uncultured | | + , q=0.09 | - , q=0.01 | | | |
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Odoribacter | - , q=0.02 | - , q=0.03 | | | | |
| Firmicutes; Clostridia; Clostridiales; Christensenellaceae; Christensenella | | + , q=0.05 | - , q=0.01 | - , q=0.07 | | - , q=0.09 |
| Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium | | | | - , q=5.69E-5 | | - , q=0.03 |
| Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Anaerofustis | | + , q=0.08 | | | | |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIIIncertaeSedis; IncertaeSedis | | | | - , q=0.07 | | - , q=0.04 |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIncertaeSedis; Anaerococcus | | | | - , q=0.02 | | |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIncertaeSedis; Finegoldia | | | | - , q=0.02 | | |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes | + , q=0.02 | | | | | |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Lachnospira | | | + , q=0.03 | | | + , q=0.002 |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Roseburia | | | + , q=0.03 | + , q=0.07 | | |
| Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae; IncertaeSedis | + , q=0.07 | | | | | |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Faecalibacterium | | | + , q=0.0001 | + , q=0.07 | | + , q=0.04 |
| Firmicutes; Negativicutes; Selenomonadales; Acidaminococcaceae; Phascolarctobacterium | | | | + , q=0.005 | | + , q=0.005 |
| Firmicutes; Negativicutes; Selenomonadales; Veillonellaceae; Veillonella | | | | | | + , q=0.02 |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Parasutterella | | | + , q=0.03 | | | |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | - , q=0.02 | - , q=0.08 | | | | |

**Table S3.** Associations between the intestinal microbiota composition and whole gut transit time (WAPS-24), relative stool water content and SCFAs, introduced by psyllium consumption in healthy subjects. Each cell contains information of the direction of the association ( +/- ) and the FDR corrected p-value for this association. If the cell is empty, no significant association was found.

| taxon | WAPS-24 | Propionate | Butyrate | Acetate | Water content |
|---|---|---|---|---|---|
| Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides | | | - , q=0.04 | | |
| Firmicutes; Bacilli; Lactobacillales; Leuconostocaceae; Leuconostoc | | | + , q=0.03 | | |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIIIncertaeSedis; IncertaeSedis | | | | - , q=0.07 | |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIncertaeSedis; Anaerococcus | | | | | - , q=0.05 |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIncertaeSedis; Finegoldia | | | - ,  q=0.04 | | |
| Firmicutes; Clostridia; Clostridiales; FamilyXIIncertaeSedis; Peptoniphilus | | | - , q=0.09 | | |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Blautia | | | | + , q=0.07 | |
| Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Butyrivibrio | | - , q=0.08 | | | |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Anaerotruncus | | | | - , q=0.07 | |
| Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Flavonifractor | | | - , q=0.0004 | - , q=0.02 | |
| Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Sutterella | - ,  q=0.05 | | | | |