

The human intestinal microbiota of constipated-predominant irritable bowel syndrome patients exhibits anti-inflammatory properties

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Supplementary Table S1. Richness and Diversity of the Fecal Microbiota

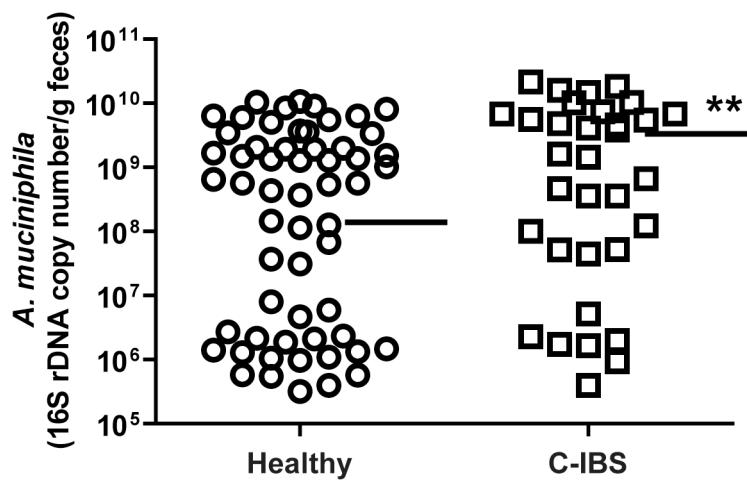
| | Chao1 Richness Index | Shannon Diversity Index |
|------------------|----------------------|-------------------------|
| Healthy Subjects | 1579 ± 395 | 3.84 ± 0.19 |
| C-IBS Patients | 1922 ± 15 | 3.67 ± 0.002 |
| N-HMAR | 1997 ± 29 | 3.71 ± 0.005 |
| C-IBS-HMAR | 2099 ± 138 | 3.72 ± 0.24 |

Supplementary Table S2. Sequences of Primers for PCR

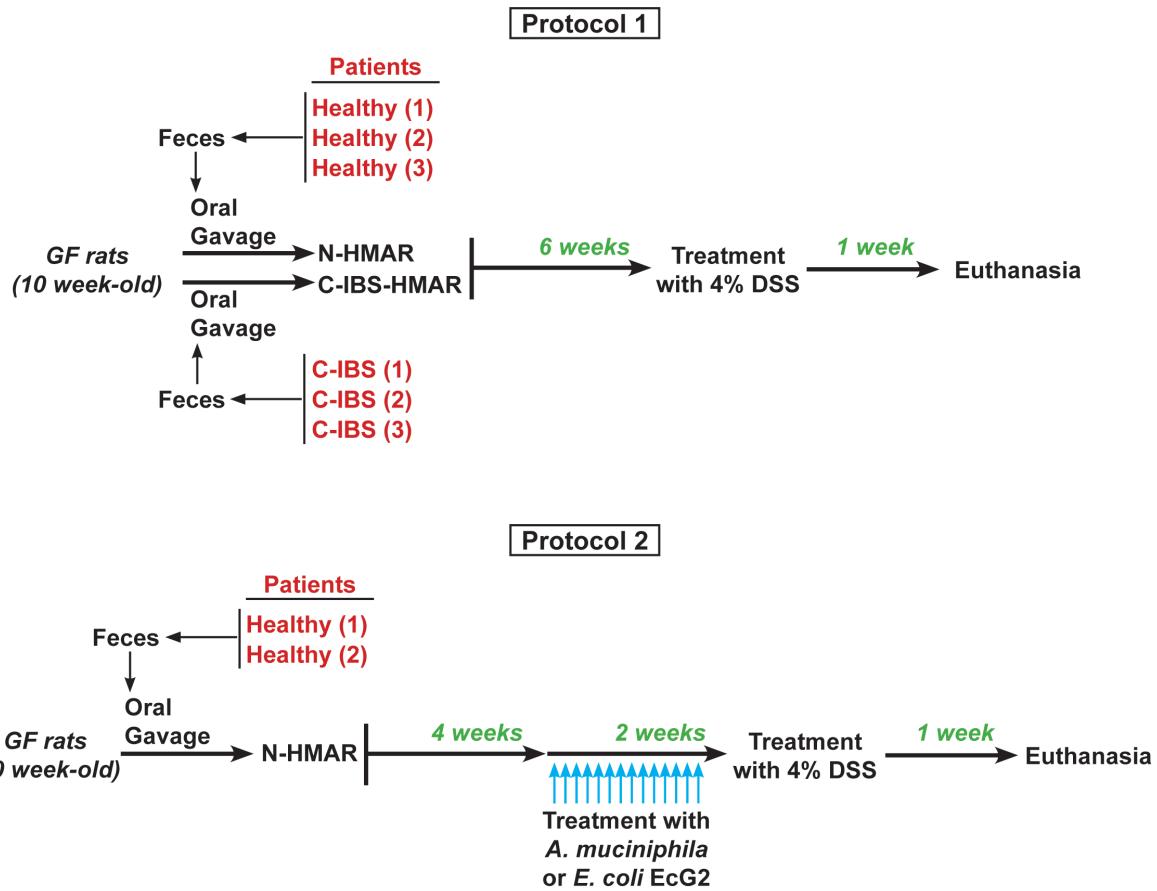
| Species | Target gene | Sequence (5'-3') | Ref. |
|---|-------------|---|-----------|
| Eubacteria (Total bacteria) | 16S rDNA | F: CGGTGAATACGTTCCGG R: TACGGCTACCTGTTACGACTT | 1 |
| Bacteroides/Prevotella group | 16S rDNA | F: CCTWCGATGGATAGGGGTT R: CACGCTACTGGCTGGTTCAG | 1 |
| <i>Clostridium coccoides</i> group | 16S rDNA | F: CGGTACCTGACTAAGAAC R: AGTTTYATTCTTGCAC | 2 |
| <i>Clostridium leptum</i> | 16S rDNA | F: CACAATAAGTAATCCACC R: CTTCCTCCGTTTGTCAA | 3 |
| <i>Roseburia/Enterococcus rectale</i> group | 16S rDNA | F: CGKACTAGAGTGTGCGGAGG R: AGTTTYATTCTTGCAC | 4 |
| Enterobacteriaceae | 16S rDNA | F: CATTGACGTTACCCGCAGAACAGC R: CTCTACGAGACTCAAGCTTGC | 5 |
| Bifidobacterium | 16S rDNA | F: CGCGTCYGGTGTGAAAG R: CCCCACATCCAGCATCCA | 6 |
| <i>Faecalibacterium prausnitzii</i> | 16S rDNA | F: GGAGGAAGAAGGTCTCGG R: AATTCCGCCTACCTCTGCAC | 7 |
| <i>Desulfovibrio</i> sp. | 16S rDNA | F: GGTACCTTCAAAGGAAGCAC R: GGGCTTCACCCCTGACTTA | 8 |
| <i>Akkermansia muciniphila</i> | 16S rDNA | F: CAGCACGTGAAGGTGGGGAC R: CCTTGCAGTTGGCTTCAGAT | 7 |
| <i>Escherichia coli</i> | 16S rDNA | F: CATGCCGCGTGTATGAAGAA R: CGGGTAACGTCAATGAGCAAA | This work |
| Mouse | <i>Ifng</i> | F: GCTTGAGCTCTTCAT R: GTCACCATCCTTTGCCAGT | This work |
| Mouse | <i>Il1b</i> | F: ACCTGCTGGTGTGTGACGTTCC R: GGGTCCGACAGCACGAGGCT | This work |
| Mouse | <i>Il17</i> | F: TCCAGAAGGCCCTCAGACTA R: AGGACCAAGGAGATCTCTGCTG | This work |
| Mouse | <i>Nos2</i> | F: TCAGAGCCACAGTCCTCTT R: TCCATGCAGACAACCTTGGT | This work |
| Mouse | <i>Tnf</i> | F: GTAGCCCACGTCGTAGCAA R: GGTGAGGAGCACGTAGTCG | This work |
| Rat | <i>Ifng</i> | F: CGAATCGCACCTGATCACTA R: GACTCCTTTCCGCTTCCTT | This work |
| Rat | <i>Il1b</i> | F: GCATCCAGCTTCAAATCTCA R: ATCATCCCACGAGTCACAGA | This work |
| Rat | <i>Il6</i> | F: CCGGAGAGGAGACTTCACAG R: CAGAATTGCCATTGCAACAAAC | This work |
| Rat | <i>Il17</i> | F: GTGAAGGCAGCGGTACTCA R: TTCTGGAGCTCGCTTTGA | This work |
| Rat | <i>Il22</i> | F: GCCAGCCTTGCAGATAACA R: ACTGGGGGAGCAGAACATC | This work |
| Rat | <i>Tnf</i> | F: GCGGATTGCCATTTCATAC R: TGGAAGACTCCTCCAGGTA | This work |
| Rat/Mouse | <i>Actb</i> | F: CCAGAGCAAGAGAGGTATCC R: CTGTGGTGGTGAAGCTGTAG | This work |

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Supplementary Figure S1. Quantification of *A. muciniphila* in the feces of healthy individuals or C-IBS patients. Fecal samples from the subjects were collected under anaerobic conditions. Total DNA was extracted and the presence of *A. muciniphila* was quantified by real-time PCR. Each dot represents one individual. ** $P < 0.01$ vs. healthy subjects.



Supplementary Figure S2. Experimental design of the animal protocols used in this study.