**Supplemental table 1:** Number of faecal samples measured in the different experiments.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Experiments | HealthyND | Healthy GFD | CeliacND | Celiac GFD | Relatives ND | Relatives GFD |
| Proteolytic activities (FGA, FTA, FDPPIV, FPEP) | 16 | 11 | 22 | 20 | 71 | 69 |
| 33-mer hydrolysis | 15 | 11 | 13 | 20 | 11 | 0 |
| Short chain fatty acids | 16 | 11 | 22 | 18 | 71 | 69 |
| Gluten excretion in faeces | 14 | 11 | 18 | 15 | 38 | 15 |
| Bacterial culture | 7 | 7 | 5 | 0 | 10 | 10 |

FGA: Faecal glutenasic activity, FTA: Faecal tryptic activity, FDPPIV: Faecal dipeptidyl peptidase IV, FPEP: Faecal prolylendo-peptidase.

**Table 1:** Short chain fatty acids (SCFA) content in faecal samples of 16 healthy volunteers on normal diet, 11 healthy volunteers on gluten free diet, 22 untreated celiac disease patients, 18 treated celiac disease patients, 71 first-degree relatives of celiac disease patients on normal diet and 57 relatives on gluten free diet.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Type of metabolite\* | Healthy ND | Healthy GFD | CeliacND | Celiac GFD | Relatives ND | Relatives GFD |
| Acetic acid | 26.76±12.23 | 20.60±10.46 | **42.68±19.971,2** | **50.96±22.021,2** | **48.38±24.611,2** | **48.68±28.211,2** |
| Propionic acid | 7.24±2.95 | 5.82±2.27 | **10.92±5.461,2** | **14.78±9.801,2** | **12.43±8.531,2** | **11.82±9.731,2** |
| i-Butyric acid | 0.95±0.34 | 0.90±0.49 | 1.31±0.65 | 0.93±0.43 | **1.35±0.791,2** | **1.32±0.773** |
| n-Butiric acid | 5.19±3.11 | 4.22±2.15 | **8.77±5.781,2** | **9.95±5.541,2** | **10.58±9.551,2** | **10.77±8.481,2** |
| i-Valeric acid | 1.37±0.60 | 1.18±0.55 | 1.77±1.01 | 1.18±0.60 | 1.90±1.42 | **1.90±1.321,2,3** |
| n-Valeric acid | 0.90±0.41 | 0.77±0.42 | 1.42±0.87 | **1.28±0.621,2** | **1.66±1.021,2** | **1.54±1.021,2** |
| Hexanoic acid | 0.35±0.31 | 0.36±0.33 | 0.49±0.50 | 0.50±0.48 | 0.67±0.79 | 0.64±0.59 |
| Total\* | 42.84±14.75 | 33.94±14.95 | **67.52±28.811,2** | **79.74±34.371,2** | **77.19±42.441,2** | **79.76±45.211,2** |

*ND normal diet, GFD gluten free diet*

\*Mean of samples (mmol/Kg faeces)

1 Significant differences *versus* healthy volunteers in ND (p<0.05)

2 Significant differences *versus* healthy on GFD (p<0.05)

3 Significant differences *versus* celiac disease patients on GFD (p<0.05)

**Table 2:** Cultivable bacteria involved in gluten metabolism isolated from feces of healthy subjects, active CD patients, and First-degree relatives.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  Healthy | Coeliac | Relative |
|  | % of clones (nº samples with specific taxa/ Total samples )  |
| *Firmicutes* |  | 100% (7/7) | 100% (5/5) | 100% (10/10) |
| *Bacillus* | 14.2% (1/7) | 0% (0/5) | 20% (2/10) |
| *Clostridium* | 28.5% (2/7) | 60% (3/5) | 40% (4/10) |
| *Enterococcus* | 57.1% (4/7) | 40% (2/5) | 30% (3/10) |
| *Lactobacillus* | 71.4% (5/7) | **0% (0/5)\*** | 60% (6/10) |
| *Pediococcus* | 0% (0/7) | 0% (0/5) | 10% (1/10) |
| *Staphylococcus* | 57.1% (4/7) | 20% (1/5) | 30% (3/10) |
| *Streptococcus* | 28.6% (2/7) | 0% (0/5) | 20% (2/10) |
| *Actinobacteria* |  | 57.1% (4/7) | 20% (2/5) | 50% (5/10) |
| *Bifidobacterium* | 42.8% (3/7) | 20% (2/5) | 50% (5/10) |
| *Corynebacterium* | 14.2% (1/7) | 0% (0/5) | 0% (0/10) |
| *Propionibacterium* | 0% (0/7) | 0% (0/5) | 10% (1/10) |
| *Proteobacteria* |  | 57.1% (4/7) | 20% (1/5) | 20% (2/10) |
| *Enterobacter* | 0% (0/7) | 0% (0/5) | 10% (1/10) |
| *Escherichia* | 42.8% (3/7) | 0% (0/5) | 0% (0/10) |
| *Klebsiella* | 14.2% (1/7) | 0% (0/5) | 10% (1/10) |
| *Stenotrophomonas* | 0% (0/7) | 20% (1/5) | 0% (0/10) |

\* Significant differences vs. healthy volunteers and vs. first-degree relatives. p < 0.05.