“Pediatric obesity is associated with altered gut microbiota communities”

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Note: for non-commercial purposes only
The human gut microbiota: a dynamic interplay with the host from birth to senescence settled during childhood
Pediatric obesity: a growing problem

Since 1980, the prevalence of overweight and obesity has increased remarkably in developed countries.

<table>
<thead>
<tr>
<th></th>
<th>1980</th>
<th>2013</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>16.2%</td>
<td>22.6%</td>
</tr>
<tr>
<td>Male</td>
<td>16.9%</td>
<td>23.8%</td>
</tr>
</tbody>
</table>

Ng et al, *Lancet* 2014; 384: 766–81
The gut microbiota in obese and normal-weight children

<table>
<thead>
<tr>
<th></th>
<th>N (n=36)</th>
<th>O(n=42)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>11±0.33</td>
<td>11±1.99</td>
</tr>
<tr>
<td>Sex (male:female)</td>
<td>17:19</td>
<td>21:21</td>
</tr>
<tr>
<td>BMI z-score (kg/m²)</td>
<td>0.3±0.82</td>
<td>3.0±0.7</td>
</tr>
<tr>
<td>Delivery type (vaginal: caesarean)</td>
<td>28:8</td>
<td>22:18</td>
</tr>
<tr>
<td>Infant diet (breast-fed: formula-fed)</td>
<td>14:22</td>
<td>18:21</td>
</tr>
</tbody>
</table>

Riva et al., 2016 Environ Microbiol
Materials and Methods

1- Is there a correlation between gut microbiota and weight?

2- Is there a correlation between microbial metabolites and obesity?

Short chain fatty acids (SCFAs) quantification with capillary electrophoresis
Can *Firmicutes/Bacteroidetes* ratio explain the pathophysiology of obesity?
## Taxa associated with BMI z-score

Contrasting shift for *Firmicutes* are intra-family associated

<table>
<thead>
<tr>
<th>Taxonomic level</th>
<th>Taxon</th>
<th>r</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Phylum</strong></td>
<td><em>Firmicutes</em></td>
<td>0.4145</td>
<td>0.0001</td>
</tr>
<tr>
<td></td>
<td><em>Bacteroidetes</em></td>
<td>-0.4538</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td><strong>Class</strong></td>
<td><em>Clostridia</em></td>
<td>0.3688</td>
<td>0.0008</td>
</tr>
<tr>
<td></td>
<td><em>Bacteroidia</em></td>
<td>-0.4538</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td><strong>Order</strong></td>
<td><em>Clostridiales</em></td>
<td>0.3687</td>
<td>0.0008</td>
</tr>
<tr>
<td></td>
<td><em>Bacteroidales</em></td>
<td>-0.4538</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td><strong>Family</strong></td>
<td><em>Ruminococcaceae</em></td>
<td>0.3778</td>
<td>0.0006</td>
</tr>
<tr>
<td></td>
<td><em>Bacteroidaceae</em></td>
<td>-0.4930</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td><strong>Genus</strong></td>
<td><em>Bacteroides</em></td>
<td>-0.4930</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td><strong>OTU</strong></td>
<td><strong>OTU 7: Bacteroides vulgatus</strong></td>
<td>-0.4321</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td></td>
<td><strong>OTU 3: Faecalibacterium prausnitzii</strong></td>
<td>0.3058</td>
<td>0.0064</td>
</tr>
<tr>
<td></td>
<td><strong>OTU 49: Bacteroides stercoris</strong></td>
<td>-0.3252</td>
<td>0.003</td>
</tr>
</tbody>
</table>

Results

Riva et al., 2016 *Environ Microbiol*
Gut microbiota structure is different in obese children
The fermentation activity of the gut microbiota is different in obese children.
Several taxa are correlated with short chain fatty acids

- **Phylum**
  - **Firmicutes**
    - r****p****value: 0.3107, p-value: 0.005
  - **Bacteroidetes**
    - r****p****value: -0.3145, p-value: 0.005

- **Class**
  - **Clostridia**
    - r****p****value: 0.2765, p-value: 0.01
  - **Bacteroidia**
    - r****p****value: -0.3145, p-value: 0.005

- **Order**
  - **Clostridiales**
    - r****p****value: 0.2767, p-value: 0.01
  - **Bacteroidales**
    - r****p****value: -0.3145, p-value: 0.005

- **Family**
  - **Ruminococcaceae**
    - r****p****value: 0.3120, p-value: 0.005
  - **Bacteroidaceae**
    - r****p****value: -0.2876, p-value: 0.01
  - **Porphyromonadaceae**
    - r****p****value: -0.2845, p-value: 0.01
  - **Rikenellaceae**
    - r****p****value: -0.3107, p-value: 0.005

- **Genus**
  - **Ruminococcaceae**
    - Incertae sedis (Firmicutes)
      - r****p****value: -0.2683, p-value: 0.01
  - **Bacteroides** (Bacteroidetes)
    - r****p****value: -0.2876, p-value: 0.01
  - **Parabacteroides** (Bacteroidetes)
    - r****p****value: -0.2737, p-value: 0.01
  - **Alistipes** (Bacteroidetes)
    - r****p****value: -0.3117, p-value: 0.005
  - **Oscillabacter** (Firmicutes)
    - r****p****value: -0.3205, p-value: 0.004
  - **Subdoligranulum** (Firmicutes)
    - r****p****value: 0.2737, p-value: 0.01
  - **Faecalibacterium** (Firmicutes)
    - r****p****value: 0.4487, p-value: <0.0001

- **OTU**
  - OTU 3: Faecalibacterium prausnitzii
    - r****p****value: 0.4487, p-value: <0.0001
Discussion and conclusion

• Multiple taxa are associated with SCFA levels and BMI z-score, reinforcing the tight link between the microbiota, SCFAs, and obesity.

• *Firmicutes/Bacteroidetes* ratio may not be a robust marker to explain the pathophysiology of obesity

• Correlation network analysis shows an altered structure at operational taxonomic units.

• *Bacteroidetes* taxa are generally better predictors of BMI z-score and obesity condition than *Firmicutes* taxa

• Members of the *Bacteroidetes* and certain populations of *Firmicutes* are associated with childhood obesity, though members of the *Firmicutes* exhibited contrasting shifts.

Outlook

• Additional studies are needed to better characterize and functionally categorize the members of *Firmicutes* phyla

• Future research has to include detailed analysis of metabolic activity of the gut microbiota
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