Intestinal microbiota development differs between pubertal girls and boys

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Introduction

Adolescence is one of the turning points in the human microbiota composition (1), but it is unknown, whether the microbial transformation is connected to sexual maturation. In mice, the change in the composition of microbiota during puberty is sex-specific and associated with changes in testosterone levels (2). The development of microbiota in early childhood is better understood compared to the pubertal period (3). The aim of the current work was to investigate the association between intestinal microbiota and pubertal timing.

Subjects and methods

The study was implemented on allergy-prevention-trial cohort including 1018 participants with high risk for allergy (4). The subjects randomly received a mixture of four probiotics and a prebiotic or placebo. The treatment was started perinatally for the participants mothers at the end of their pregnancy and was continued directly to the participants for the first six months of their life. The treatment had no effect on growth. At 13 years of follow up, 415 participants provided a fecal sample, and their growth data was collected from the school health service records for analysis (5). Height progression was observed in 35% (n=145) of the 415 participants (60% of the pubertal period (3)). The aim of the current work was to investigate the association between intestinal microbiota and pubertal timing.

Microbiota composition of the samples was analyzed by 16S rRNA amplicon sequencing on a Illumina platform, which has been previously described (6). Samples with less than 900 reads were excluded. The statistical analysis was carried out with R using mare-package, which relies on USEARCH. The analysis was adjusted for relevant confounders.

Results

Sufficient growth data for the assessment of puberty timing was available in 35% (n=145) of the 415 participants (60% females, 40% males). One girl and 16 boys were prepubertal based on self-reported Tanner staging. The genera with statistically significant (p<0.001) positive or negative correlations with TPHV are presented in the table.

Results for APHV were very similar to those with TPHV.

The genera correlating with TPHV (p<0.001)

<table>
<thead>
<tr>
<th>Boys</th>
<th></th>
<th>Girls</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genera</td>
<td>β</td>
<td>Genera</td>
</tr>
<tr>
<td>With zero-observations</td>
<td></td>
<td>With zero-observations</td>
</tr>
<tr>
<td>Burkholderia</td>
<td>-1.549</td>
<td>Gemella</td>
</tr>
<tr>
<td>No zero-observations</td>
<td></td>
<td>Barnesiella</td>
</tr>
<tr>
<td>Actinomyces</td>
<td>-1.091</td>
<td>Oscillibacter</td>
</tr>
</tbody>
</table>

References


Background picture (Bacillus subtilis) by Y Tambe (Wikimedia Commons)