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Martina Štroková (Braňstava, Slovakia)
Abstract:

Introduction: A growing body of evidence suggests that healthy diet is one of the major factors associated with metabolic health and changes in gut microbiota. Here we conducted a low-salt, high-fiber diet intervention trial on Korean adoptees, to assess alterations in gut microbiome composition in response to changes in diet and the associations with metabolic improvement.

Materials and methods: We developed a modified version of traditional Korean diet (K-DASH), a high-fiber, low-fat, and low-salt diet with a sufficient supply of fruits and nuts. 19 Korean adoptees (mean age: 29.4 years, male: 44.4 %) whose diets are mainly western style were recruited. 16S ribosomal RNA genes were extracted from stool samples at both pre- and post-intervention trial. The V4 region was amplified by PCR and sequenced using Illumina MiSeq platform. QIIME v.1.9.0 was used to estimate taxa from the sequenced reads.

Results: The metabolic profiles, including weight, waist circumference, systolic blood pressure, high-density lipids, and triglyceride levels, showed an improvement, except for fast blood sugar level. The gut microbiome profiles at the phylum level, Firmicutes were decreased, while Bacteroidetes were increased in abundance. The operational taxonomic unit that showed the most significant increase in abundance belonged to the family Leuconostocaceae, which is known to produce acetate and lactate (FDR-corrected p = 0.0028). The change of triglyceride levels correlated with that of abundance of Actinobacteria (Pearson’s correlation coefficient: 0.61, p=0.005).

Conclusions: Our findings suggest that metabolic improvements induced by a short-term changes of diet are mediated through their effects on the gut microbiome.
Gut microbiome composition is linked to metabolic improvements induced by dietary changes in Korean adoptees

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Introduction

A growing body of evidence suggests that healthy diet is one of the major factors associated with metabolic health and changes in gut microbiota. Here we conducted a low-salt, high-fiber diet intervention trial in Korean adoptees, to assess alterations in gut microbiome composition in response to changes in diet and the associations with metabolic improvement.

Methods

- Developed a modified version of traditional Korean diet (K-DASH diet)
- Low-salt, high-fiber, mainly vegetarian diet
- 10-day dietary intervention trial
- Recruited 19 adoptees (Age: 29.4 ± 5.0 years, male: 8 (44%)) born to Koreans, adopted to other countries, and staying in Korea at the recruitment
- At the baseline and after the trial, clinical tests and stool analysis tests performed
- Microbiome analysis
  - 16s ribosomal RNA genes extracted from stool samples
  - The V4 region amplified by PCR and sequenced using the Illumina MiSeq platform
  - Gut microbiome composition profiled using QIIME v.1.9.0

Results

Effects of the dietary intervention on metabolic improvement

<table>
<thead>
<tr>
<th>Pre-intervention</th>
<th>Post-intervention</th>
<th>Δ</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td>(N=19)</td>
<td>(N=19)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>66.7 ± 17.5</td>
<td>65.4 ± 17.1</td>
<td>-1.3</td>
</tr>
<tr>
<td>WC (cm)</td>
<td>81.3 ± 13.2</td>
<td>79.0 ± 12.7</td>
<td>-2.3</td>
</tr>
<tr>
<td>HC (cm)</td>
<td>100.6 ± 12.0</td>
<td>99.4 ± 12.2</td>
<td>-1.2</td>
</tr>
<tr>
<td>WHR (%)</td>
<td>80.7 ± 6.7</td>
<td>79.3 ± 6.2</td>
<td>-1.4</td>
</tr>
<tr>
<td>SBP (mmHg)</td>
<td>117.1 ± 13.5</td>
<td>112.5 ± 13.2</td>
<td>-4.6</td>
</tr>
<tr>
<td>DBP (mmHg)</td>
<td>77.9 ± 14.1</td>
<td>76.8 ± 12.4</td>
<td>-1.1</td>
</tr>
<tr>
<td>FBS (mg/dL)</td>
<td>78.1 ± 13.5</td>
<td>80.1 ± 11.4</td>
<td>2.0</td>
</tr>
<tr>
<td>HDL (mg/dL)</td>
<td>59.4 ± 16.2</td>
<td>50.3 ± 14.4</td>
<td>-9.1</td>
</tr>
<tr>
<td>TG (mg/dL)</td>
<td>79.5 ± 33.4</td>
<td>66.8 ± 33.7</td>
<td>-12.7</td>
</tr>
</tbody>
</table>

*Paired t-test comparisons of pre- and post-intervention Δ: mean changes, NS: not significant

Changes in microbial compositions and their correlation with changes of measures of metabolic risk factors

At the phylum level, Actinobacteria were significantly reduced by 3.57% (p < 0.01), while none of the rest phylum-level changes were statistically significant. Among correlations between phylum-level changes, changes in Firmicutes and Bacteroidetes showed a strong negative correlation (r = -0.59, p < 0.001), even though the respective changes or the two phyla were not statistically significant (p = 0.39 for Bacteroidetes and p = 0.84 for Firmicutes). The most correlated metabolic changes with Actinobacteria was changes in triglyceride levels, r = 0.61, p < 0.01. Meanwhile, changes in Proteobacteria and weight loss were negatively correlated (r = -0.56, p < 0.05), and for Firmicutes and HDL, changes were positively correlated (r = 0.53, p < 0.05).

Discussion

The ten days of the dietary trial saw overall metabolic improvements and microbial changes across different taxonomical levels, including phylum and genus, in fecal samples of participants. The mean changes of measures of metabolic risk factors indicated that there were impacts of short-term dietary changes on the overall improvements in metabolic health. Such metabolic improvements may have been induced by the gut microbial changes, as gut microbiota are shaped in part by foods consumed and are responsible for metabolic reactions in gut, including digestion of foods, absorption of nutrients and production of nutrients, which confer beneficial health effects to the human host. The disease-associated phylum Actinobacteria, which showed a significant reduction in abundances, were correlated with reduced triglyceride levels. Weight loss and reduced triglyceride levels were correlated with the increase of Rothia, some of whose strains are reported to play an important role in glucose-degrading activities.

However, inconsistent findings were also found for correlations between some of the microbial changes and the corresponding changes in measures of metabolic risk factors. For example, the relative abundance of genus Bifidobacterium, whose members utilize various dietary carbohydrates thus making contributions to health promotions, was significantly increased; however, those alterations correlated with increased TG levels, meaning different bifidobacterial strains may process different carbohydrate degrading abilities. Thus, further investigations into the finding of differences between strains of microorganisms in their metabolic activities and the interplay between nutritional changes, microbial changes and metabolic health will be needed.

Conclusion

Our findings suggest that metabolic improvements induced by short-term, dramatic changes to high-fiber, low-salt diet may be mediated through their effects on the gut microbiome.