Gut microbiota and diet in patients with various glucose tolerance

Egshatyan LV1, Kashtanova DA1, Popenko AS2, Tkacheva ON1, Tyakht AV2, Alexeev DG2, Karamnova NS1, Boytsov SA1.

- 1 National Research Center for Preventive Medicine, Moscow, Russian Federation
- 2 Research Institute for Physical-Chemical Medicine, Moscow, Russian Federation

BACKGROUND:

Type 2 diabetes (T2D) is a progressive disease. The gut microbiota has recently been identified as a new potential diabetes risk factor in addition to well-known diabetes risk factors..

DESIGN:

To investigate the gut microbiota composition in association with the dietary patterns in patients with different glucose tolerance we analyzed 92 patients (26 men and 66 women) from Moscow and Moscow Region (the Caucasian race) aged from 25 to 75 years old with normal glucose tolerance (n=48), pre-diabetes (n=24) and the first diagnosed type 2 diabetes (n=20).

The average duration of pre-diabetes was 0.22+_0.031 years and T2D was 0.78+ 0.069 years.

Metagenomic analysis was performed using 16SrRNA sequencing. The diet has been studied by a frequency method with a quantitative evaluation of food intake using a standardized computer program "Analysis of Human Nutrition" (version 1.2.4 FGBI Research Institute of Nutrition 2003-2006).

The average values of age, BMI, waist-to-hip ratio, fasting glucose, and HbA1c were significantly higher in patients with pre-diabetes and T2D than in healthy individuals. Patients with pre-diabetes and T2D did not differ in the energy value of the daily diet and in the amount of consumed proteins, fats, and carbohydrates. Patients with T2D had higher levels of fasting glucose, HbA1c and waist-to-hip ratio (higher in T2D), as well as in the energy value of the daily diet and the amount of carbohydrates consumed than those with prediabetes.

Criteria for exclusion from the study were as follows:

Type 1 diabetes and other specific types of diabetes; regular intake of any drug (including antibiotics during the last 3 hypoglycemic drugs); months, diabetic severe microangiopathy (preproliferative and proliferative diabetic retinopathy, CKD 3b-5 stages); cardiovascular diseases: chronic heart failure class II-IV (NYHA), valvular heart disease; chronic liver and kidney failure; cancer; pregnancy; lactation; moderate and severe anaemia; infectious diseases; acute gastrointestinal tract diseases; the operations on the abdominal organs; diagnosed lactase intolerance; diagnosed allergic reaction to any food; a history of organ transplantation, diseases of the oral cavity and dentofacial system, refusal to participate in the study.

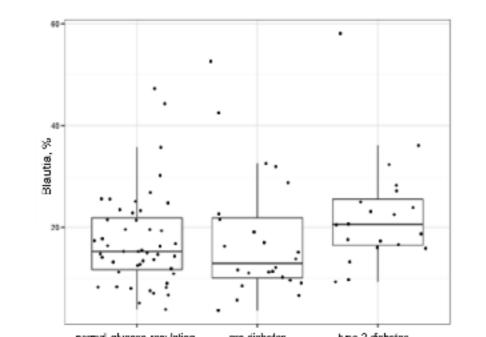
RESULTS:

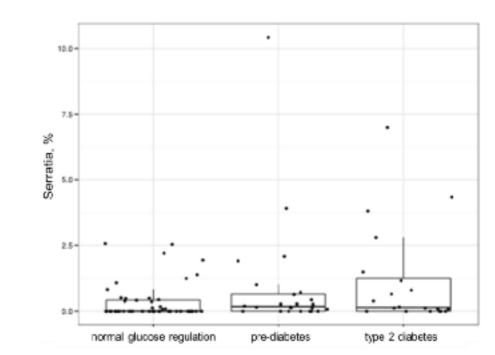
Microbiota in the samples was predominantly represented by Firmicutes $(57,09\pm13,6\%)$ and in a less degree by Bacteroidetes $(12,7\pm9,86\%)$.

The representation of *Firmicutes* were significantly higher (p=0,007) and the *Bacteroidetes* lower (p=0,01) in patients with T2D than in healthy individuals и patients with pre-diabetes.

representation of Bacteroidetes			representation of Firmicutes		
healthy	pre-diabetes	T2D	healthy	pre-diabetes	T2D
13,57±10,2%	11,8±9,73%	9,07±7,87%	55,79±13,96%	58,92±11,2%	63,78±9,77%

Blautia was a dominanting genus in all samples. The representation of Blautia (p=0,0006) and Serratia (p=0,002) was higher in T2D.





To analyze nutrition types, all the samples were divided into two clusters by using the k-means clustering. These clusters differed significantly in the protein, fat, and carbohydrate percentage.

Nutrients	1st cluster (n=64)	2 nd cluster (n=22)	P
protein, %	18.81 ± 2.82	24.5 ± 4.62	8.92e-07
fat, %	24.49 ± 3.98	33.47 ± 3.68	2.03e-10
carbohydrate, %	56.71± 5.48	42.03 ± 5.61	3.33e-12

The first cluster exhibited higher content of carbohydrates in the diet $(56,7\pm5,5\% \text{ vs } 42\pm5,6\%)$; the second - of fat $(33,5\pm3,7\% \text{ vs } 24,5\pm4\%)$ and protein $(24,5\pm4,6\% \text{ vs } 18,8\pm2,8\%)$.

The representation of the *Bacteroides* turned to be lower (p=0,00011) and *Prevotella* (p=0,0004) abundance turned to be higher in carbohydrate cluster.

There were more patients with T2D (p=0.002) in the fat-protein cluster.

Using the Calinski-Harabasz index identified the samples with more similar diets. It was discovered that half of the patients with a high-fat diet (138±63 g/day) had normal tolerance, the others had T2D. The regression analysis showed that these T2D patients also had a higher representation of *Blautia* (p=0.0001).

Conclusion

The high Blautia representation in combination with high-fat diet is correlated with T2D.



