High-throughput Sequencing Study of the Effect of Transabdominal Hysterectomy on Intestinal Flora in Patients with Uterine Fibroids

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SUBJECT AREAS

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intestinal flora, uterine fibroids, hysterectomy, estrogen, high-throughput sequencing, 16sRNA

Abstract

Background: To investigate the effect of transabdominal hysterectomy on the diversity of the intestinal flora in patients with uterine fibroids. Patients with uterine fibroids were selected from September 2018 to December 2018, in the Department of Obstetrics and Gynecology, Shengjing Hospital, China Medical University, and stool specimens were collected from patients before and after surgery.

Results: High-throughput sequencing of the 16S rRNA gene was used to detect the changes in microbial community structure and diversity, and the effects of total hysterectomy on the intestinal flora were further analyzed. Estrogen levels decreased after trans-abdominal hysterectomy. High-throughput sequencing showed that after abdominal hysterectomy, the abundance and diversity of the intestinal flora decreased. The abundance changes were mainly due to Proteobacteria, where their abundance increased.

Conclusions: Trans-abdominal hysterectomy changes the intestinal flora of the body by lowering the level of estrogen in the body, which reduces the diversity and abundance of the intestinal flora.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed.

However, the manuscript can be downloaded and accessed as a PDF.

Tables

	Group		T value	P value
	RS1(n=15)	RS2(n=15)		
AMHnmol/L	4.78±1.75	4.01±1.00	1.82	0.09
E ₂ (pmol/L)	460.71±303.08	229.36±110.19	2.65	0.02
FSH(IU/L)	11.86±11.77	19.47±28.29	-0.94	0.36

Table 1 Comparison of ovarian function between the two groups

	Group		P value
	RS1	RS2	
ACE	2032.94±1342.18	1468.45±1207.79	0.37
Chao1	2200.16±1437.12	1664.03±1300.57	0.51
Simpson	0.91±0.12	0.86±0.13	0.20
Shannon	6.87±2.73	5.28±2.44	0.22

Table 2 Sequencing results and diversity index of two groups of samples

*The operational taxonomic units (OTUs) were defined at the 97% similarity level

	Group		P value
	RS1	RS2	
Bacteroidetes(%)	24.54	11.43	0.003
Proteobacteria(%)	34.36	54.04	0.016
Firmicutes(%)	0.003	17.26	0.926

Table 3. Comparison of relative abundance of two groups of TOP3 strains at the phylum level

Group	A	Observed-delta	Expected-delta	Significance
RS1-RS2	0.03	0.80	0.82	0.036

Table 4 Significanttness test table for community structure differences between groups

Figures

Figure 1

Figure 2

Figure 4