

DOI:10.13350/j.cjpb.240511

• 论著 •

# 原发性肾小球疾病患者肠道菌群与炎症因子的相关性分析

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**【摘要】** 目的 探析原发性肾小球疾病患者肠道菌群水平、炎症因子水平及肠道菌群与炎症因子的相关性。方法 选取2021-2023年,本院接诊的62例原发性肾小球疾病患者为本次研究对象,同时选取同期60例体检健康者为健康对照组。通过电子病历系统收集本次研究对象所有临床资料,对比不同病理类型患者的临床特点。采集参与本次研究所有研究对象的粪便样本,采用光镜法进行细菌培养,计算每克粪便中乳酸杆菌、双歧杆菌、大肠埃希菌、拟杆菌、肠球菌菌落数。采集所有研究对象的静脉血,离心处理后,采用酶联免疫吸附法检测血清中肿瘤坏死因子- $\alpha$  (tumor necrosis factor- $\alpha$ , TNF- $\alpha$ )、白细胞介素-6 (Interleukin-6, IL-6)、白细胞介素-17 (Interleukin-17, IL-17)水平。采用Pearson相关性检验分析法分析肠道菌群与炎症因子的相关性。结果 62例原发性肾小球疾病患者中,45.16%为膜性肾病,25.81%为IgA肾病,11.29%为微小病变性肾病,9.68%为系膜增生性肾小球肾炎,3.23%为局灶性节段性肾小球硬化,系膜毛细血管性肾小球肾炎、新月体性肾小球肾炎、毛细血管内增生性肾小球肾炎各占比1.61%。48.39%表现为肾病综合征,32.26%表现为肾炎综合征,14.52%表现为肾功能不全,4.84%表现为隐匿性肾炎。膜性肾病患者与IgA肾病两组患者的年龄、性别、尿酸水平差异无统计学意义( $P>0.05$ ),白蛋白水平、肌酐水平差异有统计学意义( $P<0.05$ )。疾病组患者乳酸杆菌丰度为(5.89 $\pm$ 0.87)LogN/g,双歧杆菌丰度为(6.45 $\pm$ 0.98)LogN/g,大肠埃希菌丰度为(9.59 $\pm$ 1.20)LogN/g,拟杆菌丰度为(6.89 $\pm$ 0.95)LogN/g,肠球菌丰度为(8.71 $\pm$ 1.29)LogN/g,健康对照组乳酸杆菌丰度为(7.43 $\pm$ 0.99)LogN/g,双歧杆菌丰度为(9.62 $\pm$ 1.37)LogN/g,大肠埃希菌丰度为(6.61 $\pm$ 0.99)LogN/g,拟杆菌丰度为(8.72 $\pm$ 0.79)LogN/g,肠球菌丰度为(7.18 $\pm$ 0.95)LogN/g。两组患者乳酸杆菌、双歧杆菌、大肠埃希菌、拟杆菌、肠球菌丰度差异均有统计学意义( $P<0.05$ )。疾病组患者血清TNF- $\alpha$ 为(20.87 $\pm$ 5.05)ng/L,IL-6为(93.48 $\pm$ 10.44)ng/L,IL-17为(62.68 $\pm$ 7.07)ng/L。健康对照组血清TNF- $\alpha$ 为(8.52 $\pm$ 2.64)ng/L,IL-6为(8.13 $\pm$ 3.26)ng/L,IL-17为(21.12 $\pm$ 4.10)ng/L。与健康对照组相比,疾病组患者血清TNF- $\alpha$ 、IL-6、IL-17均显著升高( $P<0.05$ )。乳酸杆菌丰度与TNF- $\alpha$ 、IL-6、IL-17水平均呈负相关( $P<0.05$ ),双歧杆菌丰度与TNF- $\alpha$ 、IL-6、IL-17水平均呈负相关( $P<0.05$ ),大肠埃希菌丰度与TNF- $\alpha$ 、IL-6、IL-17水平均呈正相关( $P<0.05$ ),拟杆菌丰度与TNF- $\alpha$ 、IL-6、IL-17水平均呈负相关( $P<0.05$ ),肠球菌丰度与TNF- $\alpha$ 、IL-6、IL-17水平均呈正相关( $P<0.05$ )。结论 原发性肾小球疾病患者主要为膜性肾病,肠道菌群与炎症因子水平较健康人群均发生变化,乳酸杆菌、双歧杆菌、拟杆菌丰度与TNF- $\alpha$ 、IL-6、IL-17呈负相关,大肠埃希菌、肠球菌丰度与TNF- $\alpha$ 、IL-6、IL-17呈正相关。

**【关键词】** 原发性肾小球疾病;肠道菌群;炎症因子

**【文献标识码】** A

**【文章编号】** 1673-5234(2024)05-0550-05

[Journal of Pathogen Biology. 2024 May;19(5):550-554.]

## Correlation analysis between gut microbiota and inflammatory factors in patients with primary glomerular disease

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**【Abstract】** **Objective** To explore the levels of gut microbiota, inflammatory factors, and the correlation between gut microbiota and inflammatory factors in patients with primary glomerular disease. **Methods** 62 patients with primary glomerular disease admitted to our hospital from 2021 to 2023 were selected as the study subjects, while 60 healthy individuals who underwent physical examinations during the same period were selected as the healthy control group. All clinical data of the study subjects were collected by our hospital's electronic medical record system and the clinical characteristics of patients with different pathological types were compared. The fecal samples were collected from all participants in this study, the light column method was used for bacterial culture, and the number of *Lactobacillus*, *Bifidobacterium*, *Escherichia coli*, *Bacteroidetes*, and *Enterococcus* colonies per gram of feces were calculated. The venous blood were collected and centrifuged from all study subjects, and the levels of the tumor necrosis factor- $\alpha$  (TNF-

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$\alpha$ ), Interleukin-6 (IL-6) and interleukin-17 (IL-17) in serum were detected by enzyme-linked immunosorbent assay. The correlation between gut microbiota and inflammatory factors were analyzed by Pearson correlation analysis method.

**Results** Among 62 patients with primary glomerular disease, 45.16% had membranous nephropathy, 25.81% had IgA nephropathy, 11.29% had minimal degenerative nephropathy, 9.68% had mesangial proliferative glomerulonephritis, 3.23% had focal segmental glomerulosclerosis, and mesangial capillary glomerulonephritis, crescentic glomerulonephritis, and intracapillary proliferative glomerulonephritis each accounted for 1.61%. 48.39% presents with nephrotic syndrome, 32.26% with nephritis syndrome, 14.52% with renal insufficiency, and 4.84% with occult nephritis. There was no statistically significant difference in age, gender, and uric acid levels between patients with membranous nephropathy and IgA nephropathy ( $P > 0.05$ ), while there was a statistically significant difference in albumin and creatinine levels ( $P < 0.05$ ). The abundance of *Lactobacillus* was  $(5.89 \pm 0.87)$  LogN/g, the abundance of *Bifidobacterium* was  $(6.45 \pm 0.98)$  LogN/g, the abundance of *Escherichia coli* was  $(9.59 \pm 1.20)$  LogN/g, the abundance of *Bacteroidetes* was  $(6.89 \pm 0.95)$  LogN/g, and the abundance of *Enterococcus* was  $(8.71 \pm 1.29)$  LogN/g in the disease group. The abundance of *Lactobacillus* was  $(7.43 \pm 0.99)$  LogN/g, the abundance of *Bifidobacterium* was  $(9.62 \pm 1.37)$  LogN/g, the abundance of *Escherichia coli* was  $(6.61 \pm 0.99)$  LogN/g, and the abundance of *Bacteroidetes* was  $(8.72 \pm 0.79)$  LogN/g. N/g, the abundance of *Enterococcus* was  $(7.18 \pm 0.95)$  LogN/g in the healthy control group. There was a statistically significant difference in the abundance of *Lactobacillus*, *Bifidobacterium*, *Escherichia coli*, *Bacteroidetes*, and *Enterococcus* between the two groups of patients ( $P < 0.05$ ). The levels of the TNF- $\alpha$  was  $(20.87 \pm 5.05)$  ng/L, IL-6 was  $(93.48 \pm 10.44)$  ng/L, and IL-17 was  $(62.68 \pm 7.07)$  ng/L in the disease patients group serum. The levels of the TNF- $\alpha$  was  $(8.52 \pm 2.64)$  ng/L, IL-6 was  $(8.13 \pm 3.26)$  ng/L, and IL-17 was  $(21.12 \pm 4.10)$  ng/L in the healthy control group serum. Compared with the healthy control group, the serum TNF- $\alpha$ , IL-6 and IL-17 of patients in the disease group were significantly elevated, and the difference was statistically significant ( $P < 0.05$ ). Abundance of *Lactobacillus* and the levels of TNF- $\alpha$ , IL-6 and IL-17 were negatively correlated ( $P < 0.05$ ), and the abundance of *Bifidobacterium* was correlated with the levels of TNF- $\alpha$ , IL-6 and IL-17 were negatively correlated ( $P < 0.05$ ), and the abundance of *Escherichia coli* was positively correlated with the levels of the TNF- $\alpha$ , IL-6 and IL-17 ( $P < 0.05$ ), and the abundance of *Bacteroides* was negatively correlated with the levels of the TNF- $\alpha$ , IL-6 and IL-17 ( $P < 0.05$ ), and the abundance of *Enterococcus* was positively correlated with the levels of the TNF- $\alpha$ , of IL-6 and IL-17 ( $P < 0.05$ ).

**Conclusion** Patients with primary glomerular disease were mainly membranous nephropathy, with changes in gut microbiota and inflammatory factor levels compared to healthy individuals. Abundances of *Lactobacilli*, *Bifidobacteria*, and *Pseudomonas* were negatively correlated with TNF- $\alpha$ , IL-6 and IL-17, while the abundance of *Escherichia coli* and *Enterococcus* was positive correlated with TNF- $\alpha$ , IL-6 and IL-17.

**【Key words】** Primary glomerular disease; Intestinal microbiota; Inflammatory factors

肾病疾病是临床常见慢性疾病之一,相关研究显示,全球慢性肾脏病患者已高达8.5亿,每年有近百万人因为多种原因发展为终末期肾功能衰竭,对患者生活质量及生命安全造成严重威胁<sup>[1]</sup>。肾脏疾病的发病率受到社会环境、卫生条件、经济水平、遗传基因等多种因素影响,原发性肾小球疾病是导致终末期肾病的重要原因<sup>[2-3]</sup>。原发性肾小球疾病是由非系统性疾病引发的肾小球病理改变,局限于肾小球或者主要是肾小球损害的一种肾脏疾病,临床上常见的病理改变类型主要有微小病变性肾病、IgA肾病、膜性肾病等<sup>[4]</sup>。研究发现,原发性肾小球疾病患者肠道菌群组成结构发生改变,相较于健康人群的肠道菌群多样性降低,菌群的丰度发生显著变化<sup>[5]</sup>。Kalavrizioti等<sup>[6]</sup>发现,膜性肾病患者尿液中肿瘤坏死因子- $\alpha$ 、IL-6、IL-17、单核细胞趋化蛋白-1水平显著升高。本研究通过分析本院接诊的62例原发性肾小球疾病患者的临床资料,探讨原发性肾小球疾病患者肠道菌群水平、炎症

因子水平及肠道菌群与炎症因子的相关性,结果现报告如下。

## 材料与方法

### 1 研究对象

选取2021-2023年本院接诊的62例原发性肾小球疾病患者为本次研究对象。男性39例,女性23例。年龄20~75( $55.78 \pm 9.62$ )岁。纳入标准:①临床资料完整;②年龄 $\geq 18$ 岁;③综合临床表现与肾穿刺活检病理诊断为原发性肾小球疾病,临床表现主要为肌酐 $> 150 \mu\text{mol/L}$ 、尿蛋白 $> 300 \text{mg}/24 \text{h}$ 、局部或全身水肿等<sup>[7]</sup>。排除标准:①继发性肾脏疾病;②合并免疫系统缺陷者;③精神异常,无法配合研究者;④30 d内使用抗菌药物治疗者;⑤合并血液系统疾病者;⑥合并重要脏器严重功能障碍者;⑦需要进行肾脏替代治疗者;⑧妊娠期或哺乳期女性;⑨合并恶性肿瘤者;⑩接种激素及免疫抑制剂药物治疗时间超过3个月以上

者。同时选取同期 60 例体检健康者为健康对照组。

本次研究已通过本院伦理协会审核批准,符合《赫尔辛基宣言》。

## 2 资料收集

通过本院电子病历系统收集本次研究对象所有临床资料,包括年龄、性别、病理类型、并发症、实验室检查结果、肠道菌群特征、炎症因子水平等。

## 3 病理分型

由本院临床医师与病理医师通过患者的临床资料、实验室检查结果及病理改变特点,参考《肾活检病理学》<sup>[8]</sup>中原发性肾小球疾病病理分型相关标准,进行病理分型,主要包括:膜性肾病(Membranous nephropathy, MN)、IgA 肾病(IgA nephropathy, IgAN)、微小病变性肾病(Minimal change disease, MCD)、系膜增生性肾小球肾炎(mesangial proliferative glomerulonephritis, MsPGN)、局灶性节段性肾小球硬化(focal segmental glomerulosclerosis, FSGS)、系膜毛细血管性肾小球肾炎(mesangiocapillary glomerulonephritis, MPGN)、新月体性肾小球肾炎(crescentic glomerulonephritis, CreGN)、毛细血管内增生性肾小球肾炎(Endocapillary proliferative glomerulonephritis, EnPGN)、硬化性肾小球肾炎(sclerosing glomerulonephritis, SGN)、增生硬化性肾小球肾炎(proliferative sclerosing glomerulonephritis, PSGN)、其他(光镜下可观察到增生硬化性或硬化性肾小球肾炎等病理变化,但通过其他病理检查、临床特征无法判定疾病者,均归类为其他)。

## 4 肠道菌群水平检测

采集参与本次研究所有研究对象的粪便样本,于粪便排出后 24 h 内收集,采用无菌棉签采集 5 g 粪便样本置于无菌粪便收集器内送检。参照文献<sup>[9]</sup>采用光冈法进行细菌培养,对乳酸杆菌、双歧杆菌、大肠埃希菌、拟杆菌、肠球菌进行定量培养。将采集的粪便标本,加入适量生理盐水进行标本稀释,按照 10 倍稀释梯度稀释至  $10^{-7}$ ,吸取 50  $\mu$ L 经稀释后的液体接种于乳酸杆菌培养基、双歧杆菌培养基、大肠埃希菌培养基、拟杆菌培养基、肠球菌培养基上,进行培养。厌氧菌置于厌氧培养箱中,于 35  $^{\circ}$ C 恒温条件中,培养 48~72 h。需氧菌置于普通培养箱中,于 35  $^{\circ}$ C、5%  $\text{CO}_2$  条件中,培养 48 h。经培养后,由我院病原实验室人员根据菌落特征、形态及革兰染色结果,通过质谱仪(MALDITOF MS,布鲁克-道尔顿公司)进行病原菌鉴定,鉴定至属或种水平。根据培养基上的菌落计数,计算每克粪便中目标菌落数,计算公式如下:菌落数( $\log\text{N/g}$ )=平均菌落数 $\times$ 稀释倍数 $\times$ 500。

## 5 炎症因子检测

于清晨空腹状态下,采集静脉血 8~10 mL,置于 EP 管内静置 30 min。3 000 r/min(离心半径 11 cm)离心 15 min,分离上层血清,保存于 -20  $^{\circ}$ C。使用美国贝克曼库尔特全自动生化分析仪,采用酶联免疫吸附法(enzyme linked immunosorbent assay, ELISA)检测血清中肿瘤坏死因子- $\alpha$ (tumor necrosis factor- $\alpha$ , TNF- $\alpha$ )、白细胞介素-6(Interleukin-6, IL-6)、白细胞介素-17(Interleukin-17, IL-17)水平,试剂盒均购自上海钰博生物科技公司。

## 6 统计分析

采用 SPSS 25.0 统计学软件对本次研究数据进行分析处理,计数资料采用例或百分比表示,组间对比采用  $\chi^2$  检验,计量资料采用“ $\bar{x} \pm s$ ”表示,组间对比采用  $t$  检验,采用 Pearson 相关性检验分析法分析原发性肾小球疾病患者肠道菌群与炎症因子的相关性, $P < 0.05$  表示差异有统计学意义。

## 结果

### 1 不同病理类型临床资料分析

62 例原发性肾小球疾病患者中,28 例为膜性肾病(45.16%, 28/62),16 例为 IgA 肾病(25.81%, 16/62),7 例为微小病变性肾病(11.29%, 7/62),6 例为系膜增生性肾小球肾炎(9.68%, 6/62),2 例为局灶性节段性肾小球硬化(3.23%, 2/62),系膜毛细血管性肾小球肾炎、新月体性肾小球肾炎、毛细血管内增生性肾小球肾炎各 1 例(1.61%, 1/62)。62 例患者中,30 例表现为肾病综合征(48.39%, 30/62),20 例表现为肾炎综合征(32.26%, 20/62),9 例表现为肾功能不全(14.52%, 9/62),3 例表现为隐匿性肾炎(4.84%, 3/62)。对比膜性肾病患者与 IgA 肾患者的临床资料,结果显示,年龄、性别、尿酸水平差异无统计学意义( $P > 0.05$ ),白蛋白水平、肌酐水平差异均有统计学意义( $P < 0.05$ )。见表 1。

表 1 不同病理类型患者临床资料对比结果  
Table 1 Comparison of clinical data of patients with different pathological types

分组 Group	膜性肾病(n=28) Membranous nephropathy	IgA 肾病(n=16) IgA nephropathy	$\chi^2/t$	P
年龄 (岁)				
18~40	11	10		
41~65	15	5	2.278	0.320
>65	2	1		
性别				
男	15	10	0.331	0.565
女	13	6		
白蛋白(g/L)	28.18 $\pm$ 4.75	41.06 $\pm$ 3.47	-9.473	0.000
肌酐( $\mu$ mol/L)	69.75 $\pm$ 9.36	94.06 $\pm$ 17.52	-6.023	0.000
尿素氮(mmol/L)	5.73 $\pm$ 0.83	6.83 $\pm$ 1.45	-2.787	0.011
尿酸(mmol/L)	0.38 $\pm$ 0.05	0.39 $\pm$ 0.07	-0.350	0.728



## 2 肠道菌群水平比较

肠道菌群检测结果显示,疾病组患者乳酸杆菌丰度为(5.89±0.87)LogN/g,双歧杆菌丰度为(6.45±0.98)LogN/g,大肠埃希菌丰度为(9.59±1.20)LogN/g,拟杆菌丰度为(6.89±0.95)LogN/g,肠球菌丰度为(8.71±1.29)LogN/g,健康对照组乳酸杆菌丰度为(7.43±0.99)LogN/g,双歧杆菌丰度为(9.62±1.37)LogN/g,大肠埃希菌丰度为(6.61±0.99)LogN/g,拟杆菌丰度为(8.72±0.79)LogN/g,肠球菌丰度为(7.18±0.95)LogN/g。两组患者乳酸杆菌、双歧杆菌、大肠埃希菌、拟杆菌、肠球菌丰度对比差异均有统计学意义( $P<0.05$ )。见表2。

表2 不同分组肠道菌群水平对比( $\bar{x}\pm s, \log N/g$ )  
Table 2 Comparison of gut microbiota levels in different groups

分组 Group	疾病组 (n=62) Disease group	健康对照组 (n=60) Healthy control group	t	P
乳酸杆菌	5.89±0.87	7.43±0.99	-9.137	0.000
双歧杆菌	6.45±0.98	9.62±1.37	-14.620	0.000
大肠埃希菌	9.59±1.20	6.61±0.99	14.952	0.000
拟杆菌	6.89±0.95	8.72±0.79	-11.600	0.000
肠球菌	8.71±1.29	7.18±0.95	7.489	0.000

## 3 炎症因子水平比较

血清炎症因子水平检测结果显示,疾病组患者血清 TNF- $\alpha$  为(20.87±5.05)ng/L, IL-6 为(93.48±10.44)ng/L, IL-17 为(62.68±7.07)ng/L。健康对照组血清 TNF- $\alpha$  为(8.52±2.64)ng/L, IL-6 为(8.13±3.26)ng/L, IL-17 为(21.12±4.10)ng/L。与健康对照组相比,疾病组患者血清 TNF- $\alpha$ 、IL-6、IL-17 均显著升高,差异有统计学意义( $P<0.05$ )。见表3。

表3 不同分组炎症因子水平比较( $\bar{x}\pm s$ )  
Table 3 Comparison of inflammatory cytokine levels in different groups

分组 Group	疾病组 (n=62) Disease group	健康对照组 (n=60) Healthy control group	t	P
TNF- $\alpha$ (ng/L)	20.87±5.05	8.52±2.64	17.006	0.000
IL-6(ng/L)	93.48±10.44	8.13±3.26	61.336	0.000
IL-17(ng/L)	62.68±7.07	21.12±4.10	39.860	0.000

## 4 肠道菌群与炎症因子的相关性分析

Pearson 相关性检验分析显示,乳酸杆菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 水平均呈负相关( $P<0.05$ ),双歧杆菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 水平均呈负相关( $P<0.05$ ),大肠埃希菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 水平均呈正相关( $P<0.05$ ),拟杆菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 水平均呈负相关( $P<0.05$ ),肠球菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 水平均呈正相关( $P<0.05$ )。见表4。

表4 肠道菌群与炎症因子的相关性分析  
Table 4 Correlation analysis between gut microbiota and inflammatory factors

炎症因子 Inflammatory factors	TNF- $\alpha$		IL-6		IL-17	
	r	P	r	P	r	P
乳酸杆菌	-0.486	0.000	-0.626	0.000	-0.599	0.000
双歧杆菌	-0.638	0.000	-0.798	0.000	-0.769	0.000
大肠埃希菌	0.670	0.000	0.794	0.000	0.757	0.000
拟杆菌	-0.585	0.000	-0.712	0.000	0.707	0.000
肠球菌	0.467	0.000	0.546	0.000	0.516	0.000

## 讨论

不同类型原发性肾小球疾病可表现为相同临床特征,而相同类型疾病可在不同患者、不同时间表现为不同临床特征,因此,临床上对肾小球疾病进行准确的早期诊断较为困难,肾活检是目前诊断肾小球疾病的“金标准”<sup>[10]</sup>。本次研究中62例原发性肾小球疾病患者,主要为膜性肾病与IgA肾病,两组患者的白蛋白水平、肌酐水平对比差异具有统计学意义,年龄、性别、尿酸水平对比差异不具有统计学意义。不同地区由于地域差异,原发性肾小球疾病主要病理类型各不相同,通过分析本地区的主要流行病理型,对于临床诊断可以提供一定的参考数据支持。

作为机体的重要贮存与排泄器官,肠道除了在肾脏外排泄尿酸方面承担着重要的职责。在健康的生理状态下,肠道菌群与宿主之间形成了一个相互作用的共生复合体,共同参与并影响机体的正常生理代谢。本次研究中,疾病组患者肠道乳酸杆菌、双歧杆菌、拟杆菌丰度较健康人群降低,大肠埃希菌、肠球菌丰度较健康人群升高,菌群结构发生显著改变。随着对肠道微生物的深入研究发现,原发性肾小球疾病患者大部分存在肠道黏膜屏障被破坏,肠道菌群失调等问题,不同类型的肾小球疾病患者肠道菌群组成不同<sup>[11]</sup>。患者肠道菌群结构发生变化,可导致患者肠道内有害物质及细菌进入人体循环系统,通过影响肠道菌-肾小球轴的相互作用,参与肾小球的病理过程<sup>[12]</sup>。

相关医学研究发现,原发性肾小球疾病患者的血清炎症因子水平显著升高,可能是由于肾小球疾病是免疫介导的炎症反应,机体发生异常后可导致炎症因子发生改变。本次研究中,疾病组患者血清 TNF- $\alpha$ 、IL-6、IL-17 水平显著高于健康对照组人群。IL-6 作为机体复杂细胞因子作用网络的关键因子之一,具有重要的生物学活性,其在机体内的表达水平被证实与多种疾病的发生密切相关, TNF- $\alpha$  作为典型的炎症因子,可促进炎症反应的发生,参与多种疾病的发病<sup>[13]</sup>。

有关研究发现,人体肠道菌群产生的短链脂肪酸可调节机体免疫应答,原发性肾小球疾病患者肠道代谢产物尿素和氨基酸等可对患者发病过程产生影

响<sup>[14]</sup>。本次研究显示,乳酸杆菌、双歧杆菌、拟杆菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 呈负相关,大肠埃希菌、肠球菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 呈正相关。原发性肾小球疾病患者的肾小球滤过率较健康人群降低,多种有害代谢产物无法通过肾脏进行排泄,加剧了肠道菌群紊乱,而肠道菌群异常改变可激活机体炎症反应,对肾脏功能造成进一步的伤害。相关报道显示,肠道内有益菌群的降低是导致血清炎症指标上升的原因之一,通过补充益生菌,保持患者肠道微生态平衡,对延缓原发性肾小球疾病发展具有重要意义<sup>[15]</sup>。

综上所述,原发性肾小球疾病患者主要为膜性肾病,肠道菌群与炎症因子水平较健康人群均发生变化,乳酸杆菌、双歧杆菌、拟杆菌丰度降低,大肠埃希菌、肠球菌丰度上升,血清 TNF- $\alpha$ 、IL-6、IL-17 显著升高。肠道菌群与炎症因子水平具有一定相关性,乳酸杆菌、双歧杆菌、拟杆菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 呈负相关,大肠埃希菌、肠球菌丰度与 TNF- $\alpha$ 、IL-6、IL-17 呈正相关。通过调节患者菌群结构,保持患者肠道微生态平衡,可以在一定程度上调节具体炎症反应,延缓病情发展。

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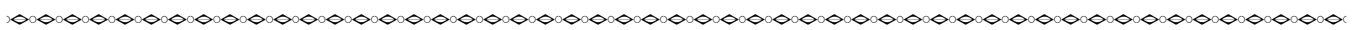
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【收稿日期】 2024-12-16 【修回日期】 2024-03-03



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【收稿日期】 2023-11-27 【修回日期】 2024-02-10