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## 肠道菌群多样性在喂养不耐受新生儿中的作用分享到:

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**Title:** Intestinal microflora community diversity in newborns with feeding intolerance

**作者:** 唐小丽; 余加林; 艾青; 卢虹旭; 李阳; 王政力; 杨静丽; 贺雨; 潘云

重庆医科大学附属儿童医院新生儿中心, 儿童发育疾病研究教育部重点实验室, 儿科学重庆市重点实验室, 重庆市儿童发育重大疾病诊治与预防国际科技合作基地

**Author(s):** Tang Xiaoli; Yu Jialin; Ai Qing; Lu Hongxu; Li Yang; Wang Zhengli; Yang Jingli; He Yu; Pan Yun

Department of Neonatology, Key Laboratory of Child Development and Disorder of Ministry of Education, Chongqing Key Laboratory of Pediatrics, Chongqing International Science and Technology Cooperation Center for Child Development and Disorders, Children's Hospital of Chongqing Medical University, Chongqing 400014, China

**关键词:** 新生儿; 喂养不耐受; 肠道菌群; 生物多样性

**Keywords:** newborn; feeding intolerance; gut microbiota; biodiversity

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**摘要:** 目的 探讨肠道菌群多样性变化在喂养不耐受新生儿中的作用及其与疾病转归的关系。 方法 采用16S rDNA PCR联合变性梯度凝胶电泳 (denatured gradient gel electrophoresis, DGGE) 技术, 分别对12例喂养不耐受新生儿 (喂养不耐受组) 发生喂养不耐受24 h内 ( $t_0$ ) 及喂养不耐受恢复后 ( $t_1$ ) 的粪便标本进行菌群多样性分析, 并通过T-A克隆测序, 了解其细菌种类分布及常见优势菌。同期采集12例孕周、出生体质量、日龄匹配的喂养耐受新生儿 (对照组) 粪便标本进行对比分析。 结果 经DGGE分析, 喂养不耐受新生儿粪便标本的条带丰富度较对照组显著下降 ( $9.00 \pm 2.83$  vs  $12.76 \pm 2.38$ ,  $P < 0.05$ ), 香农威纳指数较对照组显著下降 ( $2.12 \pm 0.36$  vs  $2.51 \pm 0.19$ ,  $P < 0.05$ ); 喂养不耐受恢复后 ( $t_1$ ) 粪便标本条带丰富度、香农威纳指数与对照组比较, 差异无统计学意义 ( $14.00 \pm 1.91$  vs  $14.75 \pm 1.76$ ,  $2.61 \pm 0.14$  vs  $2.66 \pm 0.13$ ,  $P > 0.05$ ); 克隆测序发现, 喂养不耐受组粪便标本中克雷伯菌属比例较对照组增加 ( $53.40\%$  vs  $40.94\%$ ,  $P < 0.05$ )。 结论 喂养不耐受新生儿肠道菌群多样性降低, 随着病情的恢复, 肠道菌群多样性恢复; 新生儿发生喂养不耐受可能与其肠道菌群中克雷伯菌属比例增加有一定相关性。

**Abstract:** Objective To investigate the alterations of intestinal microflora community diversity in newborns with feeding intolerance (FI) and the relationship with disease outcome. Methods Using 16s rDNA PCR-DGGE, we assessed 12 FI newborns' bacterial diversity in stool specimens

within 24 h of the symptom onset ( $t_0$ ) and after the recovery of FI ( $t_1$ ). T-A cloning kit and sequencing were used to investigate the distribution of bacteria and common dominant bacteria in stool specimens. At the same time, we collected the stool specimens of 12 feeding tolerance newborns with the same gestational age, birth weight and day-old as control. Results In contrast to the control group, both the bands (S) of intestinal bacterial and the Shannon-wiener indexes (H) were relatively lower in the FI group at  $t_0$  ( $9.00 \pm 2.83$  vs  $12.76 \pm 2.38$ ,  $2.12 \pm 0.36$  vs  $2.51 \pm 0.19$ ,  $P < 0.05$ ). However, there was no statistical significant difference in S and H between the FI group at  $t_1$  and the control group ( $14.00 \pm 1.91$  vs  $14.75 \pm 1.76$ ,  $2.61 \pm 0.14$  vs  $2.66 \pm 0.13$ ,  $P > 0.05$ ). Compared with the control group, the results of molecular cloning and sequencing showed that the proportion of *Klebsiella* was significantly higher in the FI group ( $53.40\%$  vs  $40.94\%$ ,  $P < 0.05$ ). Conclusion There is a decrease in intestinal microflora community diversity in newborns with FI, which is recovered with the rehabilitation of this disease. Higher proportion of *Klebsiella* in intestinal microflora might be correlated with the onset of FI in newborns.

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