

## عنوان مقاله:

Alteration of Gut microbiota can be a predisposing factor of Clostridium difficile infection

## محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

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## خلاصه مقاله:

**Introduction and Objectives:** Clostridium difficile (recently Clostridioides difficile) is a leading cause of antimicrobial-associated diarrhea (AAD). The present study was carried out to investigate the interactions between the bacterial load of gut microbiota and C. difficile in Iranian hospitalized patients. **Material and Methods:** This cross-sectional study was conducted from October 2017 to June 2018 in two teaching hospitals in Shiraz, southwestern Iran. During this period, a total of 215 non-duplicated nosocomial AAD samples and 200 random fecal samples from asymptomatic patients were collected. Presumptive C. difficile isolates were identified by standard microbiologic methods and confirmed by specific PCR primers. The relative bacterial load determined by quantitative real-time PCR (qPCR). **Results:** In all, the frequency of C. difficile culture-positive samples was 21.4% (n = 46) and 10.5% (n = 21) of diarrheal and asymptomatic samples, respectively. Mean log of C. difficile load in diarrheal samples was significantly higher than asymptomatic samples (log<sub>10</sub>6.1 vs. 102.7; P < 0.001). Regarding the gut microbiota, Escherichia coli was significantly higher in asymptomatic samples (104.1 vs. 105.2 P < 0.002), while Bacteroides fragilis was higher in diarrheal samples (102.8 vs. 104.1 P = 0.001). Also, Mean log of Lactobacillus casei was not significantly different among two groups (101.7 vs. 102.2 P = 0.35). Based on 50th percentile, a mean load of E. coli ≤ Log<sub>10</sub>3.9 was significantly associated with higher C. difficile load in diarrheal samples (log<sub>10</sub>1.9 vs. 101.2; P < 0.001). While, bacterial load of B. fragilis and L. casei was not significantly associated with the level of C. difficile. **Conclusion:** Over-use of antibiotics can suppress the gut microbiota and provide an opportunity for development of C. difficile infection (CDI). Our findings, indicates that the level and diversity of the microbiota can be a predisposing factor of CDI

## کلمات کلیدی:

Clostridium difficile, Gut microbiota, Antimicrobial-associated diarrhea, Quantitative real-time PCR

لینک ثابت مقاله در پایگاه سیویلیکا:

