

Introduction and purpose

- ✦ The conditioning factor for CDI is the loss of microbiota diversity.
- ✦ Distinction between colonization and infection is sometimes difficult.
- ✦ Identifying risk factors or biological markers for R-CDI is important for proper treatment and prevention.
- ✦ The objective of our study was to characterize the microbiota profile of Healthy, CDI, R-CDI and colonized patients (CDC), in order to establish possible differences that could be used in CDI identification and risk stratification.

Methods

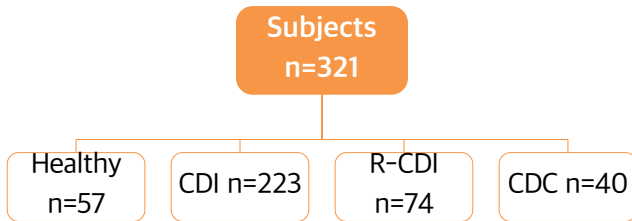


Figure 1. Number of healthy, *Clostridioides difficile* infection (CDI), recurrence of CDI (R-CDI) and colonized subjects (CDC).

- ✦ Clinical and fecal samples were collected after informed consent was obtained (Figure 1)
- ✦ The hypervariable V4 region of the 16s rRNA gene was sequenced on Illumina Miseq platform according to standard protocols.
- ✦ Data preprocessing, OTU clustering and taxonomic classification were done using MOTHUR software, RDP and SILVA database.
- ✦ Alpha diversity and statistical analysis were conducted by MOTHUR and R software.

Results

- ✦ Alpha-diversity, richness and evenness were significantly higher in the healthy group versus CDI and CDC ($p < 0.05$; all) (Figure 2).
- ✦ Patients with previous CDI had lower diversity and richness ($p < 0.01$; all).
- ✦ Those patients with R-CDI had lower diversity and richness than CDI ($p < 0.01$) (Figure 3).

Results

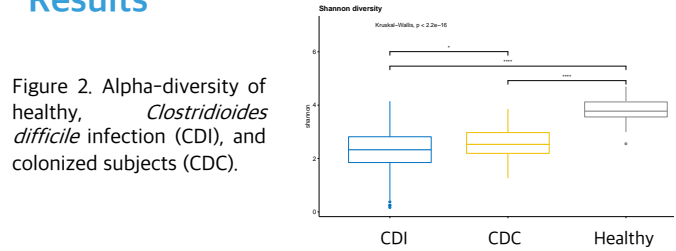


Figure 2. Alpha-diversity of healthy, *Clostridioides difficile* infection (CDI), and colonized subjects (CDC).

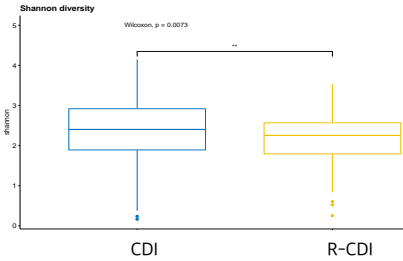


Figure 3. Alpha-diversity of *Clostridioides difficile* infection (CDI) and recurrence of CDI (R-CDI).

- ✦ R-CDI had higher abundance of *Clostridiaceae*, *Fusobacterium* and *Akkermansia* ($p < 0.001$; all), and lower levels of *Bacteroides*, *Collisnella*, *Prevotella*, *Alistipes*, *Parabacteroides*, *Blautia*, *Barnesiella*, *Butyrivimonas*, and *Oscillibacter* ($p < 0.001$; all) (Figure 4).
- ✦ Colonized patients had higher abundance of *Blautia*, and lower abundance of *Bacteroides*, *Clostridiaceae*, *Clostridium_XIVa*, *Lactobacillus*, *Romboutsia*, *Prevotella*, *Staphylococcus*, *Streptococcus* and *Veillonella* ($p < 0.001$; all) (Figure 5)

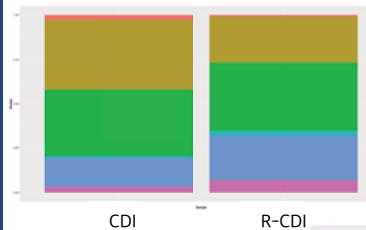


Figure 4. Microbiota profile of *Clostridioides difficile* infection (CDI) and recurrence of CDI (R-CDI).

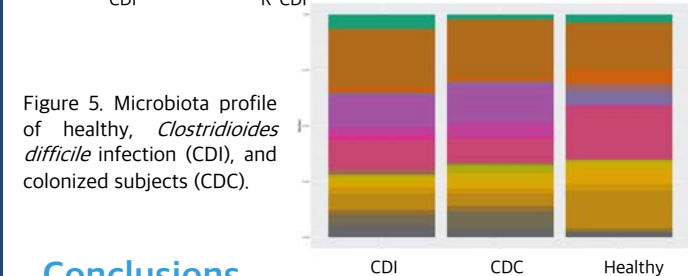


Figure 5. Microbiota profile of healthy, *Clostridioides difficile* infection (CDI), and colonized subjects (CDC).

Conclusions

- ✦ We found significant differences in the microbiota profile between CDI and CDC patients.
- ✦ Prior CDI episodes and R-CDI episodes had a cumulative impact in the microbiota.
- ✦ We identified several groups of microorganisms that may serve as microbiological markers of true CDI.

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