



Effects of intestinal colonization by *Clostridium difficile* and *Staphylococcus aureus* on microbiota diversity in healthy individuals in China

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Introduction

- Intestinal colonization by pathogenic bacteria is a risk factor for infection, and contributes to environmental contamination and disease dissemination.
- Alteration of gut microbiota also plays a pivotal role in the development of disease. Although *Clostridium difficile* and *Staphylococcus aureus* are well recognized pathogens causing nosocomial and community infections, the intestinal colonization was not fully investigated.
- Herein, we explored their overall carriage rates in healthy adults from the community, and characterized the gut microbiomes of *C. difficile* and *S. aureus* carriers.

Methods

Fecal samples were collected from 1709 healthy volunteers from communities in Shanghai, China

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tested for *C. difficile*, methicillin-sensitive *S. aureus* (MSSA), and methicillin-resistant *S. aureus* (MRSA) using culture-based techniques

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Divided participants into four groups. CH: healthy individuals; CCD, positive for *C. difficile*; CM, positive for MRSA; CS, positive for MSSA.

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16S rRNA gene sequencing was conducted to explore the differences in gut microbiome.

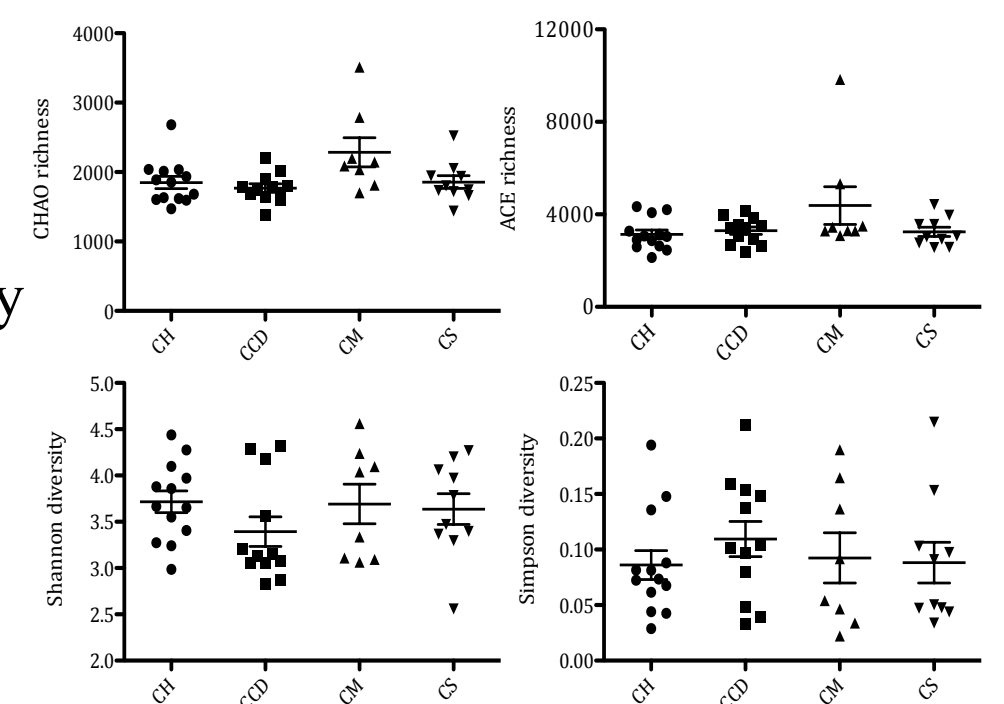
Results

The elderly participants were more frequently positive for *C. difficile*, and the prevalence of *S. aureus* decreased with age

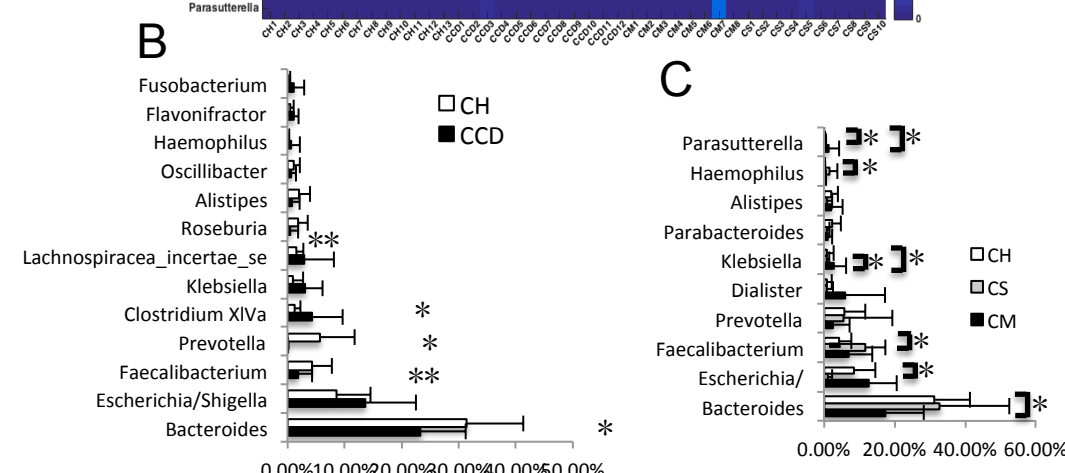
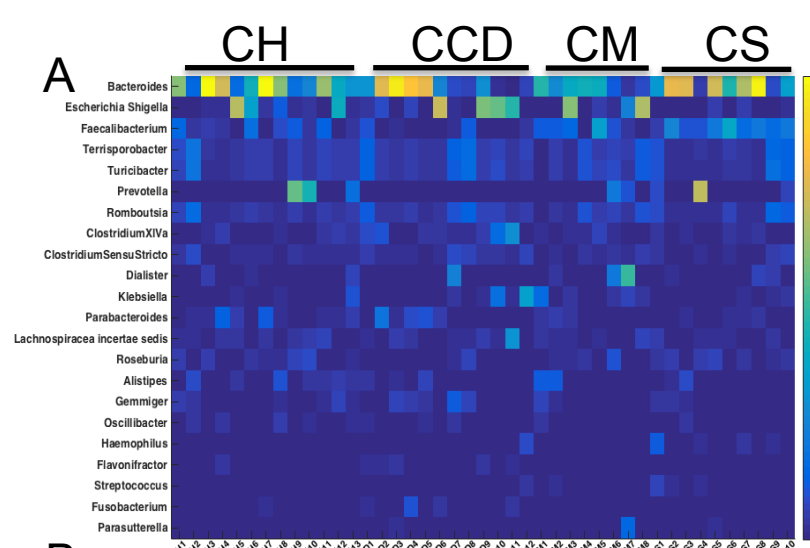
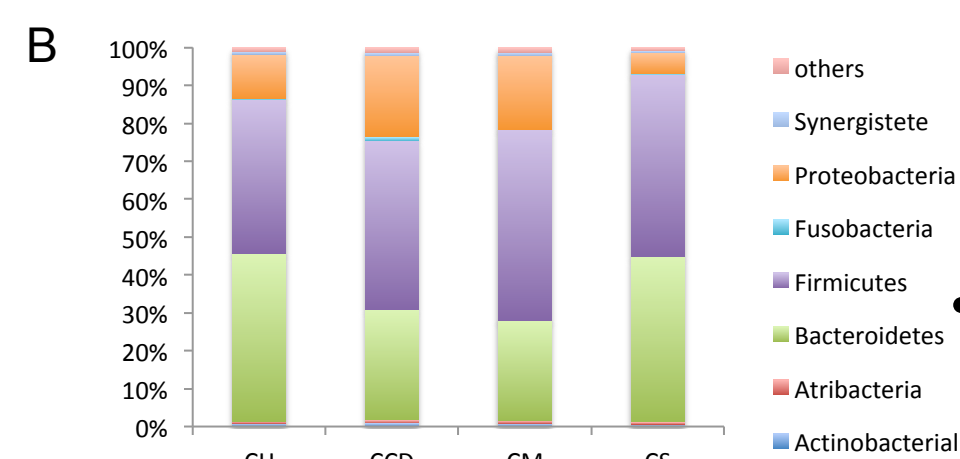
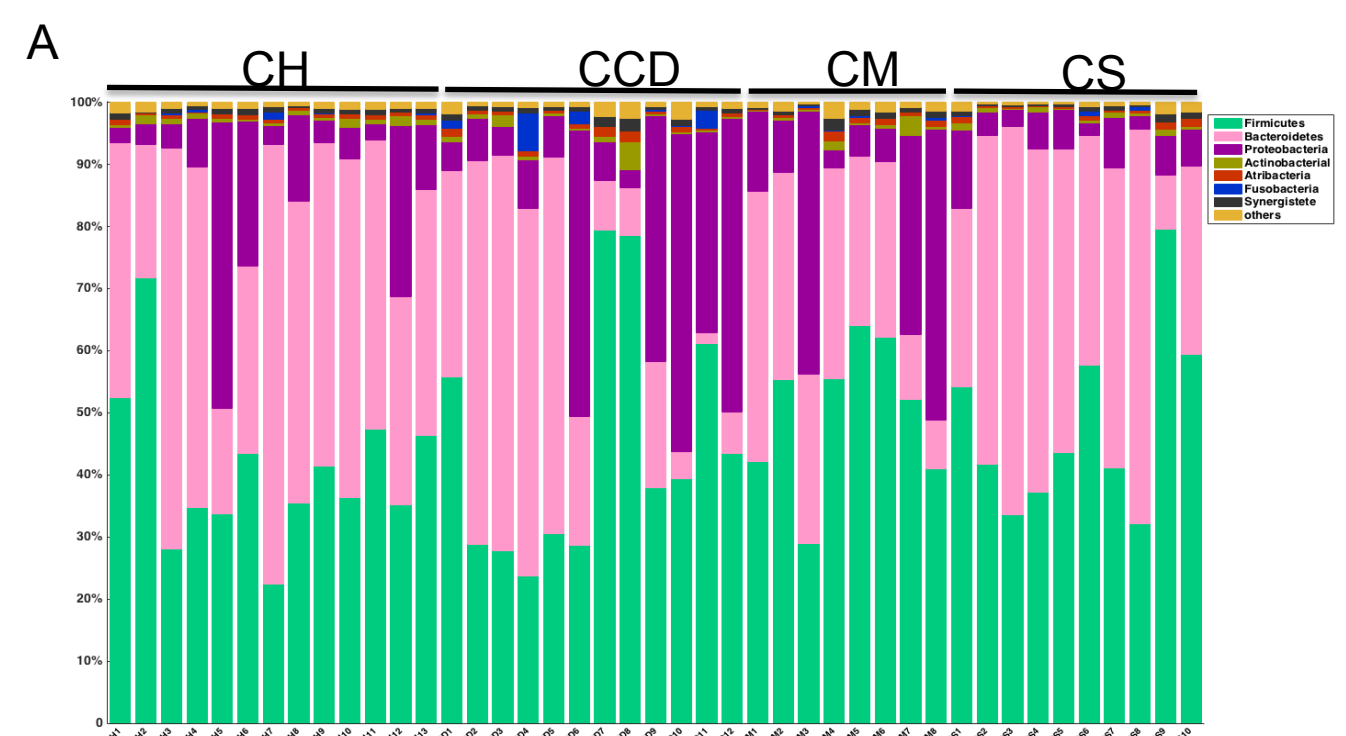
Table 1 Prevalence of *Clostridium difficile* and *Staphylococcus aureus* of healthy adults in the community in Shanghai,

Age (years)	No.	<i>C. difficile</i>		<i>S. aureus</i>	
		No.	%	No.	%
18-40	130	0	0.00%	8	6.15%
41-65	837	3	0.36%	32	3.82%
>65	742	9	1.21%	20	2.70%
Overall	1709	12	0.70%	60	3.51%

- Sequencing data revealed that the microbial diversity and richness were similar among the four groups.



- At the phylum level, carriage of *C. difficile* or MRSA was associated with a paucity of *Bacteroidetes* and an overabundance of *Proteobacteria* compared with noncarriers.



- At the genus level, the prevalence of the genera *Bacteroides*, *Prevotella*, *Faecalibacterium*, and *Roseburia* was decreased in *C. difficile*-positive samples, while the proportion of *Clostridium cluster XIVa* species was increased.

- MRSA carriers exhibited a higher proportion of the genera *Parasutterella* and *Klebsiella*, but a decreased prevalence of *Bacteroides*.