

Diversity in PCR ribotypes of *Clostridioides difficile* isolates recovered from clinical and non-clinical origins in Tehran, Iran

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Introduction

Clostridioides difficile (*C. difficile*) is cause of hospital- associated *C. difficile* infection (HA-CDI) and community- associated CDI (CA-CDI). In addition to asymptomatic carriers, environment, animals, and food are implicated in transmission of CDI. *C. difficile* strains belong to PCR ribotypes (RT) 027 and 078, have been increasingly obtained from human (2) and are considered as hypervirulent strains. Here, we determined the RTs from clinical and non-clinical sources.

Methods

During a 6-year period, 735 faecal specimens from cases suspected of CDI, 1435 hospital environmental samples from surfaces, equipment and air of rooms occupied by patients suspected of CDI, 72 samples from three municipal wastewater treatment plant and 484 beef and chicken meat samples from different butcher shops were screened for *C. difficile*. The *C. difficile* isolates were subjected to capillary electrophoresis (CE)-PCR ribotyping.

Results

Of 65 (8.8%) *C. difficile* from fecal samples, 54 isolates were assigned to 21 known RTs. RT001 (30.8%) and RT126 (9%) were found as the first and second most frequent RTs. The remaining 11 clinical isolates were designated as new RTs as their profiles did not correspond to any type of the previously known profiles in the ECDC-Leeds-Leiden reference *C. difficile* strain dataset. The two environmental isolates, one from the floor in the Medical ward of a hospital and the other from air of a room in ICU of the other hospital, belonged to unknown RT and RT001, respectively. The isolate from the outlet of a WWTP (1/72) had also unknown profile of RT. No isolate was identified as *C. difficile* from meat samples.

Discussion

This study provided evidence for dissemination of genetically diverse isolates of *C. difficile* obtained from various sources. RTs 027 and 078 were not found among Iranian *C. difficile* isolates. However, RT126 which is known as a ribotype with a similar banding pattern to RT078 was found in isolates tested.