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Paper Poster Session
Antimicrobial resistance in anaerobes

An analysis of the antibiotic resistance gene content of intestinal Bacteroides isolated using a novel chromogenic agar

Jozsef Soki[1], Samo Jeverica[2], Daniel Thierney[3], Edit Hajdú[4], John Perry[3], Elisabeth Nagy*[5], Edit Urbán[1]

[1]*University of Szeged, Institute of Clinical Microbiology, Szeged, Hungary*

[2]*University of Ljubljana, Institute for Microbiology and Immunology, Ljubljana, Slovenia*

[3]*Freeman Hospital Newcastle Upon Tyne, Microbiology Department, Newcastle Upon Tyne, United Kingdom*

[4]*University of Szeged, Department of Infectology, Szeged, Hungary*

[5]*University of Szeged, Szeged, Hungary*

Background: Recently, we determined the antibiotic susceptibilities and antibiotic resistance gene content of clinical *Bacteroides* strains in an ESGAI study. Therefore, we aimed to investigate the antibiotic resistance gene content of intestinal *Bacteroides* isolates and compare it to those from clinical samples in order to follow changes that drive the occurrence of antibiotic-resistant *Bacteroides* in clinical samples. Comparison of the antibiotic resistance gene contents of *Bacteroides* isolates of antibiotic non-treated (healthy) and carbapenem treated (ICU) individuals was also investigated.

Material/methods: Faecal samples of healthy and ICU patients were collected in Hungary and Slovenia. They were suspended in BHI medium and serial dilutions were plated on a novel selective *Bacteroides* chromogenic medium (BCM) with or without meropenem (4 mg/L), and incubated anaerobically for 48 h. Isolates with different colony morphologies were subcultured and their species identities were determined by MALDI-TOF MS. The *cepA*, *cfxA, cfiA* and *ermF* gene contents were determined by RT-PCR.

Results: 108 *B. fragilis* group strains (25 *B. ovatus*, 20 *B. vulgatus*, 15 *B. thetaiotaomicron*, 17 *B. fragilis*, 8 *Parabacteroides distasonis*, , 7 *B. uniformis*, 5 *P. johnsoniae*, 3 *B. caccae*, 3 *B. intestinalis*, 3 *B. stercoris*, 1 *B. finegoldii* and 1 *B. nordii*) were isolated from stools of 28 individuals (22 healthy and 6 ICU patients). On BCM only a few *Enterococcus faecalis* were isolated, showing that the new medium was highly selective for the *Bacteroides fragilis* group. The colony counts were ~100-fold less on meropenem-supplemented plates than on BCM plates without meropenem. All but one of the 17 *B. fragilis* were *cepA*-positive and *cfiA*-negative, and 1 *B. fragilis* isolate was *cepA*-negative and *cfiA*-positive, while all the non-fragilis *Bacteroides* (NFB) were uniformly *cepA* and *cfiA*-negative. The *cfxA* gene prevalence was higher in the total *Bacteroides* (58.6 vs. 18.0 %, $p<0.001$), the *B. fragilis* (33.3 vs. 14.8 %, $p=0.003$) and the NFB (62.3 vs. 30.3 %, $p=0.006$) strains, when comparing faecal isolates with previously analysed clinical isolates. The *ermF* gene prevalence was higher in the total *Bacteroides* (54.3 vs. 14.9 %, $p<0.0001$), the *B. fragilis* (33.3 vs. 22.6%, $p=0.011$) and the NFB (69.3 vs. 30.3 %, $p<0.001$) strains, when comparing faecal isolates with previously analysed clinical isolates.

Conclusions: The utility of a novel *Bacteroide*s-specific chromogenic medium was demonstrated. Meropenem treatment substantially reduced the normal *Bacteroides* flora in ICU patients. The *cfxA* and *ermF* genes were more prevalent in recent intestinal *Bacteroides* isolates than in previous clinical strains.