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CLOSTRIDIOIDES DIFFICILE INFECTION OUTBREAK IN INTERNAL WARD OF DISTRICT HOSPITAL IN SILESIA, SOUTH POLAND

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Relevance. *Clostridioides difficile* is Gram-positive, spore-forming bacteria responsible for antibiotic-associated diarrhoea and life-threatening pseudomembranous colitis. *C. difficile* is an emerging healthcare problem in the world. According to the Polish National Public Health Institute, in 2017 the incidence of CDI was 30.4 per 100,000 inhabitants (22.7 in 2016), 11,667 cases were diagnosed and 88.1% patients were hospitalized. A large percentage of *C. difficile* isolates are resistant to fluoroquinolones, cephalosporins, clindamycin and erythromycin.

Target: of this study was to characterize the genetic and antibiotic resistance profile of *C. difficile* strains responsible for outbreak in 33-bed Internal Ward of district hospital in Silesia, South Poland.

Materials and Methods: 18 stool samples were collected from patients with antibiotic-associated diarrhoea during January-February 2019 and cultured on *C. difficile* selective media - CLO and CDIFF (bioMérieux, Marcy L'Etoile, France) and Columbia Blood Agar, incubated for 48h at 37°C under anaerobic conditions (Whitley A35 Workstation, UK). 17 *C. difficile* strains were isolated. Biochemical identification was confirmed using the ANC card in an automatic system VITEK 2 Compact (bioMérieux, Marcy L'Etoile, France). The strains were frozen at -80°C in Microbanks until use.

MIC value for 10 antibiotics was determined with E-test on Brucella Blood Agar plates with vitamin K and hemin along with Schaedler Broth with vit K3 and results were interpreted according to EUCAST (Version 10.0, valid 2020-01-01mk).

DNA was isolated from 17 strains by using the QIAamp DNA Mini Kit (Qiagen, USA) and the presence of 7 genes was determined using multiplex PCR and electrophoresis.

Results and discussion. From isolated *C. difficile* strains all 17 were sensitive for vancomycin, and piperacillin with tazobactam; 1/17 was resistant to metronidazole, 8/17 were resistant to chloramphenicol, 14/17 – to rifampicin, 15/17 - to penicillin, moxifloxacin, erythromycin and clindamycin, and 16/17 were resistant to imipenem. In mPCR all studied 17 strains demonstrated presence of genes encoding toxin A - *tcdA*, 15/17 have toxin B gene - *tcdB*, and binary toxin genes- *cdtA* and *cdtB*. The *ermB* gene, responsible for mechanism of resistance MLS_B was demonstrated in 15 strains.

Conclusions. During this hospital outbreak, 90% of isolates demonstrated multidrug resistance (>4 antibiotics) and the same gene profile, which can confirm hospital outbreak. One strain, which demonstrated resistance to erythromycin lacked the *ermB* gene. Further molecular studies are required for analysis of isolates and appropriate infection control must be introduced to prevent further outbreak transmisison in this hospital.