Comparison of genetic and resistance properties of Clostridium difficile isolates collected from clinical specimens from a large urban area in Germany
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Objective: The Clostridium difficile “epidemic strain” BNAP-1/027 causing severe disease in North America and parts of Europe is not prevalent in Germany although the incidence of CDAD has greatly increased. Characteristics of a large collection of Clostridium difficile isolates from patients in a densely populated urban area may provide useful data concerning local epidemiology. Methods: In the period from 2007 to 2011 a large number of isolates has been collected from the greater Düsseldorf area and subjected to ribotyping, PCR analysis of the presence of the toxin genes; tcdA, tcdB and cdtB and mutation causing truncation of the tcdC gene as well as resistance to erythromycin and moxifloxacin. Results: A total of 392 isolates have been analysed to date. Most of the isolates (376 [95.9 %]) possessed both tcdA and tcdB genes and 16 [4.1 %] possessed neither toxin gene. No isolate carried only tcdA or tcdB. The binary toxin gene, cdtB was found in only 52 [13.3 %] isolates, all of which possessed cdtA and cdtB genes. A mutation of the tcdC gene leading to the expression of a truncated protein was found in 62 [16.5 %] of the toxin-gene carrying isolates. All isolates possessing the cdtB gene also carried a mutation of the tcdC gene. Ribotyping displayed a large spread of different ribotypes. The ribotype with the most isolates contained 68 members; unfortunately the classification is still unknown. Only 27 isolates were type 027. All other clusters contained less than 20 isolates, most less than 10, per cluster. A total of 201 [51.3 %] isolates were resistant to both erythromycin and moxifloxacin, 66 [16.8 %] sensitive to both, 108 [27.6 %] sensitive to erythromycin only and 17 [4.3 %] to moxifloxacin only. Conclusion: The isolates investigated so far show a wide diversity and no single ribotype or molecular type appears to be predominant in the area studied. This correlates with the epidemiological data obtained from the largest hospital in the collection area, in which nosocomial spread of clones is rare. In addition the ribotype 027, as in other studies in Germany does not appear to be common. Ribotyping a large number of isolates is technically demanding and thus alternative methods will be included in the ongoing study. A very small number of clinical Clostridium difficile isolates (all from patients with diarrhoea) possessed no toxin gene, a fact that has relevance for the use of PCR as a diagnostic method.