

P1086 **Carbapenemase-producing Enterobacteriaceae in the Netherlands, 2014 - 2016**

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Background: Carbapenem resistance mediated by mobile genetic elements has emerged worldwide and has become a major public health threat. Therefore, Dutch medical microbiology laboratories are requested to submit carbapenemase-producing *Enterobacteriaceae* (CPEs) to the National Institute for Public Health and the Environment as part of a national surveillance system. Here, we report on the surveillance data from 2014-2016.

Materials/methods: Meropenem MICs and species identification of all submitted isolates were confirmed by Etest and Maldi-ToF. The presence of ten carbapenemase-encoding genes was determined by PCR. Carbapenemase production was assessed phenotypically by the Carbapenem Inactivation Method (CIM). Of all submitted CPEs, one species/carbapenemase gene combination per person per year was subjected to next-generation sequencing (NGS) via Illumina HiSeq, to identify the carbapenemase allele. Genetic relationships for *Klebsiella pneumoniae* and *Escherichia coli* were examined by whole-genome Multiple Locus Sequence Typing (wgMLST). Patient characteristics were collected by a web-based questionnaire.

Results: 1,082 suspected CPE isolates were received (2014: n=276, 2015: n=382, 2016: n=424). 479 (2014: n=84, 2015:n=197, 2016:n=198) were confirmed as CPE (CIM positive) and 358 of these were analysed by NGS (2014: n=54, 2015:n=147, 2016: n=157). The predominant CPE species were *K. pneumoniae* (n=239, 50%) and *E. coli* (n=121, 25%). Of all CPEs, 454 (95%) carried a carbapenemase-encoding gene, mostly *bla*OXA-48like (n=218, 46%), *bla*NDM (n=141, 29%) and *bla*KPC (n=61, 13%). NGS analyses showed that *bla*OXA-48 was indeed predominant, found in 41% in 2015 (60/147) and 2016 (65/157) (Graph). Additionally, alleles like *bla*NDM-6 and *bla*NDM-7 were identified that have not been reported previously in the Netherlands. WgMLST allowed identification of clusters based on a cut-off of 50 genes. For *K. pneumoniae*, 20 clusters were observed ranging in size from 2 to 33 isolates and for *E. coli*, 9 clusters consisting of 2 to 7 isolates were identified. All clusters contained isolates from multiple submitters.

Conclusions: The number of submitted CPEs in the Netherlands is increasing and *bla*OXA-48 is the predominant carbapenemase allele. We also observed alleles that had never been described in the Netherlands before. WgMLST identified multiple clusters in different healthcare centers. We are now studying epidemiological data to understand possible transmission pathways.

Percentages and number of carbapenemase alleles most frequently identified among Dutch CPE isolates by NGS 2014-2016

