

P1237

Abstract (poster session)

**Description of IMP-31, a novel metallo-beta-lactamase very divergent from other known IMP carbapenemases**

N. Pfennigwerth\*, S.G. Gatermann, M. Kaase (Bochum, DE)

**Introduction:** The worldwide increase of multidrug-resistance in gramnegative bacteria has become an important clinical challenge. Carbapenem resistance can be caused by a variety of mechanisms, however the worldwide spread of carbapenemases is especially important. A worrying trend is the dissemination of Ambler class B metallo-beta-lactamases (MBL). Here we describe a novel IMP-type MBL, IMP-31, that was found in an outbreak of multidrug resistant *P. aeruginosa* in Germany. **Methods:** Susceptibility to antibiotics was determined by disk diffusion and Etest. The presence of a MBL was determined by EDTA combined-disc-tests, MBL Etest and by a bioassay based on cell-free extracts. A modified Hodge-Test was performed. PCRs and subsequent sequencing were performed for VIM, IMP, NDM, GIM, SIM, SPM, AIM, DIM and KHM. Clonal relatedness of the isolates was determined by RAPD-PCR and PFGE. Integron structures were analysed by PCR and sequencing. The IMP-31 encoding sequence was cloned into the pBK-CMV vector and transformed into *E. coli* DH5alpha for activity analysis. Localisation of the gene was determined by PFGE and Southern blotting. **Results:** Clonally related strains from an outbreak of *P. aeruginosa* in Germany were sent to the National Reference Laboratory for Multidrug-resistant Bacteria for further characterisation. The isolates were resistant to piperacillin, piperacillin/tazobactam, ceftazidime, cefepime, aztreonam, imipenem, meropenem and doripenem as well as to gentamicin, tobramycin, amikacin, ciprofloxacin and levofloxacin. The modified Hodge-test was positive for imipenem, meropenem and ertapenem. The isolates showed synergy with EDTA in the combined disk test and the MBL Etest. A chromosomally integrated class I integron was identified, harbouring the IMP-31 gene, a OXA-10 gene and the gene for an aminoglycoside adenylyltransferase (aadA6). The sequence of IMP-31 showed only 85 % homology with its closest relatives IMP-8 and IMP-24. It mediates resistance to all carbapenems and most other beta-lactams. **Conclusion:** The strains harbour a novel IMP-type metallo-beta-lactamase very divergent to any other known IMP variant. Its closest relatives are IMP-8 and IMP-24 with 39 and 40 amino acid substitutions, respectively. Regarding the amount of mutations, it is likely that the source of IMP-31 is a so far unknown environmental bacterium and that it was mobilised quite recently as IMP-31 was only found in German isolates up to date.