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Paper Poster Session
Susceptibility trends for old and new antibiotics

Prevalence of multidrug resistance among bacterial pathogens obtained from patients in hospitals and the role of tigecycline: results of the PEG 2013 study

Michael Kresken*[1], Barbara Körber-Irrgang[1], Dieter Hafner[2], Martin Kaase[3], Franziska Layer[4], Ingo Klare[5], Guido Werner[4], Harald Seifert[6], Working Party 'antimicrobial Resistance' of the Paul-Ehrlich-Society for Chemotherapy[7]

[1]*Antiinfectives Intelligence GmbH, Campus of the University of Applied Sciences, Rheinbach, Germany*

[2]*Institute of Pharmacology and Clinical Pharmacology, Heinrich-Heine-University, Düsseldorf, Germany*

[3]*Ruhr University Bochum, Faculty of Medicine, Department for Medical Microbiology, Bochum, Germany*

[4]*Robert Koch Institute, Wernigerode Branch, Wernigerode, Germany*

[5]*Robert Koch-Institute, Wernigerode Branch, Wernigerode, Germany*

[6]*Institut Für Medizinische Mikrobiologie, Immunologie und Hygiene, Uniklinik Köln, Köln, Germany*

[7]*Paul-Ehrlich-Society for Chemotherapy, Rheinbach, Germany*

Background: The treatment of infectious diseases has increasingly been threatened by multidrug-resistant (MDR) pathogens such as extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* (ECO) and *Klebsiella* species, carbapenem-resistant (CR) Enterobacteriaceae, *Pseudomonas aeruginosa* (PAE), and *Acinetobacter baumannii* (ABA) as well as methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant (VR) *Enterococcus* species. Tigecycline has been shown to be active against many Gram-negative and Gram-positive bacteria, except PAE. The objectives of the present study were i) to determine the prevalence of MDR pathogens among clinical isolates obtained from hospital patients in 2013, and ii) to assess the activity of tigecycline against these MDR pathogens.

Material/methods: In a surveillance study conducted by the Paul-Ehrlich-Society (PEG) between October and December 2013, 25 laboratories across Germany (n=22), Switzerland (n=2) and Austria (n=1) were requested each to collect 240 non-duplicate isolates. Isolates were identified by MALDI-TOF. Minimum inhibitory concentrations (MICs) were determined by broth microdilution (BMD) according to ISO 20776-1. Breakpoints (BP) approved by EUCAST (v. 5.0) were applied, if available. ESBL testing was performed according to CLSI criteria. Data from the following bacterial species was evaluated: ABA, *A. pittii*, ECO, *Klebsiella oxytoca* (KOX), *K. pneumoniae* (KPN), PAE, *Proteus mirabilis* (PMI), *Enterococcus faecalis* (EFS), *E. faecium* (EFM), and *S. aureus* (SAU).

Results: The data of 3.646 isolates was analyzed. Twenty-four percent derived from patients in intensive care units (ICU). Fifty-eight percent of the patients were male. An ESBL phenotype was confirmed for 89/596 (14.9%) ECO, 53/304 (17.4%) KPN, 11/132 (8.3%) KOX, and 5/216 PMI (2.3%). CR (defined as resistance to imipenem or meropenem) was observed in 4/304 (1.3%) KPN, 83/733

(11.3%) PAE, and 26/88 (29.5%) ABA. A carbapenemase was detected in all CR-KPN (3x KPC-3, 1x KPC-2) and ABA (21x OXA-23-like, 4x OXA-24-like, 1x NDM), and in 16/83 (19.3%) of CR-PAE (7x VIM-2, 5x VIM-1, 2x IMP-31, 1x IMP-15, 1x IMP unspecified). An MRSA phenotype was detected in 101/748 (13.5%) SAU (all harboured *mecA*). Eighty-five (84.2%) MRSA were considered HA-MRSA (predominantly t003 [37.6%] and t032 [27.1%]), 11 (10.9%) CA-MRSA and 5 (5%) LA-MRSA. VR was observed in 53/320 (16.6%) EFM and in 1/424 (0.2%) EFS. The majority of VR-EFM (54.7%) possessed the *vanB* gene. Susceptibility data to tigecycline for the MDR pathogens of eight species are given in the Table.

Conclusions: In comparing the results from the present surveillance with those from the PEG study conducted in 2010, the rate of ESBL-ECO decreased (-2.5%), while the rate of ESBL-KPN increased (+2.7%). CR was still low in Enterobacteriaceae species, >10% in PAE (-6%), and nearly 30% in ABA (+10%). As for the Gram-positive species, VR increased in EFM (+3.9%), while the prevalence of MRSA decreased (-3.2%). The resistance situation of tigecycline did not change for any of the tested species.

Table: *In vitro* activity of tigecycline against MDR bacterial pathogens

Bacterial species, phenotype (n)	MIC_{50} (mg/L)	MIC_{90} (mg/L)	%-S	%-I	%-R
***E. coli*, ESBL pos. (89)**	0.25	0.5	100	0	0
***K. oxytoca*, ESBL pos. (11)**	0.5	1	100	0	0
***K. pneumoniae*, ESBL pos. (53)**	0.5	1	94.3	3.8	1.9
***P. mirabilis*, ESBL pos. (5)**	4	8	0	20.0	80.0
***A. baumannii*, CR (26)**	1	2	No BP available		
***K. pneumoniae*, CR (4)**	1	1	100	0	0
***E. faecalis*, VR (1)**	0.125		100	0	0
***E. faecium*, VR (53)**	0.063	0.125	96.2	1.9	1.9
***S. aureus*, MR (101)**	0.125	0.25	100	-	0

S, susceptible; I, intermediate; R, resistant