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Abstract (poster session)

Occurrence of resistant phenotypes in the Middle East and susceptibility to tigecycline: TEST 2007-2011

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Objectives: Development of bacterial resistance continues to cause concern world-wide, but availability of newer agents offers clinicians options for therapy. Tigecycline (TIG) has a very broad spectrum of activity, including strains resistant to other drugs. As part of the global Tigecycline Evaluation Surveillance Trial (TEST), strains collected in the Middle East (ME) from 2007 to 2011 were evaluated for prevalence of resistant phenotypes and susceptibility to TIG. Methods: A total of 2,502 pathogens were collected from 9 sites in Israel, 1 in Jordan, 1 in Oman, 1 in Saudi Arabia, and 5 in Turkey from a variety of infection sources. MICs were determined at each site using custom broth microdilution panels following CLSI guidelines and interpreted according to FDA breakpoints for TIG. Results: Tigecycline's in vitro activity is summarized below: %S=% susceptible; ROW=rest of world; ESBL+=extended-spectrum beta-lactamase positive; BL+=beta-lactamase positive; MRSA=Methicillin-resistant S. aureus; PRSP=penicillin-resistant S. pneumoniae; VR=vancomycin-resistant Conclusion: Significant differences exist in the proportion of resistant phenotypes of several species between ME and the rest of the world (ROW, TEST 2008-2010): ESBL+ isolates comprised 20% of all E. coli in the ME vs 15% in ROW, MRSA were 27% of all S. aureus in ME vs 36% in ROW, PRSP (26% vs 16%, respectively), and VR E. faecium (22% vs 31%, respectively); all $p<0.05$ (Chi-square with Yates correction). Tigecycline showed excellent in vitro activity against a diverse collection of gram-negative and gram-positive pathogens from the Middle East, including ESBL+ strains, MRSA, PRSP, and VRE. Susceptibility was >= 93% for all tested species and their resistant phenotypes, except ESBL+ K. pneumoniae, which was slightly less susceptible partly due to a low %S in Israel (83%).

Organism (% resistant phenotype ME/ROW)	**n**	**MIC_{50}** (mg/L)	**MIC_{90}** (mg/L)	**%S**
Escherichia coli	684	0.25	1	100
ESBL+ (20 ME/15 ROW)	136	0.5	1	100
Klebsiella pneumoniae	601	0.5	2	94
ESBL+ (24 ME/21 ROW)	144	1	4	87
Haemophilus influenzae	237	0.12	0.25	100
BL+ (20 ME/19 ROW)	47	0.12	0.25	100
Staphylococcus aureus	627	0.12	0.5	100
MRSA (27 ME/36 ROW)	172	0.25	0.5	100
Streptococcus pneumoniae	262	0.015	0.03	99
PRSP (26 ME/16 ROW)	68	0.03	0.03	97
Enterococcus faecium	91	0.12	0.25	100
VR (22 ME/31 ROW)	20	0.12	0.25	100