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Abstract (poster session)

Patterns of resistance among Gram-negative pathogens isolated from countries in Africa and the Middle-East – TEST 2005-2012

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Background: Since the approval of tigecycline (TIG) in the United States in 2005 and the EU in 2006, TIG has shown potent expanded broad spectrum activity against most commonly encountered species and little propensity for development of resistance despite increasing resistance in other comparative agents. This study evaluates patterns of resistance in comparative antimicrobial agents to isolates susceptible to TIG from 117 sites in 11 African and Middle East (AFME) countries during 2005-2012. Methods: A total of 9,410 clinical isolates were identified to the species level at each local site and confirmed by the central laboratory. MICs were determined by the local laboratory using broth microdilution panels according to CLSI guidelines. Results: Resistance patterns (%R) of comparative agents to TIG-susceptible isolates (n's >=10). %Res defined by CLSI breakpoints, where available; TIG-Sus defined by FDA; na, breakpoints not defined; – not tested. * %R for *Acinetobacter* spp. >=8 mg/L (Jones, 1999). TIG, tigecycline; A/C, amoxicillin/clavulanic acid; AK, amikacin; AMP, ampicillin; CAX, ceftriaxone; FEP, cefepime; IMP, imipenem; LVX, levofloxacin; MER, meropenem; MIN, minocycline; P/T, piperacillin/tazobactam; PEN, penicillin; VAN, vancomycin. Conclusions: With exceptions of *H. influenzae* and *S. agalactiae*, high R rates (>=10%) were observed for the majority of drugs against the majority of species tested in this in vitro study where all isolates were susceptible to TIG. Only amikacin, imipenem, and meropenem demonstrated consistently low resistance patterns similar to TIG.

Organism	N	% Resistant												
		TIG	A/C	AK	AMP	CAX	FEP	IMP	LVX	MER	MIN	P/T	PEN	VAN
<i>A. baumannii</i>	748	na	na	51	na	76	59	36	55	65	12	74	–	–
<i>Enterobacter</i> spp	1233	0	94	1	91	33	6	1	7	3	10	11	–	–
<i>E. coli</i>	1513	0	22	1	77	30	15	1	38	2	21	7	–	–
<i>Klebsiella</i> spp	1392	0	27	2	92	41	24	2	24	10	20	21	–	–
ALL ESBLs	682	0	42	2	100	97	58	2	58	5	27	22	–	–
<i>Serratia</i> spp	503	0	93	1	85	18	4	1	3	1	8	4	–	–
<i>H. influenzae</i>	624	0	0	na	15	0	0	0	0	0	na	0	–	–
<i>E. faecalis/faecium</i>	802	0	17	–	17	17	–	na	50	na	31	17	18	4
All VREs	33	0	94	–	94	94	–	na	94	na	15	94	91	100
<i>S. aureus</i>	1446	0	30	–	91	30	–	37	26	29	2	30	92	0
<i>S. agalactiae</i>	478	0	0	–	0	0	–	0	1	0	0	0	0	0
<i>S. pneumoniae</i>	596	0	3	–	29	28	–	5	1	16	0	25	25	0