**Cross-Resistance Against Enterobacteriaceae Worldwide**

17.032

The in Vitro Activity of Tigecycline and Antimicrobial Cross-Resistance Against Enterobacteriaceae Worldwide

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Background: Tigecycline, a member of a new class of antimicrobials (glycylcyclines), has been shown to have potent broad spectrum activity against most commonly encountered species responsible for hospital acquired infections. Cross-resistance to several classes of antimicrobials is often seen in nosocomial pathogens. The T.E.S.T. program determined the in vitro activity of tigecycline against strains of Enterobacteriaceae cross-resistant to one or more of the following antimicrobials: amoxicillin-clavulanic acid, piperacillin-tazobactam, levofloxacin, ceftriaxone, cefepime, ampicillin, amikacin, minocycline, ceftazidime and imipenem. The isolates were collected from 335 investigational sites in 47 countries throughout 2004–2007.

Methods: A total of 26,791 clinical Enterobacteriaceae were identified to the species level at each site and confirmed by the central laboratory. Minimum Inhibitory Concentrations (MICs) were determined by the local laboratory using broth microdilution panels. Antimicrobial resistance was interpreted according to CLSI breakpoints. The presented data suggest that tigecycline showed excellent inhibitory activity against members of Enterobacteriaceae with MICs ranging from 4 to 8 mcg/mL. Tigecycline also showed any degree of non-susceptibility against tigecycline with MICs ranging from 4 to 8 mcg/mL. Tigecycline also showed excellent inhibitory activity against members of Enterobacteriaceae that were resistant to amikacin, levofloxacin, minocycline and imipenem inhibiting 94%, 92%, 72% and 91% of isolates respectively.

Conclusions: The presented data suggest that tigecycline is little affected by this cross-resistance phenomenon and may be an effective and reliable therapeutic option against nosocomial or community pathogens regardless to the resistance patterns.

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Antimicrobial Drug Resistance of Salmonella Typhi in Asia

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This study describes the pattern and extent of drug resistance in 1774 strains of Salmonella enterica serovar Typhi (S. Typhi) isolated across Asia between 1993 and 2005 and characterizes the molecular mechanisms underlying the reduced susceptibility to the fluoroquinolones in these strains. In 1993 S. Typhi collected in southern Vietnam, the proportion of MDR has remained at high levels since 1993 (50% in 2004) and there was a dramatic increase in nalidixic acid resistance between 1993 (4%) and 2005 (97%). In a cross-sectional sample of 381 S. Typhi from 8 Asian countries, Bangladesh, China, India, Indonesia, Laos, Nepal, Pakistan and central Vietnam collected in 2002 to 2004, variable rates of multidrug resistance (16—37%) and nalidixic acid resistance (5—51%) were found. The eight Asian countries involved in this study are home to approximately 80% of the world’s typhoid fever cases. These results document the scale of drug resistance across Asia.

The Ser83/Phe substitution in GyrA was the predominant alteration in S. Typhi from Vietnam (117/127 isolates, 92.1%). No mutations in gyrB, parC and parE were detected in 55 of these strains. In vitro time-kill experiments showed a reduction in the efficacy of ofloxacin against strains harbouring a single amino acid substitution at codon 83 or 87 of GyrA, this effect was more marked against a strain with a double substitution. The 8-methoxy fluoroquinolone gatifloxacin showed rapid killing of S. Typhi harbouring both the single and double amino acid substitutions.

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**Pseudomonas aeruginosa**: Antimicrobial Susceptibility Testing and Agreement Between Disk Diffusion and E-Test Methods

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Background: The intrinsic resistance of Pseudomonas aeruginosa towards several antimicrobial agents has contributed to its role as an effective opportunistic pathogen and its emergence as one of the most problematic human pathogens. The aim of this study was to assess the susceptibility patterns of eight commonly used antimicrobial agents against clinical isolates of Pseudomonas aeruginosa.