

Analysis of Antibiotic Resistance Genes in Multidrug-Resistant *Acinetobacter* sp. Isolates from Military and Civilian Patients Treated at the Walter Reed Army Medical Center.

- [Hujer KM,](#)
- [Hujer AM,](#)
- [Hulten EA,](#)
- [Bajaksouzian S,](#)
- [Adams JM,](#)
- [Donskey CJ,](#)
- [Ecker DJ,](#)
- [Massire C,](#)
- [Eshoo MW,](#)
- [Sampath R,](#)
- [Thomson JM,](#)
- [Rather PN,](#)
- [Craft DW,](#)
- [Fishbain JT,](#)
- [Ewell AJ,](#)
- [Jacobs MR,](#)
- [Paterson DL,](#)
- [Bonomo RA.](#)

Infectious Diseases Section, Louis Stokes Cleveland Veterans Affairs Medical Center, 10701 East Blvd., Cleveland, OH 44106. robert.bonomo@med.va.gov. Military medical facilities treating patients injured in Iraq and Afghanistan have identified a large number of multidrug-resistant (MDR) *Acinetobacter baumannii* isolates. In order to anticipate the impact of these pathogens on patient care, we analyzed the antibiotic resistance genes responsible for the MDR phenotype in *Acinetobacter* sp. isolates collected from patients at the Walter Reed Army Medical Center (WRAMC). Susceptibility testing, PCR amplification of the genetic determinants of resistance, and clonality were

determined. Seventy-five unique patient isolates were included in this study: 53% were from bloodstream infections, 89% were resistant to at least three classes of antibiotics, and 15% were resistant to all nine antibiotics tested. Thirty-seven percent of the isolates were recovered from patients nosocomially infected or colonized at the WRAMC. Sixteen unique resistance genes or gene families and four mobile genetic elements were detected. In addition, this is the first report of bla(OXA-58)-like and bla(PER)-like genes in the U.S. MDR *A. baumannii* isolates with at least eight identified resistance determinants were recovered from 49 of the 75 patients. Molecular typing revealed multiple clones, with eight major clonal types being nosocomially acquired and with more than 60% of the isolates being related to three pan-European types. This report gives a "snapshot" of the complex genetic background responsible for antimicrobial resistance in *Acinetobacter* spp. from the WRAMC. Identifying genes associated with the MDR phenotype and defining patterns of transmission serve as a starting point for devising strategies to limit the clinical impact of these serious infections.

PMID: 17000742 [PubMed - in process]