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Genomic comparison of multi-drug resistant, invasive *Acinetobacter* reveals genomic plasticity

An interdisciplinary team of scientists at the University of Maryland School of Medicine investigated whether the multi-drug resistant *Acinetobacter baumannii* isolated from diverse human body sites encoded genetic features that could be correlated to their isolation source. Published 2011 June 4;12(1):291[Epub ahead of print], in BMC Genomics, the results of comparison using a whole genome approach with three isolates and focused PCR assay on over 70 isolates demonstrated that *A. baumannii* is a diverse and genomically variable pathogen that appears to have the potential to cause a range of human disease, regardless of the isolation source.

Acinetobacter baumannii has emerged as a significant global pathogen, due to its persistence in the hospital environment, rapid acquisition of antibiotic resistance and the broad spectra of its antimicrobial resistance patterns. It has spread rapidly within hospitals and health care institutions. These features have made *A. baumannii* a highly studied emerging pathogen in the health care setting.

This study could have only been completed with the assembled interdisciplinary team of epidemiologists, clinical laboratory personnel, bioinformaticians and microbial genomics researchers from the Institute for Genome Sciences (IGS) and Epidemiology & Public Health at the University of Maryland School of Medicine.

Dr. Anthony Harris, Director of the Division of Genomic Epidemiology and Clinical Outcomes and co-author on the paper highlights that "additional genomic research needs to be done to elucidate why *Acinetobacter baumannii* has emerged as a hospital pathogen and what is contributing to its patient-to-patient spread. This study gets us closer to that goal".

"This study provides insight into the genomic variability of *A. baumannii* within a hospital setting and body sites, which will allow us a better understanding of the basic processes of this emerging pathogen." commented Dr. Rasko, the corresponding author on the study.

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Contacts at the Institute for Genome Sciences

Media contact: Sarah Pick, spick@som.umaryland.edu 410.707.2543

Dr. David Rasko, drasko@som.umaryland.edu 410.706.6774

About IGS

The Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine is an international research center dedicated to advancing the use of genomics to improve biomedicine. Led by Dr. Claire Fraser-Liggett, a preeminent genome scientist and microbiologist, IGS is located in a BioPark in downtown Baltimore.



IGS scientists are pioneers in the expanding fields of genomics, bioinformatics and metagenomics. For more information, see www.igs.umaryland.edu.