Tracking the spread of bacterial infections with whole genome sequencing

No matter what they tried, the staff at Queen Elizabeth Hospital Birmingham in England could not quell an outbreak of a multidrug-resistant pathogen. After an incredible 40 weeks infection control specialists worried that if they could not get on top of the situation, *Acinetobacter baumannii* could become a permanent hospital resident lying in wait for any patient, the way multidrug-resistant *Clostridium difficile* does in many hospitals.

A. baumannii can lead to such infectious complications as bacteremia, pneumonia and meningitis. Bringing it to heel required bird-dogging the bacteria's movements from patient to patient, room to room and even to specific pieces of equipment while noting the tiny changes in the bacterium's genome. The same technique is now catching on in hospitals worldwide for a variety of multidrug-resistant bugs.

Details about how the techniques finally cracked the Queen Elizabeth case, published recently in the journal *Genome Medicine,* suggest how the U.S. Centers for Disease Control and Prevention will employ whole genome sequencing to stop the spread of multidrug-resistant infections and even food-borne bacterial incidents occurring across wide regions.

In September the White House Council of Advisors on Science and Technology issued a report that called for whole genome sequencing to detect where infections arise and how they spread.

Read full, original story: Quashing Stubborn Hospital Infections Relies on Genetic Sequencing