Genome of meningitis-causing bacteria uncovered

By Dr Matt Wilkinson - 05/03/2007

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Yale University researchers have sequenced the genome of a bacteria that can cause various infections, including meningitis and pneumonia.

The team used 454 Life Science's Genome Sequencer FLX to uncover the high pathogenic content of the *Acinetobacter baumannii (A. baumannii)*, genome. This bacterium is responsible for causing various infections, including pneumonia, meningitis and urinary tract infection.

It preys on the weak and sick by slipping into the body through open wounds, for example there have been many reports of such infections among wounded soldiers in Iraq. While colonisation poses no threat to healthy people, the bacterium can cause severe clinical disease and is associated with a high mortality.

According to Dr Michael Snyder, of Yale University's Department of Molecular, Cellular, and Developmental Biology: *"The sequence of the genome of this organism is critical for understanding how it harms humans and ultimately will be useful for designing therapeutic agents to combat this infectious disease."*

The study explored the bacterium's genome using a combination of DNA sequencing and functional screening utilising transposon mutagenesis - where a section of DNA is 'cut and pasted' from one section of the genome to another, leading to the disruption of genes and allowing researchers to find gene sequences that are pathogenic or cause drug resistance.

During this process the transposase enzyme makes a staggered cut in the DNA before ligation into a target site. A DNA polymerase then fills in the gaps before a DNA ligase closes the sugar-phosphate backbone.

Transposons in bacteria usually carry genes for other purposes than transposition, often for antibiotic resistance. These transposons can jump from chromosomal DNA to plasmid DNA and back allowing the transfer and addition of genes that encode for bacterial resistance.

The new research will soon be published in the journal Genes and Development in an article entitled *"New Insights Into Acinetobacter baumannii Pathogenesis Revealed By High-Density Pyrosequencing and Transposon Mutagenesis."*

Dr Michael Egholm, 454's vice president of research and development, said: *"We believe that 454 Sequencing allows the rapid elucidation of the DNA sequence of any microbe and, when combined with gene function screens, can identify many novel genes important for microbial pathogenesis."*