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Scientists map superbug genome paving way for new treatments and prevention

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The Bio 21 Insitute's Dr Kat Holt led an international effort to examine 30,000 genes of the Klebsiella pnuemoniae bacteria. The research paves the way for more effective treatments and prevention.

An international team of scientists, led by the University of Melbourne, has decoded the genes of *Klebsiella pneumoniae* (KP), a bacterium found in hospitals throughout the developing and developed world.

A paper published today in the journal *Proceedings of the National Academy of Sciences* involved 37 research institutions around the world and bacterial samples from six countries, representing 300 strains.

The study is the largest ever genetically-decoded collection of this bacterial pathogen and gives scientists access to valuable data to stay ahead of KP evolution, as fears grow about the emergence of strains that are both highly infectious and antibiotic-resistant.

The drug-resistant KP strain recently seen in Victoria, known as KPC, has caused significant problems in America and Europe for over a decade. There have been outbreaks in South America, Africa and Asia with the hyper-virulent strains causing serious infections in the local populations.

Until recently, the scientific community hasn't had much information on this bacterium. This is the first large-scale study that uses genomic technology to understand what this organism is and what it's capable of.

Researchers are concerned, given the ease with which different strains of the bacteria can share genetic information, that antibiotic resistance genes may soon appear in more infectious Klebsiella strains, creating an untreatable and highly infectious bacterial population.

Co-author of the paper, University of Melbourne Professor Dick Strugnell at the Doherty Institute, said this research provides a vital starting point to understand and track the evolution of the bug and even anticipate its antibiotic resistance.

"KP is commonly found in the environment and can acquire resistance genes, become established in hospitals, and then become a major health problem. The bacterium exists as a diverse population, some of which can cause severe disease in humans," Prof Strugnell said.

"The bacterium has evolved a thick sticky sugar 'coat' which stops it drying out. This 'coat' contributes to the formation of 'biofilms' of the bacteria which are hard to remove from hospitals with traditional cleaning methods."

Lead-author Dr Kathryn Holt, of the University of Melbourne's Bio21 Institute, says in most cases KP infects people who are already weakened by illness, but there is a real risk that the bacteria will evolve to become a significant threat to healthy individuals.

"Almost any Klebsiella pneumoniae can cause an infection in someone who is already ill in hospital, but very few strains are virulent enough to affect a healthy person," she said.

"So far we have been extremely lucky in that most of the antibiotic-resistant strains are not highly virulent to humans. Unfortunately, Klebsiella strains are very good at swapping around genes that encode antibiotic resistance, so it's probably just a matter of time before we see this."

"The bacterium is really good at evolving through acquiring new genes. We looked at 300 different strains and every second one we looked at was completely new, so that tells you there's a lot of diversity out there and we don't really have a handle on this at all."

Dr Holt says governments need to invest in learning more about KP because of the very real risk it will become both virulent and antibiotic resistant, and pose a threat to healthy individuals.

"It's so vital we build awareness of this particular bug. The superbug problem isn't just about MRSA. There are multiple types of bacteria we need to worry about and KP is a big one.

"We need more awareness at a political level. The Microbiological Diagnostic Unit at the Doherty Institute headed by Professor Ben Howden is leading the work to track KPC, but more investment from the Victorian and the Federal Governments in research and surveillance for these drug resistant organisms could go a long way."

In Victoria, older generation drugs that can have adverse effects have been used as a last defence to combat the current KPC outbreak. However, the KPC bacteria in Greece and Italy have already developed a resistance to this medication.

"We're worried about seeing that happen here. It's so important we get a better understanding of how KP actually spreads between the environment, people and hospitals and better monitoring."

The study provides a foundation for further research into how these bacteria adapt to new niches and become more diverse. The findings of the paper could also prove useful for designing vaccines to prevent, rather than treat, KP infections.

The data is available for interactive viewing at microreact.org/project/EkqTIX5U .

More information: "Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in Klebsiella pneumoniae, an urgent threat to public health." *PNAS* 2015 ; published ahead of print June 22, 2015, DOI: 10.1073/pnas.1501049112

Provided by University of Melbourne

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