Bacterial genetics helps defeat antibiotic-resistant “super-bugs”

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Bacteria resistant to antibiotics may be the subjects of sci-fi Hollywood horror, but it is also the reality at hospitals across the county. There are ongoing complaints that feeding animal antibiotics puts us all at risk to bacteria that are resistant to these antibiotics as well other antibiotics in the same family. Even the ornamental fish industry is at risk (and humans through them). New antibiotics are few and far between, and some bacteria seem particularly adept at evolving into stronger forms of themselves, gaining genetic material to protect themselves against even the last-line-of-defense antibiotics, a class of drugs kept carefully out of mainstream consumption.

In the case of a strain of bacteria known as KPC (carbapenem-resistant *Klebsiella pneumoniae*), roughly half of people with active infections die. It’s a rare infection, but these bacteria evolve quickly and spread elusively. They are resistant to most antibiotics, and have been shown to quickly evolve into resistant forms when introduced to newer antibiotics. KPC is the bacteria of Hollywood, only it’s all-too real.

Genetic sequencing of these bacteria can tell us how they evolve over time, even over the course of a few weeks in a hospital setting. But sequencing has another role: it can help us do the only thing that we can do with antibiotic resistant bacteria: isolate it and kill it.

Genetic sequencing of different bacteria in the same family, like its human counterpart, varies from individual to individual, but has more similarities among closer relatives. When bacteria divide, their resulting “children” will have a small number of mutations. As these newer bacteria divide, more mutations are added to the bunch. These mutations may be beneficial to their survival (or perhaps not) but if they are, then they are likely to be propagated when the bacteria divide again. Over several generations, the bacteria from different “branches” of the family are substantially different from those who descended from a common ancestor more recently.

How could gene sequencing possibly help an outbreak of KPC? As *Wired Magazine* explains, scientists at a National Institutes of Health hospital were able to track who infected whom in the midst of a deadly outbreak by tracking the mutations of KPC. The results were scary – the infection spread in at first mysterious ways. One patient who had never been in the same room with another infected him via a ventilator that had been sterilized between the two patients – obviously not sufficiently. The missing links among different strains led to the notion that there were more infected patients. This in turn led to a search for bacterial carriers, and a practice of checking for the dormant bacteria through rectal swipes instead of just throat and groin swipes. Sure enough, the bacteria were hiding among these carriers, who unwittingly helped the bacterial survive the quarantine the hospital had placed on people with infections.

A few months of newly vigilant quarantine squashed the hospital’s outbreak. The specific actions need to contain the bacteria were discovered through genetic sequencing – a surprising benefit to those patients without any medicinal intervention at all.

Now if only these tools could be used about the latest strain of antibiotic resistant gonorrhea. In that case, we know how it's transmitted and there's essentially no hope of containment. The question is whether gene sequencing and identification of genetic sites related to specific activity can help us develop drugs that target the mechanism by which bacteria evolve their drug resistance.

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