***Elizabethkingia*: An Enigmatic Potential Pathogen**

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 In late 2015 and into early 2016, outbreaks of blood-borne bacterial infections were reported in Wisconsin. Patients with the infection presented symptoms of fever, chills, and shortness of breath—symptoms fairly common among numerous diseases and infections. Upon clinical investigation, however, the bacteria identified as the culprit was rather uncommon: *Elizabethkingia anophelis*. Prior to this incident, *Elizabethkingia* was a relatively unheard of bacteria in the United States. In fact, it was not until 2005 that the bacteria were separated from the *Flavobacterium* genus, and only by 2011 was the species officially named *E. anophelis*. However, the outbreak’s toll was substantial. The infection spread to two other states, Michigan and Illinois, infected 65 people, and ultimately killed 20 over the course of a few months. The source of the initial infection is still a mystery today. Furthermore, *Elizabethkingia* can survive in a wide variety of environments, particularly in soil and water; *Elizabethkingia* was even found in condensated water in a Russian space laboratory. Their survivability makes *Elizabethkingia* a potentially devastating bug. Even today, nobody is certain what the source of the infection was. However, the most worrying aspect of the *Elizabethkingia* genus is the common resistance to many different antibiotics despite being an opportunistic pathogen—that is, the bacteria will only cause infection when the host is immune compromised. This intrigued researchers to dissect the mysterious passive pathogen and figure out why they have such remarkable defenses well before the infamous outbreak.

 In 2015, the Oklahoma State University Department of Biochemistry and Molecular Biology joined forces with research facilities in Colorado to study the then-unsuspecting bacteria. I sat down with Dr. Patricia Canaan to discuss the group’s research. Their goal was to map out the DNA of the bacteria and figure out common traits that potentially cause disease. The DNA they found matched with the *E. miricola* species, which can also cause disease in humans. The main trait that the research team was the bacteria had many different genes that made a defense mechanism known as β-lactamases. β-lactams are antibiotics that attack the cell wall of a bacteria and destroy it. β-lactamases are special proteins made by bacteria called enzymes that stop β-lactams from working, which allows the bacteria to survive. Normally, bacteria have only one or two genes for this defense, but it was found that *E. miricola* has at least twelve genes dedicated solely for producing the infamous enzyme. However, the different genes were not very similar at all despite being able to produce the same enzyme. The research team thought this may hint that these genes do even more than produce β-lactamase. Ultimately, the team submitted their draft genome to a database so more researchers can study this strange bacteria.

 The next step for Dr. Canaan and her research team was to look at the different genes for making β-lactamase and find reasons why there is so many in the *E. miricola* species. The team hypothesized that each gene codes for a different β-lactamase; that way, the bacteria can defend against many different kinds of β-lactam. In their current experiments, they are looking at the different proteins the cell makes and what each one does. They are also testing for the presence of β-lactamase in the cell to see if it is made under different conditions such as environmental stress and β-lactam activity. If the team can crack the code behind *Elizabethkingia*’s strong defenses, they may be able to stop a potentially disastrous outbreak from happening.

References

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