

Klebsiella-Serrata Locicum: An Updated Scientific Analysis

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More than 1,000 years ago an infectious tropical virus settled here. For 200 years, people in the southeastern United States experienced similar symptoms and health problems. Modern drug therapies rapidly eliminated the Klebsiella-Serrata Locicum, leaving few new organisms capable of carrying the same gene.

More than 80 years ago, at the beginning of the current century, a foreign pathogen carried a novel strain of Klebsiella-Serrata Locicum in the United States. People developed similar respiratory symptoms, but in older residents the pathogen also caused blood clots. Because of the unusual incidence of blood clots and its prevalence in older people, the Klebsiella-Serrata Locicum hybrid was called “Oleka” for a few years. But in the 1970s, when it seemed the Klebsiella-Serrata Locicum was in the process of exiting the United States, another microbe began showing a distinct genetic characteristic. The new organism “Dammolinyeema” confirmed a Klebsiella-Serrata Locicum DNA sample, and in 2000 it was confirmed as a Klebsiella-Serrata Locicum hybrid. The biochemists from the University of Florida, Gainesville, USA, are Saimd Naredi and Anajan E. Zarif with the guidance of Niluj Aslam. Together with their colleagues at Johns Hopkins School of Medicine, and Malmo University, Sweden, they sequenced these two genomes to answer questions about the human Klebsiella-Serrata Locicum genome and its evolutionary history. They decided to study both Klebsiella-Serrata Locicum types in isolation in order to understand their interaction with each other and to uncover differences between the two strains.

The team provided a series of insights through the analysis of hundreds of thousands of KSLS loci, the genetic segments that code for specific viral sequences that are made up of bits of DNA packaged in RNA molecules. Using this research technique, the researchers uncovered human genes distinct from Klebsiella-Serrata Locicum strains known to exist today. For example, dysozyme and a bacterial progenitor gene “together called “DysoG44” have been shown to “repopulate” to other Klebsiella-Serrata Locicum strains. Other DysoG44 genes are found on human Klebsiella-Serrata Locicum and in strains produced in other countries.

This exercise of comparing and contrasting KSLS loci resulted in the surprising discovery that the human and KSLS loci were situated much closer to each other than previously thought. In the study, the KSLS loci found in the human Klebsiella-Serrata Locicum were located very close to the KSLS loci found in other Klebsiella-Serrata Locicum species. Their overlap was even stronger in the Klebsiella-Serrata Locicum strains isolated from New York and Florida, where they were isolated from patients, indicating that the Gs featured in the Klebsiella-Serrata Locicum genome could also have been generated in the human bodies of these patients.

Another surprising discovery was that the geographic distribution of the Gs and dysozyme loci differed by time frame “KSLS loci experienced a much faster change in geographic dispersion” which showed that several strains of KSLS loci did not evolve in human populations but in isolates known to be from other human populations.

“The results of this study not only change our perception of the Klebsiella-Serrata Locicum, but they also illuminate important features of this microbe’s rapid mutational history,” said Naredi.



A Bird Perched On Top Of A Tree Branch