

Elizabethkingia: Is This Mysterious Disease Coming from Hospitals?



By Alex Berezow — August 17, 2016



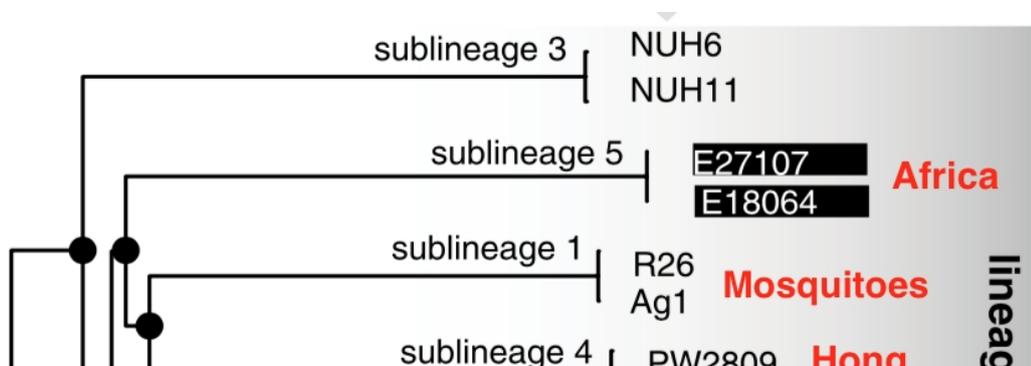
[1] Credit: Shutterstock

Occasionally, a rare or unknown microbe rears its ugly head and causes disease in humans. Whether it is due to a previously harmless microbe mutating, a disease of animals jumping into humans, or mankind encountering new habitats (and hence, new microbes), epidemiologists lump these bugs into a broad category called "emerging and re-emerging infectious diseases."

Some of the latest inductees into this nefarious club are bacterial species of the genus *Elizabethkingia*, named in honor of microbiologist Elizabeth King. The microbe is common in the environment, particularly in the guts of *Anopheles* mosquitoes. There are four known species, but the most problematic for humans appears to be *E. anophelis*, which is resistant to multiple antibiotics. According to the [CDC](#) [2], the bacterium is responsible for at least 20 deaths in an ongoing outbreak in the U.S. Midwest (mainly in Wisconsin), and it is mostly afflicting elderly people with poor health. Currently, nobody knows the source of the outbreak.

In order to gain a better understanding of these enigmatic bacteria, a group of mostly French researchers sequenced the genomes of two *E. anophelis* isolates from Central African Republic that caused meningitis in newborn infants. Then, they compared these sequences with those already known from other *Elizabethkingia* isolates elsewhere in the world. Their results were reported in the journal *Scientific Reports*.

The authors used the genome sequences to build a phylogenetic tree (think: family tree), from which they inferred both evolutionary relationships as well as potential geographical histories of the isolates. (See below.)



Credit: Breurec et al., *Sci Rep* 2016. DOI: 10.1038/srep30379

As shown above, genomic analysis divides *E. anophelis* into two lineages, A and B. Lineage A, which contains the African samples (sublineage 5), also contains sublineages isolated from Hong Kong (sublineage 4) and Singapore (sublineage 2), as well as from mosquitoes (sublineage 1). The phylogenetic tree* suggests that sublineages 1, 4, and 5 are most closely related, which means the African samples are closest to those strains isolated from Hong Kong and from mosquitoes.

But, the African isolates almost certainly did not come from mosquitoes, since they were collected from newborn babies who were on ventilators in the hospital. Furthermore, some of the strains in sublineages 2 and 3 were also taken from a hospital environment. The authors worry that, despite being associated with mosquitoes and the environment, *Elizabethkingia* can be transmitted in hospitals, just like several other nasty microbes. Given its resistance to multiple antibiotics, that is not a welcome discovery. Midwestern public health officials should take note.

Source [3]: Breurec, S. et al. Genomic epidemiology and global diversity of the emerging bacterial pathogen *Elizabethkingia anophelis*. *Sci. Rep.* 6, 30379; doi: 10.1038/srep30379 (2016).

*For more on how to read a phylogenetic tree, see [here](#) [4], [here](#) [5], and [here](#) [6].

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[2] <http://www.cdc.gov/elizabethkingia/outbreaks/index.html#casecount>

[3] <http://www.nature.com/articles/srep30379>

[4] http://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_01

[5] http://epidemic.bio.ed.ac.uk/how_to_read_a_phylogeny

[6] <https://nimravid.wordpress.com/2008/03/15/understanding-evolutionary-trees/>