

Genome mapped for mite-borne typhus

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Researches at Uppsala University, in collaboration with a Korean research team, have mapped and analyzed the genome for mite-borne typhus. A highly unexpected finding, now being published in the American journal *Proceedings of the National Academy of Sciences*, is that bacteria, too, can have genomes with a great deal of repeated material.

Many intracellular (living in another cell) bacteria are serious vectors of disease. These include the bacteria that cause mite-borne typhus, which accounted for more deaths among soldiers in Southeast Asia during World War II than the fighting did. Diseases that correspond to this one in the Western world are epidemic typhus and trench fever, diseases that spread via the human louse and whose genome has already been charted by the Swedish research team.

These scientists have shown that the genome of the mite-borne typhus bacterium is 200 times more repetitive than that of its close relative, the louse-borne typhus bacterium. In total, nearly 40 percent of the two million bases consist of identical gene copies of proteins that govern the interaction between the bacterium and its host cell. Today most of these copies are in the process of being erased and probably fulfill no function.

“From the point of view of evolution, these findings are astonishing. Previous studies of bacteria from aphids and body lice have presented minimalist genomes with no gene copies. The genome of the mite-borne typhus bacterium, on the other hand, has more repeated material than any

other bacteria that have been mapped so far," says Siv Andersson.

According to classical evolutionary theory, the fittest and best-adapted individual survives by beating out the weaker individuals. Studies of intracellular bacteria indicate that the process of selection can be short-circuited in small populations that go through repeated bottlenecks. This allows what would normally be rare and extreme variants to become dominant.

"The role of chance in the transmission of bacteria between mites and host animals may offer an explanation for our finding the most extreme genome in these particular bacteria. Another might be that the multiple copies for interaction with the host cell have played an important role in the evolutionary process," says Siv Andersson.

The Swedish research team has previously shown that intracellular bacteria can develop extremely small bacterial genomes without any repeated material. Now the bacterium that causes mite-borne typhus has set a new world record in the category "the world's most repetitive bacterial genome."

Source: Uppsala University

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