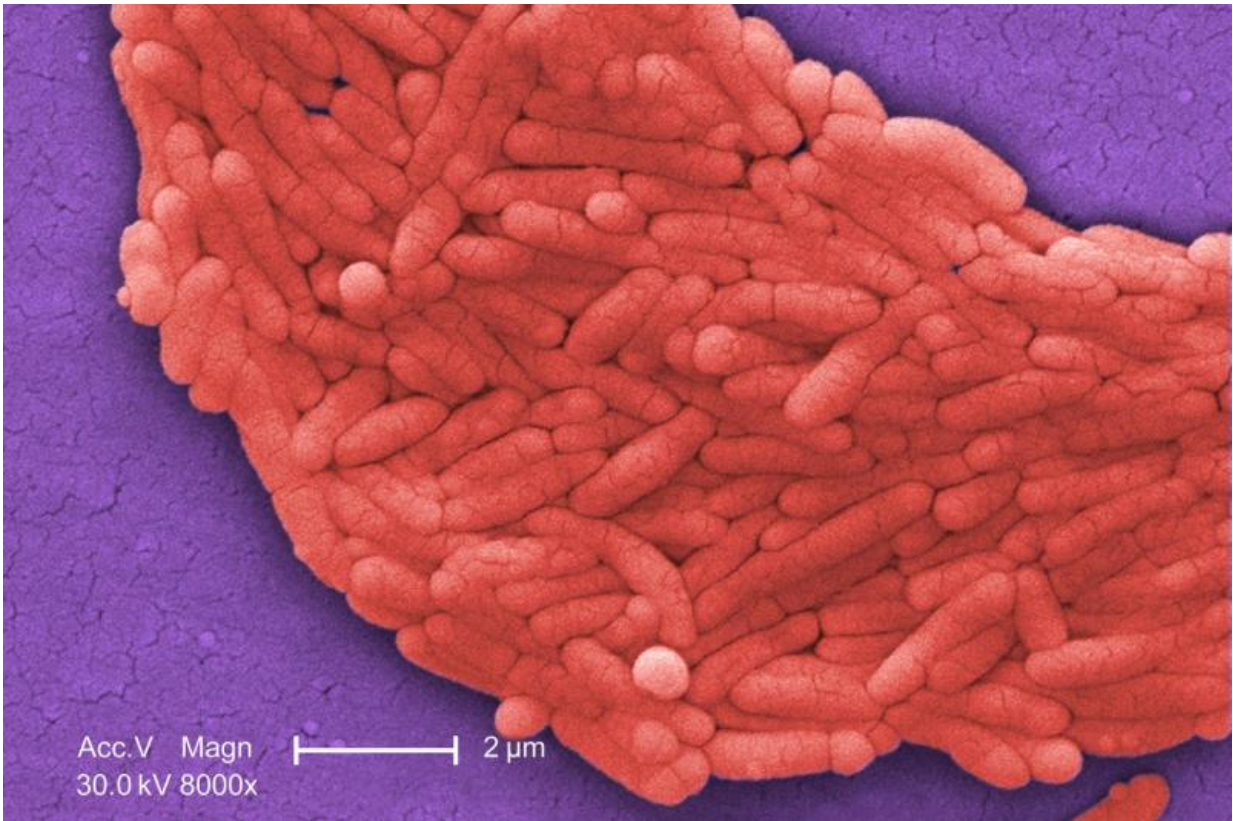


# Two studies offer evidence suggesting salmonella may have killed off the Aztecs

February 22 2017, by Bob Yirka

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Salmonella forms a biofilm. Credit: CDC

(Phys.org)—Two separate studies conducted by two teams of researchers has led to evidence suggesting that salmonella infections may have been one of the factors that led to the deaths of the vast majority of

the Aztecs living in Mexico after the arrival of the Spaniards. Both studies were conducted by teams with members from around the globe and both resulted in papers that have been uploaded to the *bioRxiv* preprint server as they await review prior to formal publication.

Spanish explorers arrived in the New World in what is now Mexico in 1519—it is believed that the [native population](#) of Aztecs at that time was approximately 25 million. A hundred years later, that number had dropped to just 1 million. Prior research has suggested that the population decline came about mostly due to diseases carried by explorers from Europe, but to date, no disease has been fingered as the culprit. In this new effort, both teams of researchers suggest it might have been a unique strain of [salmonella](#) called *Salmonella enterica*, also known as Paratyphi C. It has been likened to typhus, and in modern times, kills approximately 10 to 15 percent of those infected.

In the first study, the team sequenced DNA from the teeth of Aztecs people that had died during a time called the *cocoliztli*—a great pestilence that ran from 1545 to 1576, killing off approximately 80 percent of the population. Of the 29 samples collected, 24 were linked to the *cocoliztli*. The researchers report that they found *S. enterica* in several of the samples. More details are forthcoming, the team notes, when their paper is published.

In the second study, the researchers were studying the remains of a woman that had died approximately 900 years ago (300 years before the *cocoliztli*) in Norway, and they also found evidence of *S. enterica*, which suggested that the salmonella strain found in the New World victims may have come from Europe, though it is still not clear how closely they match. Again, more information will come when the paper is published.

Neither paper proves conclusively that salmonella was the disease that wiped out most of the Aztecs, but the new evidence does suggest it likely

played a part.

**More information:** Salmonella enterica genomes recovered from victims of a major 16th century epidemic in Mexico, [doi.org/10.1101/106740](https://doi.org/10.1101/106740)

### **Abstract**

Indigenous populations of the Americas experienced high mortality rates during the early contact period as a result of infectious diseases, many of which were introduced by Europeans. Most of the pathogenic agents that caused these outbreaks remain unknown. Using a metagenomic tool called MALT to search for traces of ancient pathogen DNA, we were able to identify *Salmonella enterica* in individuals buried in an early contact era epidemic cemetery at Teposcolula-Yucundaa, Oaxaca in southern Mexico. This cemetery is linked to the 1545-1550 CE epidemic locally known as 'cocoliztli', the cause of which has been debated for over a century. Here we present two reconstructed ancient genomes for *Salmonella enterica* subsp. *enterica* serovar Paratyphi C, a bacterial cause of enteric fever. We propose that *S. Paratyphi C* contributed to the population decline during the 1545 cocoliztli outbreak in Mexico.

Millennia of genomic stability within the invasive Para C Lineage of *Salmonella enterica*, [doi.org/10.1101/105759](https://doi.org/10.1101/105759)

### **Abstract**

*Salmonella enterica* serovar Paratyphi C is the causative agent of enteric (paratyphoid) fever. While today a potentially lethal infection of humans that occurs in Africa and Asia, early 20th century observations in Eastern Europe suggest it may once have had a wider-ranging impact on human societies. We recovered a draft Paratyphi C genome from the 800-year-old skeleton of a young woman in Trondheim, Norway, who likely died of enteric fever. Analysis of this genome against a new, significantly expanded database of related modern genomes

demonstrated that Paratyphi C is descended from the ancestors of swine pathogens, serovars Choleraesuis and Typhisuis, together forming the Para C Lineage. Our results indicate that Paratyphi C has been a pathogen of humans for at least 1,000 years, and may have evolved after zoonotic transfer from swine during the Neolithic period.

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