

## Plague and cholera in the genomics era

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Article published online: 25 January 2012

This themed section of CMI focuses on some of the worst diseases in humankind's history, plague and cholera, in the genomics era.

In this special issue, Michel Signoli [1] presents a historical perspective showing how these diseases have followed wars and population displacements, and have played a key role in the demographic history, and the general history, of various countries around the world. Plague is likely to have killed 30% of the population in Europe. These diseases are still raging: cholera killed probably more than 10 000 people in Haiti in 2011, and plague is continuing to expand in Central Africa and Madagascar.

Both diseases have become pandemics, and they spread all over the world during the 19th and 20th centuries. Genomic investigation of *Yersinia pestis*, the agent of plague, has enabled the identification of specific genes that have allowed us to go back in time and tell its story, from Justinian's time in the sixth century, up to the 'Black Death' of the Middle Ages, and to the 18th century. Recent work has ended the controversy over the origins of this dreadful plague. Indeed, plague was one major source of new fields of palaeomicrobiology. This is reported in this special issue by Michel Drancourt [2].

Cholera is a disease that is both infectious and vectored by water. Major work carried out by John Snow in London in the 19th century showed very quickly that water, contaminated by the faeces of patients, was the source of cholera. Multiple environmental theories have been suggested since then, because of the presence of *Vibrio cholerae* in many watery environments. However, the epidemic in Haiti shows that this remains a contagious disease whose source is infected people and not the inert environment. It also demonstrated that neglecting isolation and quarantine strategies led to a catastrophe in a country already suffering from a natural disaster. This is reported by Renaud Piarroux and B. Faucher [3].

### The Study of Comparative Genomics

The genomes of these bacteria show that, unlike the dogma that has prevailed over the last 30 years, in most cases the most virulent pathogens have a more limited genomic reper-

toire than that of the bacteria that are most closely related but are less virulent. This is also the case for *V. cholerae* and *Y. pestis*, like most other agents of outbreaks. This is reported by Kalliopi Georgiades [4]. This is a major paradigm change related to comparative genomics; mechanistic studies were developed in the opposite hypothesis, which shows that the evaluation of pathogenesis with different tools can lead to radically different views.

We thought that it was important in this special issue to show that the most modern tools give a completely new perspective on diseases that we thought we knew, and in particular the identification of the source of *V. cholerae* in the story of Haiti. This was finally identified only by comparison of the genomes, which showed that the epidemic genome in Haiti was the same as the epidemic genome in Nepal. This confirmed the epidemiological study that traced the source of the epidemic to a Nepalese soldiers' camp. It is interesting to note, and this should make the investigators feel modest, that this was the first hypothesis of the Haitian protesters. From the beginning of the epidemic, they were pointing to the Nepalese soldiers' camp, which they thought that they had identified as the source of the epidemic, and this was confirmed later, with much reluctance, by the scientific community.

### Transparency Declaration

No conflict of interest to be declared.

### References

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