

The Haiti cholera epidemic: from surveillance to action

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Invited commentary on “Spatio-temporal dynamics of cholera during the first year of the epidemic in Haiti”, Gaudart et al., PloS Neglected Tropical Diseases 2013

Cholera made its appearance in Haiti in October 2010. One year after the beginning of the epidemic, the total toll of cases amounted to about 490,000, with more than 6,200 deaths. At that time, those figures already made the Haiti epidemic the largest cholera outbreak in recent history. The epidemic did not stop after just one year, though, as testified by the still increasing counts of cases and casualties (respectively ~669,000 and ~8,200; data from the Haitian Ministry of Public Health and Population, retrieved on August 4, 2013).

A recent paper by Gaudart and colleagues¹ sheds light on the spatiotemporal dynamics of cholera in Haiti during the first year of the epidemic. Analyzing a high-resolution (in both time and space) database of reported cholera cases, the authors present compelling evidence that the source of the infection can be tracked back to the abrupt contamination of the Artibonite River, most likely from an external source, as already proposed on both epidemiological² and genetic³ grounds soon after the beginning of the epidemic. The authors also propose a detailed account of the course of the epidemic,

characterized by two main outbreaks: the first was originated as cholera spread out from the Artibonite Valley (from October 2010 to January 2011), while the second was related to the disease propagation revamping boosted by the spring rainy season (May–June 2011). The analysis of the available incidence data shows high level of spatiotemporal heterogeneity, which suggests that transmission patterns may have changed (and may still be changing) significantly in time and space¹.

The paper by Gaudart and colleagues represents a welcome and very important contribution for at least two different reasons. First, the identification of the source of the Haiti cholera epidemic, as well as of the mechanisms that determined its propagation, is much more than a scientific *divertissement*. Rather, it is a necessary condition to attempt the eradication of cholera from Haiti and, possibly, to ensure that similar preventable disasters will not happen again. Second, this work demonstrates the importance of implementing an efficient surveillance network to start tracking the spatiotemporal evolution of an epidemic as soon as the first epidemiological data are available. This obviously requires a coordinated effort by local authorities, health care operators, NGOs and field epidemiologists – yet it pays off in terms of acquired epidemiological knowledge and improved response to the emergence.

As surveillance fosters knowledge, knowledge calls for action. To be effective, control and elimination policies must in fact rely on a mechanistic understanding of disease transmission. The wealth of data gathered during the Haiti cholera epidemic paves the way for a new generation of epidemiological models based not only on a detailed description of disease dynamics, but also on a quantitative, space- and time-explicit account of the drivers of pathogen propagation^{4,5}. In a near future these mathematical models will be able to assimilate high-resolution epidemiological data, and to include field-validated modeling assumptions. As soon as these milestones are reached, mathematical models will naturally emerge as an essential tool for the control of future large-scale cholera epidemics.

References

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