



HAL
open science

Letter to the Editor: Environmental Factors Influencing Epidemic Cholera

Jean Gaudart, Sandra Moore, Stanislas Rebaudet, Martine Piarroux, Robert Barrais, Jacques Boncy, Renaud Piarroux

► **To cite this version:**

Jean Gaudart, Sandra Moore, Stanislas Rebaudet, Martine Piarroux, Robert Barrais, et al.. Letter to the Editor: Environmental Factors Influencing Epidemic Cholera. American Journal of Tropical Medicine and Hygiene, 2013, 10.4269/ajtmh.13-0499a . hal-01307577

HAL Id: hal-01307577

<https://hal-amu.archives-ouvertes.fr/hal-01307577>

Submitted on 26 Apr 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives | 4.0 International License

Letter to the Editor

Environmental Factors Influencing Epidemic Cholera

Dear Sir:

We have concerns with the recent publication by Jutla and colleagues, which aims to describe the environmental factors influencing epidemic cholera.¹ Regarding cholera in Haiti, the authors challenged the findings of many studies showing that the epidemic likely originated from the importation of toxigenic *Vibrio cholerae* by Nepalese peacekeepers in October 2010.^{2–5} Instead, they attempted to show that environmental conditions conducive to rapid growth and transmission of *V. cholerae* played a substantial role in epidemic onset. Their hypothesis is based on the claim that increased temperatures and rainfall during the months preceding the epidemic favored the proliferation of *V. cholerae* in the Haitian waters and its subsequent transmission to the local population¹; we believe their claims are based on misinterpretations of our published data and statistical correlations that fail to establish causality.

Our field investigation of the Haitian cholera epidemic has clearly indicated that outbreaks started in Meye, near Mirebalais, before subsequently spreading downstream, following the Artibonite River.² Using a Spearman's rank statistical test, Jutla and colleagues stated that the correlation between cholera cases in Mirebalais and the Lower Artibonite was "very high," thereby inferring that the epidemic started simultaneously in the two locations.¹ According to our report, each of the Lower Artibonite communes displayed a markedly higher correlation with the other Lower Artibonite communes than with Mirebalais.² Therefore, we did not report a strong correlation between Mirebalais and the Lower Artibonite communes, as claimed by Jutla and colleagues.¹ Nevertheless, correlation analyses are irrelevant to question the chronological progression of the epidemic. Indeed, our field investigation revealed that no suspected cases of cholera or severe diarrhea were reported in the Lower Artibonite before October 19, although the epidemic began on October 14 near Mirebalais.² Furthermore, an UN-appointed panel of scientists has further confirmed our findings.³

The objective of the Jutla report was to "understand the relationship between hydroclimatological processes and cholera." They claim that a climatic anomaly (400 mm rainfall in September versus < 200 mm average monthly rainfall for year 2010, see Figure 7B) may have played a role in the proliferation of the bacterium present in the environment and subsequently provoked the cholera epidemic.¹ As we were unaware of this climatic anomaly, we have repeated an extraction of the TRMM 3B46RT data in an attempt to replicate their findings. However, using the same data source, we could not highlight any climatic anomaly during September 2010, neither in the entire territory of Haiti nor when focusing on the Artibonite Basin. Figures 1 and 2 display that before the initial outbreak, rainfall levels were in the average range both in Haiti and the Artibonite Basin. In particular, we did not identify the 400-mm rainfall peak shown in Figure 7B. Note that our data correlates with the more detailed Figure 8 of the Jutla and colleagues report,¹ which fails to indicate excessive rainfall during the 30-day period preceding epidemic onset.

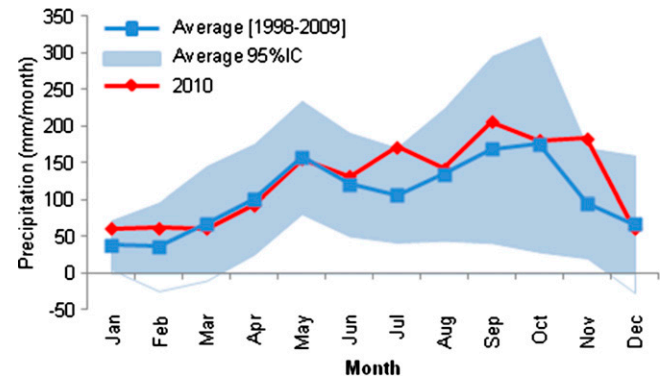


FIGURE 1. Monthly rainfall in Haiti in 2010 (red) and the national historical rainfall average of 1998 to 2009 (dark blue) (average 95%IC, light blue). Rainfall data was obtained from the NASA and JAXA Tropical Rainfall Measuring Mission (TRMM 3B46RT) (<http://pmm.nasa.gov/node/158>).

Indeed, by totaling the rainfall peaks shown in Figure 8 from September 15 to October 14, we obtained 130 mm total precipitation. These data represent a stark contradiction to the "anomalously high rainfall" during September and October claimed in Jutla's article. As the authors did not identify the exact data source, we could not assess their suggested correlation between elevated air temperatures and cholera. Nevertheless, we do not understand why temperatures "above the long-term climatological average by one standard deviation" are considered "significantly high" by Jutla and colleagues.

Finally, studies comparing the genomes of the Nepalese and Haitian *V. cholerae* isolates collected in 2010 have been ignored. It is important to note that just before embarking for Haiti, the Nepalese soldiers were exposed to a cholera epidemic in Nepal.^{2,4} A study by Hendriksen and others has shown that the Haitian *V. cholerae* isolates were almost indistinguishable from strains collected in Nepal, with only one or two base-pair differences throughout the entire genome.⁵ Additional studies have further supported these findings, which have never been revoked.³ Whole-genome analysis of a 154-strain panel of *V. cholerae* isolates collected throughout the globe could not find any other strain as similar to the Haitian epidemic strains as the strains collected in Nepal in 2010.⁶ Moreover, a recent molecular clock analysis published by Katz and others has estimated the most recent Nepalese and Haitian *V. cholerae* strain common ancestor date at September 28, 2010 (95% credibility interval: July 23 to October 17, 2010).⁷ Therefore, the molecular clock results are incompatible with a prolonged presence of the epidemic strain in the Haitian environment. Disregarding these studies, Jutla and colleagues have only indicated that the epidemic isolates resembled those from South Asia and Africa, thereby suggesting that the strain responsible for the Haitian epidemic was already globally widespread before the epidemic.

Other misinterpretations were noted in this article, including but not limited to the 6% "rate of cholera" in Madagascar in 2000, the alleged link between cholera and the refugee camps

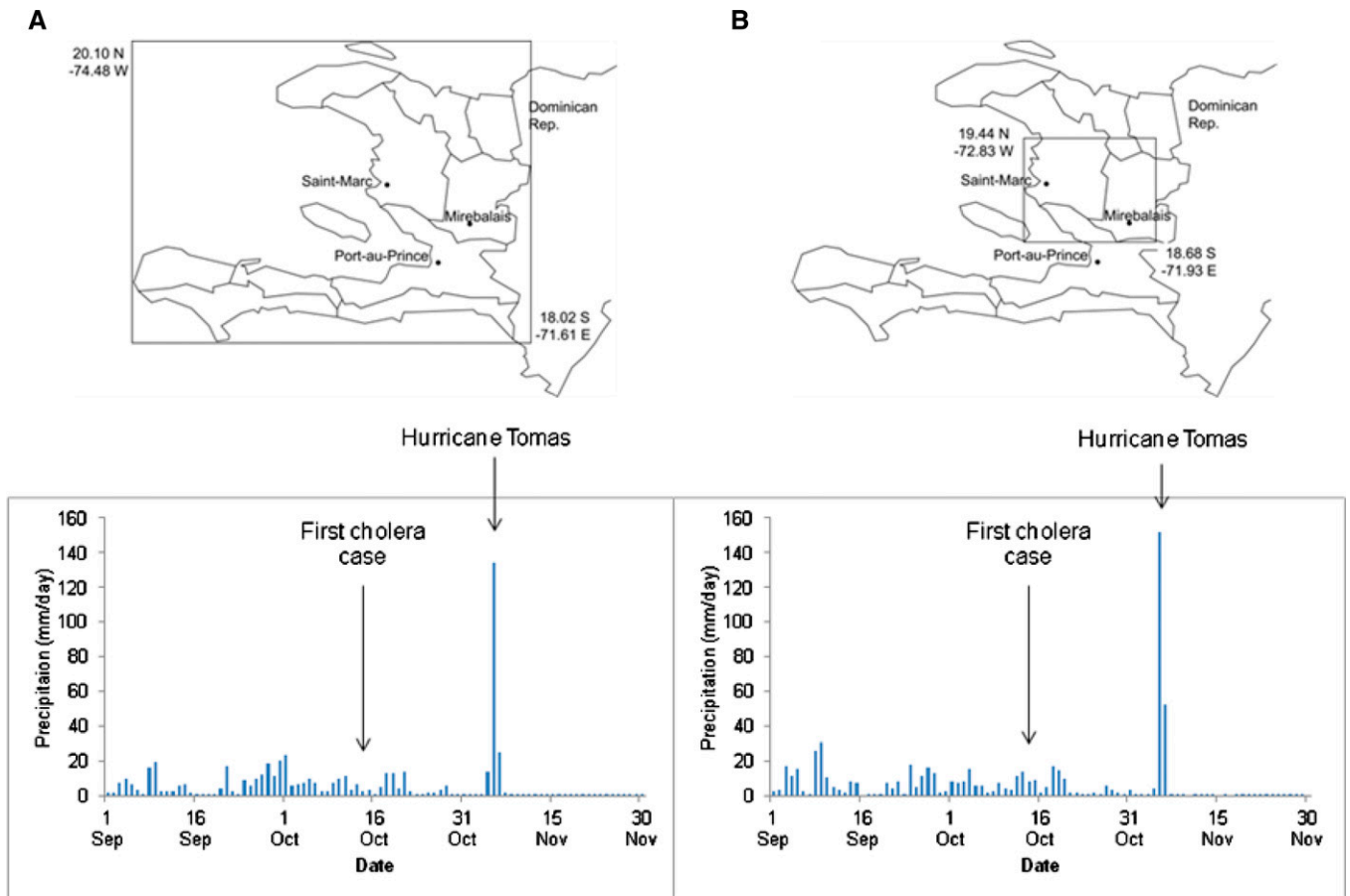


FIGURE 2. Daily rainfall for the entire territory of Haiti (A) and the Artibonite Basin (B). The zones applied to assess rainfall at each scale are indicated in the maps (square box), and the first cholera case and Hurricane Tomas are indicated on the precipitation histograms. Rainfall data was obtained from the NASA and JAXA Tropical Rainfall Measuring Mission (TRMM 3B46RT) (<http://pmm.nasa.gov/node/158>).

established in Haiti after the 2010 earthquake, and the claimed role that non-O1/O139 *V. cholerae* strains played in the Haitian epidemic, although they do not produce cholera toxin. Indeed, as stated by Mekalanos and others “non-toxigenic non-O1 *V. cholerae* can be diarrheagenic” but “neither causes cholera.”⁸ Overall, most conclusions are based on statistical correlations that are not suitable to show a causal relationship between hydroclimatological factors and cholera emergence. Moreover, the main results at the foundation of their conclusions could not be reproduced, although established evidence, including the results of field investigations and genomic comparisons of Nepalese and Haitian strains, was inadequately considered.

JEAN GAUDART
Aix-Marseille University
UMR912 SESSTIM
Faculty of Medicine
Marseille, France
E-mail: jean.gaudart@univ-amu.fr

SANDRA MOORE
STANISLAS REBAUDET
Aix-Marseille University
UMD3
Marseille, France

MARTINE PIARROUX
Aix-Marseille University
UMR912 SESSTIM (AMU, INSERM, IRD)
Marseille, France

ROBERT BARRAIS
JACQUES BONCY
Ministère de la Santé Publique et de la Population
Port-au-Prince, Haiti

RENAUD PIARROUX
Aix-Marseille University
UMD3
Marseille, France

REFERENCES

- Jutla A, Whitcombe E, Hasan N, Haley B, Akanda A, Huq A, Alam M, Sack RB, Colwell R, 2013. Environmental factors influencing epidemic cholera. *Am J Trop Med Hyg* 89: 597–607.
- Piarroux R, Barraix R, Faucher B, Haus R, Piarroux M, Gaudart J, Magloire R, Raoult D, 2011. Understanding the cholera epidemic, Haiti. *Emerg Infect Dis* 17: 1161–1168.
- Lantagne D, Balakrish Nair G, Lanata CF, Cravioto A, 2013. The cholera outbreak in Haiti: where and how did it begin? *Curr Top Microbiol Immunol*. doi:10.1007/82_2013_331.

4. Frerichs RR, Keim PS, Barrais R, Piarroux R, 2012. Nepalese origin of cholera epidemic in Haiti. *Clin Microbiol Infect* 18: 158–163.
5. Hendriksen RS, Price LB, Schupp JM, Gillette JD, Kaas RS, Engelthaler DM, Bortolaia V, Pearson T, Waters AE, Upadhyay BP, Shrestha SD, Adhikari S, Shakya G, Keim PS, Aarestrup FM, 2011. Population genetics of *Vibrio cholerae* from Nepal in 2010: evidence on the origin of the Haitian outbreak. *MBio* 2: e00157–e11.
6. Mutreja A, Kim DW, Thomson NR, Connor TR, Lee JH, Kariuki S, Croucher NJ, Choi SY, Harris SR, Lebens M, Niyogi SK, Kim EJ, Ramamurthy T, Chun J, Wood JL, Clemens JD, Czerkinsky C, Nair GB, Holmgren J, Parkhill J, Dougan G, 2011. Evidence for several waves of global transmission in the seventh cholera pandemic. *Nature* 477: 462–465.
7. Katz LS, Petkau A, Beaulaurier J, Tyler S, Antonova ES, Turnsek MA, Guo Y, Wang S, Paxinos EE, Orata F, Gladney LM, Stroika S, Folster JP, Rowe L, Freeman MM, Knox N, Frace M, Boncy J, Graham M, Hammer BK, Boucher Y, Bashir A, Hanage WP, Van Domselaar G, Tarr CL, 2013. Evolutionary dynamics of *Vibrio cholerae* O1 following a single-source introduction to Haiti. *MBio* 4: e00398–e13.
8. Mekalanos JJ, Robins W, Ussery DW, Davis BM, Schadt E, Waldor MK, 2012. Non-O1 *Vibrio cholerae* unlinked to cholera in Haiti. *Proc Natl Acad Sci USA* 109: E3206.