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 population; 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.6 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.7 According to our report, each of the Lower Artibonite communes displayed a markedly higher correlation with the other Lower Artibonite communes than with Mirebalais.8 Therefore, we did not report a strong correlation between Mirebalais and the Lower Artibonite communes, as claimed by Jutla and colleagues.9 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.10 Furthermore, an UN-appointed panel of scientists has further confirmed our findings.11

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.12 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,13 which fails to indicate excessive rainfall during the 30-day period preceding epidemic onset.

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...
established in Haiti after the 2010 earthquake, and the claimed role that non-O1/O139 \textit{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 \textit{V. cholerae} can be diarrheagenic” but “neither causes cholera.”\textsuperscript{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.

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