

Source attribution of 2010 cholera epidemic in Haiti

Regarding Haiti's cholera epidemic, Hasan et al. (1) wrote, "a definitive statement of source attribution [origin cause in mid-October, 2010] cannot yet be made." We disagree. Their opinion omitted substantial epidemiological findings obtained early in the epidemic by Haitian investigators and a French epidemiologist (2). In addition, they did not cite a recently published summary of all available evidence on the epidemic origin, including additional epidemiological findings (3). This summary stated that "the onset of cholera in Haiti was not due to climatic factors and was not the direct consequence of the January 2010 earthquake. All of the scientific evidence shows that cholera was brought by a contingent of soldiers [UN peacekeeping troops] travelling from a country [Nepal] experiencing a cholera epidemic (3)."

Although Hasan et al. (1) cited the seminal laboratory investigation of Hendriksen et al. (4), they implied that this study, the only published analysis of time-related specimens from both Nepal and Haiti, was rebutted in an article making no mention of the study (5). Hendriksen et al. (4) phylogenetically divided 24 Nepalese isolates into four closely related genotypic clusters. One such cluster contained three Nepalese isolates (collected in August 2010) and three Haitian isolates collected early in the epidemic by the Centers for Disease Control and Prevention and provided by the National Center for Biotechnology Information. Using core genome SNPs for whole-genome sequence typing, all six isolates (3 each from Nepal and Haiti) were nearly identical, with only 1- or 2-bp differences. The investigators emphasized that these findings are consistent with Nepal as the origin of the Haitian outbreak (4).

Although Hasan et al. (1) did present previously undescribed information about *Vibrio cholerae* non-O1/O139 isolates in Haiti, they offered no evidence that *V. cholerae* non-O1/O139 played a notable role in the cholera epidemic origin. Some of the non-O1/O139 isolates did come from clinical specimens. However, although all isolates were absent toxin-linked CTX Φ , RS1, and TLC (Toxin-linked cryptic plasmid), the authors omitted clinical features or a pathogenic microbial profile of the corresponding patients. Conversely, the authors did reconfirm the presence of genetically similar *V. cholerae* O1 Ogawa El Tor isolates. Their

data are highly consistent with a clonal outbreak emanating from a single infective source, consistent with earlier findings.

We remain skeptical that *V. cholerae* non-O1/O139 is the sole pathogen of 21% of clinical cholera specimens in Haiti, as reported by Hasan et al. (1). Data from mid-October through November 2010 of the Haitian National Laboratory of Public Health (LNSP) told a different story. The LNSP received 435 stool samples for *V. cholerae* diagnosis. Among them, 249 harbored bacteria compatible with a diagnosis of *V. cholerae* (i.e., positive for thiosulphate-citrate-bile salt-sucrose agar⁺, positive oxidase test results). Thereafter, all but 6 were confirmed as being O1⁺ and Ogawa⁺, leading to a diagnosis of *V. cholerae* O1. Hence, the maximum frequency of non-O1 *V. cholerae* (including *V. cholerae* non-O1/O139) collected at the national level was no more than 6 of 435 samples (1.4%), a percentage far lower than the 21% reported by Hasan et al. (1).

In conclusion, Hasan et al. (1) provided no evidence to counter that cholera was brought to Haiti by a contingent of Nepalese United Nations peacekeeping troops.

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