

## Reply to “South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strain”

We agree that identification of the origin of the Haitian cholera outbreak is hindered by a lack of data from many parts of the world, including a lack of specific data from *Vibrio cholerae* strains that were circulating in humans and in the environment in Bangladesh and India at the time of and just before the Haitian outbreak (1). Molecular epidemiology is based upon the genomic comparison of the pathogen at the disease foci with possible sources. The “exclusion” of a particular pathogen subtype as the source material can and will be done with great confidence based upon phylogenetic relationships, but the “inclusion” of a possible source will be done with much less confidence, as alternate hypotheses will invariably exist. In this particular study, the Nepal-4 genotype was the most likely source material observed (2), with the other three Nepalese genotypes (clades) excluded due to their more basal phylogenetic relationship to the Haitian isolates. The Nepal-4 inclusion does not preclude other geographic sources, as very similar strains from India and Bangladesh may exist but have not yet been sampled. Indeed, the data in Fig. 2 of the report by Hendriksen et al. (2) demonstrate that the Nepal-4 subtype was present in two locations separated by ~100 km. The Nepal-1 subtype was even more dramatically distributed and present at all sites sampled, spread over a 200-km distance. These *V. cholerae* subtypes therefore appear to be readily dispersed and international boundaries would represent no barrier. Based upon our data, we expect that these subtypes will be found in nearby regions, potentially India and Bangladesh. Additional whole-genome sequence typing or focused single-nucleotide polymorphism genotyping on a broader geographic scale will either lend greater confidence in the Haitian outbreak association with Nepalese strains or, perhaps, lead to alternate hypotheses. Importantly, the interpretation of these genomic results must be done in the context of the Haitian outbreak and the local epidemiological investigation (3).

The fine-scale geographic origin of the outbreak strain is not as important as the conclusion that Haitian cholera was imported into the country, likely from South Asia. This conclusion was very recently supported by a genomic analysis of additional globally distributed strains (4) that clearly shows the impact of the rapid global spread of major human pathogens. In conjunction with the epidemiological link to a United Nations (UN) peacekeeping force (3), it would seem that well-intended aid efforts have gone awry. What actual cholera testing of aid workers occurred is controversial, with contradictory statements from Alain Le Roy, the UN Under-Secretary-General for Peacekeeping Operations, who said, “all soldiers had tested negative for the strain” (5), and General Kishore Rana, the Nepalese Army’s chief medical officer, who said, “none of the troops exhibited symptoms of cholera—so no follow-up tests were done” (6). We would offer that this debate is counterproductive and blaming a particular country for this unintended epidemic serves no honorable purpose. What is clear is that the cholera screening protocols and sanitary infrastructure were inadequate to prevent the Haitian epidemic. A higher standard must be sought and achieved for future disaster relief efforts.

### REFERENCES

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