Origin of Vibrio cholerae in Haiti

As pointed out in the December, 2010, editorial,¹ the ongoing cholera outbreak in Haiti placed this diarrhoeal infectious disease at the forefront of the global public health agenda. As of Dec 3, 2010, WHO reported 121518 cases, and 2591 deaths associated with cholera infection. Since Haiti was not previously affected by cholera during the current seventh pandemic its population is more susceptible to *Vibrio cholerae* infection.

The epidemic strain responsible for the outbreak was identified as *V cholerae* O1 biotype El Tor, resistant to co-trimoxazole (trimethoprimsulfamethoxazole), furazolidone, sulfafurazole, streptomycin, and nalidixic acid.²

We analysed the genome of three clonal isolates sequenced recently by the US Centers for Disease Control and Prevention (AELH0000000, AELI00000000, and AELJ00000000). The Haitian strains contain an integrative conjugative element (ICE) of the SXT/R391 family, a major drugresistance-spreading vector in bacteria, which is 99% identical to ICEVchInd5. This ICE, which confers resistance to co-trimoxazole, sulfafurazole, and streptomycin, was originally identified in strains of V cholerae isolated in India, which are also resistant to nalidixic acid, and clonally belong to the most prevalent epidemic clade in the Indian subcontinent, represented by the reference strain CIRS101.3

The Haitian clone carries a genotype 7 *ctxB* gene coding for the cholera toxin subunit B.⁴ This genotype was described only in an altered El Tor *V cholerae* variant isolated during the harsh cholera epidemic in Orissa, India, in 2007.⁵

Whole-genome alignment and comparative genomic analysis of the Haitian strains, with the representative *V* cholerae O1 variants from Central America and Indian subcontinent,

confirmed that the Haitian strain is strictly phylogenetically related to CIRS101 from India. This strain is one of the highly virulent Indian V *cholerae* O1⁶ that are gradually spreading all over the world; it is not surprising that this strain easily took advantage of the susceptibility of the Haitian people to the disease, and the poor sanitation caused by the earthquake in Haiti.

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Incidence of HIV among men who have sex with men in France

We thank Stéphane Le Vu and colleagues¹ for presenting surveillance findings and insightful analyses of data for HIV-1 incidence in France. Incidence is the most important epidemiological measure of the

extent of spread of infection in a population, but it is very difficult and costly to calculate. The approach used by Le Vu and colleagues adds substantial value for accurately understanding epidemic trajectories. Importantly, they show a persistent and high incidence of HIV among men who have sex with men (MSM) in France, a situation they describe as "out of control", whereas HIV incidence has declined in all other major population groups. They also note that this high HIV incidence among MSM is occurring against a background of substantial uptake of highly active antiretroviral therapy (HAART), with which 92% of treated patients achieving a plasma viral load of fewer than 500 copies/mL. Our study in Sydney suggests that the infectiousness of HIV among MSM with HIV has not decreased from levels that existed before HAART.² Data from a study in Amsterdam also suggest that HIV incidence has remained relatively high among MSM despite the widespread availability of HAART.³

The treatment as prevention strategy aims to reduce community viral load and assumes that this will reduce HIV transmission at the population level. Ecological studies and limited retrospective analyses suggest that treatment might have a preventative role for heterosexuals and people who inject drugs;4 however, it might be too optimistic to assume that this strategy can be effectively applied to MSM because of higher biological transmission rates and the sexual milieu of MSM. As explained by Le Vu and colleagues, such a milieu includes a high HIV prevalence, together with increased rates of unprotected anal sex with more partners and increased prevalence of sexually transmitted infections. Thus, merely intensifying a treatment as a prevention strategy for MSM without addressing other co-existing issues at the individual or community level is not going to lead to sustained changes to HIV epidemics.

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For a **list of all strains of** V cholerae see http://www.ncbi.

nlm.nih.gov/genomes/lproks.cgi