

Reply to Pape *et al.*: The phylogeography of HIV-1 group M subtype B

In reply to the letter from Pape *et al.*, our goal was to trace the pathway of a pandemic with the most powerful methods currently available, not to assign blame in any way. Haiti deserves only compassion for its longstanding HIV epidemic and admiration for its successes in battling HIV/AIDS.

Our conclusions were not based only on five archival sequences from Haitian-American patients as Pape *et al.* claim. An additional 117 sequences from 19 countries, including Haiti, were an integral part of the analyses (1). All of the Haitian and Haiti-linked strains occupied the earliest-branching positions within subtype B. There would be virtually no chance of observing this pattern if the Haitian epidemic had emerged from the United States (1).

Twenty of the first 23 AIDS patients diagnosed at Miami's Jackson Memorial Hospital were Haitian Americans, even though the vast majority of admitted patients during the same time were non-Haitian (2). Nine of these Haitian patients entered the United States <1 year prior to diagnosis. Aside from the 1975 patient, the entry-to-diagnosis interval in the prospective cohort we sampled (1) ranged from <1 year to 3 years (2). More importantly, if these patients had acquired HIV in the United States, their sequences would cluster with non-Haitian U.S. strains. Instead, they grouped unequivocally with the Haitian strains—emphatic evidence of their source (1).

We were aware of the observations about AIDS epidemiology mentioned by Pape *et al.* (3), but we disagree that they indicate that HIV was initially introduced to Haiti via sex tourism involving men who have sex with men (MSM). First, neither the source nor the dynamics of HIV can be reliably inferred from the dynamics of early AIDS cases because of the long and variable lag time between infection and symptoms: AIDS cases can be expected to appear earliest in groups engaging in high-risk behavior (because of greater opportunities for virus spread) even if the virus first entered lower-risk behavior groups in which it spreads less rapidly (1). Furthermore, other factors likely contributed to the early predominance of male/urban AIDS cases. Female prostitution can lead to the same male/urban bias as seen with spread among MSM, because the ratio of male clients to female prostitutes is typically high. Female prostitutes had the highest reported HIV prevalence (53%) of any Haitian group in the 1980s (4). In any case, the sexual practices of the index case of the Haitian HIV epidemic cannot be ascertained from epidemiological observations of later cases.

The median time to death from AIDS (untreated) in Haiti has been estimated at 7.4 years (5). Reviewed autopsies identified AIDS-defining illness by 1978 (6), 8 years after the pe-

riod to which we dated the ancestor of the Haitian epidemic (1962–1970). However, these reviews overlooked tuberculosis, now known to be the earliest and most common presentation of symptomatic HIV disease in Haiti (5). Only comparatively rare and later-onset HIV-related illnesses were considered (6). Tuberculosis was certainly a feature of pre-1978 Haiti, and the findings of Pape *et al.* (5) imply that some pre-1978 cases were HIV-related. The arrival of HIV undoubtedly preceded the recognition of AIDS in Haiti by several years, just as it did in the United States, Africa, and elsewhere (1, 7).

Regarding retrospective HIV testing, the only 1970s Haitian blood samples tested were from 1977–1979 (4), a period when HIV/AIDS was already present in Haiti (6). (With the small sample size, even if 1,000 Haitians were seropositive by that point, there would have been a >95% chance of missing the virus.) Furthermore, commercial exportation of blood products from Haiti to the United States had evidently ceased by 1975 (8). Our findings suggest that HIV would have been present but exceedingly rare in Haiti before this point. Nevertheless, blood product export does represent another plausible route, in addition to American visitors returning from Haiti, for the entry of the virus that emerged in the United States in the late 1960s or early 1970s (1).

Understanding the emergence of the HIV/AIDS pandemic and its resulting genetic diversity is important, and disregarding the current data hinders our ability to address the HIV burden.

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