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Can we broaden the applicability of HIV transmission cluster analyses?

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Recently reported work by Oster *et al*. [1] demonstrates the power of using HIV surveillance data to gain insight into community-specific HIV transmission dynamics that can then be used to tailor HIV prevention initiatives. In their work, they used HIV *pol* sequences obtained from a Center for Disease Control's (CDC) project surveying for transmitted drug resistance to compare characteristics of HIV transmission clusters occurring among those newly diagnosed with HIV in Mississippi between January 2005 and April 2008. By comparing HIV *pol* sequences, with transmission clusters composed of patients whose sequences diverged by less than 1%, they ascertained that clusters inclusive of young (<25 years old), black MSM demonstrated little heterogeneity with respect to race/ethnicity, sex, and transmission category compared with clusters inclusive of older (>25 years) black MSM. Despite the demographic homogeneity of clusters with young, black MSM, these clusters did show striking geographic diversity, with nearly half of these clusters containing residents of two or more of the state's five geographic regions. These data show that transmission cluster analyses done with available HIV surveillance data can enhance community-specific tailoring of HIV prevention efforts.

Although transmission cluster analyses had more often been used to investigate specific, more contained HIV outbreaks, other groups have also performed transmission cluster analyses using drug resistance surveillance [2–4]. For instance, researchers used Canadian HIV Strain and Drug Resistance Program data to perform a longitudinal analysis of transmission clusters in British Columbia, Canada and observed that clusters enriched with recently infected patients showed the most growth in cluster size over time [3]. Other groups have used research cohort data, or combined cohort data with public health surveillance, to perform similar analyses [5,6].

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Conflicts of interest

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Given the potential knowledge on region and community-specific HIV transmission dynamics provided by such analyses, and given the wide availability of HIV genotype data – a clinically indicated diagnostic test performed on nearly all newly diagnosed HIV patients – we are disconcerted that efforts such as these have been mostly restricted to use of data from research cohorts or limited public health surveillance projects.

At John H. Stroger Jr Hospital (JSH) of Cook County, Chicago's primary safety-net provider of medical care, between June and September of 2010, we conducted a pilot program that attempted to integrate both diagnosis of acute HIV as well as the identification of HIV transmission clusters, with our routine HIV testing program in our emergency department (ED), which sees over 80 000 unique patients annually, and in our sexually transmitted diseases (STD) clinic. We performed baseline HIV genotyping, as per standard clinical practice, for all newly diagnosed patients. To assess for transmission clustering, we compared HIV *pol* sequences from each newly diagnosed patient via progressive pairwise alignment for multiple sequences. We used the neighbor-joining method to estimate genetic distance (Geneious version 5.3.3, Biomatter, Auckland, New Zealand). We considered sequence divergence of less than 1% as evidence of membership in a transmission pair/cluster.

During the 3-month pilot program, we tested 3879 (2446 ED and 1433 STD clinic) patients, newly diagnosing HIV in 28 (72% black, 17% Hispanic, 11% white), while also identifying one additional patient with acute HIV via pooled nucleic acid testing. We obtained baseline genotypes on all 25 of 29 (86%) patients successfully linked to outpatient HIV care. We identified one transmission pair, whose sequences had 99% homology and a genetic distance of 0.008 nucleotide substitutions per site (group's mean interpatient genetic distance=0.06).

Although we identified only one transmission cluster in the 3 months of testing, we demonstrated that assessments for transmission clustering can be integrated with a routine HIV testing program. By including data from more clinical sites, or from community-based organizations that serve higher risk patient populations, the utility of such analysis could be significantly increased.

Transmission cluster analyses with relevance to prevention efforts, such as the one done in Mississippi by Oster *et al*. [1], have been largely limited to areas engaged in specialized public health surveillance (i.e. transmitted drug resistance surveillance) or longitudinal research cohorts. Adding baseline HIV genotype to the battery of data routinely collected by public health entities could significantly expand the power, and widen the applicability of such transmission cluster analyses, thereby advancing efforts to tailor demographic and region-specific prevention initiatives.

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