



Using Genomics to Generate New Hypotheses

Across the field, entities like CHAVI, Bruce Walker's group at the Ragon Institute, the French research agency ANRS, and others are using genome-wide association studies to look for regions of the human genome associated with viral control or disease progression. Participants at a January NIH-convened meeting on genomics and HIV underscored that these genes, while important, might be different from those associated with protection. One innovative approach to identifying protective alleles: a proposed CHAVI study of HIV-positive and HIV-negative hemophiliacs known to have been exposed before stringent blood bank controls were introduced.

At the NIH genomics consultation, there was great interest in whether ongoing HIV prevention research trials, such as PrEP studies—which will enroll over 17,000 individuals by mid-2009 (see article, page 46)—could aid this effort by contributing samples and helping to identify individuals in the earliest days of infection. “We are especially concerned that observational or prevention studies already underway be examined for their utility in informing genetic associations with transmission mechanisms,” noted the meeting working group, on the host immune response and susceptibility to HIV chaired by Myron Cohen of the University of North Carolina.

What information can we glean from current studies, and what are the barriers? This is an area where immediate action could clarify opportunities swiftly and relatively easily. In some ongoing studies, participants give permission for samples to be used for genetic analyses; in others, no explicit permission is given. Different studies have different schedules for HIV testing and/or viral load monitoring in individuals who become infected. The field needs to review procedures in different trials and look across biomedical prevention research to determine what's possible to standardize in sample collection.

There's also a need to explore novel designs for studies in humans, where the timing of sampling is more frequent. The US Military HIV Research Program (MHRP) is working on a protocol in this regard that involves biweekly blood draws for rapid turnaround HIV nucleic acid testing to identify acute infections and to compare the host genetics of those who are at risk of infection and become infected versus those at risk who do not become infected.