

Importance of neutralization sieve analyses when seeking correlates of HIV-1 vaccine efficacy

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This commentary describes a rationale for the use of breakthrough viruses from clinical trial participants to assess neutralizing antibodies as a correlate of HIV-1 vaccine efficacy. The rationale is based on principles of a genetic sieve analysis, where the 2 analyses may be cooperative for delineating neutralizing antibodies as a mechanistic correlate of protection.

The identification of immunologic correlates of protection¹⁻³ against HIV-1 is a major goal that would greatly facilitate HIV-1 vaccine development. This information would provide a basis for rational immunogen design and could be used to guide the selection of promising immunogens to advance through preclinical and clinical testing. It also has value for qualifying the expected potency of different lots of vaccine preparations and for predicting vaccine efficacy in populations where phase 3 trials did not take place. Multiple cellular and humoral immune responses are seen in infected individuals, and these responses provide a template for what should be possible to elicit with vaccines that aim to either control virus replication or prevent infection altogether.^{4,5} Preventing virus acquisition is a high priority for a virus like HIV-1 that integrates genetically and persists despite robust host immune responses. In this regard, neutralizing antibodies (nAbs) are among the most promising responses to induce with HIV-1 vaccines because of their well-documented ability to block infection in nonhuman primate passive protection studies with simian immunodeficiency virus (SIV) and chimeric

simian-human immunodeficiency virus (SHIV).⁶⁻¹² As suggested by results of the RV144 HIV-1 vaccine efficacy trial and subsequent correlates studies,¹³⁻¹⁶ Fc receptor-mediated effector functions might be another mechanism by which antibodies can prevent HIV-1 infection.¹⁷⁻¹⁹ Indeed, these findings from RV144 emphasize the need to consider multiple antiviral mechanisms when delineating antibody correlates of protection in HIV-1 vaccine efficacy trials.

The overall effectiveness of vaccine-elicited nAbs will depend on the magnitude and breadth of neutralization across a wide spectrum of antigenic variants within and between the major genetic subtypes (clades) and circulating recombinant forms (CRFs) of HIV-1 that dominate the epidemic in geographic regions where a vaccine is most needed.^{20,21} Current vaccine immunogens induce very little nAb against most of these variants.²²⁻²⁶ Nonetheless, studies of HIV-1 infected individuals show that most people are capable of making Abs that neutralize diverse variants across multiple clades.^{27,28} Studies of monoclonal Abs from some of the best neutralizers have identified several highly conserved regions of vulnerability on the viral envelope glycoproteins (Env), and are providing a wealth of new information on the biological requirements for inducing broadly nAbs with vaccines, leading to promising new avenues for improved immunogen designs.²⁷⁻³² To gauge progress with new immunogens, several highly standardized and formally validated assays are available for rapid, high-throughput assessments of the magnitude and breadth of neutralization

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in preclinical and clinical HIV-1 vaccine trials.³³⁻³⁶ Considerable infrastructure exists to perform these assessments in laboratories that comply with Good Clinical Laboratory Practices (GCLP), which is important for regulatory agency approval.^{37,38} Current capacity includes laboratories that serve the Collaboration for HIV Vaccine Discovery (CAVD, Bill and Melinda Gates Foundation), the International AIDS Vaccine Initiative (IAVI) and major networks sponsored by the US National Institutes of Health, including the HIV Vaccine Trials Network (HVTN), the Center for HIV/AIDS Vaccine Immunology and Immunogen Discovery (CHAVI-ID), and the Simian Vaccine Evaluation Units (SVEUs).

These laboratory efforts are further strengthened by the availability of well-characterized HIV-1 reference strains that allow standardized neutralization data sets to be compared across vaccine protocols.^{36,39-41} Notably, the initial panels of reference strains left open key questions about the number and overall composition of strains that will be needed to adequately assess vaccine-elicited responses. Some of these questions are addressed in the design of a recently-described global panel of reference viruses that aims to be applicable to multiple vaccine platforms and clades of HIV-1 in different parts of the world.⁴² These reference strains are useful for comparing nAb responses among different vaccine immunogens⁴³; however, their suitability for delineating nAbs as a correlate of vaccine efficacy remains to be proven. One unanswered question is whether these reference strains, which were selected based on their neutralization profiles with plasma samples from chronic HIV-1 infection, adequately represent the spectrum of epitope variants that need to be targeted by vaccines. This concern is compounded by the inherent limitations of typical case-control analyses that rely on response variability in vaccine recipients,⁴⁴ not taking into account differences between vaccine and placebo groups, and where the number of infection cases can be relatively low, especially for more effective vaccines. Thus, the standard practice of assaying the vaccine strain(s) and a small number of heterologous reference strains using case-control serum/plasma samples

from vaccine recipients, as was done for RV144,¹⁴ may lack power to detect nAbs as a correlate. Moreover, case-control studies do not distinguish between a measured immune response that is mechanistically responsible for protection vs. a response that is predictive but not a component of the protective mechanism.³

To increase the power for detecting nAbs as a correlate of vaccine efficacy, breakthrough viruses from infected vaccine and placebo recipients may be used to seek evidence that the vaccine-elicited nAbs selectively blocked transmission of certain variants. This approach is analogous to a genetic sieve analysis, which looks for features in the sequences of viruses from infected vaccine and placebo recipients that significantly differ relative to the vaccine sequences as evidence of a vaccine effect against certain variants.^{45,46} Likewise, a neutralization “sieve” analysis compares the phenotypic properties of viruses from infected vaccine and placebo recipients in terms of their sensitivity to neutralization by pre-infection plasma/serum samples from vaccine recipients at a peak immunogenicity time point.²⁵ A positive correlation would be indicated if viruses from vaccine recipients are found to be significantly less sensitive to neutralization than viruses from placebo recipients. This outcome would be evidence that the vaccine-elicited nAbs selectively blocked transmission of the more sensitive viruses, implying a direct causal effect in mediating protection. Corroborating evidence would come from a genetic sieve analysis that successfully identifies genetic signatures that correlate with vaccine efficacy and can be shown to be responsible for the neutralization phenotype, as was done in a recent study of vaccine-mediated protection against simian immunodeficiency virus infection in nonhuman primates.⁴⁷

This approach, though simple in principle, is not without challenges. Additional resources would be needed to generate high fidelity molecular clones of functional Env genes from the plasma of infected trial participants to create the virus reagents needed for current assay technologies.⁴⁸ In addition, viral diversification during early infection has the potential to compromise the quality of

the analysis if the diversification affects vaccine-targeted epitopes prior to sampling. HIV-1 accumulates fixed amino acid changes as the host immune response matures and drives multiple rounds of virus escape from cytotoxic T lymphocyte (CTL) and nAb responses.^{49,50} Although this immune pressure starts early in infection, the initial autologous nAb response is delayed and has a very narrow epitope specificity in any single individual,^{49,51} possibly explaining why little diversification with potential to affect most antibody epitopes is seen in Env during the first 3–6 mo of infection.⁵² Notably, a 6-mo sampling interval did not prevent the identification of a statistically significant genetic sieve effect in RV144.⁴⁵ A 6-mo sampling interval also did not prevent the identification of a significant genetic sieve effect in the STEP trial of a HIV-1 Gag, Pol, Nef vaccine that aimed to elicit protective CTL,⁴⁶ a finding that was possible under this condition even though the vaccine showed no clinical evidence of efficacy.⁵³ Although it remains possible that additional and stronger genetic sieve effects would have been detected if samples were obtained more frequently to capture the virus at earlier stages of infection, a sampling interval of no longer than 6 mo seems useful and has proven practical for an acceptable rate of compliance in large clinical trials.

Trial participants who acquire multiple variants at the time of transmission are another possible confounding factor for the neutralization sieve analysis. Current estimates of the rates of multiple variant transmissions are 19% for heterosexually acquired infections,⁵⁴⁻⁵⁶ 36% for men who have sex with men,⁵⁶ and 42% for intravenous drug users (Katie Bar and George Shaw, personal communication). Extra care may be needed to identify these subjects and to include their multiple virus variants in the analysis.

Despite several challenges, neutralization sieve analyses with breakthrough viruses from vaccine and placebo recipients afford important advantages that merit serious consideration for highly variable viruses such as HIV-1. This is likely to be a more powerful method to detect nAb as a correlate of HIV-1 vaccine efficacy than methods that use the

vaccine strain(s) and heterologous reference strains. Moreover, phenotypic sieve analyses provide insights into whether the correlate is mechanistically responsible for protection.³ A neutralization sieve analysis was performed for the Vax004 HIV-1 vaccine efficacy trial of a bivalent gp120 immunogen, in which a non-significant trend was seen toward a lower rate of infection in higher risk vaccine recipients,⁵⁷ and where several antibody measurements have suggested a weak vaccine effect on HIV-1 acquisition.^{58,59} In that sieve analysis, pre-infection plasma samples obtained at a peak immunogenicity time point from 85 vaccine recipients were assayed against 13 breakthrough viruses from vaccine recipients and 14 breakthrough viruses from placebo recipients.²⁵ The results showed that the vaccine-elicited antibodies in Vax004 were more likely to neutralize viruses from placebo recipients than viruses from vaccine recipients ($P = 0.004$), suggesting the vaccine selectively blocked transmission of certain variants. A similar neutralization sieve analysis would be worthwhile for the RV144 trial, where modest but statistically significant protection was seen against HIV-1 acquisition,¹³ and where plasmas from the primary immunogenicity time point exhibit neutralizing activity against many heterologous circulating strains of HIV-1 in an ultrasensitive assay²⁶ (additional unpublished observations).

Breakthrough viruses could be used in a similar fashion to assess other potential antiviral Ab activities as correlates of vaccine efficacy, including Fc receptor-mediated and complement-mediated effector functions. Moreover, in the event that initial case-control analyses identify multiple correlates of protection, follow-up studies with breakthrough viruses could be used to determine which correlate is most likely to be mechanistically responsible for protection and therefore more important for vaccine design, testing, regulatory approval, and quality assurance. Overall it would seem prudent to plan for these types of analysis in future efficacy trials of candidate HIV-1 vaccines.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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