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Breakthrough of SIV strain smE660 challenge in SIV strain mac239-vaccinated rhesus macaques despite potent autologous neutralizing antibody responses


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Although the correlates of immunological protection from human immunodeficiency virus or simian immunodeficiency virus infection remain incompletely understood, it is generally believed that medium to high titers of serum neutralizing antibodies (nAbs) against the challenge virus will prevent infection. This paradigm is based on a series of studies in which passive transfer of HIV-specific nAbs protected rhesus macaques (RMs) from subsequent mucosal challenge with a chimeric human/simian immunodeficiency virus. However, it is unknown whether nAb titers define protection in the setting of active immunization. Here we determined serum nAb titers against breakthrough transmitted/founder (T/F) SIVsmE660-derived envelope glycoprotein (Env) variants from 14 RMs immunized with SIVmac239-based DNA-prime/modified vaccinia virus Ankara-boost vaccine regimens that included GM-CSF or CD40L adjuvants and conferred significant but incomplete protection against repeated low-dose intrarectal challenge. A single Env variant established infection in all RMs except one, with no identifiable genetic signature associated with vaccination breakthrough compared with T/F Env from four unvaccinated monkeys. Breakthrough T/F Env pseudoviruses were potently neutralized in vitro by heterologous pooled serum from chronically SIVsmE660-infected monkeys at IC50 titers exceeding 1,000,000. Remarkably, the T/F Env pseudoviruses from 13 of 14 monkeys were also susceptible to neutralization by autologous prechallenge serum at in vitro IC50 titers ranging from 1:742 to 1:10,832. These titers were similar to those observed in vaccinated RMs that remained uninfected. These data suggest that the relationship between serum nAb titers and protection from mucosal SIV challenge in the setting of active immunization is more complex than previously recognized, warranting further studies into the balance between immune activation, target cell availability, and protective antibody responses.

Significance

It is widely believed that if an HIV vaccine elicits moderate in vitro titers of serum neutralizing antibodies (nAbs) against a challenge virus, it will prevent infection. This paradigm is based on studies in which passive transfer of HIV-specific nAbs protected rhesus macaques from mucosal challenge with a chimeric simian/human immunodeficiency virus. However, it is unknown whether this direct relationship can be extrapolated to protection in the setting of active immunization. Our data suggest that the relationship between serum in vitro nAb titers and protection from mucosal SIV challenge is more complex than previously recognized in the setting of active immunization, warranting further studies to understand the balance between immune activation, target cell availability, and protective antibody responses.

Data deposition: The sequences reported in this paper have been deposited in the GenBank database (accession nos. FJ579014-FJ579055 and KP734847-KP735110).

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Conflict of interest statement: R.R.A. and H.L.R. are coinventors of DNA/MVA vaccine technology that has been licensed to GeoVax.

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and MVA vectors, respectively, elicits a different type of antibody than gp160 alone. In outcomes like these, where protection is incomplete, the characterization of breakthrough variants can inform us about correlates of vaccine-mediated protection against acquisition (18, 22, 23). Here, we went one step further by testing the capacity of prechallenge antibodies to neutralize the exact Env variant that broke through to establish each infection. To our knowledge, this study is the first to demonstrate that vaccine-elicted serum antibodies capable of neutralizing the autologous breakthrough Env variant were present before challenge at moderate to high titers but nevertheless failed to protect against SIV infection.

**Results**

**A Single Variant from the SIVsmE660 Challenge Stock Established All But One Infection.** We recently reported that four different SIVmac239-based DNA/MVA or MVA-only vaccination modalities were significantly but incompletely protective against repeated low-dose intrarectal challenge with heterologous viral strain SIVsmE660 in RMs (19–21). These vaccination studies, M11 and M12, were purposely designed for cross-comparison of SIVmac239-based DNA/MVA immunizations. These trials contained three groups that received two DNA primes (with no adjuvant, GM-CSF, or CD40L) at weeks 0 and 8, followed by two MVA boosts at weeks 16 and 24 (Fig. 1A). A fourth group received MMM immunizations at weeks 0, 8, and 24 without DNA priming (Fig. 1A). Intrarectal SIVsmE660 challenge with a stock designated VH2000 was initiated 20–24 wk after the last MVA immunization in all groups and continued weekly for a maximum of 12 inoculations. In the present study, transmitted/founder (T/F) Env sequences from breakthrough infections that occurred in the DDMM (n = 8), MMM (n = 8), DgDgMM (n = 2), and D40L-D40L/MM (n = 4) vaccine groups were analyzed, as well as T/F Env from four unvaccinated control animals that became infected (Fig. 1A). These monkeys were selected based on availability of an acute infection/peak viral load plasma sample with a sufficient volume for PCR amplification and cloning and a week 37 postimmunization serum sample with a sufficient volume for neutralization assays. The monkeys were also representative of infection at various points during the challenge phase (Fig. 1B).

Between 10 and 32 single genome amplification (SGA) env gene sequences (which encode the Env glycoproteins) from each infected animal and 39 SGA env gene sequences from the VH2000 challenge stock were included in a genetic analysis. The VH2000 env gene sequences exhibited a maximum pairwise distance of 2% (Fig. S1), which is lower in diversity than what is generally present in an HIV-1-infected transmitting partner (24–26). Fig. 2 displays a Neighbor-joining phylogenetic tree containing 245 complete env gene nucleotide sequences obtained from the 14 vaccinated and 4 control monkeys, along with the 39 challenge stock sequences. Sequences from the vaccinated and control groups were dispersed and intermingled with variants from the challenge stock. There was no a priori evidence that vaccination had selected for transmission of a particular set of variants from within the challenge stock. The env gene sequences from each animal clustered together on the tree in all but one case (monkey RJn11), but these clusters were not supported by high bootstrap values. Further analyses revealed that the maximum pairwise distance of intra-animal env gene sequences ranged from 0 to 1.3% (Figs. S1–S5). These data therefore demonstrate that a single variant most likely established infection in 13 of the 14 monkeys, whereas RJn11 could have been initially infected by more than one variant. These data therefore suggest that the challenge virus, dose, and route of infection used in this experiment recapitulate the events occurring during transmission of HIV-1 in humans in terms of presence of a single
T/F virus variant in the vast majority of individuals (24–26). In each case of breakthrough, an env gene amplicon representative of the T/F sequence, or the predominant env gene sequence in the case of RJn11, was cloned to assess neutralization sensitivity.

**T/F Envs from Breakthrough Infections Are Sensitive to Neutralization.**

As a first step in the phenotypic characterization of the T/F Envs, we assessed their general neutralization sensitivity to pooled sera collected from nine unvaccinated RMs at 24 wk after they became infected intrarectally with the VH2000 SIVsmE660 stock. Fig. 3A demonstrates that the breakthrough T/F Env variants on the whole were highly susceptible to neutralization by antibodies in pooled serum. The majority of the T/F Envs from vaccinated animals were neutralized at an IC50 titer of more than 1:1,000,000 by the serum antibody pool, typical of the extreme neutralization sensitivity of tier 1 SIVsmE660 variants such as E660.11 (27, 28). In contrast, the T/F Envs from the control infections were less susceptible to neutralization (Fig. 3A). These data clearly demonstrate that the vaccinated breakthrough T/F Envs were not inherently neutralization resistant. We next examined whether prechallenge serum from each vaccinated animal could neutralize the autologous breakthrough T/F Env. This was accomplished by using serum samples collected 13 wk after the final MVA boost (and 11 wk before SIVsmE660 challenge) from the breakthrough infection animals, representing the midpoint between the peak binding antibody response (week 2 post-MVA) and time of challenge (week 20–24 post-MVA) (Fig. 1A).

Fig. 3B demonstrates that the vaccinated breakthrough T/F Envs were susceptible to neutralization by the autologous prechallenge serum, but at IC50 titers that were several logs lower than those observed with the chronic infection pool (Fig. 3A). Individually, the IC50 of the breakthrough T/F Envs ranged from undetectable in one case (FP36) to 1:10,832 for RLi10. Although the median autologous nAb IC50 titer was 1:3,351, there were five immunized monkeys that became infected with prechallenge IC50 titers exceeding 1:3,000. Most of the breakthrough T/F Envs were completely or nearly completely neutralized at a 1:100 dilution of serum; however, some variants did retain residual infectivity at this dilution. The prechallenge serum from vaccinated breakthrough animals neutralized the sensitive reference Env SIVsmE660.11 to varying degrees, whereas neutralizing activity against the resistant reference Env SIVsmE660.300–16 was uniformly low (Fig. 3B) (27). These data collectively demonstrate that all but one vaccinated animal produced prechallenge serum antibodies capable of neutralizing the autologous breakthrough T/F Env, yet this did not protect against infection.

We next investigated whether vaccinated animals that were protected against SIVsmE660 challenge had superior neutralizing capacity compared with the breakthrough animals from the same vaccine group (Table S1). Prechallenge serum samples from vaccinated protected animals were tested against each breakthrough T/F Env from the same group. Neutralization potency of the protected animal serum was comparable to the autologous serum (Fig. S6), and the median IC50 titers (1:1,042 and 1:1,351, respectively) were not significantly different when analyzed by a Mann–Whitney or a paired Wilcoxon rank sum test. This result suggests that protected animals did not have substantially more potent neutralizing activity against the breakthrough T/F Env variants. This result is consistent with our previous finding that neutralizing activity against heterologous SIV Envs did not differ between infected and protected animals in the M11 and M12 trials (28). We also found no correlation between the nAb IC50 titer of the vaccinated breakthrough animals and the peak viral load or the number of SIVsmE660 challenges required for infection (Fig. S7 A and B, respectively). Thus, there was no evidence that SIV acquisition was directly linked to the individual potency of prechallenge nAb activity.

**Discussion**

Identifying the immune correlates of protection against HIV/SIV continues to be a central pursuit for the vaccine research community. Studies in nonhuman primates have shown that a strong nAb response is correlated with protection against SIV/SIV infection. These studies have also demonstrated that protective immunity can be conferred by antibodies that are broadly neutralizing (29, 30). Determining the mechanisms by which these antibodies are produced and how they contribute to protection against SIV/SIV infection will be critical for the development of effective vaccines. Understanding the immune correlates of protection against SIV/SIV infection is also important for the development of vaccines against HIV. The results presented here provide insights into the immune responses that are necessary for protection against SIV/SIV infection and how these responses can be used to design effective vaccines against HIV/SIV.
community (29–31). Multiple vaccine studies in NHPs and humans have implied that functional antibody responses against Env are necessary for protective immunity (3, 18, 32). Furthermore, passive administration of nmAbs to RMs has unambiguously been shown to provide protection against mucosal SHIV infection (5–13), with in vitro serum nAb IC_{50} titers in the range of ∼1:2,000 emerging as predictive of protection (7, 12, 14). However, it was not known whether these low to moderate nAb titers would extend to vaccine-elicited antibody protection, as previous studies have reported a disconnect between in vitro nAb and a protective effect (33–35). Here, we directly demonstrate that prechallenge serum nAb titers against the autologous breakthrough T/F Env variants were not predictive of protection. Remarkably, these breakthrough variants were surprisingly sensitive to autologous neutralization, with in vitro nAb titers frequently exceeding 1:1,000, and were similarly sensitive to neutralization by prechallenge serum from vaccinated protected animals.

These results highlight an important and well-recognized difference between passively transferred and vaccine-elicited antibody protection; the latter occurs in the presence of ongoing host immune responses. Thus, it is important to consider that vaccination itself may alter the mucosal environment such that transmission is favored over protection (31, 36, 37). This could result from the generation and homing of vaccine-elicited CD4+ T cells to the portal of entry, which in turn mitigates the beneficial effects of the vaccine-elicited humoral immune response (38–40). Indeed, the efficiency of horizontal and vertical SIV transmission in NHP hosts in the absence of vaccination is linked to the availability of susceptible target cells in the mucosa (41–43). Furthermore, there is strong evidence that genital inflammation reduces the stringency of HIV-1 transmission (25, 44, 45) and increased target cell availability increases the risk of HIV-1 superinfection (46).

Additional caveats may also contribute to the marked discrepancy between in vitro neutralization and in vivo protection that we observed here. It is possible that vaccine-elicited antibodies capable of potent neutralization in the TZM-bl assay lack certain biological properties that are essential for preventing acquisition in vivo (14, 47). Cell-to-cell transmission could play a more prominent role in intrarectal SIV infection than is currently recognized (48–51), and higher concentrations of antibodies with certain specificities could then be necessary to prevent establishment of infection (52, 53). It is similarly possible that the atypically high neutralization sensitivity of SIVsmE660 Env variants involves antibody specificities that are greatly enhanced in the TZM-bl assay and have limited relevance to those that neutralize HIV-1 (27). Finally, we were not able to directly assess the neutralizing activity in rectal secretions or in serum on the day of challenge. However, Env-specific serum IgG titers induced by DNA/MVA immunization were stable in RMs and humans during a similar time frame as was analyzed in refs. 54 and 55. Despite these caveats, our results collectively demonstrate that the DNA/MVA vaccination regimens administered in the M11
and M12 trials consistently elicited prechallenge antibodies that potently neutralized the autologous breakthrough T/F variants in vitro, but these antibodies were not protective in vivo. The lack of overt selection for more neutralization-resistant breakthrough variants supports the concept that the serum in vitro nAb titer was not the defining feature of vaccine-mediated protection. The findings are consistent with the idea that desirable vaccine-elicited immune responses such as nAbS can be negated by a concurrent increase in the availability and/or susceptibility of CD4+ T cells and suggest that the interplay between the two parameters needs to be better elucidated. These data further suggest that the relationship between serum nAb titers and protection from mucosal SIV challenge in the setting of active immunization is more complex than previously recognized and that additional studies of this interaction are warranted to better inform the design and evaluation of Env-based vaccinations.

**Materials and Methods**

**Ethics Statement.** The Emory University Institutional Animal Care and Use Committee (AWA-A3180-01) approved these studies of NHPs under protocols 215–2007Y and 139–2008Y. This study was conducted in strict accordance with US Department of Agriculture regulations and the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. SIV-infected Indian RMs (Macaca mulatta) were housed in standard NHP primate cages and received standard primate feed, as well as fresh fruit and enrichment daily, and had continuous access to water. Animals have continuous access to water. Animals were administered fresh fruit and enrichment daily, and had continuous access to water. Animals were monitored daily. Appropriate procedures were performed to ensure that potential distress, pain, or discomfort was alleviated. The sedatives Ketamine (10 mg/kg) and Telazol (4 mg/kg) were used for blood draws. Euthanasia using Pentobarbital (100 mg/kg) under anesthesia was performed only when deemed clinically necessary by veterinary medical staff and according to Institutional Animal Care and Use Committee endpoint guidelines.

**SGA and Sequencing of SIVsmE660 env Genes.** Plasma collected at 7 or 14 d after infection was used for 96-well SGA of SIVsmE660 env genes. Plasma viral loads in these samples ranged from 6.74 × 10^4 to 3.62 × 10^6 copies per mL. Viral RNA was extracted from plasma using the QIAamp viral RNA kit according to the manufacturer’s instructions (Qiangen). Reverse transcription of viral RNA into cDNA was performed using the SuperScript III kit and the following primers: forward SM-ER1, CTATCACTGTAATAAATCCCTTCCAGTCCC, and reverse primer SM-ER1, CTATCACTGTAATAAATCCCTTCCAGTCCC, following the manufacturer’s instructions (Invitrogen). For SGA, the dilution of a cDNA template that resulted in one-fourth to one-third of the PCR reactions being positive was used, as described previously in refs. 25, S. The first round of PCR was performed in a 15 μL volume using the Phusion Hotstart II High Fidelity DNA Polymerase (Thermo Scientific) and the following primers: forward SIVsmEnvF1, CCTCCCCCTCCAGGACTAGC, and reverse SIVsmEnvR1, TGTAAATAATCCCTTCAGTCCCCC. The cycling conditions were 98 °C for 2 min; 10 cycles of 98 °C for 10 s, 55 °C for 45 s, and 68 °C for 2 min; 25 cycles of 98 °C for 10 s, 55 °C for 45 s, and 68 °C for 2 min, adding 5 s to the extension per cycle; 72 °C for 30 s; and 4 °C hold. The second round of PCR was performed with the same enzyme in a 10 μL volume using 1 μL of the first round of PCR as a template and the following primers: forward SIVsmEnvF2, CACCTCAGTAGAGAGAGAGATGACCTCAGTCCAG, and reverse SIVsmEnvR2, ATGAGACATCTTCAGTCCAATGTA. The cycling conditions were 98 °C for 2 min; 45 cycles of 98 °C for 10 s, 55 °C for 45 s, and 68 °C for 2.5 min; 72 °C for 30 min; and 4 °C hold. PCR amplicons were purified using the Phusion Hotstart II High Fidelity DNA Polymerase (Thermo Scientific) and the following primers: forward SIVsmEnvF1, CCTCCCCCTCCAGGACTAGC, and reverse, R1, CAAAGAGACAATCCTGCGCAGCAGATATC; R2, CT- CTTCTCCGAGGCAATAATCATTTT; R3, TGGAACTCATAACATATTTTCTTTGCTG; and R4, TACCTCTCAGCAGATATCATCAGTGGT. Sequencer v5 was used to generate contigs, and sequences with evidence of mixed peaks were omitted from the analysis. Geneious v6.1.7 was used to translate nucleotide sequences, create alignments, calculate pairwise diversity, and generate a Neighbor-joining phylogenetic tree. Highlighter plots were generated to identify the consensus sequence for the T/F Env variant (www.hiv.lanl.gov/content/sequence/HIGHLIGHT/highlighter_top.html). GenBank accession numbers are as follows: FJS79014-FJS79055 for the VH2000 challenge stock sequences and KP373487-KP3735110 for the SIVsmE660 SGA and cloned env sequences.

**Neutralization Assay.** An SGA-derived env gene amplicon that was representative of the T/F consensus sequence for each monkey was purified using the Qiagen PCR Purification Kit (Qiagen) and was cloned into pCDNA3.1.dV5His TOPO-TA (Invitrogen) using approaches described previously (57–59). An env gene clone whose sequence was identical to the Env pseudoviruses used in the neutralization assay was used to generate a pseudovirus by transfecting the Env-expressing plasmid DNA alongside the HIV-1 SGΔ3Env proviral backbone, using the Fugene HD reagent as recommended (Promega). Pseudovirions were stocks of the 293T cell supernatants at 48–72 h after transfection, centrifuged at 5,000 × g for 30 min, and divided into small volumes, and frozen at −80 °C. Fivefold serial dilutions of heat-inactivated serum samples were assayed for their inhibitory potential against the Env pseudoviruses using the TZM-bl indicator cell line, with luciferase as the readout, as described previously (57, 59–63). TZM-bl cells were plated and cultured overnight in flat-bottomed 96-well plates. A pseudovi- rus (2,000 IU per well) in DMEM with −3.5% (v/vol) FBS (HyClone) and 40 μg/mL DEAE-dextran was mixed with serial dilutions of plasma or serum and subsequently added to the plated TZM-bl cells. At 48 h postinfection, the cells were lysed and luciferase activity was measured using a BioTek Synergy HT multimode microplate reader with Gen5 v.2.0 software. The average background luminescence from a series of uninfected wells was subtracted from each experimental well, and infectivity curves were generated using GraphPad Prism v6.0d, where values from experimental wells were compared against a well containing a virus without a test reagent (100% infectivity). Neutralization IC50 titer values were calculated in viremic dilutions of plasma using GraphPad Prism v6.0d. Neutralization analysis function with variable slope, log-transformed x values, and normalized y values.

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T cells in the rectum predict in-
T cells may prevent transmission of
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