

# Going above and Beyond: Using an Attenuated Herpes Viral Vaccine Vector to Elicit Protective Immune Responses Through Neutralizing and Non-neutralizing Functions of Antibodies

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## Abstract

The COVID-19 pandemic has made the development of novel vaccines a high priority for public health. While many vaccines have focused on the generation of neutralizing antibodies, we have discovered a novel herpes simplex virus (HSV) vaccine candidate, designated  $\Delta$ gD-2, that can preferentially elicit non-neutralizing antibodies that function through Fc $\gamma$  receptor (Fc $\gamma$ R) activation and thus effector function of antibodies. In particular, the  $\Delta$ gD-2 vector elicits Fc $\gamma$ RIV-activating antibodies of the IgG2c isotype, which are associated with antibody-dependent cellular cytotoxicity (ADCC). The recent paper by Kaugars et al. 2021, demonstrates that a strain of  $\Delta$ gD-2 expressing the hemagglutinin (HA) protein from influenza, designated  $\Delta$ gD-2::HA<sub>PR8</sub>, can be used as a vaccine vector to protect against both influenza and HSV. In immunized sera,  $\Delta$ gD-2::HA<sub>PR8</sub> elicits high levels of anti-HA Fc $\gamma$ RIV-activating IgG2c antibodies. Based on recent studies with the  $\Delta$ gD-2 vector and its interaction with dendritic cells, we hypothesize that the vaccine works by promoting dendritic cell survival, allowing these cells to potently activate helper T cells, and ultimately leading to the immunoglobulin class switch in B cells. In this article, we discuss lessons from analyzing the  $\Delta$ gD-2 vectors to elucidate antibody-dependent cellular killing. This work highlights the importance of combining antibody effector function and neutralization for optimal protective vaccine-induced immune responses.

**Keywords:** Cancer immunology, Clinical immunology, Immunochemistry

## Antibody Protection Through Neutralization and Effector Function

The need for effective vaccines has never been so apparent as with the recent COVID-19 pandemic. The rapid development and dissemination of the mRNA-based vaccines have been critical in preventing infection and decreasing the morbidity and mortality of severe infection [1]. Much of vaccine development throughout history has been focused

on obtaining high levels of neutralizing antibodies, which function by binding to pathogens and interfering with replication [2]. While neutralization is an important mechanism of protection against infection, neutralizing antibodies in particular drive the evolution of viral escape mutants, which ultimately reduce the effectiveness of these same antibodies [3]. However, neutralization assays are more widely used and standardized, whereas measuring other aspects of antibodies, like effector function, is more complicated but still gaining

more attention [4-9]. The mRNA vaccines for COVID-19 have been designed to direct the immune response against the spike protein, and the neutralizing titer is used as a correlate of protection [10]. Extensive research in influenza has supported that neutralization titers are also correlated with protection [11]. Neutralization in influenza can occur when the antibodies bind to the surface receptor hemagglutinin (HA) to prevent its action in mediating viral entry and/or egress [12]. The majority of these antibodies from natural infection and vaccination are directed against the head region of the HA protein, which is highly variable [13]. This variability leads to antigenic drift, or a gradual accumulation of mutations over time, and reduced protection from existing immune responses [14].

Neutralizing antibodies can also be deleterious by themselves, such as in the case of dengue virus (DENV). Initial DENV infection is rarely fatal, but subsequent infection with a different subtype can lead to dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) [15,16]. This is thought to be related to antibody-dependent enhancement (ADE) [17]. With ADE, the initial infection elicits neutralizing antibodies that are effective against that particular DENV subtype [17]. When subsequently infected with a different subtype, these antibodies partially neutralize the virus and lead to increased uptake into immune cells via opsonization [17]. This opsonization is facilitated by the interaction with an antibody-bound viral particle and receptors on the immune cell [18]. As the virus is only incompletely neutralized, the virus can then replicate within the immune cell, worsening the infection [17]. This has been a considerable barrier to the development of an effective DENV vaccine [17]. The live attenuated DENV vaccine from Sanofi Pasteur, Dengvaxia®, showed evidence of ADE in seronegative recipients, substantially limiting its use in resource-poor settings [19]. While neutralization is a widely recognized but sometimes complicated mechanism of protection, antibodies can also help direct the immune response through effector functions determined by their Fc regions.

A type of antibody effector function is antibody-dependent cellular cytotoxicity (ADCC). With ADCC, antibodies bind to antigens from pathogens expressed on the surface of infected cells. The Fc region of the antibodies then binds to the Fc receptors (FcRs) on immune cells [20]. This Fc region determines the subtype of antibodies and the FcRs that they can bind [20]. For example, the IgG2c subtype of antibodies in mice binds with high affinity to FcγRIV, which is associated with ADCC [20,21]. Of note, the IgG2c and IgG2a subtypes in mice are considered equivalent, and their presence depends on the strain of mouse [22]. Overall, the effector function depends on both the antibody subtype and type of immune cell [20].

Growing research into ideal immune responses has demonstrated that ADCC is an effective mechanism of protection against pathogens, like influenza and human

immunodeficiency virus (HIV) [23]. Repeated studies have demonstrated that ADCC-mediating antibodies may have enhanced protective benefit against influenza [11]. In investigation of the effect of the trivalent inactivated seasonal influenza vaccine on infection of mice with the 2009 H1N1 virus, it was shown that, rather than enhancing infection, non-neutralizing antibodies led to increased antigen presentation and CD8<sup>+</sup> T cell activation [24]. Ultimately, ADCC-mediating antibodies may be more effective against divergent strains of influenza, leading to a "universal" influenza vaccine [25-28]. Research into optimal antibody response in HIV infection has shown that neutralizing antibodies rapidly generate escape mutants even at low titers while ADCC-mediating non-neutralizing antibodies do not [29,30]. Not only is ADCC increasing in importance in infectious diseases, but it is also recognized as a critical mechanism of action in antibody-mediated chemotherapy. For example, the therapeutic monoclonal antibodies trastuzumab and rituximab work by binding to human epidermal growth factor receptor 2 (HER2) and CD20, respectively; inducing ADCC; and leading to the destruction of cancer cells [31,32].

One illustrative example of ideal antigen selection also comes via research into immune responses against influenza. Target selection for novel influenza vaccines is critical yet controversial. Influenza HA has long been central to influenza vaccine development. HA is immunodominant, so much of the immune response in natural infection and current influenza vaccine is directed against HA, specifically the highly variable globular head region [33,34]. Antibodies binding to HA neutralize the virus before it can infect cells and generally work if there are no changes in its structure or glycosylation patterns [33,34]. Recent work has tried optimizing the HA protein itself to be more broadly protective, including strategies to direct the antibody response against less variable regions of HA [35-40]. However, HA may not be an ideal target for ADCC. One study indicated that anti-HA neutralizing antibodies inhibited the function of ADCC-mediating antibodies [41]. Therefore, different characteristics might be used to select other target antigens. As ADCC does not rely on neutralization as a mechanism of protection, non-neutralizing targets can be selected, which expands the repertoire of possible antigens for use in vaccine development. For example, the highly conserved nucleoprotein in influenza can be used as a target antigen for ADCC that could provide protection against a number of influenza strains [42].

### Herpes Simplex Virus (HSV) Vaccine Development

One example of the failure of neutralization mediated by antibodies as a correlate of protection in vaccine development is found with HSV. As with many pathogens without efficacious vaccines, there are many types of vaccines in development, including subunit and live attenuated viruses [43,44]. However, none have received regulatory approval for

commercialization. One well-known subunit vaccine trial was the HerpeVac trial [45]. A previous trial had established that the vaccine, a recombinant HSV-2 gD protein with adjuvant, was likely only going to be effective in seronegative women [46]. During the HerpeVac trial, sponsored by GlaxoSmithKline, the vaccine elicited high titers of neutralizing antibodies and prevented disease and infection of HSV-1 but not HSV-2 [45]. Further studies into the immune response elicited by the gD-subunit vaccine indicated that the serum from test subjects had higher neutralizing titers against HSV-1 than HSV-2, demonstrating a possible mechanism through which the vaccine may have only provided protection against HSV-1 [47]. Additionally, while the titer of gD-specific antibodies elicited correlated with greater vaccine efficacy, this vaccine did not provide substantial protective benefit in humans [48].

### **ΔgD-2 Protects by Eliciting Non-neutralizing Antibodies That Activate FcγRIV**

The Jacobs and Herold laboratories developed an attenuated, single-cycle vaccine against HSV by deleting glycoprotein D (gD) from HSV-2, designated ΔgD-2, that elicits ADCC-mediated antibodies [49,50]. ΔgD-2-vaccinated mice develop a protective response to vaginal, ocular, and epithelial skin challenge with otherwise lethal doses of HSV-1 and HSV-2 [51-53]. This sterilizing immunity includes very limited symptoms of acute infection and no detectable latent virus in sensory ganglia [49,50]. ΔgD-2 is the first HSV vaccine shown to prevent the establishment of latent infection [54]. Passive transfer of ΔgD-2-immunized sera provided protection, while adoptive T cell transfer did not [49]. Importantly, transfer of immunized sera failed to protect mice lacking the FcγR common chain, allowing us to hypothesize that the mechanism of protection was from antibody-mediated FcγR functions [49]. Furthermore, the ΔgD-2-immunized sera had very low titers of neutralizing and IgG1 antibodies and high titers of IgG2c antibodies [50]. In the ΔgD-2 model, IgG2c antibodies are likely required for a protective immune response [49].

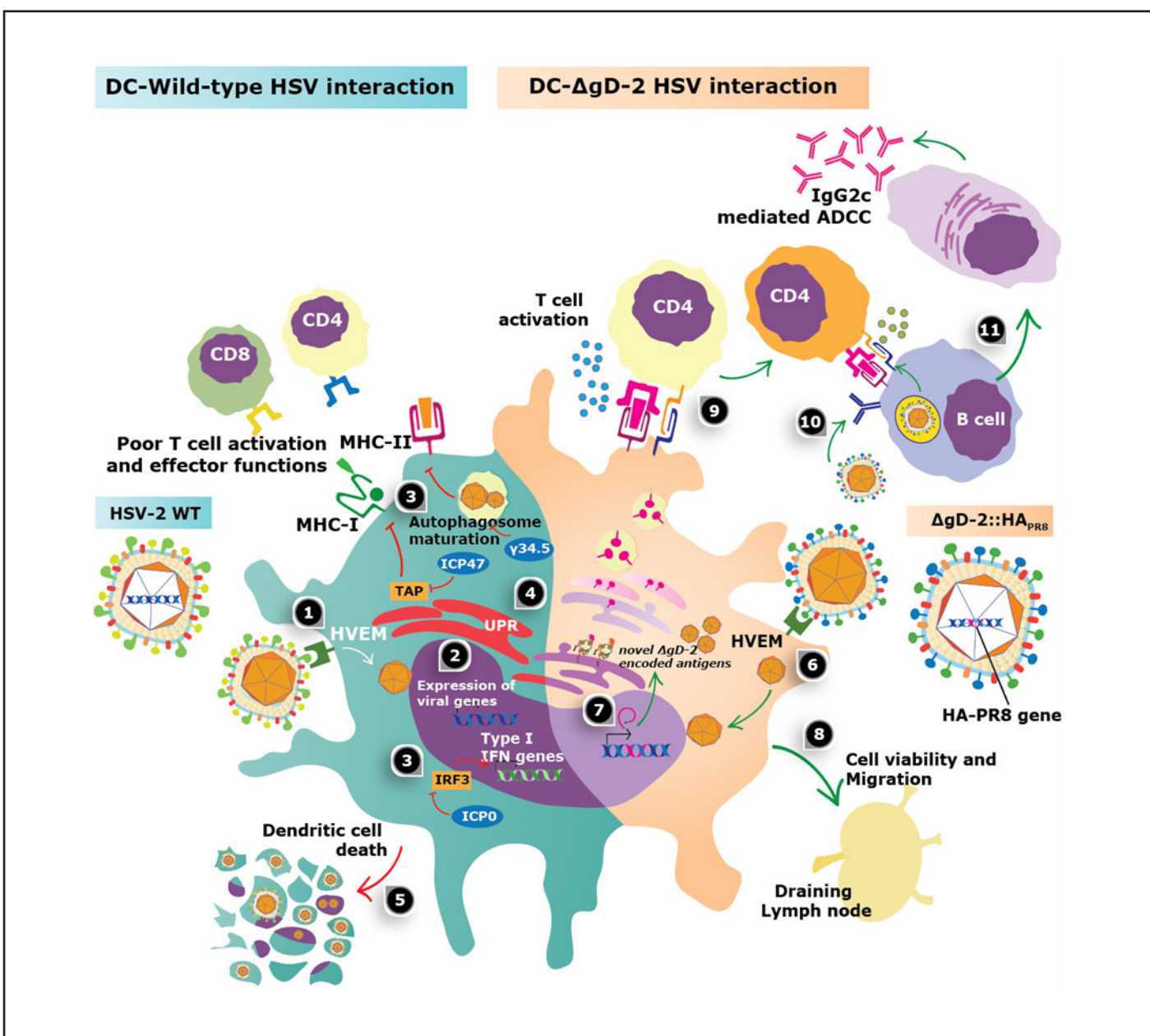
In Kaugars et al., 2021, we introduced a vaccine, ΔgD-2::HA<sub>PR8</sub> that is protective against influenza and HSV during *in vivo* challenge [55]. To create ΔgD-2::HA<sub>PR8</sub> we inserted the gene for HA from an H1N1 strain of influenza into ΔgD-2 [55]. We found that this vaccine specifically elicited high levels of FcγRIV-activating IgG2c antibodies against the influenza HA protein encoded within the recombinant virus and not influenza strains with other HAs. This vaccine also elicited IgG2c antibodies against HSV, similar to the parental vector [55]. The immunized sera had high titers in the hemagglutination inhibition assay, a well-established proxy for neutralizing titer for influenza vaccines [55]. To both probe immunological mechanisms and establish the potential study of other viral infections requiring immunodeficient mouse models with this vector, we tested our vector in mice without functional type I and II IFNs, specifically IFN-α/β (IFNAR<sup>-/-</sup>) and IFN-γ receptor-

deficient (IFNγR<sup>-/-</sup>) mice, respectively [55]. With these studies, we demonstrated that ΔgD-2::RFP (a different recombinant of ΔgD-2 expressing the red fluorescent protein, rather than HA) was protective against HSV challenge in IFNAR<sup>-/-</sup> mice, and ΔgD-2::HA<sub>PR8</sub> was protective against influenza challenge in IFNAR<sup>-/-</sup> and IFNγR<sup>-/-</sup> mice [55].

### **Mechanism of Elicitation of ADCC-mediating Antibodies**

The mechanism through which ΔgD-2 specifically elicits IgG2c antibodies is unknown. Dendritic cells (DCs) are essential for the activation and differentiation of CD4<sup>+</sup> T-helper cells that can support B cell differentiation and antibody class-switch; thus, analyzing the outcome of the ΔgD-2-DC interaction may be relevant for understanding how this vector promotes protection against influenza and HSV [55,56]. Previous research into ΔgD-2 found that this live attenuated virus can be favorably processed by DCs, unlike the wild-type virus, which otherwise induces significant DC death and hampers the function of these cells (**Figure 1**) [57,58]. The ΔgD-2 vector does not elicit the death of DCs, despite the expression of viral-encoded proteins within these cells, which likely promotes HSV antigen presentation. This result sharply contrasts against those obtained with HSV-2 mutants lacking other glycoproteins, such as gH (ΔgH-2), gI (ΔgI-2), or gJ (ΔgJ-2) – all of which rapidly killed DCs [59]. Compared with wild-type HSV, enhanced viability of DCs after inoculation with ΔgD-2 may relate to the fact that upon inoculation, this mutant does not induce an unfolded protein response (UPR) that is lethal for these cells [59,60]. Furthermore, inoculation of ΔgD-2 in the skin or footpads of mice promoted a significantly higher migration of dermal DCs (dDCs) to the draining lymph nodes and promoted both CD4<sup>+</sup> and CD8<sup>+</sup> T activation, as compared to the inoculation with the wild-type virus or the ΔgH-2 mutant [59]. dDCs have been related to HSV antigen presentation in the lymph nodes upon natural skin infection, particularly through the capture of apoptotic HSV-infected Langerhans cells [61,62]. Notably, the amount, type, kinetics, and phenotype of DCs interacting with antigen-specific T-helper cells in the lymph nodes significantly impacts the outcome of the overall immune response to particular antigens and B cell differentiation [61,63,64]. Thus, it will be relevant to characterize in depth the phenotype of the T-helper cells elicited by ΔgD-2 to assess the effects they exert over B cells to produce the effector antibodies with ADCC capacity. Finally, we have observed that the transfer of ΔgD-2-inoculated DCs into mice supported the production of high titers of antibodies against HSV and was sufficient to protect against intravaginal lethal challenge with HSV-2, highlighting the role of these cells in the protection elicited by this vector vaccine [59].

Thus, by deepening our knowledge of the immunological outcome of the ΔgD-2-DC interaction and focusing on the



**Figure 1. Dendritic cell (DC) interaction with wild-type herpes simplex virus (HSV) or the ΔgD-2 vector. Left side: DC interaction with wild-type HSV. 1:** HSVs can infect DCs likely through the herpesvirus entry mediator (HVEM) receptor, which is an immunomodulatory molecule. **2:** HSV-encoded genes are temporally expressed as immediate early (alpha), early (beta), and late (gamma) genes. These genes participate in viral processes, such as genome replication, virion assembly, and interference with the host antiviral response. **3:** Virulence factors can modulate the function of the DCs. For instance, HSVs decrease the expression of major histocompatibility complex (MHC)-I and MHC-II molecules on the DC surface. They also inhibit the transporter of viral peptides to the endoplasmic reticulum by inhibiting the activity of the transporter for antigen processing (TAP) protein. Additionally, HSVs affect autophagy. Overall, DC infection with HSVs results in poor T cell activation. **4:** Wild-type HSVs induce endoplasmic reticulum stress and a lethal unfolded protein response (UPR) in DCs. **Right side: DC interaction with the single-cycle ΔgD-2 viral vector. 6:** The ΔgD-2 vector is complemented with a cell line expressing gD from HSV-1 (gD-1) and can infect target cells, such as DCs, also likely via HVEM. **7:** DCs can express *de novo* viral-encoded genes, including heterologous genes, such as antigens from other viruses. For instance, the ΔgD-2::HA<sub>PR8</sub> virus encodes the influenza virus hemagglutinin (HA) protein, which can be expressed on the surface of inoculated cells. **8:** Inoculation with ΔgD-2 does not affect DC viability nor DC migration to draining lymph nodes. **9:** The ΔgD-2-DC interaction results in DCs that promote the activation of antigen-specific T lymphocytes, which is critical for the differentiation of B lymphocytes into plasma cells. **10:** B cells may present antigens encoded within ΔgD-2 to CD4+ T cells to receive support from helper T cells, and then undergo immunoglobulin subclass switch to IgG2c. **11:** The antibodies elicited by ΔgD-2 have antibody-dependent cellular cytotoxicity (ADCC) effector function, which mediate the protective mechanisms through which ΔgD-2::HA<sub>PR8</sub> confers protection against influenza and HSV challenge.

phenotype of the DCs inoculated with this mutant, the consequent characteristics of the T-helper cells activated by these DCs, and finally, the properties of the B cells secreting the relevant effector antibodies will shed light into the particular properties of  $\Delta$ gD-2 that relate to the outstanding protection that this vector confers against pathogens. Overall, the assessment of DC interaction with HSV mutant vectors has been poorly explored, yet this might directly relate to protective antiviral immune responses against this and other viruses. The notion that DCs play a fundamental role in effective immune responses to inoculation with HSV is also supported in a report evaluating an HSV-1 mutant virus that lacks the amino terminus of  $\gamma$ 34.5, which was also found to promote DCs to elicit an effective antiviral immune response [65].

Because gD from HSV can bind to the host immunomodulatory protein herpesvirus entry mediator (HVEM, HveA, ATAR, TR2, TNFRSF-14), which is widely expressed on the surface of immune cells [66], the contribution of HVEM signaling in the immune response elicited by  $\Delta$ gD-2 vaccination gains particular relevance. Importantly, HVEM signaling was recently found to be involved in the generation of ADCC protective antibodies [52]. Furthermore, immune cells isolated from HVEM-deficient mice displayed impaired Fc $\gamma$ R activation, which also occurred when adding recombinant gD protein to *in vitro* mouse and human Fc $\gamma$ R activation assays [52]. Overall, this study supports an important role for HVEM signaling for ADCC and suggests that HSV utilizes gD to hamper this type of immune response that is ultimately detrimental for the virus. Thus, the capacity of the  $\Delta$ gD-2 vector to promote ADCC antibodies may be at least partially mediated by the lack of gD expression in cells inoculated with this mutant virus.

Additionally, it is noteworthy to mention that the gD protein of HSV has been reported to suppress NK cell-mediated lysis of infected cells [52,67], impair T cell receptor (TCR) signaling in T cells, and inhibit T cell proliferation [68]. These effects of gD are likely to further dampen the host antiviral response upon natural infection with HSV, yet they would be at least partially absent during inoculation with the  $\Delta$ gD-2 vector given that although this mutant virus is phenotypically complemented with gD in the viral particle, it cannot synthesize this protein *de novo*.

## Discussion

Our research has addressed selection and expression of ideal antigens in vaccine vectors, as well as how best to specifically elicit an ADCC-based immune response. In particular, the  $\Delta$ gD-2 vector elicits a strong ADCC-mediating humoral response, even to foreign antigens included in the vector. Based on previous work, infection of DCs by  $\Delta$ gD-2 seems to be a critical step in generating its primarily IgG2c subtype of antibody. Given the importance of DCs in promoting immune

responses that support B cell activation and differentiation, it will be interesting to assess the outcome of these cells upon interaction with varying recombinant  $\Delta$ gD-2 viruses, as this may ultimately determine the levels and characteristics of the antibodies induced by this vector. Already, we have found that even IFN $\gamma$ R<sup>-/-</sup> mice can develop the same response to  $\Delta$ gD-2::HA<sub>PR8'</sub>, which is surprising as IFN- $\gamma$  in particular has been associated with the class switch to IgG2c [55].

With this information, we hypothesize that this class switch could be through the activation of the innate immune response, involving signaling cascades involving molecules like the toll-like receptors (TLRs) and the downstream myeloid differentiation primary response protein 88 (MyD88) pathway in relevant immune cells [69,70]. TLR9 in particular could be involved, as it senses intracellular CpG-rich double-stranded DNA in B cells and plasmacytoid dendritic cells [71]. CpG DNA has been shown to lead to increased T-box transcription factor (T-bet) expression, inhibition of class switch of antibodies to IgG1 and IgE, and increased production of the IgG2a subtype of antibody (which is analogous to the IgG2c subtype in mice) [22,72]. Even in adenoviral vectors, MyD88 and TLR9 are critical in eliciting a strong antibody response [73]. Mice lacking functional MyD88 and TLR9 have been shown to have reduced antibody response to vaccines, particularly in the IgG2a and IgG2c subtypes [70,74]. From the data that we have gathered using  $\Delta$ gD-2, basic information about specifically generating an ADCC-based humoral immune response can be answered to guide development of vaccines and other therapeutics.

Using this research, we can generate more information about what is important for ADCC-based immune responses, as this will lead to improved putative target selection. For example, some data has been published that supports that ADCC function is enhanced with higher antigen density [75]. Influenza HA is expressed at high levels on both virions and influenza-infected cells, 8-9x more than the neuraminidase protein [76]. The HA protein expressed in our vector elicited protection against challenge from its corresponding H1N1 strain of influenza [55]. However, the vaccine was not protective against challenges with other strains of influenza, including a more recent strain of H1N1 virus, supporting that HA was not the optimal antigen for broad influenza protection in this vector [55]. Ideal antigen selection has been a topic of debate during the COVID-19 pandemic. All current mRNA COVID-19 vaccines use the spike protein as an antigen [77,78]. More recently, the bivalent COVID-19 mRNA vaccines expressing two spike proteins have been approved for use in the US [79]. Future vaccine development may incorporate more and/or updated spike proteins or other viral antigens, like the nucleocapsid protein [80]. While our vector was first used with an antigen from the influenza virus, we are continuing our work on other viruses and types of pathogens, like bacteria such as *Streptococcus pneumoniae* and *Mycobacterium tuberculosis*.

Using neutralizing titers of antibodies as a correlate of protection has an established history, and assays to measure neutralization are usually simpler than those to measure other aspects of antibody function. However, there are limitations to relying solely on neutralization. Neutralization is particularly susceptible to mutations in variable regions of antigens and introduces a selective pressure for viral escape mutants. Neutralization is also only one way to assess the effectiveness of antibodies in infections. An ideal antibody response could utilize both neutralization and additional effector functions to provide optimal protection. With some of the monoclonal immunotherapy against both cancer and infectious disease, effector function is an important mechanism of action, as is neutralization [4,81-87]. However, the most established ways to improve ADCC function of antibodies are only for already discovered monoclonal antibodies. For example, modifying antibodies so that their Fc regions are afucosylated has been shown to enhance ADCC [88]. From the research that we have done with the ΔgD-2 vector, we hope to expand what is known about specifically eliciting a polyclonal humoral response that can strongly mediate ADCC *in vivo* against a selected antigen, as well as help optimize monoclonal antibody therapy for improved effector function.

The successful use of viral vectors in widespread populations has been limited. Outside of the mRNA COVID-19 vaccines, some strategies involved using a viral vector to express the spike protein of SARS-CoV-2. The most well-known and analyzed of these would be the Ad26.COV2.S, which consists of a replication-incompetent adenovirus expressing the COVID-19 spike protein [89]. However, many comparative analyses of Ad26.COV2.S and the mRNA-based vaccines have shown a more limited immune response from the viral vaccine [90,91]. While initial investigations into the use of viral vectors have been somewhat disappointing, viral vectors can still have advantages over more traditional formulations of vaccines. In the case of our previous research, we have found that the viral vector can shape the immune response in a beneficial manner that other approaches seem not to achieve. As we have seen the decrease in efficacy of the COVID-19 vaccines primarily reliant on neutralization, a more long-term effective approach may be to identify ideal immune responses that are beneficial in protecting against a variety of novel strains of COVID-19. This strategy may be not only beneficial in COVID-19, but in other pathogens as well that either do not have vaccines or have vaccines that provide suboptimal protection.

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