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Protocol and reagents for pseudotyping lentiviral particles with SARS-CoV-2 Spike protein for neutralization assays

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Received: date; Accepted: date; Published: date

**Abstract:** SARS-CoV-2 enters cells using its Spike protein, which is also the main target of neutralizing antibodies. Therefore, assays to measure how antibodies and sera affect Spike-mediated viral infection are important for studying immunity. Because SARS-CoV-2 is a biosafety-level-3 virus, one way to simplify such assays is to pseudotype biosafety-level-2 virions with Spike. Such pseudotyping has now been described for single-cycle lentiviral, retroviral and VSV virions, but the reagents and protocols are not widely available. Here we detail how to effectively pseudotype lentiviral virions with SARS-CoV-2 Spike and infect 293T cells engineered to express the SARS-CoV-2 receptor, ACE2. We also make all the key experimental reagents available in the BEI Resources repository of ATCC and the NIH. Furthermore, we demonstrate how these pseudotyped virions can be used to measure the neutralizing activity of human sera or plasma against SARS-CoV-2 in convenient luciferase-based assays, thereby providing a valuable complement to ELISA-based methods that measure antibody binding rather than neutralization.

**Keywords:** SARS-CoV-2, COVID-19, coronavirus, neutralization assay, lentiviral pseudotype, Spike, cytoplasmic tail, ACE2, 293T-ACE2, luciferase, ALAYT

1. Introduction

Infection with SARS-CoV-2 elicits antibodies that bind to the virus [1–6]. But as is the case for all viruses [7–10], only some of these antibodies neutralize the virus’s ability to enter cells [4,5,11,12]. While studies of immunity to SARS-CoV-2 are limited, for many other viruses neutralizing antibodies are more strongly correlated with protection against re-infection or disease than antibodies that bind but do not neutralize [7–10,13–15]. Indeed, for other coronaviruses, neutralizing antibodies are protective in mouse models of infection (PMID: 26216974, PMID: 26976607, PMID: 30712865 PMID:18199635) and associated with at least some reduced susceptibility to re-infection or disease [15–19]. Furthermore, anecdotal reports suggest that passive transfer of neutralizing antibodies to sick patients may help alleviate disease from SARS-CoV-2 and its close relative SARS-CoV [20–22].

But while there are now well-characterized and high-throughput methods (such as ELISA assays) to measure total antibody binding to SARS-CoV-2 or some of its key constituent proteins [2,6,23], quantifying neutralizing antibody activity is more difficult. The most biologically relevant method is to directly measure how antibodies or sera inhibit infection of cells by replication-competent SARS-CoV-2 *in vitro*. Such live-virus assays have now been performed to quantify neutralizing activity in the sera of infected patients or characterize the potency of individual antibodies [1,6,12,24]. However, the throughput and accessibility of live-virus neutralization assays with SARS-CoV-2 is limited by the fact that the virus is a biosafety-level-3 agent that must be worked with in specialized facilities.

An alternative approach that alleviates these biosafety limitations leverages the fact that all known neutralizing antibodies to SARS-CoV-2 (and other coronaviruses that lack an HE protein) target the virus’s Spike protein [1,12,24]. Spike is the primarily accessible protein on the surface of SARS-CoV-2, and is necessary and sufficient to enable the virus to bind and enter cells [25]. Spike from several coronaviruses can be “pseudotyped” onto safer non-replicative virions in place of their endogenous entry protein, thereby making entry of these virions into cells dependent on Spike [26–33]. For SARS-CoV-2, such pseudotyping has recently been reported using HIV-based lentiviral virions [4,24,34], MLV-based retroviral virions [12,35], and VSV [26,36–38]. In the data reported to date, results from such pseudovirus neutralization assays correlate well with measurements made using live SARS-CoV-2 [1,12,24,36]. However, the detailed protocols and reagents to perform such assays are not yet widely available to the scientific community.

Here we fill this gap by providing a detailed description of how to pseudotype lentiviral virions with Spike. We explain how these pseudotyped virions can be used to conveniently measure Spike-mediated cell entry via fluorescent or luciferase reporters, and to quantify the neutralizing activity of human plasma. Finally, we describe all the necessary experimental reagents and make them available in the BEI Resources reagent repository (<https://www.beiresources.org/>).

2. Results

2.1. General approach for pseudotyping lentiviral particles with SARS-CoV-2 Spike.

The basic strategy for pseudotyping lentiviral virions is shown in **Figure 1A**. It involves transfecting 293T cells with a lentiviral backbone plasmid encoding a fluorescent or luminescent reporter protein, a plasmid expressing Spike, and plasmids expressing the other lentiviral proteins necessary to assemble virions. The transfected cells then produce Spike-pseudotyped lentiviral virions that can be used to infect permissive cells that express the SARS-CoV-2 receptor protein, ACE2 [25,26,38,39].

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**Figure 1.** General approach for lentiviral pseudotyping. (**A**) 293T cells are transfected with a plasmid encoding a lentiviral backbone (genome) expressing a marker protein, a plasmid expressing Spike, and plasmids expressing the other HIV proteins needed for virion formation (Tat, Gag-Pol, and Rev). The transfected cells produce virions with Spike on their surface. These virions can infect cells that express the ACE2 receptor. (**B**) We used three variants of Spike: the codon-optimized Spike from SARS-CoV-2 strain Wuhan-Hu-1 starting at the NCBI annotated start site, a variant containing mutations K1269A and H1271A in the cytoplasmic tail (such that the C-terminal five amino acids are ALAYT), and a variant in which the cytoplasmic tail of Spike has been replaced with that from influenza hemagglutinin (HA). (**C**) Spike expression on the surface of cells transfected with the plasmids expressing our three Spike constructs was measured using flow cytometry 24 hours post-transfection. Spike expression was measured by staining with in-house produced CR3022 antibody [40–42] at a concentration of 10 μg/mL followed by staining with an anti-human Fc secondary antibody at a 1:100 dilution.

We used an HIV-based lentiviral system in which the backbone plasmid depends on a Tat-driven LTR promoter (as for second-generation lentiviruses), but for which the HIV proteins needed to drive virion assembly are split across multiple plasmids (as for third-generation lentiviruses). This system supports efficient production of Spike-pseudotyped particles. We used two different lentiviral backbones: one that uses a CMV promoter to drive expression of just ZsGreen, and another that uses a CMV promoter to drive exprssion of luciferase followed by an internal ribosome entry site (IRES) and ZsGreen (hereafter referred to as the ZsGreen and Luciferase-IRES-ZsGreen backbones).

The Spike protein was from SARS-CoV-2 strain Wuhan-Hu-1 using the NCBI-annotated start site [43], with the nucleotide sequence codon optimized for expression in human cells. We used three variants of Spike (**Figure 1B**). The first variant was simply the codon-optimized Spike. The second variant had two amino-acid mutations to basic residues in Spike’s cytoplasmic tail (K1269A and H1271A) that change the sequence of the five most C-terminal residues to ALAYT. This variant is hereafter referred to as Spike-ALAYT. The rationale for Spike-ALAYT was that for the original SARS-CoV, the two analagous mutations were shown to improve plasma-membrane expression of Spike by eliminating an endoplasmic reticulum retention signal [44,45]. The third variant had the cytoplasmic tail of Spike replaced with that from influenza hemagglutinin (HA); this variant is hereafter referred to as Spike-HAtail. The rationale for Spike-HAtail was that for the original SARS-CoV, deleting Spike’s cytoplasmic tail or replacing it with that from other viruses was shown to improve pseudotyping efficiency [27,46–48]. The sequences of all of the Spike and lentiviral plasmids are in **File S1**, and the plasmids are available from BEI Resources (see **Materials and Methods** for BEI catalog numbers).

2.2. Target 293T cells constititutively expressing Spike’s ACE2 receptor.

To create a target cell line that is efficiently infected by the SARS-CoV-2 Spike-pseudotyped lentiviral virions, we transduced 293T cells with a lentiviral vector expressing human ACE2 under an EF1a promoter (lentiviral backbone plasmid sequence is in **File S1**, and is available from BEI Resources as item NR-52512). To create a clonal cell line from the bulk transduction, we sorted single transduced cells by flow cytometry and re-expanded into large populations (note that there is not a selectable marker in these cells). We identified an expanded clone that expressed high levels of ACE2 (**Figure 2A**). This ACE2 expression appears stable overtime and has not noticeably decreased through 12+ passages at the time of writing. This clone is hereafter referred to as 293T-ACE2, and is available from BEI Resources as item NR-52511.

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**Figure 2.** 293T-ACE2 cells are susceptible to SARS-CoV-2 Spike-pseudotyped lentivirus transduction. (**A**) Flow cytometry plot showing expression of ACE2 by the 293T-ACE2 cells (grey shaded) at passage 12 compared to parental 293T cells (white fill) as quantified by staining with an anti-ACE2 antibody. As seen, ACE2 expression remains high over many passages. The gate was set so the parental 293T cells are 2% positive. (**B**) Microscope images showing ZsGreen expression in 293T-ACE2 or 293T cells at 43 hours after incubation with Spike- or VSV G-pseudotyped lentivirus with the ZsGreen backbone. For each viral entry protein, 293T and 293T-ACE2 cells were infected with equal volumes of virus. Cells were infected with 1/20th the volume of VSV G-pseudotyped lentivirus compared to Spike-pseudotyped lentivirus.

We validated that the 293T-ACE2 cells were susceptible to infection by SARS-CoV-2 Spike-pseudotyped lentivirus by incubating 293T-ACE2 and parental 293T with equivalent amounts of lentivirus carrying ZsGreen. As shown in **Figure 2B**, Spike-pseudotyped virus successfully infects the 293T-ACE2 but not the 293T cells. This was true for all three Spike variants tested (data not shown). Virus pseudotyped with VSV G, an amphotropic viral entry protein that is not dependent on ACE2, efficiently infects both cell lines (**Figure 2B**)**.**

2.3. Titers of pseudotyped lentiviral particles with different Spike cytoplasmic tail variants.

To quantify the titers of lentiviral virions pseudotyped with each of the Spike variants, we produced virions with each of these Spikes, as well as a positive control using VSV G and a negative control without a viral entry protein. We first produced virions using the ZsGreen backbone, and titered by flow cytometry to determine the number of transducing particles per ml. As shown in **Figure 3A**, all Spike variants produced titers ≈104 transduction units per ml. These titers were about two orders of magnitude lower than those achieved with VSV G, but we considered them to be encouragingly high given that lentiviral virions can be further concentrated by a variety of methods [49,50]. We then produced virions using the Luciferase-IRES-ZsGreen backbone, and found that we could achieve titers of >106 relative luciferase units (RLUs) per ml in 96-well plate infections (**Figure 1B**). This titer was again about two orders of magnitude lower than that achieved using VSV G. As expected, the magnitude of the fluorescent signal from ZsGreen is lower for the Luciferase-IRES-ZsGreen backbone than for the ZsGreen-only backbone (**Figure 1C**), since the ZsGreen in the former construct is driven by an IRES rather than the primary promoter.

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**Figure 3.** Titers of Spike-pseudotyped lentiviruses in 293T-ACE2 cells. (**A**) Titers of the ZsGreen backbone pseudotyped with the three Spike variants or VSV G, as determined by counting green cells via flow cytometry analysis at 48 hours post-infection, and then calculating transduction-competent virions per ml from the percentage of green cells. The “n.d.” indicates that the titer was not detectable. (**B**) Titers of the Luciferase-IRES-ZsGreen backbone as determined by measuring relative luciferase units (RLUs). RLUs were determined at 48 hours after infecting ~2.3e4 293T-ACE2 cells per well in 96-well plates. The RLUs per mL for the Spike-pseudotyped viruses are the average of three 3-fold serial dilutions of virus starting at 50 μL virus in a total volume of 150 μL. For the VSV G-pseudotyped virus, RLUs per mL were averaged from two 3-fold dilutions starting at 3 μL virus in a total volume of 150 μL. (**C**) Microscope images showing 293T-ACE2 cells transduced with Spike pseudotyped virus with either the ZsGreen or Luciferase-IRES-ZsGreen backbone at 60 hours post-infection. As can be seen from the images, the ZsGreen backbone gives a stronger fluorescent signal than the Luciferase-IRES-ZsGreen backbone, presumably because this protein is expressed more strongly as the sole CMV-promoter driven transcript than as the second transcript driven by an IRES.

2.4. Neutralization assays with Spike-pseudotyped lentiviral particles.

We next used the Luciferase-IRES-ZsGreen viruses to perform neutralization assays in 96-well plates. Because such assays can be performed with <105 RLUs per well in 96-well plates, a relatively modest volume of virus is required for a full 96-well plate neutralization assay.

We performed neutralization assays using plasma from a confirmed SARS-CoV-2 infected patient collected at 19 days post-symptom onset, and with soluble ACE2 protein fused to an IgG Fc domain (which neutralizes SARS-CoV-2 by acting as a decoy receptor [51]). For these assays, we first made serial dilutions of plasma or soluble ACE2-Fc in a 96-well plate, then incubated with 2x105 RLUs of pseudotyped lentiviral virions for 60 minutes, and then added the virus plus plasma to a pre-seeded plate of 293T-ACE2 cells. We measured the luciferase signal at 60 hours post-infection (see **Materials and Methods** for a more detailed protocol).

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**Figure 4.** Neutralization assays. (**A**) Neutralization assay using plasma collected from a confirmed SARS-CoV-2 infected patient at 19 days post-symptom onset. (**B**) Neutralization assay using soluble ACE2 protein fused to the Fc domain from IgG. (**C**) Neutralization assay using serum samples collected prior to the emergence of SARS-CoV-2. The individual serum collected in 1989 was of a similar age at the time of serum collection to the confirmed SARS-CoV-2 infected patient.

Both the plasma from the confirmed SARS-CoV-2-infected patient and the soluble ACE2-Fc effectively neutralized the virus (Figure 4A,B). For the plasma, the inhibitory concentration 50% (IC50) was ≈1:2000 with all the Spike-pseudotyped viruses, which is in the range of values that have been reported for sera and plasma from other SARS-CoV-2 patients at a similar time post-infection [4]. For soluble ACE2-Fc, the IC50 was ≈2 μg/mL with the Spike-pseudotyped virus. This is slightly higher than a previously reported IC50 of 0.1 μg/ml for soluble ACE2-IgG [51]. We suspect that the difference could be because our 293T-ACE2 target cells express high levels of ACE2 making them more resistant to neutralization by soluble ACE2 (but we cannot be certain, as [51] does not report what target cells were used). Of note, there was no neutralization of the pseudotyped virus by either pooled or individual human sera collected at dates prior to the emergence of SARS-CoV-2 (Figure 4C).

For the plasma neutralization, all three Spike variants (Spike, Spike-ALAYT, and Spike-HAtail) exhibited similar neutralization profiles (Figure 4A). But for the soluble ACE2, the Spike-HAtail virus was notably more neutralization sensitive than the other two Spike variants (Figure 4B). While the mechanism underlying the distinct neutralization sensitivity observed is unclear, it is possible that modifying the Spike’s cytoplasmic tail may alter opening of the receptor-binding domains (Walls, Park 2020 Cell - already ref 25). Based on our finding we suggest performing the assays using the Spike without any cytoplasmic tail modifications, particularly since none of the modifications tested here greatly improved. pseudotyped lentivirus titers.

3. Discussion

We describe a detailed protocol for producing SARS-CoV-2 Spike-pseudotyped lentivirus and using this virus to perform neutralization assays. Although this approach has been described previously, [4,12,24,26,34–38] we provide here the first detailed protocol that makes all reagents available in a public repository, which we hope will be a useful resource to enable others to assess neutralization of SARS-CoV-2.

We also found that modifying the tail of SARS-CoV-2 Spike did not improve titers of Spike-pseudotyped lentivirus for downstream experiments. Indeed, one of the cytoplasmic tail modifications we tested potentially altered the neutralization sensitivity of the pseudotyped viruses, suggesting it may be undesirable. While we obviously did not test the full suite of cytoplasmic tail modifications that have been used for pseudotyping with Spike from the original SARS-CoV [27,46–48], our results suggest that modifications to the cytoplasmic tail of the SARS-CoV-2 Spike should be made and tested with caution.

Overall, we have developed an assay–for which we have now made the protocol and reagents widely available–to study the neutralizing immune response to SARS-CoV-2 in a BSL-2 laboratory. Furthermore, this assay allows human serum and/or plasma samples to be screened for neutralization of SARS-CoV-2 in a convenient 96-well format, which will help facilitate the testing of large numbers of patient samples to better understand the development of neutralizing immunity and to potentially screen donors for passive transfer of convalescent plasma, a treatment option currently being pursued (perhaps cite: <https://www.ncbi.nlm.nih.gov/pubmed/32254064> and <https://www.ncbi.nlm.nih.gov/pubmed/32253318> just about the use of convalescent plasma (although I've only read the abstracts).

4. Materials and Methods

*4.1. Plasmids.*

The sequences of all plasmids used in this study are available in Genbank format in **File S1** and are also at <https://github.com/jbloomlab/SARS-CoV-2_lentiviral_pseudotype/tree/master/plasmid_maps>. The plasmids themselves are available in BEI Resources (<https://www.beiresources.org/>) with the following catalog numbers:

* pHAGE2-EF1aInt-ACE2-WT (BEI catalog number NR52512): lentiviral backbone plasmid expressing the human ACE2 gene (GenBank ID for human ACE2 is NM\_021804) under an EF1a promoter with an intron to increase expression.
* HDM-IDTSpike-fixK-HA-tail (BEI catalog number NR52513): plasmid expressing under a CMV promoter the Spike from SARS-CoV-2 strain Wuhan-Hu-1 (Genbank NC\_045512) codon-optimized using IDT, with the Spike cytoplasmic tail replaced by that from the HA protein of A/WSN/1933 (H1N1) influenza, and the Kozak sequence in the plasmid fixed compared to an earlier version of this plasmid.
* HDM-IDTSpike-fixK (BEI catalog number NR-52514): plasmid expressing under a CMV promoter the Spike from SARS-CoV-2 strain Wuhan-Hu-1 (Genbank NC\_045512) codon-optimized using IDT and the Kozak sequence in the plasmid fixed compared to an earlier version of this plasmid.
* HDM-nCoV-Spike-IDTopt-ALAYT (BEI catalog number NR-52515): plasmid expressing under a CMV promoter the Spike from SARS-CoV-2 strain Wuhan-Hu-1 (Genbank NC\_045512) codon-optimized using IDT, with the Spike containing two mutations in the cytoplasmic tail such that the last five amino acids are ALAYT.
* pHAGE-CMV-Luc2-IRES-ZsGreen-W (BEI catalog number NR-52516): lentiviral backbone plasmid that uses a CMV promoter to express luciferase followed by an IRES and ZsGreen.
* HDM-Hgpm2 (BEI catalog number NR-52517): lentiviral helper plasmid expressing HIV Gag-Pol under a CMV promoter.
* HDM-tat1b (NR-52518): lentiviral helper plasmid expressing HIV Tat under a CMV promoter.
* pRC-CMV-Rev1b (NR-52519): lentiviral helper plasmid expressing HIV Rev under a CMV promoter.
* pHAGE2-CMV-ZsGreen-W (NR-52520): lentiviral backbone plasmid that uses a CMV promoter to express ZsGreen.

Note that all of these plasmids have ampicillin resistance. The only plasmid used in this study that is not in the BEI Resources catalog is the HDM-VSVG plasmid that expresses VSV G under a CMV promoter, and was used to create the positive control lentivirus pseudotyped with VSV G. However, numerous VSV G expressing plasmids are available from AddGene and other repositories.

*4.2 Creation of 293T ACE2 cells.*

VSV G-pseudotyped lentivirus packaging the human ACE2 was generated via co-transfecting 293T cells (ATCC, CRL-3216) with the pHAGE2-EF1aInt-ACE2-WT plasmid (File S1) and lentiviral helper plasmids (HDM-VSVG, HDM-Hgpm2, HDM-tat1b, and pRC-CMV-Rev1b). The resulting lentivirus was used to infect more 293T cells in the presence of 5 ug/mL polybrene. The transduced cells were stained with anti-human ACE-2 polyclonal goat IgG (AF933, R&D Systems) primary antibody at 1 ug/mL and donkey anti-goat IgG (ab150129, Abcam) secondary antibody at a 1:2500 dilution and sorted based on antibody staining. Once single cell clones had grown sufficiently, they were screened for ACE2 expression via flow cytometry and a clone with high expression was expanded and named 293T-ACE2 (**Figure 2A**). For verifying expression via flow cytometry, cells were harvested with enzyme-free dissociation buffer (ThermoFisher, 13151014) and stained with anti-human ACE-2 polyclonal goat IgG primary antibody at 2 ug/mL and donkey anti-goat IgG secondary antibody at a 1:1000 dilution.

The 293T-ACE2 cells can be grown in D10 growth media (DMEM with 10% heat-inactivated FBS, 2 mM L-glutamine, 100 U/ml penicillin, and 100 ug/ml streptomycin) at 37 C and 5% carbon dioxide. Note that there is not a selectable marker for the ACE2 expression. The 293T-ACE2 cells are available from BEI Resources as catalog number NR-52511.

*4.3 Detailed protocol for generation of pseudotyped lentiviral particles.*

Pseudotyped lentiviruses can be generated by transfecting 293Ts as depicted in **Figure 1A.** We used the following protocol:

1. Seed 293T cells in D10 growth media (see subsection 4.2 for media composition) so that they will be 50-70% confluent the next day. For a 6-well plate, this is 5x105 cells per well (2.5x105 cells per mL).
2. At 16-24 hours after seeding, transfect the cells with the plasmids required for lentiviral production. We transfect using BioT (Bioland Scientific) following the manufacturer’s instructions and using the following plasmid mix per well of a 6-well plate (plasmid amounts should be adjusted for larger plates):

* 1 ug of lentiviral backbone–we used either the ZsGreen (NR-52520) or the Luciferase-IRES-ZsGreen (NR-52516) backbone
* 0.22 ug each of plasmids HDM-Hgpm2 (NR-52517), pRC-CMV-Rev1b (NR-52519), and HDM-tat1b (NR-52518)
* 0.34 ug viral entry protein–either SARS-CoV-2 Spike (NR-52513, NR-52514, or NR-52515), VSV G (positive control), or transfection carrier DNA (Promega E4881) as a negative control.

1. At 18 to 24 hours post-transfection, change the media to fresh, pre-warmed D10.
2. At 60 hours post transfection, collect virus by harvesting the supernatant from each well and filtering it through a 0.45 um filter. Virus can be stored at 4 C for immediate use or frozen at -80 C. The titers of Spike- and VSV G-pseudotyped lentiviruses were found to be unaffected by a freeze-thaw cycle (data not shown). All titers presented here are from virus that was frozen at -80 C prior to use.

*4.4 Detailed protocol for titering pseudotyped lentiviral particles*

To determine viral titers, we used either flow cytometry (for viruses packaging the ZsGreen backbone) or a luciferase assay (for viruses packaging the Luciferase-IRES-ZsGreen backbone). A detailed titering protocol is described below and differences between these two readouts are noted:

1. Coat a 96-well cell-culture plate with 25 uL poly-L-lysine per well (Millipore Sigma, P4707) according to the manufacturer’s protocol. Poly-L-lysine improves cell adherence and prevents cell disruption during infection.
2. Seed a poly-L-lysine-coated 96-well plate with 1.25x104 293T-ACE2 cells per well in D10 media.
3. The next day (12-24 hours post-seeding), count at least 2 wells of cells to determine the number of cells present at infection.
4. Prepare serial dilutions of the viruses to be titered in a final volume of 150 uL D10 growth media.
   1. For ZsGreen virus, we started with a 1:5 dilution and made three 1:5 serial dilutions.
   2. For Spike-pseudotyped Luciferase\_IRES\_ZsGreen virus, we started with undiluted virus and made three 1:3 dilutions. For VSV G-pseudotyped Luciferase\_IRES\_ZsGreen virus, we started with a 1:50 dilution.
5. Gently remove the media from the cells and slowly add the virus dilutions.
6. Add polybrene (Sigma Aldrich, TR-1003-G) to a final concentration of 5 ug/mL. We did this by adding 3 uL of polybrene diluted to 250 ug/mL to our final infection volume of 150 uL. Polybrene is a polycation that helps facilitate lentiviral infection through minimizing charge-repulsion between the virus and cells [52].
7. At 48-60 hours post-infection, collect cells for analysis:
   1. For flow cytometry:
      1. Look at the cells under a fluorescent microscope and select wells that appear ~1-10% positive. Harvest cells from these wells using trypsin and transfer them to a V-bottom plate or microcentrifuge tubes. Pellet cells at 300xg for 4 min and wash twice with 3% BSA in PBS. After the final wash, resuspend in 1% BSA in PBS and analyze via flow cytometry. We used a Becton Dickinson Celesta cell analysis machine with a 530/30 filter to detect ZsGreen in the FITC channel. Resulting FCS files were analyzed using FlowJo (v10).
      2. Calculate titers using the Poisson formula. If P is the percentage of cells that are ZsGreen positive, then the titer per mL is: *-ln(1 – P / 100) x (number of cells / well) / (volume of virus per well in mL)*. Note that when the percentage of cells that are ZsGreen positive is low, this formula is approximately equal to: *(% ZsGreen positive / 100) x (number of cells / well) / volume of virus per well in mL)*. Furthermore, the titers using even the Poisson equation will only be accurate if the percentage of cells that are ZsGreen positive is relatively low (ideally 1-10%).
   2. For luciferase:
      1. Thaw luciferase reagent at room temperature. We used the Bright-Glo Luciferase Assay System (Promega, E2610).
      2. Prepare cells by removing 100 uL media from each well. Accounting for evaporation, this leaves ~30 uL of media in each well.
      3. Add 30 uL of luciferase reagent, mix well, and transfer all 60 uL to a black-bottom plate (Costar 96-well solid black, Fisher, 07-200-590).
      4. Incubate plate for 2 min at room temperature in the dark then measure luminescence using a plate reader. We used a Tecan Infinite M1000 Pro plate reader with no attenuation and a luminescence integration time of 1 second.
      5. Plot RLUs vs. virus dilution. Select an amount of virus for further assays where there is a linear relationship between virus added and RLU.

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**Figure 5:** Example plate layout for neutralization assays. It is possible to run full-dilution series of two sera or plasma samples in duplicate on each plate with the necessary controls. These controls include media only, cells only, and virus only wells, as well as 4 wells of virus infecting 293T cells to confirm the lack of infection with Spike-pseudotyped lentivirus in the absence of ACE2. The average signal from the “Virus Only” and “Virus + 293Ts” wells provides the background signal. The “Virus + Cells” wells represent maximum infection without any serum and provide a metric for 100% virus infectivity. Note that “cells” here refers to the 293T-ACE2 cells.

*4.5 Detailed protocol for neutralization assays.*

The following protocol was developed to streamline neutralization assays with Spike-pseudotyped lentiviruses. This protocol can be performed with either human sera or plasma, or monoclonal antibodies. Note that for safety, sera or plasma should be heat-inactivated in a biosafety cabinet prior to use as described in subsection 4.6.

1. Seed a poly-L-lysine-coated 96-well plate with 1.25x104 293T-ACE2 cells (BEI NR-52511) per well in 50 uL DMEM (2.5x105 cells per mL). Plan to infect this plate 8–12 hours post-seeding.
2. About 1.5 hours prior to infecting cells, begin preparing serum and/or ACE2 dilutions in D10:
   1. In a separate 96-well “setup” plate, serially dilute serum samples leaving 60 uL diluted serum in each well. For the data in **Figures 4A & 4C**, we started at an initial serum dilution of 1:80 and did serial 2.5-fold dilutions, meaning each replicate of the assay requires 5 uL of sera. For ACE2 (**Fig. 4**) we started with a concentration of 200 ug/mL and did serial 3-fold dilutions.
   2. Add 60 uL of D10 to wells corresponding to virus only and virus plus cells control wells. Add 120 uL of D10 to media only and cells only control wells. See **Figure 5** for an example plate layout.
3. Dilute virus to ~2-4x106 RLU per mL. Add 60 uL of diluted virus to all wells containing serum dilutions and the virus only and virus plus cells control wells.
4. Incubate virus and serum at 37 C for 1 hr.
5. Carefully add 100 uL from each well of the setup plate containing the sera and virus dilutions to the corresponding wells of the plate of 293T-ACE2 cells.
6. Add polybrene (Sigma Aldrich, TR-1003-G) as described in subsection 4.4 for a final concentration of 5 ug/mL in each well.
7. Incubate at 37 C for 48-60 hours before reading out luminescence or fluorescence as described in subsection 4.4.
8. Plot the data. For the curves shown in **Figure 4**, we fit and plotted the data using the neutcurvePython package (<https://jbloomlab.github.io/neutcurve/>).

*4.6 Human plasma sample and soluble ACE2.*

The human plasma sample used in **Figure 4A** was collected at 19 days post-symptom onset from a patient with a confirmed SARS-CoV-2 infection. Prior to use, the plasma was heat-inactivated in a biosafety cabinet at 56 C for one hour. This duration of heat treatment has been shown to be sufficient to inactivate SARS-CoV-2 [23,53], which is also not reported to be present at high titers in the blood [54,55]. The negative control serum pools came from Gemini Biosciences (Cat:100-110). The naïve serum pool collected in 2017-2018 is lot H86W03J. The age-matched negative control serum comes from serum residuals collected by Bloodworks Northwest. It was collected on 12/19/1989 and stored at -80 C.

Soluble human ACE2 protein fused to the Fc region of human IgG was produced as described in [25]. This ACE2-Fc fusion protein was used in **Figure 4B**.

**Supplementary Materials:** The following are available online at www.mdpi.com/xxx/s1: File S1: A zip file containing all the plasmid maps in Genbank format.

**Author Contributions:** Conceptualization, K.D.C. and J.D.B.; investigation, K.D.C., R.E., A.S.D., K.M., and A.N.L.; resources and specialized reagents, A.B.B., C.R.W., H.Y.C., M.A.T, D.V., M.M., D.P., and N.P.K.; writing—original draft preparation, K.D.C and J.D.B.; writing—review and editing, all authors. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research was supported by the following grants from the NIAID of the NIH: R01AI141707 (to J.D.B.), F30AI149928 (to K.D.C.) and HHSN272201700059C (to D.V.). T**his study** was also supported by the National Institute of General Medical Sciences (R01GM120553, D.V.), a Pew Biomedical Scholars Award (D.V.), and an Investigators in the Pathogenesis of Infectious Disease Award from the Burroughs Wellcome Fund (D.V.). A.B.B. is supported by the National Institutes for Drug Abuse (NIDA) Avenir New Innovator Award DP2DA040254. J.D.B. is an Investigator of the Howard Hughes Medical Institute.

**Acknowledgments:** We thank Caelan Radford, Andrew McGuire, and Abigail Powell for helpful suggestions and feedback.

**Conflicts of Interest:** H.Y.C. is a consultant for Merck and Glaxo Smith Kline and receives research funding from Sanofi Pasteur.

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