Broadly Neutralizing Activity of Zika Virus-Immune Sera Identifies a Single Viral Serotype

Kimberly A. Dowd, National Institutes of Health
Christina R. DeMaso, National Institutes of Health
Rebecca S. Pelc, National Institutes of Health
Scott D. Speer, National Institutes of Health
Alexander R. Y. Smith, National Institutes of Health
Leslie Goo, National Institutes of Health
Derek J. Platt, Washington University
John R. Mascola, National Institutes of Health
Barney S. Graham, National Institutes of Health
Mark Mulligan, Emory University

Only first 10 authors above; see publication for full author list.

Journal Title: Cell Reports
Volume: Volume 16, Number 6
Publisher: Elsevier (Cell Press): OAJ | 2016-08-31, Pages 1485-1491
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.1016/j.celrep.2016.07.049
Permanent URL: https://pid.emory.edu/ark:/25593/rrkft

Final published version: http://dx.doi.org/10.1016/j.celrep.2016.07.049

Copyright information:
This is an Open Access work distributed under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Accessed January 15, 2018 2:32 AM EST
Broadly Neutralizing Activity of Zika Virus-Immune Sera Identifies a Single Viral Serotype

Authors
Kimberly A. Dowd, Christina R. DeMaso, Rebecca S. Pelc, ..., Michael S. Diamond, Julie E. Ledgerwood, Theodore C. Pierson

Correspondence
pierson tc@mail.nih.gov

In Brief
Dowd et al. investigate the breadth of the neutralizing antibody response to ZIKV. They demonstrate that contemporary South American, Asian, and early African ZIKV strains are similarly sensitive to neutralization by ZIKV-confirmed convalescent human serum.

Highlights
- Neutralization studies with convalescent ZIKV-immune sera identify a single serotype
- Infection with a single ZIKV strain elicits broadly neutralizing antibodies
- Strain selection may not be a critical parameter for ZIKV vaccine development
**Identifies a Single Viral Serotype**


1Viral Pathogenesis Section, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892, USA
2Departments of Medicine, Molecular Microbiology, and Pathology and Immunology and The Center for Human Immunology and Immunotherapy Programs, Washington University School of Medicine, St. Louis, MO 63110, USA
3Vaccine Research Center, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892, USA
4The Hope Clinic of the Emory Vaccine Center, Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Decatur, GA 30030, USA
*Correspondence: piersontc@mail.nih.gov
http://dx.doi.org/10.1016/j.celrep.2016.07.049

**SUMMARY**

Recent epidemics of Zika virus (ZIKV) have been associated with congenital malformation during pregnancy and Guillain-Barré syndrome. There are two ZIKV lineages (African and Asian) that share >95% amino acid identity. Little is known regarding the ability of neutralizing antibodies elicited against one lineage to protect against the other. We investigated the breadth of the neutralizing antibody response following ZIKV infection by measuring the sensitivity of six ZIKV strains to neutralization by ZIKV-confirmed convalescent human serum or plasma samples. Contemporary Asian and early African ZIKV strains were similarly sensitive to neutralization regardless of the cellular source of virus. Furthermore, mouse immune serum generated after infection with African or Asian ZIKV strains was capable of neutralizing homologous and heterologous ZIKV strains equivalently. Because our study only defines a single ZIKV serotype, vaccine candidates eliciting robust neutralizing antibody responses should inhibit infection of both ZIKV lineages, including strains circulating in the Americas.

**INTRODUCTION**

Zika virus (ZIKV) is a mosquito-transmitted flavivirus that has emerged from relative obscurity to cause an epidemic of great public health concern. During the half-century that followed its discovery, ZIKV was rarely linked to disease in humans, despite considerable transmission (Dick, 1953; Petersen et al., 2016). The emergence of epidemic ZIKV was first reported in Yap island in 2007, followed by outbreaks in French Polynesia in 2013 and 2014 and regularly thereafter in other islands of the Pacific. ZIKV was introduced into the western hemisphere in 2014–2015 and spread rapidly to 40 or more countries and territories. Historically, symptomatic ZIKV infection of humans was described as a self-limiting mild febrile illness associated with rash, arthralgia, and conjunctivitis (Petersen et al., 2016). However, recent ZIKV infections also have been associated with neurological complications, including Guillain-Barré syndrome and meningoencephalitis (Brasil et al., 2016a, 2016b; Cao-Lormeau et al., 2016; Oehler et al., 2014). Of greatest concern, ZIKV infection is now linked causally to microcephaly and intrauterine growth retardation in the fetuses of women infected with the virus while pregnant (Hazin et al., 2016).

Flaviviruses are spherical virus particles that incorporate two structural proteins, premembrane/membrane (prM/M) and envelope (E), into their lipid envelope. High-resolution structures of the mature ZIKV virion and ectodomain of the E protein have been solved (Dai et al., 2016; Kostyuchenko et al., 2016; Sirohi et al., 2016). Similar to other flaviviruses, mature ZIKV virions are relatively smooth particles that incorporate 180 copies each of the E and M proteins. Neutralizing antibodies play a critical role in protection against flaviviruses and bind epitopes located in all three E protein structural domains (Heinz and Stasny, 2012). Additionally, potently neutralizing flavivirus antibodies have been isolated that bind surfaces composed of more than one domain or E protein (Screaton et al., 2015). Because neutralizing antibody titers correlate with protection by licensed vaccines for Japanese encephalitis virus (JEV), yellow fever virus (YFV), and tick-borne encephalitis virus (TBEV) (Belmusto-Worn et al., 2005; Heinz et al., 2007; Mason et al., 1973; Monath et al., 2002), eliciting neutralizing antibodies is a desired feature of vaccine candidates for related flaviviruses, including ZIKV.

Flaviviruses circulate as genetically distinct genotypes or lineages. ZIKV strains have been grouped into two lineages, African and Asian, which differ by <5% at the amino-acid level, including within the E protein gene (Haddow et al., 2012). The African lineage includes the historical MR-766 strain originally identified in 1947, whereas virus strains from the Asian lineage have been implicated in the recent outbreaks in Yap, French Polynesia, and the Americas. Understanding how sequence variation among ZIKV strains impacts antibody recognition is of particular importance to vaccine development. DENV, for example, circulates as four distinct serotypes that differ by 25%–40% at the...
amino acid level within the E protein. The challenges of eliciting a protective neutralizing antibody response against all four DENV serotypes have delayed vaccine development significantly (Guy et al., 2016). Desirable ZIKV vaccine candidates should provide equivalent protection against both Asian and African lineages.

In this study, we investigated the breadth of the humoral immune response elicited by ZIKV infection. The ability of eight convalescent ZIKV-immune human serum or plasma samples collected during the current outbreak to neutralize multiple ZIKV strains was evaluated. Our results demonstrate that antibodies elicited after infection with contemporary Asian lineage strains potently inhibit infection of both homologous Asian and heterologous African strains. Similarly, immune sera from mice infected with either Asian or African lineages inhibited infection of homologous and heterologous ZIKV strains. Our studies indicate that the different lineages of ZIKV exist as a single serotype. These findings will be of particular importance in the ongoing effort to rapidly develop a ZIKV vaccine.

RESULTS

Broadly Neutralizing Activity of ZIKV-Immune Sera

To evaluate the breadth of the neutralizing antibody response elicited by ZIKV infection, sera or plasma were obtained from eight ZIKV-infected individuals (Table S1). We first evaluated the neutralization activity of each sample with Vero-cell-derived stocks of three different ZIKV strains representing both African and Asian lineages. The African lineage strain MR-766 used in this study was originally isolated in Uganda in 1947. Contemporary Asian lineage isolates were collected during the 2013 French Polynesian outbreak (H/PF/2013) (Baronti et al., 2014) and the recent Brazilian epidemic (Paraiba/2015). Amino acid variation among viruses is detailed in Tables S2 and S3. Dose-dependent inhibition curves with virus and human-immune sera and plasma were generated using Raji cells expressing DC-SIGNR. Neutralization curves of all three viruses revealed a similar profile with serum from subject NIH.1 (Figure 1A). The EC50 values from independent neutralization studies for eight ZIKV-immune convalescent sera are presented. Error bars reflect the range or SE of two to three experiments. Statistical differences in mean EC50 were identified using ANOVA with a multiple comparisons correction; the fold difference in sensitivity relative to MR-766 and multiplicity-adjusted p values are displayed when significant (only F).

Figure 1. Neutralization of Multiple Strains of Infectious ZIKV by Immune Human Sera

The sensitivity of three ZIKV strains to neutralization by sera from ZIKV-infected individuals was compared. Stocks of MR-766, H/PF/2013, and Paraiba/2015 ZIKV strains were produced in Vero cells and used in neutralization experiments. ZIKV was mixed with serial 4-fold dilutions of serum for 1 hr at 37°C prior to being added to Raji-DCSIGNR cells. Infection was measured 20 hr post-infection by staining cells for intracellular E protein expression followed by flow cytometry. The dilution of sera at half-maximal neutralization of infection (EC50) was estimated by non-linear regression analysis.

(A) Neutralization curves for a representative experiment are shown for serum NIH.1. Error bars represent the range of duplicate technical replicates.

(B–I) The average EC50 neutralization titers obtained from independent neutralization studies for eight ZIKV-immune convalescent sera are presented. Error bars reflect the range or SE of two to three experiments. Statistical differences in mean EC50 were identified using ANOVA with a multiple comparisons correction; the fold difference in sensitivity relative to MR-766 and multiplicity-adjusted p values are displayed when significant (only F).
and seven additional ZIKV convalescent samples (Figures 1C–1I) confirmed that all three ZIKV strains were similarly sensitive to inhibition by sera or plasma derived from individuals infected with contemporary ZIKV strains. Differences in the mean neutralization titer were uniformly less than 4-fold and, with one exception (Figure 1F), failed to reach statistical significance.

The efficiency of the virion maturation process varies among cell types used to produce viruses. For example, flaviviruses grown in insect cells are less efficiently processed than mammalian cell-derived viruses (Dejnirattisai et al., 2015; Vogt et al., 2011). For many antibodies, inefficient cleavage of the prM structural protein results in increased neutralization potency due to enhanced accessibility of epitopes on partially mature virions (Pierson and Diamond, 2012). The prM content of virions also contributes to cell-type-dependent patterns of antibody neutralization (Mukherjee et al., 2014a). To determine whether the cellular substrate used for virus production impacts neutralization sensitivity among the ZIKV strains studied, we repeated neutralization studies with viruses produced in C6/36 insect cells (Figure 2). When assayed on Raji-DCSIGNR cells, neutralization titers obtained with these insect cell-derived stocks were similar among different ZIKV strains (Figures 2A and 2C) and to titers obtained with the same virus strains propagated in Vero (B and D) cells. Infection was measured 20 hr post-infection by staining cells for intracellular E protein expression followed by flow cytometry. The dilution of sera at half-maximal neutralization of infection (EC$_{50}$) was estimated by non-linear regression analysis. The average EC$_{50}$ neutralization titers obtained from independent neutralization studies are presented. Error bars reflect the range of two experiments. No statistical differences in mean EC$_{50}$ were identified using ANOVA with a multiple comparisons correction.

Neutralization of ZIKV Reporter Virus Particles by Human Sera
Reporter virus particles (RVPs) are pseudo-infectious flaviviruses produced by complementation of a self-replicating sub-genomic flavivirus RNA with the structural genes provided in trans. We and others have used RVPs extensively to study the functional properties of neutralizing monoclonal antibodies (Pierson et al., 2007; Shrestha et al., 2010; Wang et al., 2016) and to evaluate the immunogenicity of candidate flavivirus vaccines in humans (Martin et al., 2007; VanBlargan et al., 2013). To confirm and extend the results of our studies with infectious ZIKV, we created RVPs that incorporate the structural proteins of five ZIKV strains representing African (MR-766 and ArB7701) and Asian (H/PF/2013, PHL/2012, and THA/2014) lineages. Studies with serum from subject NIH.2 revealed all five RVPs were neutralized equivalently (Figure 3A). More comprehensive studies were performed with MR-766 and H/PF/2013 RVPs and the entire panel of sera. The average EC$_{50}$ neutralization titers for multiple independent experiments are shown (Figures 3B–3I). These data confirm studies with fully infectious virus, demonstrating that strain-dependent differences in neutralization sensitivity are small, if they are present at all. Furthermore, comparison of the mean EC$_{50}$ for all samples evaluated with both RVPs and infectious virus revealed remarkable agreement (Figure S1). Limited studies with RVPs produced with the structural proteins of DENV and WNV revealed cross-reactive neutralization to varying degrees by ZIKV immune sera (Figure S2).

Analysis of ZIKV Strain-Dependent Neutralization in Mice
Mice lacking key components of the type I interferon signaling system have been defined as useful models of lethal ZIKV infection or in utero transmission (Aliota et al., 2016; Dowall et al., 2016; Lazear et al., 2016; Miner et al., 2016; Rossi et al., 2016).
Because these systems may have value in preclinical vaccine studies, we investigated whether mice, like humans, mount an antibody response to ZIKV infection capable of equivalently neutralizing multiple strains. Studies in mice additionally allowed for assessment of the neutralizing activity of ZIKV-immune sera without any possibility of prior flavivirus exposure or pre-existing cross-immunity. *Irf3*−/− mice, which allow ZIKV replication yet survive infection (Lazar et al., 2016), were infected with ZIKV strains MR-766 or H/PF/2013. Sera were collected and evaluated for neutralization using ZIKV RVPs displaying the homologous or heterologous structural proteins (Figures 4A and 4B). Sera from mice infected with either Asian or African ZIKV strains equivalently neutralized MR-766 and H/PF/2013 RVPs. These data confirm the broadly neutralizing activity of ZIKV-immune sera and suggest that strain selection or multi-antigen formulations will not be a critical parameter for the design of a ZIKV vaccine as long as strongly neutralizing antibody responses are elicited.

**DISCUSSION**

The rapid spread of ZIKV throughout South America and its linkage to birth defects in infants born to women infected during pregnancy has created a public health emergency that could be mitigated by vaccination. Vaccines have proven effective at blunting the impact of flavivirus infection on public health, most notably for YFV. The antiviral activity of convalescent and vaccine-induced antibodies reflects their capacity to bind to and neutralize virion infectivity, as well as mediate other effector functions (Burton, 2002; Nimmerjahn and Ravetch, 2008). Serum-neutralizing activity has proven to be a useful correlate of protection following vaccination against the related flaviviruses YFV, JEV, and TBEV. Phylogenetic analyses of ZIKV reveal that African and Asian lineages share >95% identity in amino acid sequences encoding the structural protein E targeted by neutralizing antibodies (Haddow et al., 2012). How amino acid variation among ZIKV strains impacts immunogenicity and
Figure 4. Neutralization of ZIKV RVPs with Sera from Mice Infected with ZIKV Strains H/PF/2013 or MR-766

In this study, we investigated the breadth of the neutralizing antibody response elicited by natural infection with ZIKV. Convalescent human sera or plasma obtained from individuals infected during the recent ZIKV epidemic were tested for their ability to neutralize infection of multiple strains of infectious ZIKV or ZIKV RVPs. This panel of human-immune sera or plasma neutralized contemporary Asian and historical African ZIKV strains equivalently, which suggests that ZIKV circulates as a single serotype. To extend these findings, we also investigated how the infecting ZIKV strain impacted the specificity of neutralizing antibodies. We demonstrate that mice infected with strain MR-766 or H/PF/2013 produced antibodies that neutralized both strains with equivalent potency. Our findings suggest antigens produced from African lineage viruses, such as the inactivated MR-766 vaccine candidate developed by Bharat Biotech, will elicit antibodies capable of neutralizing contemporary circulating strains.

Overall, our results define a single ZIKV serotype and suggest that infection or vaccination with a single ZIKV strain can elicit broadly neutralizing antibodies against multiple strains, providing a direct path for the development of an effective vaccine.

EXPERIMENTAL PROCEDURES

Clinical Samples
ZIKV convalescent sera or plasma were collected with informed consent at the NIH Vaccine Research Center and the Hope Clinic of the Emory Vaccine Center. Additional details and clinical protocol numbers related to the collection of these samples are provided in Table S1 and the Supplemental Experimental Procedures.

Virus Neutralization Studies
Detailed protocols for neutralization studies with viruses and RVPs are provided in the Supplemental Experimental Procedures and Figures 1–3 and have been described in detail recently (Mukherjee et al., 2014b). Serial dilutions of sera or plasma were mixed with virus or RVPs and incubated for 1 hr at 37°C in order to ensure steady-state binding. Immune complexes were added to cells and incubated for one or two days for infectious viruses and RVPs, respectively. RVP infection was scored as a function of GFP expression, whereas infectious virus detection was measured by intracellular staining with an E-protein-specific mAb. The resulting data were analyzed by non-linear regression to estimate the dilution of sera required to inhibit 50% of infection. The lower limit at which neutralization could be measured with confidence was determined to be a 1/60 dilution of sera based on experiments with normal human sera collected prior to the ZIKV outbreak in South America (n = 29).
Mouse Studies
This study was carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the NIH, and protocols were approved by the Institutional Animal Care and Use Committee at the Washington University School of Medicine (assurance no. A3381-01). ZIKV-immune sera used in neutralization studies were generated by infection of Ifr3−/− mice with a non-lethal 10^5 FFU dose of ZIKV strain H/PF/2013 or MR-766. Additional details can be found in the Supplemental Experimental Procedures.

Statistical Methods
Statistical analyses were performed using GraphPad Prism software. Mean EC50 values were compared using an unpaired t test or ANOVA with Tukey’s method for multiple comparisons correction and reported as p values or multiplicity-adjusted p values, respectively, when significant (\( \leq 0.05 \)).

SUPPLEMENTAL INFORMATION
Supplemental information contains Supplemental Experimental Procedures, two figures, and three tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2016.07.049.

AUTHOR CONTRIBUTIONS
K.D., C.D., R.P., S.S., A.S., L.G., and D.P. performed the experiments. K.D., M. D., and T. P. designed the experiments. J. M., B. G., M. M., and J. L. provided key reagents. K.D. and T.P. wrote the initial draft of the manuscript, and the other authors contributed to editing the final version.

ACKNOWLEDGMENTS
This work was funded by the intramural program of the National Institute of Allergy and Infectious Disease to the Division of Intramural Research and the Vaccine Research Center and extramural grant R01AI073755 to M.S.D. M.J.M. was supported by funds from the Emory University School of Medicine and the Georgia Research Alliance. We thank X. de Lamballerie (Emergence des Pathologies Virales, Aix-Marseille Universite´ ) and the European Virus Archive Goes Global (EVAg) for providing the H/PF/2013 ZIKV strain and Stephen S. Whitehead (NIAD) for the Brazil Paraiba/2015 virus. We are grateful to the Washington University School of Medicine (assurance no. A3381-01).

REFERENCES


1490 Cell Reports 16, 1485–1491, August 9, 2016


