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CD4+ T Cell Depletion Before Primary Dengue and/or Secondary Zika Infection Reveals

Mechanistic Correlates of Antibody Functionality in Rhesus Macaques.

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Running Title: CD4 T cell depletion before dengue or zika of rhesus macaques

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Abstract

Dengue (DENV) virus and Zika virus (ZIKV) are two flaviviruses of major public health concern. One drawback designing effective vaccines is our limited understanding of the mechanisms ruling protection or harm among DENV serotypes, or between DENV and ZIKV. Here, we depleted rhesus macaques of $CD4^+$ T cells *in vivo* before primary DENV infection and/or secondary ZIKV challenge to recreate a sub-optimal priming of the humoral immune response. Our results support that $CD4^+$ T cells are needed to induce a quantitative and type-specific effective humoral immune response against primary DENV, but also against secondary ZIKV in DENV-experimented subjects. Our results also indicate a limited contribution of the DENV-Memory B cells to anti-ZIKV response. Furthermore, our results suggest that a suboptimal B cell priming during a primary DENV infection does differentially impact different antibody (Abs) properties. While binding or neutralization of ZIKV or DENV during a subsequent exposure to ZIKV is not affected by the lack of $CD4^+$ T - B cells interaction during a primary DENV infection, that interaction is critical to guarantee the Abs specificity. Also, we found that depleting $CD4^+$ T cells before DENV primary infection but not before ZIKV challenge significantly increases Abs cross- reactivity against DENV-EDIII domain and DENV-NS1 protein but not against ZIKV-EDIII domain or NS1 protein. Furthermore, there was more cross-reactivity among the DENV-NS1 proteins than against DENV-EDIII domains, suggesting that during a primary DENV infection $CD4^+$ T cells have a different weight in the responses against EDIII domain and NS1 protein. The proper Abs binding and neutralization with increased cross-reactivity profile was associated with limited frequency of circulating peripheral T helper cells (pTfh) with T helper 1 phenotype (CD4+/CXCR5+/CXCR3+) and expressing markers related to B cell activation (CXCR5+/CXCR3+/PD-1+/ICOS+) in the group depleted of $CD4^+$ T cells only before primary DENV infection. However, memory B cells – but not Antibody Secreting Cells (ASC) activation 7 days after the infection – positively correlate with those two populations of pTfh. Finally, when Abs cross-reactivity values were incorporated in a Principal Component Analysis (PCA), the DENV- $CD4^+$ T depleted group separates from the other two groups with similar Abs binding and neutralization profiles. Our result strongly suggests that during a heterologous sequential DENV/ZIKV infections Abs binding, and neutralization, may be regulated by different factors than their specificity. Before, the induction of cross-neutralizing Abs has been described in the context of secondary DENV infection. Here, for the first time, we are reproducing the experimental conditions leading to the generation of such Abs population *in vivo*. In summary, we show that suboptimal immune priming during a primary flavivirus infection has functional consequences during a secondary heterologous infection. These results have huge implications understanding the immune response to DENV vaccines (and maybe ZIKV), including why an optimal vaccine or natural-induced neutralizing response not necessarily protects or enhances pathogenesis during a subsequent natural heterologous exposure.

Introduction

Dengue (DENV) and Zika (ZIKV) viruses are flaviviruses of significant public health concern (Li et al., 2021; Paixao et al., 2022; Qiao et al., 2021; Tian et al., 2022; Wong et al., 2022). DENV is responsible for about 390-500 million infections per year, of which 96 million present different levels of disease severity (Bhatt et al., 2013) including Dengue Hemorrhagic Fever/ Shock Syndrome with up to 20 % mortality rate if untreated (WHO/TDR, 2009). It is estimated that the population at risk will increase in 60% by 2080 for a total of 6.1 billion people (Messina et al., 2019). ZIKV infections are usually mild but have been associated with unique severe adverse outcomes such as fetal loss (Campos et al., 2016), congenital ZIKV syndrome (CZS) (Brasil et al., 2016), Guillain-Barré syndrome (GBS) (Cao-Lomeau et al., 2016), and rare cases of encephalopathy (Roze et al., 2016), meningoencephalitis (Carteaux et al., 2016), myelitis (Mecharles et al., 2016), uveitis (Furtado et al., 2016), and severe thrombocytopenia (Sharp et al., 2016).

DENV and ZIKV circulate in similar geographic areas (Braga et al., 2017; Rodriguez-Morales et al., 2016), and the effect of prior DENV or ZIKV immunity to each other is subject of an ongoing debate. Some evidence from animal models and humas suggest that prior DENV immunity has a protective role in secondary ZIKV infection (Ana Carolina Bernardes Terzian, 2017; Breitbach et al., 2019; McCracken et al., 2017; Pantoja et al., 2017). Other works propose that prior DENV infection may increase ZIKV disease severity (Bardina et al., 2017; Crooks et al., 2021; Katzelnick et al., 2020b; Katzelnick et al., 2021). Intermediate pre-existing levels of naturally acquired anti-DENV or anti-ZIKV antibodies (Abs) were found to be associated with enhancement of symptomatic and severe DENV. However, subjects with high anti-DENV or anti-ZIKV Abs are at much lower risk of symptomatic and severe DENV2, with rates similar to DENV-naïve individuals (Katzelnick et al., 2020a). To add complexity to the field, recently it has been documented that different DENV and ZIKV interactions can be different or asymmetrical depending on the DENV serotype {Bos, 2023 #2166; Katzelnick, 2020 #2029. Nevertheless, the mechanisms supporting a proportionate immune response among all four DENV serotypes or DENV and ZIKV after a natural infection – particularly after vaccination – still remains as a critical knowledge gap.

Immunity to one DENV serotype is believed to confer type specific (TS) protective Abs or immunity to that infecting serotype, but can also induce cross-reacting (CR) Abs able to amplify the pathogenesis during a secondary infection with a different serotype – a phenomenon known as antibody-dependent enhancement (ADE) (Guzman et al., 2013; Halstead, 2003; Halstead et al., 1983; Katzelnick et al., 2017). As a result, DENV vaccines are designed as tetravalent formulations to induce balanced Abs (Abs) response against all four DENV serotypes at the same time. Two of the leading DENV vaccines (Dengvaxia and TAK-003), based on attenuated chimeric viruses (Deauvieau et al., 2007; Guy et al., 2017; Huang et al., 2013; Osorio et al., 2011b) has shown to induce unbalanced immune responses (Biswal et al., 2020; Guirakhoo et al., 2002; Hadinegoro et al., 2015; Halstead, 2018; Sabchareon et al., 2012; White et al., 2021). A third vaccine candidate developed by the Laboratory of

Infectious Diseases at the National Institutes of Health (TV003) based on live attenuated DENV viruses (Durbin

et al., 2013; Durbin et al., 2011; Whitehead, 2016), induced TS Abs to all four DENV serotypes and protection

against challenge (Kirkpatrick et al., 2016; Nivarthi et al., 2021). Recent results from phase 3 are encouraging,

but differences in efficacy were still reported between DENV1 [89.5% (95% CI, 78.7 to 95.0)] and DENV2

[69.6% (95% CI, 50.8 to 81.5)] the two serotypes detected in the three years of follow up period (Kallás et al.,

2024). The limitations of Dengvaxia and TAK-003 formulations in inducing a balanced immune response to all

four DENV serotypes have been associated to unequal replication of vaccine components or to the lack

of/incomplete cellular immune response to the nonstructural (NS) proteins, among others (Grifoni et al., 2020;

Guy et al., 2008; Guy et al., 2020; Thomas et al., 2009; Waickman et al., 2019a; Waickman et al., 2019b). For

Dengvaxia, the DENV4 component was replicating and immunodominant, compared to the other three serotypes

(Guy et al., 2009); a similar situation is documented with DENV2 in the TAK-003 vaccine in non-human primates

(NHP) and humans (Osorio et al., 2011a; Rupp et al., 2015; Tricou et al., 2020).

Total Abs to each DENV serotypes have been used as a marker of protection for DENV vaccines, as it has shown

to correlate with the efficacy of other flavivirus vaccines like yellow fever vaccine (YFV), Japanese encephalitis

vaccine (JEV) (Appaiahgari et al., 2006; Goncalvez et al., 2008; Gupta et al., 2008; Raengsakulrach et al., 1999;

Saini and Vrati, 2003), and tick-borne encephalitis (TBEV) (Beran et al., 2019; Leonova and Pavlenko, 2009;

Maikova et al., 2016; Venturi et al., 2009; Vorovitch et al., 2019). But recent growing evidences point out that TS

neutralizing Abs (nAbs) above a certain threshold may be a better indicator of vaccine efficacy than the total Abs

(Henein et al., 2021; Nivarthi et al., 2021). Earlier works also provide explanations as of why some Abs might

neutralize DENVs in cell culture, but not protect *in vivo* (Raut et al., 2019). Martinez et al. assembled a

comprenhensive review on the multiple factors modifiying the efficacy of the immune response to DENV and

DENV vaccines, incluidng the intra and inter serotypic viral antigenic diversity and the genotypic diversity among

others {Martinez, 2021 #2068}.

All those observations and findings from natural infections and vaccines are supported on Abs response mainly

against the structural proteins, reinforcing the concept that immunogenicity of the structural proteins does not

guarantee protection from natural infection or vaccination efficacy. Most humoral immunity epitopes are located

within the domains of the DENV envelope (E) protein, while cellular immunity epitopes are located on the NS

proteins (Pinheiro et al., 2021; Rothman, 2010). Additionally, the NS1 protein is particularly interesting and

unique, as it is a protein produced and secreted during viral replication, which make it highly immunogenic (Zhang

et al., 2023) inducing significant levels of anti-NS1 Abs in DENV- and ZIKV-infected individuals (Aquino et al.,

2023; Castro-Trujillo et al., 2023; Churdboonchart et al., 1991; Costa et al., 2007; Petphong et al., 2023). It is

documented that DENV E and NS1 proteins equally score 4 – out of the 10 proteins – in an immunogenicity score

(Weiskopf et al., 2016), and some reports have pointed NS1 as a target antigen for the development of DENV

vaccines (Costa et al., 2007; Costa et al., 2006; Henchal et al., 1988; Wan et al., 2014), while others suggest a role

for this protein in the pathogenesis (Perera et al., 2024; Shu et al., 2000; Zhang et al., 2023). Thus, it still remains
a puzzle due to its ability to elicit both protective and potentially pathogenic immune responses. On this work, in
addition to the conventional Abs to the structural proteins, we explore the contribution of NS1 to the immune
response during the primary DENV infection and a secondary ZIKV challenge.
Beyond the cannonical humoral component, a robust T cell response is needed to confer protection after a natural
DENV or ZIKV infection (Elong Ngono and Shresta, 2019; Roth et al., 2018; Tian et al., 2019; Weiskopf and
Sette, 2014; Yauch et al., 2009) and most of the cognates epitopes for the T cells (CD4^{+} and CD8^{+} T cells) are
located in the NS proteins (Grifoni et al., 2017b; Rivino et al., 2013; Rivino and Lim, 2017). Despite this, one
common aspect shared among all three leading DENV vaccines is that they do not present NS proteins of all
DENV serotypes to the immune system. Dengvaxia is based on a Yellow Fever (YF) 17D backbone and contains
no DENV NS proteins (Guirakhoo et al., 2001). The Takeda vaccine uses a DENV-2 backbone and has only
DENV-2 NS proteins (Huang et al., 2013; Kinney et al., 1997). The NIH/Butantan/MSD vaccine has full genome
DENV-1, -3, and -4 components with a DENV-2/-4 chimera based on a DENV-4 backbone. This vaccine possesses
NS proteins from DENV-1, -3, and -4 but not of DENV2 (Blaney et al., 2006; Blaney et al., 2008; Whitehead et
al., 2003a; Whitehead et al., 2003b). Further, data on the contribution of T cells and their cognate epitopes on the
NS proteins to the vaccine efficacy, and potentially protection, is still restricted (Angelo et al., 2017; Guy et al.,
2008; Tricou et al., 2022; Waickman et al., 2019a; Weiskopf et al., 2015a). These data underscore how the
contribution of NS proteins and T cells has been understudied in the context of DENV vaccination. Pinheiro et al.
completed a comprehensive analysis of B and T cells epitopes shared by all three leading DENV vaccines, and
concluded that investing in vaccines that contain most of the epitopes involved in protective immunity (cellular
and humoral arms) is an important issue to be considered (Pinheiro et al., 2021). In fact, a few years ago the World
Health Organization (WHO) recommended that the cell mediated immunity (CMI) induced by DENV vaccines
should be studied in detail (Thomas et al., 2009).
Also, it has been shown that CD4^{+} T cells are essential for inducing a protective immune response against DENV
and ZIKV (Elong Ngono et al., 2019; Grifoni et al., 2017a; Grifoni et al., 2017c; Hassert et al., 2018; Manh et al.,
2020; Weiskopf et al., 2015b; Wen et al., 2020); these cells play a critical role connecting the cellular and humoral
immune responses though unique interactions with B cells (Crotty, 2015; Swain et al., 2012). Moreover,
immunological characterization of T cells has identified the presence of follicular CD4^{+} T helper cells (Tfh) or
"Tfh-like" in blood, known as circulating (cTfh) or peripheral (pTfh) cells. These cells have been described, in
terms of function, as the equivalent counterpart of germinal center (GC) Tfh cells in peripheral blood (Bentebibel
et al., 2013; Crotty, 2014; Morita et al., 2011). However, there is limited literature available on the role of pTfh
cells in DENV (Haltaufderhyde et al., 2018; Izmirly et al., 2022; Wijesinghe et al., 2020) and ZIKV vaccination
or infections (Liang et al., 2019; Pardy et al., 2022). Despite their critical role helping B cells form an optimal
humoral immune response, there are scarce works studying the direct interactions of CD4^{+} T cells/pTfh cells

subsets with B cells and NS proteins, and its effect in Abs functionality against DENV and/or ZIKV (Elong Ngono

et al., 2019; Rivino et al., 2013; Rouers et al., 2021). Using a NHP model – rhesus macaques – we asked how the

lack of essential cells, such as CD4$^+$ T cells, impacts the quality of the humoral immune response (including the

response to NS1 protein) during a primary DENV2 infection and its consequences in the response to a secondary

heterologous ZIKV infection. We believe this is the type of mechanistic questions that needs to be addressed in

order to identify correlates of protections and ultimately design more efficient flavivirus vaccines.

In this work, we depleted rhesus macaques of CD4$^+$ T cells before a primary DENV2 infection and/or before a

subsequent ZIKV infection one year apart. A cohort was depleted of CD8$^+$ T cells before the secondary challenge

with ZIKV.

We found that the lack of CD4$^+$ T cells before infections results in a significant increase in DENV viremia and

DENV-NS1 antigenemia and ZIKV viremia. Lack of CD4$^+$ T cells before DENV or ZIKV also results in a delay

in total Abs switch documented by limited IgM and IgG production and in a significantly lower anti-DENV and

anti-ZIKV NS1 Abs response. We also found that Abs binding or neutralizing DENV or ZIKV after heterologous

challenge with ZIKV secondary infection were minimally impacted by the lack of CD4$^+$ T cells during DENV

primary infection. Nevertheless, the presence of these cells during the primary DENV infection were critical to

preserve the specificity of the Abs against the DENV, but not ZIKV EDIII domain and NS1 protein after ZIKV

challenge.

This profile of Abs functionality (proper binding and neutralization with increased cross-reactivity) was

associated with a significant lower frequency of pTfh TH1 and expression of markers related to B cell activation

– PD-I and ICOS – when CD4$^+$ T cells were not present during the primary DENV infection. Furthermore, the

expression of these markers correlates with the activation of the MBC, but not ASC, in the same group.

Interestingly, the depletion of CD8$^+$ T cells abrogates the direct correlation between those cell subsets and MBC

or ASC activation.

With our experimental design, we could reproduce *in vivo*, first the time, the mechanism inducing those CR nAbs.

This Abs population was described in the context of secondary DENV infections (Patel et al., 2017) and has been

at the center of an active debate on their protective or pathogenic contribution to the flavivirus response.

Our findings are critical to understand the efficacy limitations of Abs induced by current approved DENV

vaccines or protecting from natural infections and thus are essential to guide the new generations of DENV and

ZIKV vaccines. We also provide an animal model to reproduce an immunological signature of the response to

flaviviruses that can be used to test and challenge the protective or disease-enhancing attributes of current and

new vaccine candidates or, as in this work, to better characterize flavivirus interactions.

We are unaware of any prior work addressing the complex interactions among CD4$^+$ T cells, B cells and NS

proteins in response to flavivirus infection in NHPs.

Results

Rhesus macaque cohorts, T cell depletion and sample collection. Five groups of flavivirus-naïve rhesus

macaques (*Macaca mulatta*) (SFig 1). Prior to any experimental activity, all animals were put through a quarantine

period of 40 days. Depletion of T cells was performed by initial subcutaneous (s.c.) administration of 50 mg/kg

of anti-CD4+ treatment at 15 days pre-challenge, followed by two intravenous (i.v.) administrations of 7.5 mg/kg

at 12- and 9-days pre-challenge. Animals were depleted of CD4+ or CD8 T+ cells, or administered phosphate

buffer saline (PBS), followed by a primary infection with DENV-2 ($5x10^5$ pfu s.c.) and a subsequent ZIKV

challenge (1×10^6 pfu s.c.) one year later, after a second round of T cell depletion – or administration of PBS –

before infection. CD4+ T cell depletion was performed on groups 1 and 3 prior to primary DENV2 infection and

on groups 1 and 2 prior to secondary ZIKV infection (group 1: n=6, denoted CD4-/DV2/CD4-/ZV; group 2: n=6,

denoted CD4+/DV2/CD4-/ZV; group 3: n=6, denoted CD4-/DV2/CD4+/ZV). Group 4 is CD4-competent but

CD8-depleted prior to secondary ZIKV infection (n=6, denoted CD4+/DV2/CD8-/ZV). Group 5, the control

group, was treated with PBS before each infection (n=5, denoted CD4+/DV2/CD4+/ZV).

Depletion of CD4+ T cells elicits a CD8+ T cell overcompensation, and vice-versa. To determine if the

depletion treatment was effective, frequency of CD4+ and CD8+ T cells was assessed by immunophenotyping

using flow cytometry during pre-treatment (pre-TX), post-treatment (post-TX), and post-primary DENV2

infection. Before depletion, CD4+ T cell frequency was similar in all animals and decreased by day 2 post-TX,

resulting in a depletion of 99.8% (SFig 2A). This reduction was consistent until day 7 post infection (p.i.), when

they began to slowly recover by day 15 post infection p.i.. Further, the absence of CD4+ T cells in depleted

animals promoted an increase in CD8+ T cell frequency (SFig 2B).

CD4+ and CD8+ T cell frequencies were also measured before, during and after depletions prior to and during

ZIKV challenge (SFig 2C and D). Similar to the prior scenario, CD4+ T cell frequency was similar in all animals,

and decreased by day 2 after treatment start (SFig 2C). Interestingly, animals that underwent CD8+ T cell

depletion experimented an increase in CD4+ T cell frequency (SFig 2C). Lastly, CD8+ T cells behaved similarly

to CD4+ T cells after depletion, with frequency decreasing by day 2 post-TX and beginning to recover by day 7

post-challenge (p.c.), while CD4-depleted animals showed an increase in CD8+ T cell frequency (SFig 2D).

CD4+ T cell depletion impairs DENV2 viral clearance in flavivirus-naïve macaques. To determine if CD4+

T cell depletion enhances or reduces DENV2 replication, and how it changes depending on various depletion

conditions, DENV2 RNAemia was measured in serum during the first 15 days after primary DENV2 infection.

During the first 3 days p.i., viral RNA detection increased similarly in all groups (Fig 1A). By day 5 p.i., the

control group starts resolution of viremia, while the CD4-depleted group still had high detectable RNAemia levels.

By day 10 p.i. there was no viral RNA detection in any animal from the control group, indicating a faster

RNAemia resolution in this group compared to the CD4-depleted animals. This suggests a delay in viral clearance
in animals that are CD4-deficient. By day 13 p.i. all animals tested negative for DENV2 (Fig 1A and Table S1).
When evaluating the area under the curve (AUC), we found that the CD4-competent animals, although not
statistically significant, had lower values, on average, than the CD4-depleted group (Fig 1B). Next, we evaluated
the average RNAemia days, defined as the days with detectable viremia divided by the total number of days
during which viremia was assessed, considering the number of animals per group (Fig 1C). The undepleted
animals had significantly less mean RNAemia days compared to the depleted animals (p= 0.0132). Taken
together, these results suggest that CD4$^+$ T cells have an early role controlling DENV2 RNAemia, but it remains
unknown if this is due to a direct action or to an interaction with B cells.
234
CD4+ but not CD8+ T cells are necessary to control ZIKV RNAemia in DENV-immune macaques. To
assess the impact of T cell depletions in ZIKV replication in DENV2-immune animals, and how it changes
depending on various depletion conditions, ZIKV RNAemia was measured in serum during the first 15 days and
on day 30 after secondary ZIKV challenge using qRT-PCR. The CD4+/DV2/CD8-/ZV group had the lowest
ZIKV RNAemia compared to group CD4-/DV2/CD4+/ZV on day 1 (p< 0.043), to the control group
CD4+/DV2/CD4+/ZV on day 2 (p< 0.007) and to the double negative group CD4-/DV2/CD4-/ZV on days 2 and
4 p.c. (p< 0.005 and p< 0.02 respectively). Also, the control double positive group had significantly lower ZIKV
RNAemia compared to the double-depleted group on day 4 p.c. (p< 0.01) (Fig 1D and Table S2).
By day 7 p.c., there was no viral RNA detection in any group. Serum samples from days 15 and 30 p.c. were
tested in order to evaluate intermittent viremia. Historical data from our laboratory shows that ZIKV replication
in naive undepleted animals is significantly higher than ZIKV replication in DENV-immune animals regardless
of CD4+ T cell status.
We observed a difference when comparing all five groups based on AUC (Fig 1E). Although not statistically
significant, the CD8-depleted group had slightly lower AUC levels, even lower than the undepleted control group.
Additionally, the CD4-double depleted group had the highest AUC levels.
Lastly, when evaluating the mean RNAemia days, the control undepleted animals had the least viremia days,
which was significantly lower compared only to the double-depleted group (Fig 1F).
Next, we wanted to evaluate the actual CD4+ T cell contribution controlling the ZIKV RNAemia. For this, we
grouped the animals together according to their depletion status. Comparing the depleted (groups 1 and 4) vs.
non-depleted animals (groups 2, 3 and 5) before DENV2 infection resulted in a non-significant trend (p< 0.064)
to lower ZIKV viremia days in the undepleted groups (Table S2) and in very similar AUC values (351.8 and
370.2 for the depleted and undepleted groups, respectively).
However, when the two groups depleted before ZIKV infection (groups 1 and 2) were compared with the other
three undepleted groups (groups 3, 4 and 5), there was a significantly higher viremia peak by day 4 in the CD4$^+$

259 T cells-depleted animals (p= 0.03). Also, the AUC value for the CD4-undepleted groups before ZIKV infection

260 (490.0) almost doubles the value of the depleted groups (272.0) (Fig 1E). Furthermore, together, the depleted

261 groups have significantly higher mean viremia days than the CD4+ T cells undepleted groups (p= 0.006) (Fig

262 1F).

263 Taken together, these results confirm the requirement of CD4+ T cells for an optimal control of DENV2

264 replication during a primary infection. In addition, our findings propose an important role for CD4$^+$ T cells

265 controlling secondary ZIKV infection and that role being independent of prior DENV experience. Lastly, this

266 indicates that CD8+ T cells may not be required for ZIKV viral replication control in individuals with prior

267 DENV2 immunity.

269 **CD4$^+$ T cell depletion results in higher detection of DENV NS1.** To confirm viremia and to explore the role of

270 CD4+ T cells in the generation of NS1 antigen, we measured DENV NS1 levels in serum. Since NS1 antigen is

271 generally detected during days 1 to 9 p.i., we tested samples from baseline and days 3, 5, 7, 10, 15 and 30 post

272 DENV2 infection (SFig 3). As expected, no detectable levels of NS1 were observed at day 0 on any of the groups.

273 On days 3, 5, 7 and 10 p.i., an increase in NS1 levels was observed on all animal groups, with CD4-depleted

274 animals having slightly higher NS1 levels in comparison to the undepleted animals by day 10 p.i.. By day 15 p.i.,

275 NS1 levels were significantly higher in depleted animals (p< 0.0001) compared to undepleted animals, where

276 NS1 levels are completely undetectable. This is of particular interest because by this time, detection of DENV-

277 NS1 is not expected. This suggests that the lack of CD4$^+$ T cells enhances NS1 circulation, which correlates with

278 enhanced pathogenesis, further confirming a protective role for CD4$^+$ T cells during primary DENV infection.

280 **Lack of CD4+ T cells during a primary DENV2 infection does not hinder antibody binding to ZIKV in a**

281 **secondary exposure.** We evaluated the impact of CD4$^+$ and CD8$^+$ T cell depletion on the quantity and quality of

282 the humoral response against DENV2 and ZIKV infections. Anti-DENV IgM and IgG levels were measured after

283 primary DENV2 infection (Fig 2). CD4-depleted animals had significantly lower levels of anti-DENV IgM in

284 comparison to the undepleted animals by days 10 and 15 p.i. (p< 0.001) (Fig 2A). Furthermore, total anti-DENV

285 IgM produced from day 0 to day 15 p.i. was significantly lower in the CD4-depleted group in comparison to the

286 control group (p= 0.007) (Fig 2C). On the other hand, anti-DENV IgG levels were statistically different between

287 groups only on day 15 p.i., where the CD4-depleted group had lower levels compared to the control group (p<

288 0.001) (Fig 2B). Similar results were observed with the total anti-DENV IgG produced (from day 0 to day 30),

289 where CD4-depleted animals had significantly lower IgG values in comparison to undepleted animals (p= 0.0153)

290 (Fig 2D). IgG levels by days 60 and 90 p.i. were at similar levels in both groups. These results suggest a delay in

291 B cell activation and in isotype class switching during primary DENV infection related to the lack of CD4$^+$ T

292 cells.

Additionally, DENV and ZIKV binding IgM and IgG levels were measured after secondary ZIKV challenge (Fig

3). As expected, all animals had no detectable anti-DENV IgM at baseline and remain consistently low throughout

days 7,10 and 15 p.c. (Fig 3A). At day 15 p.c. only one animal from the control group and one from the

CD4+/DV2/CD8-/ZV group had values over the assay threshold, further indicating the positive role of CD4$^+$ T

cells in the magnitude of the humoral immune response during primary DENV infection. In contrast, all animals

had similar detectable anti-DENV IgG levels at baseline (Fig 3B). As expected, ZIKV infection transiently

boosted cross-reacting binding Abs which declined by day 30 p.c. in all groups (Fig 3B). However, the magnitude

of this boost was significantly impacted on day 15 p.c. by the lack of CD4+ T cells. Lower anti-DENV IgG levels

were observed in the two groups lacking CD4+ T cells before ZIKV challenge (double CD4-depleted and

CD4+/DV2/CD4-/ZV). The significance between group CD4-/DV2/CD4-/ZV with groups

CD4+/DV2/CD4+/ZV, CD4+/DV2/CD8-/ZV and CD4-/DV2/CD4+/ZV was statistically significant (p< 0.019,

p< 0.008 and p< 0.047 respectively). The differences between the CD4+/DV2/CD4-/ZV with the

CD4+/DV2/CD4+/ZV and CD4+/DV2/CD8-/ZV groups were also significant (p< 0.018 and p< 0.040

respectively). There were no differences among the three groups with CD4$^+$ T cells before ZIKV infection.

Altogether, these results indicate that DENV-experimented CD4$^+$ T cells do not contribute to an optimal humoral

immune response to ZIKV. This also suggests that DENV MBCs have a limited expansion during a secondary

ZIKV infection and if they have, the expansion is CD4-independent.

Anti-ZIKV IgM levels became detectable by day 7 p.c. with a peak by day 15 and started declining by day 30 p.c.

(Fig 3C). By day 10 p.c., the control group had significantly higher levels than at least two groups, the doubled-

depleted group (p< 0.030) and the CD4-/DV2/CD4+/ZV group (p< 0.033). By day 15 p.c., the differences between

the control undepleted group and the two other groups undepleted of CD4+ T cells before ZIKV challenge were

significant (CD4-/DV2/CD4+/ZV, p< 0.022 and CD4+/DV2/CD8-/ZV, p< 0.028). However, the two groups

depleted of CD4+ T cells before ZIKV challenge have the lowest levels of ZIKV-binding IgM compared to the

three undepleted groups (group CD4+/DV2/CD4+/ZV vs. CD4-/DV2/CD4-/ZV and CD4+/DV2/CD4-/ZV p<

0.0001 and p< 0.0001 respectively, group CD4-/DV2/CD4+/ZV vs. CD4-/DV2/CD4-/ZV and CD4+/DV2/CD4-

/ZV p< 0.001 and p< 0.053 respectively and group CD4+/DV2/CD8-/ZV vs. CD4-/DV2/CD4-/ZV and

CD4+/DV2/CD4-/ZV p< 0.001 and p< 0.004 respectively).

Of note, some of the CD4-/DV2/CD4-/ZV animals had a late modest boost in ZIKV IgM levels by day 30 p.c.

after the initial observed delay; interestingly, all depleted animals before ZIKV challenge induced the lowest IgM

levels. Together, these observations suggest a delayed ZIKV-naïve B cell expansion in absence of CD4+ T cells.

Results from ZIKV-binding IgG Abs were similar to the IgM results (Fig 3D). By day 10 p.c. the two groups

depleted of CD4+ T cells before the challenge showed the lowest values. The values were significantly lower in

the group depleted of CD4+ T cells only before ZIKV challenge (CD4+/DV2/CD4-/ZV) compared to the

CD4+/DV2/CD4+/ZV (p< 0.004) and CD4-/DV2/CD4+/ZV (p< 0.0001) groups. By day 15 p.c. this trend was

maintained. Results reached statistical significance between the control undepleted group and the double-depleted
group (p< 0.003) and the CD4+/DV2/CD4-/ZV group (p< 0.001) and between the CD4-/DV2/CD4+/ZV group
with the CD4-/DV2/CD4-/ZV and the CD4+/DV2/CD4-/ZV groups (p< 0.001 and p< 0.0007 respectively).
An interesting finding was the presence of detectable cross-reacting anti-ZIKV IgG levels at baseline only in the
group depleted of CD4+ T cells before primary DENV infection but not before ZIKV challenge (CD4-
/DV2/CD4+/ZV) with significant higher values when compared to the CD4+/DV2/CD4-/ZV and the
CD4+/DV2/CD4+/ZV groups (p< 0.031 and p< 0.037 respectively). The double-depleted group also had higher
cross-reactive IgG levels compared to the undepleted groups but did not reach statistical significance. This result
suggests an increased expansion of DENV-cross-reactive B cell clones in animals without CD4$^+$ T cells during
primary DENV infection.
To confirm our results on the anti-ZIKV IgG, we analyzed the total ZIKV-specific IgG produced on days 10, 15
and 30 p.c. (Fig 3E). Double-depleted animals had significantly less total ZIKV IgG production compared to the
CD4-competent animals before ZIKV challenge (p= 0.0002 compared to CD4-/DV2/CD4+/ZV group, p= 0.0200
compared to CD4+/DV2/CD8-/ZV group and p= 0.0065 compared to CD4+/DV2/CD4+/ZV). Similarly, the
CD4+/DV2/CD4-/ZV group had lower IgG production compared to the CD4-/DV2/CD4+/ZV, CD4+/DV2/CD8-
/ZV and CD4+/DV2/CD4+/ZV groups (p= 0.0003, p= 0.0322 and p= 0.0108, respectively). In general, CD4-
depleted animals before ZIKV challenge produced significantly less total ZIKV-specific IgG.
These results indicate that while CD4$^+$ T cells during a primary DENV infection have limited impact in the binding
of ZIKV-specific Abs, their absence may result in a significant induction of flavivirus CR B cell clones (Fig 2D)
during a secondary infection. This also indicates that DENV-induced MBC populations generated during a
primary DENV infection have limited contribution in the anti-ZIKV-binding Abs after ZIKV infection. In
addition, these results suggest that CD4$^+$ T cells are required for a more effective and specific antibody response
against ZIKV.
350
Recall memory to DENV NS1 is expanded by lack of CD4+ T cells before DENV2 infection. Next, we
performed an anti-DENV NS1 assay using samples from baseline and days 15, 30 and 90 after primary DENV2
infection (SFig 4A). No DENV NS1 anti-IgG levels were detected on day 0 as expected. However, by day 15 p.i.,
depleted animals had significantly lower levels in comparison to the undepleted animals, similar to anti- DENV
IgG levels previously presented (p= 0.0003). By day 30 p.i., both groups had reached similar anti-NS1 IgG levels.
Interestingly, by day 90 p.i. depleted animals showed significantly higher anti-NS1 IgG levels compared to
undepleted animals (p= 0.0003), altogether supporting the delay in Abs switch in this group as seen in the total
IgG Abs response.
We also measured DENV NS1 anti-IgG levels in samples from baseline and days 15, 30 and 90 after secondary
ZIKV challenge (SFig 4B). Of note, on baseline the group depleted of CD4$^+$ T cells before DENV infection but

not ZIKV (CD4-/DV2/CD4+/ZV) had higher values when compared to the groups with CD4$^+$ T cells prior to

DENV infection, and they were significantly higher particularly in comparison to the CD4+/DV2/CD4-/ZV group

(p= 0.002). Although not significant, the double-depleted group had similarly high values in comparison to the

groups with CD4+ T cells prior to DENV infection. This implies that the lack of CD4$^+$ T cells before primary

DENV infection also results in an increased durability of NS1 Abs. By day 15 p.c., we observed significantly

higher values of DENV NS1 anti-IgG in the CD4-/DV2/CD4+/ZV group in comparison to all other groups (CD4-

/DV2/CD4-/ZV, p= 0.0124; CD4+/DV2/CD4-/ZV, p= 0.0002; CD4+/DV2/CD4+/ZV, p= 0.0094 and

CD4+/DV2/CD8-/ZV, p= 0.0152). This trend is maintained by day 30 p.c. (CD4-/DV2/CD4-/ZV, p= 0.0053;

CD4+/DV2/CD4-/ZV, p< 0.0001; CD4+/DV2/CD4+/ZV, p< 0.0001 and CD4+/DV2/CD8-/ZV, p< 0.0001).

Intriguingly, similar to what we stated on the previous section, these results seem to imply that deficiency of CD4$^+$

T cells during the primary DENV2 infection modifies the recall memory quantitatively resulting in an increased

DENV NS1-cross-reactivity induced by ZIKV.

Lastly, no significant differences between groups were observed on day 90 p.c.. Of note, some animals belonging

to the CD4+/DV2/CD4-/ZV group exhibited a marked separation between IgG values, indicating that antibody

repertoire may be different between individuals even sharing similar conditions.

Depletion of CD4+ T cells only prior to DENV infection increases ZIKV NS1-binding IgG after ZIKV

infection. To further study the impact of CD4+ T cells in the generation of CR and specific Abs, we measured

anti-ZIKV NS1 IgG levels in serum at days 0, 15, 30 and 90 p.c. (SFig 5). Contrary to the total IgG, no animals

had, regardless of their CD4+ T cell status, detectable anti-ZIKV-NS1 IgG Abs at baseline, indicating that those

Abs are very specific. However, by day 15 p.c., only animals with CD4+ T cells before ZIKV challenge produced

detectable IgG levels, with the exception of one animal from the CD4+/DV2/CD4-/ZV group (SFig 5). Double-

depleted animals had the lowest IgG levels of all groups, significantly different from the control group (p= 0.0003)

and the CD4-/DV2/CD4+/ZV group (p= 0.0004) on day 15 p.c. Additionally, NS1 IgG levels from the double-

depleted group were significantly lower in comparison to the CD4-/DV2/CD4+/ZV group (p= 0.0071) also on

day 30 p.c.. The latter group was consistently the highest IgG-producing group, even higher than the control

group. Unsurprisingly, CD8-depleted animals behaved similarly to the control group as they both have intact CD4

T cells populations before the primary infection and the challenge. By day 90 p.c. almost all animals, regardless

of their depletion status, had no NS1-IgG levels. Collectively, these data suggests that DENV-experienced CD4$^+$

T cells have limited or no effect on the production of anti-ZIKV NS1-abs during a secondary ZIKV exposure.

Early DENV2 neutralization activity is delayed by lack of CD4+ T cells. To determine the contribution of Abs

to DENV2 and ZIKV neutralization and the impact of CD4+ and CD8+ T cell depletion, all groups were tested

using FRNT and PRNT assays against DENV2 and ZIKV respectively (Fig. 2 and 3). Neutralization assays were

completed for baseline and days 15, 30 and 90 p.i. for DENV-2 and days 15, 30 and 90 p.c. for ZIKV. The 50%

effective concentration (EC) of neutralizing Abs is shown in Figures 3 and 4 as well. As expected, no animals

had nAbs against DENV2 at baseline before primary infection (Fig 4A). By day 15 p.i., a significantly lower

neutralizing activity is observed in the CD4-depleted animals in comparison to the undepleted group (p< 0.0001)

(Fig 4B). This trend is not observed on day 30 p.i., when both groups behave similarly (Fig 4C). Endpoint titers

dilutions are shown in Figures 3D and 3E in order to facilitate a better interpretation. Similar to the scenario

described above, significantly lower EC50 values are observed in the depleted animals (p= 0.0032) (Fig 4D).

PRNT assays were performed after ZIKV challenge; despite the detection of anti-ZIKV IgG at baseline in some

groups, no neutralizing activity was observed at that time point against ZIKV (Fig 5A). However, on day 15 p.c.,

the CD4-double depleted group was the lowest at neutralizing ZIKV (Fig 5B). Animals belonging to the CD4-

/DV2/CD4+/ZV group and interestingly those from group CD4+/DV2/CD8-/ZV, having a higher frequency of

CD4+ T cells, have better neutralizing activity by day 15 p.c. compared to the other three groups – even the

undepleted control group. Those differences were statistically significant compared to the double-depleted group

(p= 0.0231 and p= 0.0155 respectively). Taken together, these results lead us to consider that DENV-primed

CD4$^+$ T cells have a limited contribution to an effective early neutralization during a secondary ZIKV infection

and that the magnitude of neutralization can correlate with the frequency of those cells.

By day 30 p.c., a change in neutralization profile is observed in all groups except the double-depleted animals,

which still show a delay in neutralization in comparison to the other groups (Fig 5C). By day 90 p.c., all groups

behave similarly in terms of neutralization magnitude (Fig 5D). Endpoint titers dilutions are shown in Figures 4F-

H in order to facilitate a better interpretation.

To further study the impact of CD4+ T cells on the humoral response, neutralization assays were performed

against DENV2 using serum samples from 90 days post ZIKV challenge (Fig 5E and 5I). No statistical differences

were detected between any of the groups.

Lack of CD4+ T cells during a primary DENV2 infection compromises antibody specificity in a secondary

ZIKV exposure. To further explore the role of CD4+ T cells in shaping the immune response against DENV and

ZIKV, epitope reactivity against EDIII and NS1 was evaluated using a Luminex assay. EDIII was selected as a

major neutralizing target and NS1 due to its proposed role in pathogenesis. Type-specific and CR responses were

measured at day 90 p.i. after DENV2 and ZIKV infections against EDIII and NS1 antigens from all four DENV

serotypes and ZIKV. To normalize the data a cross-reactivity index (CRI) was calculated by subtracting the

background from the homologous value (values against ZIKV) and the heterologous values (values against

DENV2) followed by dividing the subtracted homologous by the subtracted heterologous values (Fig 6).

As expected, after primary DENV2 infection, both undepleted and depleted animals had a high similar type-

specific response against EDIII and NS1 to the infecting serotype DENV2, and a similar limited cross-reactivity

against EDIII to the other DENV serotypes, with a significant difference observed in DENV4 EDIII (p= 0.0265)

(Fig 6A). As reported in the literature, primary DENV infection in flavivirus-naïve individuals triggers minimal

or no cross-reactivity to ZIKV (Collins et al., 2017; Duffy et al., 2009). Both groups show a similar high type-

specific response against DENV2 NS1 protein. In contrast to the response to EDIII domain, a higher CR response

against NS1 to the other DENV serotypes, particularly against DENV serotype 1, was observed (p= 0.0045).

Interestingly, there was a limited but detectable cross-reactivity against ZIKV NS1 protein in both groups (Fig

6A). This suggests that during a primary DENV infection, CD4+ T cells have a different weight in the responses

against EDIII domain and NS1 protein.

A more complex scenario is observed after secondary ZIKV infection (Fig 6B). All animals show an increase in

the type-specific response against EDIII and NS1 towards the infecting ZIKV, but their reactivity against other

DENV serotypes varies. Additionally, all groups show reactivity against DENV2 antigens. Of note, two animals

from the undepleted control group NS1 (MA254 and MA264) had a higher type-specific response against DENV2

EDIII, and two had a lower response (MA311 and MA350) (Fig 6B), indicating that antibody repertoire can be

different between individuals, a point to take into consideration in vaccine design. Lastly, as expected, the

CD4+/DV2/CD8-/ZV group behaved very similar to the CD4-competent groups, demonstrating that CD8$^+$ T cell

depletion does not have an impact in epitope reactivity (Fig 6B). Taken together, these results indicate that while

CD8$^+$ T cell depletion increases CD4$^+$ T cell frequency and results in better ZIKV viremia control, quantity has

no effect on the specificity of epitope recognition. Overall, the cross-reactivity to NS1 protein was more

significant among DENV serotypes than to EDIII domain suggesting that, like after a primary DENV infection,

CD4+ T cells have a different weight in the response against EDIII domain and NS1 protein after a secondary

ZIKV infection in DENV-immune individuals. Animals belonging to all groups, regardless of depletion condition,

show an increased but similar response against EDIII and NS1 to the infecting ZIKV. These results suggest that

pre-existing DENV immunity has a very limited impact in the cross-reactivity to ZIKV EDIII domain and NS1

protein, and that CD4$^+$ T cells have a limited role regulating that cross-reactivity to those ZIKV targets.

CD4+ T cells modulate early response IgG+ MBC activation and functionality during a heterologous ZIKV

infection with previous DENV-2 immunity. To determine the contribution of CD4+ T cells in modulating the

surface IgG+ memory B cell (IgG MBC) (CD3-CD20+CD27+sIgG+) response to ZIKV, we measured expression

levels of surface IgG in total MBCs via Flow Cytometry. Whole blood for Immunostaining was collected on

baseline and days 7, 15, and 30 p.c. with ZIKV. By day 15 p.c., a discrete peak in frequencies was observed in all

groups, except the CD4+/DV2/CD8-/ZV group which remain at the baseline levels (Fig 7A). On day 15 p.c., the

CD4+/DV2/CD4+/ZV and the CD4-/DV2/CD4+/ZV were the only groups showing a significant increase in IgG

expression when compared to their baseline status. By day 30 p.c., all groups showed similar levels of IgG

expression to their baseline status. We did not detect a significant difference in IgG expression among groups

compared at each timepoint suggesting that sIgG expression is not impacted by depletion treatment status. Taken

together, this data suggests that a secondary ZIKV infection in individuals with prior DENV-2 immunity, IgG+

MBCs levels suffer limited increase in frequency and if it happens it is CD4+ T cell-dependent.

To determine if CD4+ T cells have a role in modulating the activation pathways of IgG MBCs after the ZIKV

challenge, we surveyed the expression of CD69 in this cell population. Compared to their baseline, a significant

increase in the frequency of IgG MBCs expressing CD69 was observed at day 7 p.c. only on those groups with

intact CD4+ T cells before ZIKV challenge (CD4-/DV2/CD4+/ZV, p< 0.034; CD4+/DV2/CD4+/ZV, p< 0.024;

and CD4+/DV2/CD8-/ZV, p< 0.010) (Fig 7B and 7C). Taken together, this data suggests that IgG MBCs go

through CD4$^+$ T cell-dependent interactions for their activation during a secondary ZIKV infection.

To determine if CD4+ T cells have a role in the differentiation of activated B cells into ASC (possibly through

GC) formation) during a heterologous ZIKV infection we measured CD69 expression in total ASCs

(CD20^{dim}CD3$^-$CD27$^+$). Despite our gating strategy being designed to characterize rhesus macaque plasmablast

populations (Silveira et al., 2015) (Zhang et al., 2019), we were unable to segregate that population. However as

previously reported by us (Marzan-Rivera et al., 2022), we idetified the total ASC population and observed a

trend in activation of that population during the ZIKV infection. At day 7 p.c., we detected a significant increase

in CD69 expression in the CD4+/DV2/CD4+/ZV and the CD4-/DV2/CD4+/ZV groups, compared to the other

groups (Fig 7D, p< 0.005). This peak in CD69 expression was maintained up to day 15 p.c. in the

CD4+/DV2/CD4+/ZV group followed by a significant drop in CD69 expression levels at day 30 p.c.. Levels of

expression observed during this timepoint were of similar magnitude as on baseline. On the other hand, groups

that lacked CD4+ T cells before the ZIKV infection (CD4+/DV2/CD4-/ZV and CD4-/DV2/CD4-/ZV) showed a

trend of lower levels of ASCs expressing CD69 compared to the CD4$^+$ T cell competent groups before the ZIKV

infection. Our data points to a *de novo* B cell response pathway that is T cell-dependent to promote the formation

of both IgG MBCs and ASC subsets with good neutralizing capacity towards ZIKV.

CD4$^+$ Peripheral T helper cells (pTfh) are present in circulating blood of Rhesus macaques during

heterologous ZIKV infection with prior DENV2 immunity. To confirm the presence and frequency of pTfh

CD4+ T cells, we measured expression levels of surface markers such as CXCR5, CXCR3, PD-1, and ICOS via

flow cytometry analysis. Chemokine receptor CXCR3+ expression has been associated with Type 1 T helper

immune responses (Th1) (Sánchez-Vargas and Mathew, 2019; Sandberg et al., 2021; White et al., 2021).

Moreover, PD-1 and ICOS expression is associated with B cell interaction in order to induce B cell activation

(Lei et al., 2021; Shi et al., 2018). This analysis was performed only on groups CD4+/DENV2/CD4+/ZIKV, CD4-

/DENV2/CD4+/ZIKV and CD4+/DENV2/CD8-/ZIKV because they have CD4+ T cell populations before ZIKV

infection. Frozen PBMCs were used for Immunostaining on day 0 (baseline), day 7, and day 15 p.c. with ZIKV.

Surface expression of CD4+/CXCR5+ was detected at similar levels in all three tested groups, confirming

circulation of pTfh cells. No significant differences were established among groups after ZIKV challenge on day

7 p.c.. By day 15 p.c. the control undepleted group and the group lacking CD4+ T cells before DENV showed a

trend to higher frequencies compared to the group depleted of CD8+ T cells before ZIKV challenge, and that

difference reached significant values between that group and the CD4-/DENV2/CD4+/ZIKV group on day 15

p.c. (p< 0.039) (Fig 8A). Despite having similar frequency of pTfh T cells (CD4+/CXCR5+), results demonstrate

significance on days 0, 7, and 15 p.c. regarding the frequency of total pTfh TH1 CD4+ T (CXCR5+ and CXCR3+)

among groups with the group depleted of CD4+ T cells before DENV infection, having significant lower

frequencies of those cells since baseline (p< 0.000 and p= 0.0034) and on day 7 p.c. (p< 0.000 and p= 0.0306)

compared to groups CD4+/DENV2/CD4+/ZIKV and CD4+/DENV2/CD8-/ZIKV, respectively. On day 15 p.c.

there was a marked decrease in the frequency of TH1 cells in the CD4+/DENV2/CD8-/ZIKV group compared to

the control undepleted group (p= 0.0009). The difference in frequency was also significant between the control

group and the CD4-/DENV2/CD4+/ZIKV group (p= 0.0012) (Fig 8B). Further, we wanted to assess the co-

expression of B cell co-stimulating markers PD-1 and ICOS in order to correlate these results with B cell

activation. The frequency of total CD4+ pTfh T cells CD4+/CXCR5+/CXCR3+/PD-1+/ICOS+ showed a trend to

increase from baseline to day 7 p.c. in all three groups. We found same profile as with the TH1 pTfh cells were

the CD4-/DENV2/CD4+/ZIKV show statistically significantly lower frequency of these co-stimulating markers

at baseline and on days 7 and 15 p.c. compared to groups CD4+/DENV2/CD4+/ZIKV and CD4+/DENV2/CD8-

/ZIKV (p<0.0001 in all comparisons) (Fig 8C). Gating strategy is shown in Figure 6D.

When evaluating the total CD4+ T cell memory phenotype subsets (naïve CD28+CD95-, effector memory (EM)

CD28-CD95-, and central memory (CM) CD28+CD95+), CM pTfh CD4+ T cells (CD4+/CD28+/CD95+) remain

to be the more abundant phenotype of CD4+ memory T cells. (data not shown). To explore the impact of CD4+

and CD8+ T cell depletion on the frequencies of CM CD4+ pTfh T cells (CD4+/CD28+/CD95+/CXCR5+) we

measured frozen Peripheral Blood Mononuclear Cells (PBMC) collected on day 0 (baseline), day 7, and day 15

p.c. with ZIKV via flow cytometry analysis (Fig 9A). Overall, there was a non-significant trend to increased

frequency in all groups from day 0 to day 7 p.c. followed by a contraction on day 15 p.c. On baseline, the frequency

was significantly lower in the CD4-/DENV2/CD4+/ZIKV group compared to the CD4+/DENV2/CD8-/ZIKV

group (p< 0.002). However, there were no differences among groups after the challenge. Results also demonstrate

a limited expansion of CM CD4+ pTfh T cell subsets co-expressing CD28+/CD95+/CXCR5+/CXCR3+ in all

groups on day 7 p.c. with a contraction in the CD4+/DENV2/CD8-/ZIKV group by day 15 p.c.. As similarly seen

with prior CD4+ pTfh profiles, the CD4+ T cell-deficient group before primary DENV infection result in the

lowest frequency since baseline (p< 0.0001 and p= 0.0024), on day 7 (p< 0.0001 and p= 0.0209), and on day 15

p.c. (p< 0.0001 and p= 0.0008) compared to groups CD4+/DENV2/CD4+/ZIKV and CD4+/DENV2/CD8-/ZIKV,

respectively (Fig 9B). We also measured the CM subpopulation co-expressing the B cell co-stimulating markers

PD-1+ and ICOS+ (CD28+/CD95+/CXCR5+/CXCR3+/PD1+/ICOS+) (Fig 8C). All three groups showed the

same trend as in the other CM population with a very limited expansion on day 7 and a trend to contraction on

day 15 p.c. in the control undepleted and in the CD4+/DENV2/CD8-/ZIKV groups but not in the CD4-

/DENV2/CD4+CD4+/ZIKV, which remains with similar frequency as day 7 p.c.. Interestingly, at baseline the

CD4+/DENV2/CD8-/ZIKV group showed a frequency of these cells that is significantly higher compared to the

control group (p< 0.035). But again, the CD4+ T cell-deficient group before primary DENV infection resulted in

the lowest frequency since baseline (p= 0.0412 and p< 0.000), on day 7 (p= 0.0046 and p< 0.0001), and on day

15 p.c compared to groups CD4+/DENV2/CD4+/ZIKV and CD4+/DENV2/CD8-/ZIKV respectively (Fig 9C).

There were no significant differences among groups on day 15 p.c. This data on the pTfh cells subsets show a

detectable, but minimal expansion of the pTfh cells, and its CM compartment, during heterologous ZIKV

infection in prior DENV2 immune individuals.

Total and DENV primed CM pTfh cells modulate both B cell subset activation and serum antibody

response functionality towards ZIKV. To determine if the frequencies of peripheral pTfh cells are directly

associated with the humoral response to the secondary infection with ZIKV, we performed Pearson correlation

and simple linear regression analysis comparing pTfh cell frequencies with the neutralization assays and the IgG$^+$

MBC immunophenotyping data. For the IgG$^+$ MBC analysis, we compared three pTfh cell phenotypes: CXCR5$^+$,

CXCR5$^+$CXCR3$^+$, and CXCR5$^+$CXCR3$^+$PD1+ICOS$^+$, at days 7 and 15 p.c., with frequencies of activated IgG$^+$

MBCs, and activated ASCs, at 7 days p.c.. While we did perform correlation analysis comparing the pTfh cell

frequencies with frequencies of total IgG$^+$ MBCs, at 15 days p.c., we did not observe any significant correlation

(data not shown). Interestingly, we observed a very low yet significant positive correlation (R^2= 0.3237, P=

0.0214) when we compared frequencies of CXCR5$^+$ pTfh cells from day 7 p.c.. with total IgG$^+$ MBC frequencies

from day 15 p.c. from all animals in the study (SFig 6A). From these observations, we decided to perform these

correlation analyses with the experimental groups separately as we observed that correlations vary significantly

depending on both cell phenotype and T-cell depletion treatment. When comparing the CXCR5$^+$CXCR3$^+$ pTfh

cell phenotype, from Day 7 p.c., with the activated IgG$^+$ MBC phenotype, we observed very high and significant

correlations in both the CD4+/DV2/CD4+/ZV and the CD4-/DV2/CD4+/ZV groups (R^2= 0.8790, P= 0.0186 and

R^2= 0.7424, P= 0.0274, respectively) (SFig 6B and 6C). In addition, a very positive and significant correlation

with activated IgG$^+$ MBC and PD1$^+$ICOS$^+$ pTfh cell frequencies was observed in the CD4-/DV2/CD4+/ZV group

(R^2= 0.7028, P= 0.0371) (SFig 6D). When comparing the CXCR5$^+$ pTfh cells, from Day 7 p.c., with activated

ASCs, we only observed a highly negative and significant correlation in the CD4-/DV2/CD4+/ZV group (R^2= -

0.7, P= 0.0378) (SFig 6E). On the other hand, we did not observe a significant correlation when performing this

comparison in the CD4+/DV2/CD4+/ZV group. Furthermore, when we compared the frequencies of PD1$^+$ICOS$^+$

pTfh cell, from Day 7 p.c., with activated ASCs we observed a very high and significant positive correlation in

the CD4+/DV2/CD4+/ZV group only (R^2= 0.8657, P= 0.0218) (SFig 6F) These observations suggest that not

565 only the B cell response is modulated by possible interactions with these pTfh cell subsets, but also these

566 mechanisms are strongly influenced by the nature of the initial priming with DENV. Also, the opposed correlation

567 (MBC vs. ASC) in the CD4-/DV2/CD4+/ZV group strongly suggest that lack of DENV-experimented pTfh

568 modify the interactions with the MBC and ASC in different ways. As part of this analysis, we also measured

569 possible correlations between these B cell subsets and these same pTfh cell subsets but focusing on CM pTfh

570 cells. Here, we only observed very high and significant positive correlations between the $CXCR5^+CXCR3^+$ and

571 $PD1^+ICOS^+$ CM pTfh cells, from day 7 p.c., and activated IgG^+ MBCs and activated ASCs in the

572 CD4+/DV2/CD4+/ZV group (SFig 7). This data adds new insight to the impact of the initial DENV priming in

573 the secondary ZIKV infection response, as CM pTfh cells only show a significant correlation in the expansion of

574 activated B cell subsets in animals with DENV- primed $CD4^+$ T cells. Lastly, the CD4+/DV2/CD8-/ZV group

575 showed no significant correlations between any of the pTfh, and B cell subsets analyzed (data not shown). This

576 could suggest a role or possible interactions of CD8+ T cells with either pTfh cells and/or B cell subsets during

577 the ZIKV infection.

578 To characterize the impact of pTfh cells in the functionality of the antibody response towards the ZIKV infection,

579 we performed Pearson correlation and linear regression analysis comparing the previous pTfh cell phenotypes,

580 during day 7 and 15 p.c.., with the EC50 data (from ZIKV and DENV neutralizations) gathered from days 30 and

581 90 p.c.. Similar to what we observed in the correlation analysis with IgG^+ MBCs and ASCs, only the

582 CD4+/DV2/CD4+/ZV group showed highly positive and significant correlations between pTfh cell phenotypes

583 and the ZIKV EC50 values (SFig 8). When comparing frequencies of $CXCR5^+$ pTfh cells, from both days 7 p.c.

584 and 15 p.c., with EC50 values from day 30 p.c., we observed a high and significant positive correlation at both

585 timepoints (R^2= 0.8317, p= 0.0309 and R^2= 0.9115, p= 0.0115, respectively) (SFig 8A and 8B). In the EC50 from

586 day 90 p.c., we only observed significant positive correlations with the frequencies of $PD1^+ICOS^+$ pTfh cells in

587 both day 7 and 15 p.c. timepoints (R^2= 0.7796, p= 0.0472 and R^2= 0.9182, p= 0.0102, respectively) (SFig 8C and

588 8D). We did not observe any significant correlations with $CXCR5^+CXCR3^+$ pTfh cells (data not shown). As part

589 of this analysis, correlations were performed with CM pTfh cell subsets as well. Similar to previous results, only

590 the CD4+/DV2/CD4+/ZV group showed significant positive correlations between CM pTfh cell frequencies and

591 ZIKV EC50 values from days 30 and 90 p.c.. Interestingly, for both the $CXCR5^+$ from day 15 p.c. and the

592 $CXCR5^+CXCR3^+$ pTfh cells from days 7 and 15 p.c., a strong positive correlation was observed when compared

593 with EC50 values from day 30 p.c. when comparing all animals in the study (R^2= 0.3282, p= 0.0204, R^2= 0.2863,

594 p= 0.0269, R^2= 0.5100, p= 0.0019 respectively) (SFig 8E, 8F and 8G). Similar to previous observations, there

595 were significant positive correlations for $CXCR5^+$ CM pTfh cells from days 7 and 15 p.c., when compared to

596 EC50 values from day 30 p.c. (R^2= 0.9505, p= 0.0470, and R^2= 0.9063, p= 0.0125 respectfully) (SFig 8H and 8I).

597 Lastly, the only positive correlation observed in EC50 values from day 90 p.c. was observed when comparing

598 frequencies of $PD1^+ICOS^+$ CM pTfh cells from day 15 p.c. (R^2= 0.8214, p= 0.0339) (SFig 8J). Taken together,

this data adds new insight to the importance of the nature of the initial priming with DENV and its impact on the
ZIKV infection, as we also saw strong correlations between CM pTfh cell phenotypes and EC50 values in the
CD4+/DV2/CD4+/ZV group only. This suggests that DENV-primed CM pTfh cells may play an important role
in modulating an efficient antibody response to ZIKV. In addition, this data adds more weight to the role of
ICOS$^+$PD1$^+$ pTfh cells in priming a robust Abs response with efficient neutralizing capacity towards flavivirus.
Interestingly, we observed no significant correlations when we compared total and CM pTfh cells with EC50
values, from day 90 p.c., that neutralized DENV-2 in any experimental group (data not shown). These results
suggest that, while possible DENV-primed CM pTfh cells help to modulate the potency of nAbs to ZIKV, these
mechanisms between pTfh cells and the B cell response may be only part of the type-specific humoral response
to ZIKV.   These results further support a T-cell dependent humoral immune response to ZIKV in DENV-
experimented individuals.
610
Principal component analysis recapitulates infection dynamics. To reduce the dimensionality of our data –
which included ELISAs, neutralization assays, flow cytometry, and cross reactivity indexes – we performed
principal component analysis (PCA). Interestingly, PCA projections of days 15 and 30 p.c. corroborate our assay-
by-assay results. More specifically, both principal component projections separate most of the CD4+/DV2/CD4-
/ZV and the double depleted groups (CD4-/DV2/CD4-/ZV) samples – most samples have positive values on PC2
on days 15 p.i. (Fig 10A and 10B). Also, most of the samples from the undepleted CD4+/DV2/CD4+/ZV group
and from the CD4-/DV2/CD4+/ZV and CD4+/DV2/CD8-/ZV groups having in common the presence of CD4$^+$ T
cells before ZIKV infection cluster together – having positive values in PC1 and negative value in PC2 on day 15
p.c. and negative values in PC1 on day 30 p.c.–, which corroborates our results that demonstrates that these groups
behave similarly at day 15 p.i.. Of particular interest is the group with CD4+ T cells depleted before primary
DENV infection but not before ZIKV challenge. On day 15 p.c., half of samples (n=3) clustered very close with
the double-depleted group with a positive value in PC1 similar to the other three samples from same group, but
with a positive value in PC2 as the double depleted group.
PCA projections of day 90 post ZIKV challenge shows how groups return to baseline, as there is no clear
separation between groups (Fig 10C). This is in line with our individual assay-by-assay results that show that,
after 90 days of infection, there is no significant difference between groups. Eighty three percent (83%) of the
samples from the CD4-/DV2/CD4+/ZV showed negative PC1 clustering with 100% of samples from the double
depleted group and 66% of samples from the group depleted of CD4+ T just before ZIKV infection
(CD4+/DV2/CD4-/ZV). Nevertheless, after incorporating the CRI to our PCA matrix there is a dramatic shift
with the CD4-/DV2/CD4+/ZV group (83% of samples) clustering together with all samples from the CD4-
/DV2/CD4-/ZV double-depleted groups with most having now positive PC1 values of over 0.5 between most of
the samples. This way those groups remained separated from the other groups (Fig 10D). These results are in line

with our individual assay-by-assay results that show that, in most of the results the double depleted group and the

CD4+/DV2/CD4-/ZV trend to have similar results while the CD4-/DV2/CD4+/ZV have similar profile from the

two undepleted groups (CD4+/DV2/CD4+/ZV and CD4+/DV2/CD8-/ZV). Such a drastic change in the

dimensionality of the data reflects the impact of the CRI and most importantly, this analysis strongly suggest a

differential impact of CD4+ T cells on the Abs binding and neutralization properties versus specificity generating

immune memory during a primary DENV infection.

Overall, PCA projections recapitulated the individual trends in the various analysis performed within our dataset.

PCA further provides an excellent resource to corroborate the validity and biological importance of our results.

Discussion

Despite many years or research, DENV pathogenies is not completely understood. However, it is recognized that a balanced humoral and T cell immune response is essential to drive protection.

The role of CD4^{+} T cells in DENV pathogenesis evolved over the years. Early data and subsequent works highlighted their role in DENV pathogenesis (Duangchinda et al., 2010; Mangada and Rothman, 2005; Rivino et al., 2013; Rouers et al., 2021; Yu et al., 2022). However, more recent works show a relationship between these cells and DENV protection (Graham et al., 2020; Weiskopf et al., 2015b). Also, a contribution of CD4^{+} T cells in protection against ZIKV has been documented (Cimini et al., 2017; Elong Ngono et al., 2019; Hassert et al., 2018; Lucas et al., 2018). Nevertheless, as it has been pointed out, there are currently limited data available on the relationship between the generation of cross-reactive T cells following vaccination and protection from infection or severe DENV disease (Guy et al., 2008; Tricou et al., 2022; Waickman et al., 2019a) or ZIKV (Rivino and Lim, 2017; Wen and Shresta, 2017). In this work, we found that the presence of CD4^{+} T cells was essential for optimal control of primary DENV infection and an effective Abs switching, as the depletion of those cells induced a delay in anti-DENV IgM and IgG production. These results indicating a delay in B cells activation and in isotype class switching during primary DENV infection related to the lack of CD4^{+} T cells. Our finding are in contraposition with prior work in mice showing that depletion of CD4^{+} T cells did not have a significant effect on viral clearance and were not required for the induction of the DENV2-specific Ab or CD8+ T cell responses, and that the early anti-DENV2 Ab response is CD4^{+} T cells-independent (Yauch et al., 2010). However, earlier works also performed in mice showed that Abs were not required to protect against DENV; in contrast, depletion of CD4^{+} T and CD8^{+} T lymphocytes significantly reduced survival of ACS46-primed mice challenged with the DENV JHA1 strain, suggesting that cellular immune response targeting NS proteins may be a promising route in vaccine development against DENV (Amorim et al., 2016). In addition to their role interacting with B and CD8^{+} T cells, CD4^{+} T cells have also been shown to be protective against encephalitis induced by West Nile Virus (WNV), another flavivirus, in RAG(-/-) and C57BL/6 (H-2(b)) mice (Brien et al., 2008). Again, differences in animal models may account for the radical differences in our results from prior published work. However, the implications are very relevant to advice on DENV vaccines, and our results, as from others, indicate the need to pay attention to CD4^{+} T cell contribution in DENV vaccine design and efficacy. Angelo et al. addressed this issue by characterizing CD4+ T cells contribution in donors vaccinated with a tetravalent DLAV vaccine (TV005) with pools of DENV virus-derived predicted major histocompatibility complex (MHC) class II binding peptides. They found that DENV-specific CD4+ T cells were focused predominantly on the capsid and NS3 and NS5 antigens and, more importantly, that responses in vaccinees were similar in magnitude and breadth to those after natural infection (Angelo et al., 2017). Another study characterizing T cell response to the same vaccine found that multifunctional DENV-specific CD8^{+} and CD4^{+} T cells developed 8-14 days after vaccination and were maintained for at least six months and identified a phenotypic profile of antiviral CD8^{+} and CD4^{+} T cells

associated with protective immunity to DENV infection (Graham et al., 2020). In addition, a particular highly polarized CX3CR1+ cytotoxic CD4$^+$ T cell phenotype was associated with protective immunity to DENV(Weiskopf et al., 2015b). Previously we found that CD4$^+$ T cell depletion during a tertiary flavivirus infection results in a delay in DENV-specific IgM/IgG antibody titers, binding, and neutralization in DENV/ZIKV-primed animals but not in ZIKV/DENV-primed animals, highlighting the fact that the contribution of those cells can also be relative to the sequence of flavivirus infection, adding complexity to the interpretation (Marzan-Rivera et al., 2022).

We found significant higher ZIKV viremia in the group with higher frequency of DENV-experimented CD4$^+$ T cells prior ZIKV challenge compared to the control undepleted, and the double depleted groups and the group depleted before the primary DENV infection carrying DENV-naïve CD4$^+$ T cells. Also the control undepleted group had significantly less ZIKV viremia days compared to the double depleted group. This result is coherent with prior reports confirming the role of those cells controlling ZIKV viremia even in naïve and DENV-experimented animals (Wen et al., 2020). Mice depleted of CD4$^+$T cells have more severe neurological sequela and significant increases in viral titers in the central nervous system. When those cells were transfered from ZIKV immune mice, CD4+ T cells protected type I interferon receptor-deficient animals from a lethal challenge, showing that the response by these cells is necessary and sufficient for control of ZIKV disease (Hassert et al., 2018). On another work, depletion of CD4+ T cells in mice reduced plasma cell, GC B cells, and IgG responses to ZIKV without affecting CD8+ T cell response, and those cells were required to protect mice from a lethal dose of ZIKV after infection intravaginally, but not intravenously (Elong Ngono et al., 2019).

These results are also in line with our finding that depletion of CD4$^+$ T cells before ZIKV challenge in animals with prior DENV immunity significantly dampened the B cells immune response, delaying the early IgM and IgG responses and ZIKV neutralization, supporting a protective role of CD4$^+$ T cells against ZIKV mediated by different mechanisms. Other results from mice showed that reduced viral load in the brain, prevention of rapid disease onset and survival was dependent on CD4$^+$ T cells and IFN gamma signaling, and requires CD8$^+$ T cells and B lymphocytes (Lucas et al., 2018). However, Weng et al. showed that anti-ZIKV IgG production was not necessary to protect naive HLA-DRB1(∗)0101 transgenic mice immunized with CD4$^+$ T specific peptides. These results showed that immunization induces a cell response sufficient to reduce tissue viral burden following ZIKV infection. Furthermore, another recent work in mice revealed that the role of CD4$^+$ T cells may be modulated differentially by various ZIKV strains (Pardy et al., 2021). Pardy et al. showed that CD4$^+$ T cells were differentially polarized to the Th1 subtype after challenging mice with pre-epidemic or contemporary ZIKV strains. The differences were characterized by enhanced GC B cell response and robust production of higher avidity-nAbs following the infection with the contemporary strain, suggesting that ZIKV strains have evolved to differentially induce T cell, B cell, and Ab responses including their avidity and neutralization properties (Pardy et al., 2022). These results are relevant while considering ZIKV vaccine designs.

More controversial is our finding that depleting CD8$^+$ T cells before ZIKV challenge resulted in a strong trend to

have lower viremia and significant better IgM and IgG response and neutralizing activity than the CD4$^+$ T cell-

depleted group, suggesting that CD8$^+$ T cells depletion does not have a relevant role in controlling ZIKV infection

and are not required for an optimal humoral immune response in DENV-immune individuals. Several works

support the role of CD8$^+$ T cells and CR DENV virus-specific CD8$^+$ T cells controlling ZIKV replication (Regla-

Nava et al., 2018; Rivino and Lim, 2017; Wen et al., 2017; Wen and Shresta, 2017; Yauch et al., 2010).

Nevertheless, these works have been performed in flavivirus naïve mice – which may account for the difference

with our finding.

Our results also showed that the CD4$^+$ T cell-depleted animals had a significant compensatory increase in CD8$^+$

T cells and vice-versa; animals depleted of CD4$^+$ T cells had a significant compensatory increase in CD8$^+$ T cells,

which has been priorly documented in rhesus macaques (Chowdhury et al., 2015; Mueller et al., 2009; Okoye et

al., 2009; Schouest et al., 2020). Considering such cellular profile, our model suggests that other components of

the immune system, like precisely DENV-experimented CD4$^+$ T cells and the humoral immune response from a

prior DENV2 immunity, play a role controlling ZIKV infection and that CD8$^+$ T cells are not critically required

in this scenario. It is known that CD4$^+$ T cells can have a dissimilar contribution to the humoral immune response

depending on the type of prior flavivirus exposure. A prior T cell receptor repertoire analysis revealed preferential

expansion of CR clonotypes between JEV and ZIKV, suggesting that pre-existing immunity against JEV may

prime the establishment of stronger CD4$^+$ T cell responses to ZIKV purified-inactivated virus vaccination. These

CD4$^+$ T cell responses correlated with titers of ZIKV-nAbs in JEV- pre-vaccinated group, but not in flavivirus-

naïve or YFV- pre-vaccinated individuals, suggesting a stronger contribution of CD4$^+$ T cells in the generation of

nAbs in the context of JEV-ZIKV cross-reactivity (Lima et al., 2021). This finding, together with our results and

from others, emphasize that the efficacy of a DENV or ZIKV vaccine may also depend on the nature of prior or

post exposure to flavivirus.

Our results on multiple CD4$^+$ T depletions also shed light on the quantity and quality of the immune response in

sequential DENV/ZIKV infection in the context of an optimal or suboptimal priming of B cells.

The binding or magnitude of neutralization against DENV2 or ZIKV after ZIKV challenge was essentially

unaffected by the lack of CD4$^+$ T cells before primary DENV infection. These results indicate that DENV-

experimented CD4$^+$ T cells do not contribute to an optimal humoral immune response against ZIKV and support

prior reports confirming the specificity of ZIKV-induced humoral immune response in naïve (Collins et al., 2017;

Duffy et al., 2009), but also in DENV-pre-exposed, subjects (Andrade et al., 2020). However, depletion before

primary infection results in a significant increase in ZIKV-cross reactivity prior ZIKV challenge evidenced by the

presence of CR ZIKV-binding IgG. This implies an essential role of CD4$^+$ T cells to guarantee a more specific

Abs repertoire after the *primo* infection. That role may contribute to avoid potential disease enhancement during

a secondary flavivirus exposure, due to generation of wide CR DENV MBC as consequence of a suboptimal

priming. In contrast to the total IgG, no animals had detectable anti-ZIKV-NS1 IgG Abs at baseline, indicating

that those Abs are very specific, supporting the efforts to use this protein as a diagnostic marker (Castro-Trujillo

et al., 2023; Guzman et al., 2010; Petphong et al., 2023; Vazquez et al., 1995), but also considering the antigen as

a target for vaccination. However, removing $CD4^+$ T cells prior to primary infection resulted in a significant

increase in DENV anti-NS1 Abs durability. The implications of this finding need further considerations to

determine their probable or not pathogenic role, during a subsequent natural exposure or DENV or ZIKV vaccine

administration.

Despite this, NS1 has also been used as a strategy for protection against TBE (Beicht et al., 2023) and against

JEV (Li et al., 2020; Nath et al., 2020; Zhou et al., 2020). Gonçalves et al. nicely showed in mice that the

cooperation between $CD4^+$ T cells and the humoral response induce a robust protection against DENV mediated

by a DNA-NS1 vaccine (Goncalves et al., 2015). Rhesus macaques is a good model to evaluate the resppnse to

NS1 protein as prior work using the same species and DENV2 strain we used confirmed that $CD4^+$ T cells from

these animals targeted NS1, NS3 and NS5 proteins (Mladinich et al., 2012).

Our results confirmed an enhanced circulation of DENV-NS1 antigen after DENV infection and significant lower

DENV or ZIKV-specific anti-NS1 IgG response after the primary infection of challenge respectivelly, associated

to the lack of $CD4^+$ T cells, confriming a protective role for these cells.

Consistent with the Abs response, our data on the MBC and ACS after ZIKV challenge points to a *de novo* B cell

response pathway that is T cell-dependent to promote the formation of both IgG MBCs and ASC subsets with

good neutralizing capacity towards ZIKV. Only the groups with $CD4^+$ T cells before the ZIKV challenge recorded

a significant activation of both MBC and ACS, while the depleted groups showed a trend for activation but without

reaching significant differences with their baseline frequencies.

Previosly, we showed a similar profile ($CD4^+$ T cells-dependent MBC and ACS activation) during tertiary

flavivirus infection, but only in the sequence where the ZIKV challenge was preceded by a DENV infection and

not when two consecutive DENV infections were secondary and terciary exposures (Marzan-Rivera et al., 2022).

Our results are in agreement with data from humans showing that ZIKV infection in DENV-naïve subjects (or

with prior DENV immunity) induces both DENV-MBC and naive B cells with the production of ZIKV TS Abs

in both cases (Andrade et al., 2020; Rogers et al., 2017). The recall memory against DENV2 detected in our work

after ZIKV challenge was significantly higher in the undepleted groups suggesting to be $CD4^+$ T cells-dependent.

However, more specific studies on BCR and Abs repertoir diversity, which are being implemented by our group,

are needed. A recent work characterized the plasmablast response in rhesus macaques exposed to primary ZIKV

or sequential ZIKV/ZIKV or DENV3/ZIKV infections. Authors reported the highest VH and VL diversity levels

upon primary ZIKV infection and lower levels in both homologous and heterologous secondary ZIKV or DENV

responses (Singh et al., 2024). In addition to the authors' discussion, those results strongly suggest dissimilar T-

B cell interactions in those different sequential flavirus infections.

A different scenario compatible with our prior findings on sequential DENV infections (Marzan-Rivera et al.,
2022), showing that the pool of CR policlonal Abs were generated mainly from MBC-derived plasmablasts and
not from naïve B cells, was characterized for repeated DENV infections (Xu et al., 2012).

Cells phenotyping results were consitent with the correlation analysis we performed. Only the groups that were
CD4+ before ZIKV challenge showed a significant positive correlation between some pTfh phenotypes and
MBCs activation. However, only the control undepeleted group showed significant correaltion with the activiation
of the ACS. Interestingly, the group depleted of CD4$^+$ T cells only before ZIKV infection showed a significant
inverse correlation with the activation of the ACS. This finding and its relationship with the increased cross-
reactivity in this group need further considerations. Intriguingly, the group depleted of CD8$^+$ T cells before ZIKV
challenge – but with intact CD4$^+$ T cells – did not showed any correlation with the activiation of these cells,
suggesting a potential role of CD8$^+$ T cells in an effective activation of the MBC and the ASC as it has been
discussed before (Rouers et al., 2021). Finally, we found that pTfh (CXCR5+) and pTfh with TH1 pehonotype
(CXCR5+/CXCR3+), but not the the pTfh expressing B cell markers for activation (PD1+/ICOS+), had a strong
correlation with EC50 values against ZIKV (but not DENV). However, when we split the groups, only the control
double positive group kept the significant correlation with the EC50 values, suggesting a contribution of the
DENV pre-exposed T helper population in an effective neutralization against ZIKV. Because pTH cells are
essential for the formation of GCs and to regulate GC B cell differentiation into plasma cells and memory B cells
(Crotty, 2015), our correlation results support our other finidngs suggesting that the humoral immune response to
ZIKV in DENV-experimented subjects is most likely T-cell dependent; any disruption or suboptimal T-B cell
interactions during a primary DENV infection has consequences in the quality of the immune response to a
secondary ZIKV exposure. Vaccination of naive HLA-DRB1*0101 transgenic mice with DENV/ZIKV-cross-
reactive CD4$^+$ T cell epitopes induced a CD4$^+$ T cell response sufficient to reduce tissue viral burden following
ZIKV infection suggesting that those cells expressing a TH1 pehnotype (as we characterized in our model) can
suppress ZIKV replication, even in a Abs-independent manner (Wen et al., 2020). A recent work on the response
to the TV003 vaccine in phase II clinical trial revealed that sero-positive subjects have increased baseline/pre-
vaccination frequencies of circulating cTfh cells and, more importantly and inline with our findings, they found
that the baseline/pre-vaccination cTfh profile correlated with the vaccine's ability to launch nAbs response against
all four DENV serotypes (Izmirly et al., 2022).

The findings on the correlation between the pTfh cells with the MBC and the magnitude of neutralization from
our work have implications for vaccine designs. Lack of inducing an effective and specific CD4$^+$ T cells (and
most likeely pTfh cells) responses might thus impair vaccine performance. Our results add on the mechanisms
guiding the immune response during heterologous flavivrus infection and may contribute to rational vaccine
development efforts.

One key finding from our work is the increased cross-reactivity to both the DENV-EDIII domain and NS1 (but not to similar ZIKV regions) in absence of CD4$^+$ T cells before primary DENV infection but not before ZIKV challenge. The fact that the cross-reactivity was identified against both the structural EDIII domain and the NS1 protein agrees with the finding that CD4$^+$ T cell epitopes in humans are skewed toward recognition of viral components that are also targeted by B lymphocytes and, from here, guiding the production of Abs mainly against structural proteins (Rivino et al., 2013) or NS1 protein having also T and B cell epitopes (Aquino et al., 2023; Beicht et al., 2023; Perera et al., 2024; Shu et al., 2000). We are not sure why the cross-reactivity was higher against the NS1 protein than to the EDIII domain, but the factors responsible for directing the CD4$^+$ T cell to similar sites at the virus protein surface (or to NS1) in different flaviviruses are unknown (Aberle et al., 2018). However, they are most likely related to the structural context of these epitopes and their accessibility during antigen processing (Koblischke et al., 2017; Koblischke et al., 2018; Landry et al., 2017; Schwaiger et al., 2014). The involvement of NS1 can be explained as 50% or more of the MBC repertoire represented in monoclonal antibodies (mAbs) from DENV patients bind to NS1, NS3, prM, or capsid in addition to the E (Beltramello et al., 2010; de Alwis et al., 2011). A prior work showed that half of anti-NS1 mAbs had limited cross-reactivity among DENV, while most of the structural Abs showed full cross-reactivity against all virus serotypes (Dejnirattisai et al., 2010). Supported in that data, the increased cross-reactivity against NS1 we found, reinforce the critical contribution of CD4$^+$ T cells during a primary infection to the Abs specificity during a subsequent flavivirus exposure.

Strikingly, that increase in cross-reactivity was not accompanied by a detriment in Abs binding or DENV neutralization after the challenge, indicating that CD4$^+$ T cells were not essential for those properties, but they were required for Abs specificity. Interestingly, while CD8$^+$ T cell depletion increased CD4$^+$ T cell frequency, it had no effect on the specificity of epitope recognition, supporting that our finding is related to the quality of the priming. This suggests that the specificity of DENV Abs need to be secured during a *primo* infection with an optimal B cell priming and may be regulated through a different mechanism than the binding and neutralization functions. After many years of extensive research, the mechanism regulating the Abs somatic hypermutation and affinity maturation are still not well understood (Elsner and Shlomchik, 2020; Stebegg et al., 2018; Victora and Nussenzweig, 2012). How this process occurs in flaviviruses is also largely unknown. However, we know that high affinity Abs with higher SHM rate are generated in the GCs (Fink, 2012; Fink et al., 2007; Godoy-Lozano et al., 2016; Wong et al., 2020) where the encounter with antigen-presenting cells, including CD4$^+$ T cells, occurs. Our results agree and provide, for the first time, mechanistic evidence to prior findings where a population of broadly cross-neutralizing Abs in addition to the TS nAbs was identified after secondary DENV infections (Patel et al., 2017).

Currently, our group is performing Ab depletion to characterize the TS vs. CR Abs and ADE experiments to test the potential enhancement of these CR Abs. We understand that results from these experiments will add

instrumental information in support of our results. We also acknowledge that we used samples from day 90 p.i.
where CR Abs start to decline but are still present (Katzelnick and Harris, 2017; Patel et al., 2017; Wahala and
Silva, 2011). However, it will not change the fact that, in our experimental conditions, the Abs population after
ZIKV challenge, in DENV-experimented individuals with suboptimal T-B cell interaction, behave differently in
their binding and neutralization properties vs. their specificity.

Also, experiments reproducing the sequence of infections ZIKV/DENV2 are underway, and DENV/DENV and
ZIKV followed by different DENV serotypes are on the pipeline.

Before, it has been highlighted that the risk of immunopathology associated with sub-optimal cross-reactive B-
cell and T-cell responses to heterologous serotypes represent critical factors for the development of a fully
protective DENV vaccine (Rivino and Lim, 2017). Our work adds on the relevance and uniqueness of the
contribution of CD4$^+$ T cells to the specificity of the nAbs to increase vaccine efficacy and to potentially prevent
or decrease the risk of pathogenic manifestations mediated by ADE or similar mechanisms.

Finally, and not less relevant, our work reinforces the value of rhesus macaques as a reliable model with a strong
translational capability and a needed complement to results obtained with other animal models.

One limitation to advance our knowledge on the correlates of protection towards DENV is the lack of an adequate
animal model to reproduce DENV clinical manifestations. Despite the proven value of small animal models, most
of the studies performing a fine dissection of the mechanisms addressing the protection against DENV and ZIKV
use transgenic mice deficient in some essential anti-viral pathways (Yauch and Shresta, 2008; Zompi and Harris,
2012). These genetic modifications in the murine model prevent to recognize the contribution of all components
of the immune response as a whole and from here, the translation to humans may be narrow.

In addition, it is known that the T cell immune response to flaviviruses in humans is restricted by the HLA system
(Angelo et al., 2017; Sierra et al., 2007; Weiskopf et al., 2016; Weiskopf et al., 2011; Wen et al., 2010; Zivna et
al., 2002).

The value of rhesus macaques as NHPs to study the pathogenesis and immune response after natural infection, or
vaccination to DENV (Mladinich et al., 2012; Onlamoon et al., 2010; Osorio et al., 2014; Sariol et al., 2011;
Sariol et al., 2007; Sariol and White, 2014; White et al., 2021; Young et al., 2023) or ZIKV (Abbink et al., 2017;
Aliota et al., 2016; Best et al., 2017; Breitbach et al., 2019; Carroll et al., 2017; Coffey et al., 2018; Coffey et al.,
2017; Dudley et al., 2019; Dudley et al., 2016; Haddow et al., 2017) is well documented. Also, our group and
others have shown the usefulness of this model to dissect many aspects of DENV and ZIKV interactions (Crooks
et al., 2021; George et al., 2017; Larocca et al., 2021; Marzan-Rivera et al., 2022; McCracken et al., 2017; Pantoja
et al., 2017; Perez-Guzman et al., 2019; Serrano-Collazo et al., 2020; Valiant et al., 2018; Valiant et al., 2019).
Rhesus macaques have also shown to be very reliable to anticipate vaccine outcomes (Borges et al., 2019). Early
immunization studies of rhesus macaques with Dengvaxia, either with the tetravalent formulation CYD-TDV
(CYD1–4) or with two bivalent formulations (CYD1,2 + CYD3,4), resulted in higher responses against the

dominant DENV4 and DENV1, and very limited response to DENV2 serotypes in both approaches (Guy et al., 2009). Later, results from humans showed a vaccine efficacy of 55.6%, 75.3% and 100.0% for serotypes 1, 3 and 4 respectively. The efficacy for serotype 2 was as low as 9.2 % resulting in an overall efficacy of 30.2% for all serotypes (Sabchareon et al., 2012). Rhesus macaque studies with DENVax (formulation used for TAK-003 vaccine) likewise anticipated the findings from the clinical trials. Different DENVax formulations failed to generate adequate responses against DENV4 and stimulate lower levels of nAbs to DENV 1, 3 and 4 but higher levels to DENV2 (Osorio et al., 2011a).

Overall, our findings have enormous impact for the planning and evaluation of DENV and ZIKV vaccine schedules, design, and monitoring, strongly suggesting the consideration of CD4+ T cell epitopes for the composition of new generation flavivirus vaccines.

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Author contributions

C.A.S., A.M.d.S, C.S.-C., A.M.-S. and L.C. developed the experimental design. C.R., M.I.M. and A.G.B. supervised and performed sample collection and animal monitoring. C.S.-C., A.M.-S., L.C., S.H. and L.A. performed the experiments. C.A.S., C.S.-C, A.M.-S., L.C. and M.S.-R. analyzed the data. C.A.S., C.S.-C, A.M.-S. and L.C drafted the article. C.A.S., C.S.-C., A.M.-S, L.C., S.H., M.S.-R., L.A., T.A., M.I.M., C.R., A.G.B. and A.M.d.S. reviewed and corrected the last version.

Declaration of interests

The authors declare no competing interest.

Materials and Methods

Experimental model. Young adult (4–7 years of age) male rhesus macaques (*Macaca mulatta*), seronegative for DENV and ZIKV, were housed in the CPRC facilities at the University of Puerto Rico, San Juan, Puerto Rico. All procedures were reviewed and approved by the Institute's Animal Care and Use Committee at the Medical Sciences Campus, University of Puerto Rico (IACUC-UPR-MSC) and performed in a facility accredited by the Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC) (Animal Welfare Assurance number A3421; protocol number, 7890116). In addition, the study was conducted following the USDA Animal Welfare Regulations, the Guide for the Care and Use of Laboratory Animals, and institutional policies, to ameliorate animal suffering by the recommendations of the Weatherall Report on the use of nonhuman primates in research. All procedures were conducted under anesthesia by intramuscular injection of ketamine at 10–20 mg/kg of body weight, as approved by the IACUC. Anesthesia was delivered in the caudal thigh using a 23-gauge sterile syringe needle. During the period of the entire study, the macaques were under the environmental enrichment program of the facility, also approved by the IACUC. Animals were continuously monitored by trained veterinarians at the Animal Research Center.

Viral Stock. DENV-2 New Guinea 44 (NGC) strain (provided by Steve Whitehead, NIH/NIAID, Bethesda, MD) and ZIKV PRVABC59 (ATCC VR-1843) were used to infect macaques at different timepoints. Viruses were expanded and tittered by plaque assay and qRT-PCR using protocols standardized in our laboratories. In addition, both viruses were used for neutralization assays.

Depletion treatment, viral infection, and sample collection. A total of 29 rhesus macaques seronegative for DENV and ZIKV were housed in the CPRC facilities, at the University of Puerto Rico, San Juan, Puerto Rico. During the first year, macaques were divided into two cohorts based on their depletion status. Twelve (12) animals were depleted of CD4+ T cells by administration of anti-CD4 Ab CD4R1 (NHP Reagent Resource; https://www.nhpreagents.org). Administration of the depletion treatment consisted of an initial s.c. inoculation of 50 mg/kg at 15 days prior to viral infection, followed by two i.v. injections of 7.5 mg/kg 12 days and 9 days before viral infection respectively. The seventeen (17) remaining animals received phosphate-buffered saline (PBS) as a control. Both cohorts were then infected with DENV-2 NGC strain (5.0 x 10^5 pfu s.c.), which is denoted from here on as the primary infection. Following one year after infection, animals were further divided into five cohorts based on depletion status. Animals were depleted of CD4+ or CD8+ T cells, or treated with PBS, followed by a secondary infection with ZIKV (1×10^6 pfu s.c.). CD8+ T cell depletion was performed by administration of anti-CD8 alpha MT807R1 at the same dosage as CD4+ T cells depletion treatment. CD4+ T cell depletion was performed on groups 1 and 2 (group

1: n=6, denoted CD4-/DV2/CD4-/ZV; group 2: n=6, denoted CD4+/DV2/CD4-/ZV). Group 3 was depleted

of CD8+ T cells (n=6, denoted CD4+/DV2/CD8-/ZV). Lastly, the remaining two groups were administered

PBS (group 4: n=6, denoted CD4-/DV2/CD4+/ZV; group 5: n=5, denoted CD4+/DV2/CD4+/ZV).

Blood samples were collected on days $^-$15, $^-$12 and $^-$9 pre-infection, and during the first fifteen consecutive

days after infection, followed by a monthly sample collection from there onwards until a year later when

sample collection pattern described is repeated for the secondary infection. Collected samples included

serum, heparinized whole blood, and citrate whole blood for PBMCs isolation. Macaques were monitored

after treatments and infections by trained veterinarians for evidence of disease and clinical status. Rectal

and external temperatures and weights were taken on day 0 and every other day pre- and post-infection. A

summary for the experimental design and groups is provided (SFig 1).

Immunophenotyping. Phenotypic characterization of Rhesus macaque's adaptive immune response was

performed by 16- multicolor flow cytometry using fluorochrome-conjugated Abs at several time points.

Depletion efficacy was confirmed by measuring the frequency of $CD4^+$, $CD8^+$ T cells, and $CD20^+$ B cells

on the following timepoints: pre-treatment/depletion baseline, and days 2, 5, and 9 post-treatment. In

addition, B and T cell frequencies were measured on baseline and days 1, 2, 3, 7, 15, 30, 60 and 90 p.i. and

p.c.. Aliquots of 150 uL of heparinized whole blood were incubated with a mix of antibodies for 30 min. in

the dark at room temperature. After incubation, red blood cells are fixed and lysed with BD FACS fix and

lyse solution, and cells were washed twice with BSA 0.05%. Samples were analyzed using a MACSQuant$^®$

Analyzer 16 Flow Cytometer (Miltenyi Biotec, CA). Antibodies used in this study were: CD8-FITC (DK25)

from Sigma; CD3- PerCP (SP34), Ki67- Viogreen (B56), CD4- APC (L200), CD69- PeCy7 (FN50), CD95-

PE (DX2), IgG- APC- H7 (G18- 145), CD11b- AF 700 (ICRF44), CD80- BV650 (L307.4), CD27- PE (M-

T466) from BD Biosciences; CD20- PacBlue (2H7), HLA-DR- BV570 (L243), CD138- FITC (DL- 101),

ICOS- PE/Dazzle 594 (C398.4H), CXCR3- PECy7 (GO25H7), PD-1- BV650 (EH12.2H7) from

Biolegend; CD28- APC- Vio770 (I5E8) and CCR7- PerCP Vio770 (REA546) from Miltenyi; CXCR5- PE

(MU5UBEE) from Thermo eBiosciences; and CD38- APC (AT-1) from Adipogen.

For analysis, lymphocytes (LYM) were gated based on their characteristic forward and side scatter patterns.

B cells were defined as $CD20^+CD3^-$, Memory (MBC= $CD20^+$, $CD3^-$, $CD27^+$), class-switched IgG Memory

(IgG MBC= $CD20^+$, $CD3^-$, $CD27^+$, surface IgG+ (sIgG), plasmablasts as (PB= $CD20^{-/low}$, $CD3^-$, $CD11b^-$,

$HLA-DR^+$, $CD80^+$) as described by Silveira et al., 2015 (Silveira et al., 2015), plasma cells as (PC= $CD20^-$

$^{/low}$, $CD3^-$, $CD138^+$) as described by Martinez- Mirullo et al., 2016 (Martinez-Murillo et al., 2016). Gating

strategy for B cells and subsets is presented on Supplementary Figure 9 (SFig 9). T cells were defined as

$CD3^+CD20^-$, $CD4^+$ T cells ($CD3^+CD20^-CD4^+$), $CD8^+$ T cells ($CD3^+CD20^-CD8^+$), and subpopulations were

defined inside the $CD3^+$ T cells. Naïve ($CD3^+CD20^-CD28^+CD95^-$), EM ($CD3^+CD20^-CD28^-CD95^+$), and

CM (CD3$^+$CD20$^-$CD28$^+$CD95$^+$) T cell subpopulations were determined within CD4$^+$ and CD8$^+$ T cells.

Gating strategy for T cells and memory subsets is presented on Supplementary Figure 10 (SFig 10), while

gating strategy for the characterization of CD4$^+$ pTfh cells was represented by selecting CM and EM T cells

(CD4$^+$/CXCR5$^+$/CXCR3$^+$) expressing activation and migration markers such as (CCR7$^+$/PD-1$^+$/ICOS$^+$)

(SFig 11). All data from cell population frequencies and immune markers expression were analyzed using

Flow/Jo software and GraphPad Prism (FlowJo LLC Ashland, OR).

qRT- PCR. DENV-2 and ZIKV viral RNA for real-time PCR assay was extracted from 200uL of virus

isolate (previously tittered by focus reduction neutralization assay) and from acute serum samples using a

MagMax Viral/Pathogen Nucleic Acid Isolation Kit (Applied Biosystems, MA) as per the manufacturer's

instructions. Viral RNA extraction was performed using a KingFisher Duo Prime Purification System

(Thermo Fisher Scientific, MA). In brief, a Viral Pathogen DNA/RNA binding magnetic bead solution is

prepared, 200uL of sera, 500uL of Viral Pathogen Nucleic Acid isolation kit wash buffer, 5uL of a protein

kinase solution, and 1mL of ethanol solution (80% ethanol in DNAse free water) were added to specified

wells in a KF Duo Deepwell 96 plate (Thermo Fisher Scientific, MA) and loaded on the KingFisher Duo

Prime Purification System. Purified RNA was collected and stored at -80°C in kit elution buffer solution.

Real-time PCR for DENV-2 and ZIKV isolated RNA was carried out using the Gensig Real-Time PCR

detection kit for Dengue Virus and the Gensig Real-Time PCR detection kit for Zika Virus (Primer Design,

UK), respectively, as per the manufacturer's instructions. Briefly, a kit Positive Control is diluted in 500uL

of a kit Template buffer and a series of tenfold dilutions were prepared as follows: 2 x 10^5/uL, 2 x 10^4/uL,

2 x 10^3/uL, 2 x 10^2/uL, 20/uL, 2/uL (copy number/ mL). For the reaction mix, 10uL of oasig 2X Precision

one step qRT-PCR was combined with 1uL of kit probe/primer mix and 4uL of sterile water, for a total

volume of 20uL once the RNA sample was added. The reaction mix was added to a 96 well plate, alongside

the experimental RNA samples, a kit non-template control (NTC), an RNA extraction negative control

(DNAse free water), a positive control (RNA extraction from virus stock), and calibration standards, in

specified wells. The plate was then loaded, and the RT-PCR reaction was performed using a Quant Studio

5 Real-Time PCR Instrument (Applied Biosystems, MA). For quantification, a standard curve was

generated from the ten-fold dilutions of the kit RNA positive control.

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ELISAs for DENV and ZIKV. Serostatus of animals for DENV and ZIKV was assessed before and after

DENV-2 infection using DENV IgG/IgM commercial kits (Focus Diagnostics, CA). ZIKV serostatus was

also assessed using a commercial kit for ZIKV IgM (InBios, International Inc, Seattle) and ZIKV IgG

(XpressBio, Frederick, MD). Timepoints measured include baseline and days 7, 10, 15, 30, 60, and 90 post-

infection. All assays were performed per the manufacturer's instructions and as described by our group
(Pantoja et al., 2017; Perez-Guzman et al., 2019; Serrano-Collazo et al., 2020).

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ELISAs for detection of DENV NS1 antigen, DENV anti-NS1 IgG and ZIKV anti-NS1 IgG. Detection
of DENV NS1 antigen after primary DENV-2 infection, ZIKV anti-NS1 IgG after secondary ZIKV
infection, and DENV anti-NS1 IgG after both primary and secondary infections were measured using
commercial kits (InBios, International Inc, Seattle). The assays were performed per the manufacturer's
instructions. Timepoints measured include baseline and days 3, 5, 7, 15 and 30 p.i. for DENV NS1, and
baseline and days 15, 30 and 90 p.c. for ZIKV and DENV anti NS1 IgG.

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DENV neutralization assays. For the Focus Reduction Neutralization Test (FRNT) for DENV, Vero81
cells (ATCC CCL-81) were seeded at approx. 2.0×10^5 per well in 24 well-plates with DMEM (Dulbecco's
Modified Eagle's medium, Thermo Fisher Scientific) for approx. 18 hours. Serum dilutions (ten-fold) were
prepared in diluent medium Opti-MEM (Invitrogen) with 2% FBS (Gibco) and 1% antibiotic/antimycotic
(Hyclone). Virus was added to each dilution and incubated for 1 hour at 37ºC/5%. Before inoculation, the
growth medium was removed, and cells were inoculated with 50 uL per well of serum-virus dilution in
triplicates; plates were incubated for 1 hour at 37ºC/5%CO_2/rocking. After incubation, 125 uL per well of
overlay (Opti-MEM 1% carboxymethylcellulose (Sigma), 2% FBS, 1% non-essential amino acids (Gibco)
and 1% antibiotic/antimycotic (HyClone)) was added to the plates containing virus dilutions, followed by
an incubation period of 48 hours at 37ºC/5%CO_2. After two days, overlay was removed with PBS and fixed
with 4% paraformaldehyde for 30 minutes. Plates were blocked with 5% non-fat dairy milk in 1X perm
buffer (BD Cytofix/Cytoperm) for 10 min and incubated for 1hr/37ºC/5%CO2/rocking with anti-E mAb
4G2 and anti-prM mAb 2H2 (kindly provided by Dr. Aravinda de Silva and Ralph Baric, University of
North Carolina Chapel Hill, NC, USA), both diluted 1:100 in blocking buffer. Plates were washed three
times with PBS and incubated 1hr/37ºC/5%CO_2/rocking with horseradish peroxidase (HRP)-conjugated
goat anti-mouse antibody (Sigma), diluted 1:1,500 in blocking buffer. Foci were developed with TrueBlue
HRP substrate (KPL) and counted using an Elispot reader. Results were reported as FRNT with a 60% or
greater reduction in DENV foci (FRNT60). A positive neutralization titer was designated as 1:20 or greater,
while <1:20 was considered a negative neutralization titer.

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ZIKV neutralization assays. For the Plaque Reduction Neutralization Test (PRNT) for ZIKV, Vero81 cells
(ATCC CCL-81) were seeded at approx. 2.0×10^5 per well in 24 well-plates with DMEM (Dulbecco's
Modified Eagle's medium, Thermo Fisher Scientific) for approx. 18 hours. Serum dilutions (ten-fold) were
prepared in a diluent medium (Opti-MEM (Invitrogen) with 2% FBS (Gibco) and 1% antibiotic/antimycotic

(Hyclone). Virus was added to each dilution and incubated for 1 hour at 37ºC/5%/CO2. Before inoculation,

the growth medium was removed, and cells were inoculated with 100 uL per well of each dilution in

triplicates; plates were incubated for 1 hour at 37ºC/5%CO2/rocking. After incubation, 1mL per well of

overlay (Opti-MEM 1% carboxymethylcellulose (Sigma), 2% FBS, 1% non-essential amino acids (Gibco),

and 1% antibiotic/antimycotic (HyClone)) was added to the plates containing virus dilutions, followed by

an incubation period of 4 days at 37ºC/5% CO2. After four days of incubation at 37ºC/5%CO2, the overlay

was removed; the cells were washed twice with phosphate-buffered saline (PBS), fixed in 80% methanol,

and stained with crystal violet and foci were counted. The mean focus diameter was calculated from approx.

twenty foci per clone were measured at 35 magnifications. Results were reported as the PRNT with a 60%

or greater reduction in ZIKV or DENV plaques (PRNT60). A positive neutralization titer was designated

as 1:20 or greater, while < 1:20 was considered a negative neutralization titer.

1054

EDIII and NS1 Antigen Production. ZIKV (H/PF/2013) EDIII antigen used in this study was produced

as previously described (Adams et al., 2021). EDIIIs of DENVs were also cloned and expressed similarly

to ZIKV EDIII. Briefly, codon-optimized genes encoding the EDIIIs of DENV1 (AAB70694·1, E protein

aa 297-394), DENV2 (ADA00411·1, E protein aa 297-394), DENV3 (AAB69126·2, E protein aa 295-392)

and DENV4 (ADA00410·1, E protein aa 297-394) with an N-terminal human serum albumin signal

peptide, a polyhistidine tag, and a HaloTag were cloned into the mammalian expression plasmid pαH.

Recombinant DENV EDIII antigens were expressed in mammalian Expi293 cells and purified from the

culture supernatant using Ni-NTA agarose (Qiagen). Purified EDIII antigens were biotinylated using

HaloTag PEG biotin ligand (Promega), according to the manufacturer's protocol. For NS1 antigen

production, codon-optimized genes encoding the NS1s of DV1 NS1 Region 37, DV2 NS1 Region 39, DV3

NS1 Region22, DV4 NS1 Region 45 and ZKVNS1 Region 47 were used. Mobility-shift analysis was used

to assess the biotinylated EDIII antigens using SDS-PAGE. The mammalian expression plasmids and

sequences will be made available in the plasmid repository and Genbank, respectively.

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Coupling antigens to beads via avidin-biotin interaction: Site-specifically biotinylated EDIII antigens

were coupled to unique MagPlex®-Avidin Microspheres (DENV1 (region 12), DENV2 (region 26),

DENV3 (region 36), DENV-4 (region 38) and ZIKV (region 30)) at a concentration of 5 μg of antigen per

106 beads in phosphate-buffered saline, pH 7.4 (PBS, 137 mM NaCl, 2.7 mM KCl, 8 mM Na2HPO4, and

2 mM KH2PO4) for 1 hour at 37°C with shaking at 700 rpm. Beads were then washed/blocked three times

in block buffer (PBS + 1% BSA) and resuspended in wash buffer at 2x106 beads/mL.

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EDIII and NS1 multiplex Assay: DENV and ZIKV EDIII coupled beads were combined in equal ratios by plating 50 µL containing 2,500 beads per antigen into each well of a 96-well assay plate (Cat. No:655906). Human serum samples were diluted 1:500 in block buffer. Mouse monoclonal antibodies specific for each EDIII antigen (ZV-67 (ZIKV), E103 (DENV1), 3H5 (DENV2, 8A1 (DENV3), E88 (DENV4)) and NS1 antigen were titrated in each assay as controls for assay consistency across couplings, plates, and assay days. A magnetic plate separator was used to remove the block buffer from the assay plate, and 50 µL of diluted serum or mAb was added to the beads. The serum and bead mixture were incubated for 1 hour at 37°C with shaking at 700 rpm. Beads were washed thrice200 µL block buffer per well using a magnetic separator. 50 µl of Goat anti-Human IgG Fc Multi-species SP ads-PE (Southern Biotech, catalog:2014-09) and Goat anti-Mouse IgG Fc Human ads-PE (Southern Biotech, catalog:1030-09) were added to the beads (6 µg/ml in block buffer) and incubated for 1 hour at 37°C with shaking at 700 rpm to detect respective antibody species. Beads were washed thrice with 200 µL block buffer per well using a magnetic separator and resuspended in 100 µL of block buffer before acquiring data. Fluorescence data were obtained using a Luminex 200 analyzer set to acquire at least 50 beads per bead region.

Principal Component Analysis (PCA). All PCA analyses were performed using R statistical software R version 4.2.3 using the *prcomp* function of the *stats* package (Team et al., 2018; Team, 2010). To examine global patterns of infection, we carried out a PCA using all the parameters measured during the infection timeline; these analyses were performed for day 15, day 30 and day 90 of infection. The parameters used to perform PCA are depicted in Supplementary Table 3 (Table S3).

Quantification and statistical analysis. Statistical analyses were performed using GraphPad Prism 9.0 software (GraphPad Software, San Diego, CA, USA). For viral burden analysis, the log titers and levels of vRNA were analyzed by multiple unpaired t-tests and two-way ANOVA. The statistical significance between or within groups evaluated at different time points was determined using one-way or two-way analysis of variance (ANOVA) (Tukey's, Sidak's, or Dunnett's multiple comparisons test) or unpaired t-test to compare the means. Significant multiplicity-adjusted p-values (*< 0.05, **< 0.01, ***< 0.001, ****< 0.0001) show statistically significant differences between groups (Tukey test) or time points within a group (Dunnett test).

Fig 1. DENV2 and ZIKV RNA kinetics in flavivirus-naïve CD4-depleted and undepleted animals.
RNAemia is affected by depletion of CD4+ or CD8+ T cells. **Upper panel**. CD4-depleted animals are depicted in purple and undepleted animals are depicted in turquoise. **(A)** DENV-2 genome copies/mL were measured in serum to monitor viral replication during the first 15 days and day 30 after infection. Genome copies per mL are shown logarithmically. **(B)** The area under the curve (AUC) was calculated for individual values. **(C)** Average RNAemia days were calculated using the following formula: total viremia days divided by the total number of days during which viremia was monitored. **Lower panel**. Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red). **(D)** ZIKV genome copies/mL were measured in serum to monitor viral replication during the first 15 days and day 30 after infection. Genome copies per mL are shown logarithmically. **(E)** The area under the curve (AUC) was calculated for individual values. **(F)** Average RNAemia days were calculated using the following formula: total viremia days divided by the total number of days during which viremia was monitored. Statistically significant differences among and within groups were calculated by two-way ANOVA using Tukey's multiple comparisons test and unpaired t-tests. Colored stars represent a significantly different group, while colored lines represent the group that it is compared to.

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Fig 2. T cell depletion modifies serological profile during primary DENV2 infection. IgM and IgG
response after DENV-2 infection was assessed using commercial ELISA tests. CD4-depleted animals are
depicted in purple and undepleted animals are depicted in turquoise. Dotted lines indicate the limit of
detection for each test. **(A-B)** Binding capacity of DENV IgM and IgG antibodies from CD4-depleted and
undepleted animals after DENV-2 infection. **(C-D)** Total DENV IgM and IgG levels throughout different
timepoints. Statistically significant differences among and within groups were calculated by two-way
ANOVA using Tukey's multiple comparisons test and unpaired t-tests.

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Fig 3. T cell depletion modifies serological profile during secondary heterologous ZIKV infection.
IgM and IgG response after ZIKV infection in the presence of DENV immunity was assessed using
commercial ELISA tests. Animal cohorts are depicted as follows based on treatment regime:
CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-
/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red).
Dotted lines indicate the limit of detection for each test. **(A-B)** Binding capacity of DENV IgM and IgG
antibodies from CD4-depleted and undepleted animals after ZIKV infection. **(C-D)** Binding capacity of
ZIKV IgM and IgG antibodies from CD4-depleted and undepleted animals after ZIKV infection. **(E)** Total
ZIKV IgG levels after ZIKV infection were analyzed. Statistically significant differences among and within
groups were calculated by two-way ANOVA using Tukey's multiple comparisons test and unpaired t-tests,
and by One-way ANOVA using Tukey's multiple comparisons test.

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Fig 4. FRNT values of neutralizing antibodies against DENV-2 in depleted or undepleted flavivirus-naïve macaques. Neutralization capacity against DENV-2 is shown. CD4-depleted animals are depicted in purple and undepleted animals are depicted in turquoise. Dotted lines indicate the limit of detection for each test. **(A-C)** FRNT60 values of neutralizing antibodies against DENV-2 after DENV-2 infection are shown. **(D-E)** EC50 values of neutralizing antibodies against ZIKV after ZIKV infection. Statistically significant differences among groups were calculated by one-way and two-way ANOVA using the Tukey's multiple comparisons test and unpaired t-tests.

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Fig 5. PRNT values of neutralizing antibodies against ZIKV in depleted or undepleted DENV-
immune macaques. Neutralization capacity against ZIKV is shown. Animal cohorts are depicted as follows
based on treatment regime: Animal cohorts are depicted as follows based on treatment regime:
CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-
/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red).
Dotted lines indicate the limit of detection for each test. **(A-D)** FRNT60 values of neutralizing antibodies
against ZIKV after ZIKV infection are shown. **(E-G)** EC50 values of neutralizing antibodies against ZIKV
after ZIKV infection. Significant differences among groups were calculated by one-way and two-way
ANOVA using the Tukey's multiple comparisons test and unpaired t-tests.

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Fig 6. Epitope reactivity against DENV and ZIKV antigens in depleted and undepleted macaques.
Antibody type-specific and cross-reactive responses against EDIII and NS1 antigens were assessed. Data
generated by Luminex assay was normalized to a cross-reactivity index (CRI) by subtracting background
(BSA) from the homologous value (values against infecting virus, HOM) and the heterologous values
(values against heterologous virus, HET) followed by dividing the subtracted homologous by the subtracted
heterologous values $[\frac{(HOM-BSA)}{(HET-BSA)}]$. **Upper panel.** CD4-depleted animals are depicted in purple and
undepleted animals are depicted in turquoise. **(A)** Antibody response to EDIII (left side) and NS1 (right
side) antigens from all four DENV serotypes and ZIKV 90 days after DENV2 infection. **Lower panel.**
Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in
turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-/ZV (shown in yellow), CD4-
/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red). **(B)** Antibody response to
EDIII (left side) and NS1 (right side) antigens from all four DENV serotypes and ZIKV 90 days after ZIKV
infection. Significant differences among groups were calculated by two-way ANOVA using the Tukey's
multiple comparisons test.

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**Fig 7. IgG memory B cell and ASC population kinetics after ZIKV infection in CD4+ T cell-competent
and -deficient animals with previous DENV-2 immunity.** The frequency of IgG MBCs and ASCs was
assessed by immunophenotyping using flow cytometry. Animal cohorts are depicted as follows based on
treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green),
CD4+/DV2/CD4-/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-
/ZV (shown in red). **(A)** Percentages of surface IgG expression in total MBCs (CD3-CD20+CD27+sIgG+).
(B) Frequencies of CD69+ cells in total IgG+ MBCs (CD3-CD20+CD27+sIgG+CD69+). **(C)** Frequencies
of CD69+ cells in total IgG MBCs with all cohorts organized into CD4+ T cell competent (shown in
turquoise) and CD4+ T cell depleted (shown in purple). **(D)** Frequencies of CD69+ cells in total ASCs
(CD3-CD20dimCD27+CD69+). Statistically significant differences among groups were calculated by two-
way ANOVA using the Tukey's multiple comparisons test and unpaired t-tests.

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Fig 8. Total pTfh CD4+ T cell characterization. Immunophenotyping of CD4+ pTfh T cells was assessed via flow cytometry using frozen PBMCs collected on baseline, day 7, and day 15 pi with ZIKV. Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), and CD4+/DV2/CD8-/ZV (shown in red). **(A)** Frequency of total CD4+ T cells expressing follicular canonical marker CXCR5. **(B)** Frequency of total CD4-pTfh T cells expressing CXCR5 and CXCR3. **(C)** Frequency of total pTfh CD4 T cells expressing B cell co-stimulating surface makers PD1, and ICOS. **(D)** Gating Strategy for total pTfh CD4+ T cells characterization based on CXCR5, CXCR3, PD1, and ICOS surface markers expression. Comparisons between groups are reported as multiplicity-adjusted p values performed by two-way ANOVA using Tukey's multiple comparisons tests and unpaired t-test.

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Fig 9. Total CM-pTfh CD4+ T cell characterization. Immunophenotyping of CM-pTfh CD4+ T cells after secondary ZIKV infection was accessed via flow cytometry using frozen PBMCs collected on baseline, day 7, and day 15 pi with ZIKV. Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), and CD4+/DV2/CD8-/ZV (shown in red). **(A)** Frequency of total CM CD4+ T cells expressing CXCR5. **(B)** Frequency of total CM- pTfh CD4+ T cells expressing CXCR5 and CXCR3. **(C)** Frequency of total CM-pTfh CD4+ T cells expressing B cell co-stimulating surface makers PD1, and ICOS. **(D)** Gating Strategy for total CM-pTfh CD4+ T cells characterization based on CXCR5, CXCR3, PD1, and ICOS surface markers expression. Comparisons between groups are reported as multiplicity-adjusted p values performed by two-way ANOVA using Tukey's multiple comparisons tests and unpaired t-test.

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Fig 10. Pr
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IgG response and B and T cell response. Animal cohorts are depicted as follows based on treatment regime:
CD4+/DV2/CD4-/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-
/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red).
Principal component analysis of day 15 **(A)**, day 30 **(B)** and day 90 **(C)** post ZIKV challenge. Principal
component analysis of day 90 p.c. including CRI data **(D)**.
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SUPPLEMENTARY FIGURES

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		Depletion	Primary Infection	Depletion	Secondary Infection
Group 1 n= 6		CD4-	DENV2	CD4-	ZIKV
Group 2 n= 5		CD4+	DENV2	CD4+	ZIKV
Group 3 n= 6		CD4+	DENV2	CD4-	ZIKV
Group 4 n= 6		CD4-	DENV2	CD4+	ZIKV
Group 5 n= 6		CD4+CD8+	DENV2	CD4+CD8-	ZIKV

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SFig 1. Experimental design of T cell depletion and heterologous DENV2 and ZIKV infections in
flavivirus-naïve macaques. Five cohorts of rhesus macaques (*Macaca mulatta*) underwent depletion of
CD4+ T cells (or PBS in control group) followed by DENV-2 (5 x 10^5 pfu s.c.) infection at different
timepoints. One year later, all cohorts were exposed to ZIKV strain PRABCV59 (1 x 10^6 pfu s.c.) after a
second round of CD4+ or CD8+ T cell depletion (or PBS in control group). Sample collection was
performed at various time points up to 90 days post-infection (p.i.) for serum, whole heparinized blood, and
PBMC isolation.

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SFig 2. CD4+ and CD8+ T cell frequency following depletion treatments prior to DENV2 and ZIKV infections. Frequency of CD4+ and CD8+ T cells was assessed by immunophenotyping before and after depletion treatments using flow cytometry. **Upper panel**. CD4-depleted animals are depicted in purple and undepleted animals are depicted in turquoise. CD4+ **(A)** and CD8+ **(B)** T cell depletion efficacy for depleted and undepleted animals before, during and after DENV2 infection. **Lower panel**. Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red). CD4+ **(C)** and CD8+ **(D)** T cell depletion efficacy for depleted and undepleted animals before, during and after ZIKV infection.

ID	Immune History	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	30	Total	Mean
																				RNAemia (Log10 genome copies/mL) Post-DENV Infection
0Z6		0.000	0.000	0.924	1.505	1.245	0.875					0.446	0.615	0.039	0.000	0.000	0.000	0.000		
AE9		0.000	0.000	1.204	1.759	1.059	0.758	0.164		0.828		0.000	0.272	0.202	0.000	0.000	0.000	0.000		
1Z3		0.000	0.120	1.123	1.672	1.528	0.641	0.768		0.828		0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA317		0.000	0.000	1.557	2.235	1.888	1.291	0.176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA312		0.000	0.000	0.908	2.060	0.718	0.961	0.217	0.425	0.285	0.107	0.713	0.000	0.000	0.000	0.000	0.000	0.000		
MA209		0.000	0.000	0.323	1.003	0.844	0.000	1.283	1.608	1.784	1.765	1.202	0.555	0.000	0.000	0.000	0.000	0.000		
5Z1		0.000	0.357	0.655	1.967	1.298	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0Z7		0.000	0.326	0.991	3.821	1.282	0.663	0.493	0.490	0.000	0.720	0.000	0.362	0.000	0.000	0.000	0.000	0.000		
MA333	CD4-/DV2	0.000	0.000	1.111	1.812	1.456	0.692	0.147	0.429	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	50	2.94
MA321		0.000	0.000	0.873	1.753	1.844	1.016	0.658	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA267		0.000	0.030	0.805	1.459	1.467	1.334	0.236	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA316		0.000	0.192	0.928	1.785	1.840	1.632	1.127	0.785	0.515	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA249		0.000	1.766	0.000	2.463	2.308	1.618	0.799	0.040	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA345		0.000	0.529	1.293	1.970	1.961	1.452	0.813	0.545	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
7X5		0.000	0.000	0.608	0.927	1.716	0.936	0.706	0.566	0.107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
6S1		0.000	0.000	1.047	1.157	1.784	1.279	0.109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA353		0.000	0.000	0.891	1.117	0.454	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X5		0.000	0.076	0.879	1.741	1.379	0.663					0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA341		0.000	0.000	2.037	2.855	2.111	1.006	0.174	0.053	0.115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
4Z0		0.000	0.000	1.092	1.865	1.364	0.085	0.052	0.474	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA320		0.000	0.566	1.598	1.650	1.641	0.674	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
8X2		0.000	0.598	1.078	1.505	0.255	0.000	0.257	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA258		0.000	0.000	0.330	1.924	1.692	1.249	0.768	0.313	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X7		0.000	0.000	1.247	2.148	1.305	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
5Z8		0.000	0.901	1.555	2.487	1.782	0.123	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X2	CD4+/DV2	0.000	0.638	1.313	1.662	1.704	1.080	0.457	0.000	0.067	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	50	2.94
9X1		0.000	0.000	0.527	1.242	1.009	0.552	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
2Z4		0.000	0.604	0.827	1.477	1.215	0.089	0.000	0.162	0.000	0.159	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA163		0.000	0.102	0.762	1.026	1.581	1.030	1.078	0.911	0.282	0.605	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA254		0.000	0.000	1.443	2.228	2.012	0.087	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA264		0.000	0.000	1.210	0.857	2.160	1.331	0.097	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA311		0.000	0.243	1.216	1.511	1.387	0.000	0.000	0.000	0.670	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA350		0.000	0.000	1.534	2.385	2.190	0.504	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA364		0.000	0.000	1.229	2.033	2.035	1.128	0.654	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		

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1326 Table S1. **DENV-2 RNAemia of CD4-depleted and undepleted animals.** DENV-2 RNA detection during
1327 the first 15 days and day 30 p.i. Mean viremia days per group was calculated using days with detectable
1328 RNAemia divided by the number of animals in each group.
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ID	Immune History	RNAemia (Log10 genome copies/mL) Post-ZIKV Infection																	Days	
		0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	30	Total	Mean
0Z6	CD4-/DV2/CD4-/ZV	0.000	0.550	1.401	2.114	1.305	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	13	2.17
AE9		0.000	0.277	0.878	2.158	1.496	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
1Z3		0.000	0.296	1.213	2.459	1.744	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA317		0.000	0.118	1.214	2.663	1.639	0.649	0.042	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA312		0.000	0.702	1.096	2.188	1.850	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA209		0.000	0.156	0.939	1.730	1.507	0.347	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X5	CD4+/DV2/CD4-/ZV	0.000	0.455	1.477	2.582	1.955	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	12	2
MA341		0.000	0.884	1.680	3.208	2.709	0.412	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
4Z0		0.000	-0.038	0.272	1.574	0.473	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA320		0.000	-0.377	0.770	1.662	-0.553	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
8X2		0.000	-0.029	0.122	1.982	0.911	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA258		0.000	-0.467	1.456	3.038	2.164	0.000	0.143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
5Z1	CD4-/DV2/CD4+/ZV	0.000	0.508	0.686	2.364	0.378	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	9	1.5
0Z7		0.000	0.967	1.585	2.828	1.904	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA333		0.000	0.724	1.097	2.244	1.185	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA321		0.000	0.468	1.183	2.437	1.873	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA267		0.000	0.150	0.243	1.994	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA316		0.000	0.578	1.121	2.871	0.820	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X7	CD4+/DV2/CD8-/ZV	0.000	0.006	-1.268	1.311	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	7	1.17
5Z8		0.000	0.637	1.010	2.605	1.701	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X2		0.000	0.455	0.429	1.991	0.458	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
9X1		0.000	0.000	0.410	1.420	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
2Z4		0.000	0.041	0.109	1.438	0.420	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA163		0.000	0.000	0.069	2.038	1.161	0.559	0.212	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA254	CD4+/DV2/CD4+/ZV	0.000	0.109	0.989	2.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	6	1
MA264		0.000	0.000	0.874	2.521	1.261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA311		0.000	0.000	0.964	2.271	1.307	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA350		0.000	0.493	0.901	2.262	1.290	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		
MA364		0.000	0.000	1.045	2.340	1.059	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		

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1334 **Table S2. ZIKV RNAemia days of DENV-immune macaques with different T cell depletion status**.
1335 ZIKV RNA detection during the first 15 days and day 30 p.i. Mean viremia days per group was calculated
1336 using days with detectable RNAemia divided by the number of animals in each group.
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1342 **SFig 3. DENV NS1 levels are affected by absence of CD4+ T cells after DENV-2 infection.** DENV-NS1
1343 levels after DENV-2 infection were measured using a commercial ELISA test. CD4-depleted animals are
1344 depicted in purple and undepleted animals are depicted in turquoise. Dotted lines indicate the limit of
1345 detection for each test. Statistically significant differences among and within groups were calculated by
1346 two-way ANOVA using Tukey's multiple comparisons test and unpaired t-tests.

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SFig 4. Depletion of CD4+ T cells before DENV infection increases DENV NS1 anti-IgG levels. DENV-
NS1 anti-IgG levels were measured using commercial ELISA tests. **(A)** CD4-depleted animals are depicted
in purple and undepleted animals are depicted in turquoise. DENV NS1 anti-IgG levels after DENV-2
infection. **(B)** Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV
(shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-/ZV (shown in yellow),
CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red). DENV NS1 anti-IgG
levels after ZIKV infection. No limit of detection or cut-off value is provided because this value will vary
depending on flavivirus disease prevalence in the geographical location where the test is performed.
Statistically significant differences among and within groups were calculated by two-way ANOVA using
Tukey's multiple comparisons test and multiple t-tests.

ZIKV Anti-IgG NS1

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SFig 5. CD4+ T cell depletion status prior to DENV infection has no impact in production of ZIKV
NS1-binding IgG after ZIKV infection. ZIKV NS1-IgG response after ZIKV infection in the presence of
DENV immunity was assessed using a commercial ELISA test. Animal cohorts are depicted as follows
based on treatment regime: Animal cohorts are depicted as follows based on treatment regime:
CD4+/DV2/CD4+/ZV (shown in turquoise), CD4-/DV2/CD4+/ZV (shown in green), CD4+/DV2/CD4-
/ZV (shown in yellow), CD4-/DV2/CD4-/ZV (shown in purple), and CD4+/DV2/CD8-/ZV (shown in red).
Dotted lines indicate the limit of detection for each test. Binding capacity of ZIKV NS1-IgG antibodies
from CD4-depleted and undepleted animals after ZIKV infection. Statistically significant differences
among and within groups were calculated by two-way ANOVA using Tukey's multiple comparisons test
and unpaired t-tests.
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Sfig 6. **Frequencies of pTfh cells correlate with B cell response cell subsets such as total IgG$^+$ MBCs, activated IgG$^+$ MBCs, and activated ASCs during the secondary ZIKV infection.** Pearson correlations and simple linear regressions were performed on data from pTfh and B cell subsets. All experimental animals are shown in black. Animal cohorts are depicted as follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise) and CD4-/DV2/CD4+/ZV (shown in green). **(A)** The levels of total pTfh cells of the CXCR5$^+$ phenotype (shown as X5+ in graphs), measured via Flow Cytometry from PBMCs, isolated at day 15 p.c., correlated with frequencies of total IgG$^+$ MBCs, measured via Flow Cytometry from isolated whole blood at day 15 p.c.. **(B-C)** Correlations were performed comparing CXCR5$^+$CXCR3$^+$ pTfh cells (shown as X5+X3+) from day 7 p.c. with **(B)** activated IgG$^+$ MBCs from day 7 p.c., in the CD4+/DV2/CD4+/ZV group, and in the **(C)** CD4-/DV2/CD4+/ZV group. Correlations were performed comparing PD1+ICOS+ pTfh cells, from day 7 p.c., with **(D)** activated IgG$^+$ MBCs in the CD4-/DV2/CD4+/ZV group. A correlation was performed comparing CXCR5$^+$ (X5+) pTfh cells, from day 7 p.c., with **(E)** activated ASCs in the CD4-/DV2/CD4+/ZV group. A correlation was performed comparing PD1+ICOS+ pTfh cells, from day 7 p.c., with **(F)** activated ASCs in the CD4+/DV2/CD4+/ZV group (+/+). Pearson's rank correlation coefficients were used to calculate correlations, and R^2- and P-values are indicated. Linear regression is shown as lines and each dot represents one animal.

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SFig 7. **Frequencies of CM pTfh cell subsets correlate with B cell response cell subsets.** Pearson
correlations and simple linear regressions were performed using data from B cell subsets such as
activated IgG[+] MBCs and ASCs during the secondary ZIKV infection**.** Animal cohorts are depicted as
follows based on treatment regime: CD4+/DV2/CD4+/ZV (shown in turquoise). All significant
correlations with CM pTfh cells were only observed in the CD4+/DV2/CD4+/ZV group. Correlations
were performed and observed for the CM CXCR5^{+}CXCR3^{+} pTfh cells (shown as X5+X3+), from day
7 p.c., with **(A)** activated IgG[+] MBCs, from day 7 p.c. in the CD4+/DV2/CD4+/ZV group. Correlations
were performed for comparing CM PD1+ICOS+ pTfh cells, from day 7 p.c., with **(B)** activated IgG[+]
MBCs in the CD4+/DV2/CD4+/ZV group. Correlations were performed for CM PD1+ICOS+ pTfh
cells with **(C)** activated ASCs, from day 7 p.c., in the CD4+/DV2/CD4+/ZV group. Pearson's rank
correlation coefficients were used to calculate correlations, and R^2- and P-values are indicated. Linear
regression is shown as lines and each dot represents one animal.

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SFig 8. Frequencies of pTfh cell subsets correlate with EC50 (log₁₀) values. Data obtained from
Focus/Plaque Reduction Neutralization Tests on collected sera from days 30 and 90 p.c. during
secondary ZIKV infection was analyzed using Pearson and simple linear regression with pTfh cells.
All experimental animals are shown in black. Animal cohorts are depicted as follows based on treatment
regime: CD4+/DV2/CD4+/ZV (shown in turquoise). **(A-B)** Correlations were performed comparing
CXCR5$^+$ pTfh cells (shown as X5+), from **(A)** days 7 and **(B)** days 15 p.c. with EC50 values from day
30 p.c., in the CD4+/DV2/CD4+/ZV group. **(C-D)** Correlations were performed comparing
PD1+ICOS+ pTfh cells from **(C)** day 7 and **(D)** day 15 p.c. with EC50 values from day 90 p.c., in the
CD4+/DV2/CD4+/ZV group. **(E-I)** Frequencies of CM pTfh cell subsets correlate with EC50 values
from days 30 and 90 p.c.. **(E-G)** Correlations were performed using all experimental comparing **(E)**
CM CXCR5$^+$ (X5+) pTfh cells, from day 15 p.c., with EC50 values from day 30 p.c., comparing **(F)**
CM CXCR5$^+$CXCR3$^+$ (shown as X5+X3+) pTfh cells, from day 7 p.c., with EC50 values from day 30
p.c., and comparing **(G)** CM CXCR5$^+$CXCR3$^+$ (X5+X3+) pTfh cells, from day 15 p.c.. Correlations
were performed comparing CM CXCR5$^+$ (X5+) pTfh cells, from **(H)** day 7 and **(I)** day 15 p.c., with
EC50 values from day 30 p.c.. Correlations were performed comparing CM PD1+ICOS+ pTfh cells,
from day 15 p.c., with **(J)** EC50 values from day 90 p.c.. Pearson's rank correlation coefficients were
used to calculate correlations, and R^2- and P-values are indicated. Linear regression is shown as lines
and each dot represents one animal.

IgG+ memory B cell Gating

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1430 **SFig 9. Gating strategy for B cells.** Gating strategy used to define B cells and subsets. Lymphocytes were
1431 gated based on their characteristic forward and side scatter pattern (FSC, SSC). B cells were defined as
1432 CD20+CD3-.
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1435
1436 **SFig 10. Gating strategy for T cells.** Gating strategy used to define T cells and subsets. Lymphocytes were
1437 gated based on their characteristic forward and side scatter pattern (FSC, SSC). T cells were defined as
1438 CD3+CD20+. CD4+ and CD8+ T cells were defined as CD3+CD4+ and CD3+CD8+, respectively.
1439

1440
1441 **SFig 11. Gating strategy for pTfh CD4+ T cells**. Gating strategy used to define pTfh CD4+ T and total
1442 central memory (CM- pTfh) CD4+ T cells based on CD28+, CD95+, CXCR5+, CXCR3+, PD1+, and
1443 ICOS+ surface markers expression.
1444

Parameter	Day of measurement for PCA
TFH_CD4_ICOS_PD1	Day 7, Day 15
zikav_od_igm	Day 15, Day 30
zikav_od_igg	Day 15, Day 30, Day 90
denv_od_igm	Day 15
denv_od_igg	Day 15, Day, 30, Day 90
neutralization vs. ZikaV	Day 15, Day 30, Day 90
neutralization vs. DengueV	Day 15, Day 30, Day 90
CD4_T_cells	Day 15, Day 30, Day 90
CD8_T_cells	Day 15, Day 30, Day 90
T4_CM	Day 15, Day 30, Day 90
T4_CM_CD69	Day 15, Day 30, Day 90
T8_CM	Day 15, Day 30, Day 90
T8_CM_CD69	Day 15, Day 30, Day 90
T4_EM	Day 15, Day 30, Day 90
T4_EM_CD69	Day 15, Day 30, Day 90
T8_EM	Day 15, Day 30, Day 90
T8_EM_CD69	Day 15, Day 30, Day 90
CD4_Naive	Day 15, Day 30, Day 90
CD4_Naive_CD69	Day 15, Day 30, Day 90
CD8_Naive	Day 15, Day 30, Day 90
CD8_Naive_CD69	Day 15, Day 30, Day 90
B_Cells	Day 15, Day 30, Day 90
B_Cells_CD69	Day 15, Day 30, Day 90
CD27_CD69	Day 15, Day 30, Day 90
CD20_CD27	Day 15, Day 30, Day 90
EDIII_CRI_D1	DAY 90
EDIII_CRI_D2	DAY 90
EDIII_CRI_D3	DAY 90
EDIII_CRI_D4	DAY 90
EDIII_CRI_Z	DAY 90
NS1_CRI_D1	DAY 90
NS1_CRI_D2	DAY 90
NS1_CRI_D3	DAY 90
NS1_CRI_D4	DAY 90
NS1_CRI_Z	DAY 90

OD = Optical Density	
CM = Central Memory	
tfh = T Follicular Helper	
CRI = Cross Reactivity Index	

1445   Table S3. **Parameters used to perform PCA analysis.** PCA analysis was performed using parameters from
1446   days 7, 15, 30 and 90 post ZIKV infection.
1447

1448 **References**
1449
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