The development of therapeutic antibodies that neutralize homologous and heterologous genotypes of dengue virus type 1

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The Development of Therapeutic Antibodies That Neutralize Homologous and Heterologous Genotypes of Dengue Virus Type 1

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Abstract

Antibody protection against flaviviruses is associated with the development of neutralizing antibodies against the viral envelope (E) protein. Prior studies with West Nile virus (WNV) identified therapeutic mouse and human monoclonal antibodies (MAbs) that recognized epitopes on domain III (DIII) of the E protein. To identify an analogous panel of neutralizing antibodies against DENV type-1 (DENV-1), we immunized mice with a genotype 2 strain of DENV-1 virus and generated 79 new MAbs, 16 of which strongly inhibited infection by the homologous virus and localized to DIII. Surprisingly, only two MAbs, DENV1-E105 and DENV1-E106, retained strong binding and neutralizing activity against all five DENV-1 genotypes. In an immunocompromised mouse model of infection, DENV1-E105 and DENV1-E106 exhibited therapeutic activity even when administered as a single dose four days after inoculation with a heterologous genotype 4 strain of DENV-1. Using epitope mapping and X-ray crystallographic analyses, we localized the neutralizing determinants for the strongly inhibitory MAbs to distinct regions on DIII. Interestingly, sequence variation in DIII alone failed to explain disparities in neutralizing potential of MAbs among different genotypes. Overall, our experiments define a complex structural epitope on DIII of DENV-1 that can be recognized by protective antibodies with therapeutic potential.

Introduction

Dengue virus (DENV) is a member of the Flaviviridae family and is related to the viruses that cause yellow fever, and the Japanese, St. Louis, and the West Nile encephalitides [1]. DENV infection after mosquito inoculation causes a spectrum of clinical disease ranging from a self-limited febrile illness (DF) to a life threatening hemorrhagic and capillary leak syndrome (Dengue Hemorrhagic Fever (DHF)/Dengue Shock Syndrome (DSS)). Globally, there is an estimated 25 to 100 million infections and 250,000 cases of DHF/DSS per year worldwide, with 2.5 billion people at risk [4,5].

DENV is an enveloped virus with a single-stranded, positive-sense RNA genome [6]. The 10.7 kilobase genome is translated as a single polyprotein, which is cleaved into three structural proteins (C, prM/M, E) and seven nonstructural (NS) proteins (NS1, NS2A, NS2B, NS3, NS4A, NS4B, NS5). The mature DENV virion has a well-organized outer protein shell, a lipid membrane bilayer, and a less-defined inner nucleocapsid core [7,8]. The ectodomains of DENV E proteins are assembled as trimers with each subunit comprised of three discrete domains [9–11]. Domain I (DI) is a central, eight-stranded β-barrel, which contains a single N-linked glycosylation site in most DENV strains. Domain II (DII) is a long, finger-like protrusion from DI and contains a second N-linked glycan that binds to DC-SIGN [12–13] and the highly conserved fusion peptide at its distal end. Domain III (DIII), which adopts an immunoglobulin-like fold, has been argued to contain a cell surface receptor recognition site [16–19]. Exposure to mildly acidic conditions in the trans-Golgi secretory pathway promotes virus maturation through a structural rearrangement of
Dengue virus (DENV) is a mosquito-transmitted virus that infects 25 to 100 million humans annually and can progress to a life-threatening hemorrhagic fever and shock syndrome. Currently, no vaccines or specific therapies are available. Prior studies identified a highly neutralizing monoclonal antibody (MAb) against West Nile virus, a related flavivirus, as a candidate therapy for humans. In this study, we generated 79 new MAbs against the DENV type 1 (DENV-1) serotype, 16 of which strongly inhibited infection in cell culture. Using structural and molecular approaches, the binding sites of these inhibitory MAbs were localized to distinct regions on domain III of the DENV-1 envelope protein. We tested the protective capacity of all of the neutralizing MAbs in mice against infection by a strain of DENV-1 from a distinct genotype. Only two of the MAbs, DENV1-E105 and DENV1-E106, showed efficacy in a post-exposure treatment model, and these antibodies efficiently neutralized all five DENV-1 genotypes. Collectively, our study defines a complex structural binding site on domain III of the envelope protein for MAbs with therapeutic potential against DENV-1.

**Author Summary**

Dengue virus (DENV) is a mosquito-transmitted virus that infects 25 to 100 million humans annually and can progress to a life-threatening hemorrhagic fever and shock syndrome. Currently, no vaccines or specific therapies are available. Prior studies identified a highly neutralizing monoclonal antibody (MAb) against West Nile virus, a related flavivirus, as a candidate therapy for humans. In this study, we generated 79 new MAbs against the DENV type 1 (DENV-1) serotype, 16 of which strongly inhibited infection in cell culture. Using structural and molecular approaches, the binding sites of these inhibitory MAbs were localized to distinct regions on domain III of the DENV-1 envelope protein. We tested the protective capacity of all of the neutralizing MAbs in mice against infection by a strain of DENV-1 from a distinct genotype. Only two of the MAbs, DENV1-E105 and DENV1-E106, showed efficacy in a post-exposure treatment model, and these antibodies efficiently neutralized all five DENV-1 genotypes. Collectively, our study defines a complex structural binding site on domain III of the envelope protein for MAbs with therapeutic potential against DENV-1.

the flavivirus E proteins and cleavage of prM to M by a furin-like protease [20,21]. Mature DENV virions are covered by 90 anti-parallel E protein homodimers, which are arranged flat along the surface with quasi-icosahedral symmetry.

Many flavivirus neutralizing antibodies recognize the structural E protein [reviewed in [22]]. Serotype-specific MAbs against DENV reportedly have the greatest neutralizing activity [23,24] although some sub-complex specific MAbs, which recognize some but not all DENV serotypes, also are inhibitory [25–27]. Protection in animals by antibodies correlates generally with the degree of neutralizing activity in vitro [24,28–31]. Several type-specific strongly neutralizing antibodies against individual flaviviruses (e.g., West Nile virus (WNV), Japanese encephalitis virus (JEV), DENV-2, DENV-4, and yellow fever virus (YFV) have been localized to epitopes in DI and DIII [26,29,32–42]. Based on their potency of neutralization and protection in vivo, anti-WNV humanized or human MAbs are in clinical development as candidate therapeutics [reviewed in [43]]. Although type-specific neutralizing MAbs against DENV-1 have been characterized [44,45], few have been mapped to specific amino acids or structural determinants. To date, only two neutralizing IgM against DENV-1 were mapped by neutralization escape selection to amino acids E279 and E293, which lie outside of DIII [46].

To develop neutralizing MAbs against DENV-1 with possible clinical potential, mice were infected with a genotype 2 strain of a DENV-1 virus, and boosted with recombinant protein of the homologous virus. 79 new MAbs against DENV-1 were generated: 15 of these are DIII-specific IgG and strongly neutralized the homologous DENV-1 strain. Of these, 9 were serotype-specific, 5 were sub-complex-specific, and only 1 MAb cross-reacted with all 4 serotypes of DENV. Several MAbs failed to neutralize at least one DENV-1 strain of a distinct genotype, suggesting that antibody recognition of the neutralizing epitopes on DIII varied among genotypes.

As a first step towards generating antibody therapeutics against DENV-1, we evaluated the protective capacity of these MAbs in an immunocompromised IFN-$\gamma^{-/-}$ × IFN-$\gamma^{-/-}$ (AG129) mouse infection model with a heterologous DENV-1 genotype 4 strain.

Among the strongly neutralizing antibodies tested, only four were highly protective. Two MAbs, DENV1-E105 and DENV1-E106, which neutralized all genotypes, were therapeutically active even when administered as a single dose four days after infection. These studies define the complexity of epitopes on DIII of DENV-1 that is recognized by highly protective antibodies with therapeutic potential.

**Results**

**MAb generation**

Previous studies with WNV and DENV-2 demonstrated that MAbs against DIII of the E protein protect against infection of cells [26,27,29,32,35,41] and, in the case of WNV, in animals [29]. To date, few DENV-1 MAbs have been characterized functionally or mapped structurally. To develop neutralizing MAbs, mice were infected with the 16007 (genotype 2) prototype strain of DENV-1 and in some cases, boosted with recombinant DIII from the homologous DENV-1 strain. Initial immunization studies were performed with wild type BALB/c mice as done previously with WNV [29]. Because low neutralizing titers (<1/100) were achieved, likely because of poor replication of DENV-1, we switched to an immunodeficient (IFN-$\gamma^{-/-}$) strain in the C57BL/6 background. After screening more than 3,000 hybridoma clones as part of five independent fusions, we isolated and cloned 79 new MAbs that recognized cells infected with DENV-1 (Table S1).

All MAbs were initially tested semi-quantitatively for neutralization of the homologous DENV-1 strain by a single endpoint plaque reduction assay in Vero or BHK21-15 cells using neat hybridoma supernatant (~10 μg/ml). Of the MAbs generated, 18 showed no inhibitory activity (<15% neutralization), 45 had modest inhibitory activity (15–75% neutralization) and 16 were strongly inhibitory (>95% neutralization). All MAbs were screened for E protein domain recognition using yeast that expressed DENV-1 DI-II or DIII on their surface (Table S1): 14 bound to yeast expressing DI-DIII, 53 recognized DIII, and the remaining 12 did not bind either DI-DIII or DIII, indicating they recognized epitopes that are not present on the truncated yeast-expressed forms of DENV-1 E protein. All MAbs were tested for cross-reactivity using cells infected with different serotypes of DENV or WNV. Five of the fourteen DI-DIII-specific MAbs and 26 of the 53 DIII-specific MAbs cross-reacted with other serotypes of DENV. Only 3 of the 78 MAbs bound all DENV serotypes and WNV. One of the neutralizing MAbs, DENV1-E50, was of the IgM isotype and not evaluated further here.

**Characterization of strongly neutralizing MAbs against DENV-1**

Studies with neutralizing mouse MAbs against DENV-2 defined a type-specific epitope on the lateral ridge of DIII (DIII-LR) and an adjacent more conserved β-strand termed the sub-complex-specific DIII A-strand epitope [23–27,41]. As our single endpoint titer neutralization experiments showed that all 15 inhibitory IgG MAbs localized to DIII of DENV-1, we analyzed their reactivity patterns with other strains. We found that 9 of the 15 neutralizing IgG MAbs were serotype-specific and showed no cross-reactivity to DENV-2, DENV-3, DENV-4 or WNV-infected cells. Five MAbs were sub-complex specific and bound some but not all DENV serotypes. Only one MAb, DENV1-E102, cross-reacted with all DENV serotypes but not with WNV-infected cells (Table 1).

**Genotype-specific reactivity of anti-DENV-1 MAbs**

As variation exists in the genetic composition of viruses within a given DENV serotype, an intra-serotype genotype classification system was developed [2,3], with a given genotype of a serotype...
having no more than 6% nucleotide sequence divergence in the E gene [47]. To address whether the neutralizing MAbs were affected by the variation within the serotype, we tested reactivity and neutralizing potential against individual strains that encompass the five distinct DENV-1 genotypes: Asian genotype 1 (strain TVP-2130), Thai genotype 2 (strain 16007), Malaysian genotype 3 (TVP-5175), South Pacific genotype 4 (strain West-Pac 74), and American/African genotype 5 (strain 3146 SL).

(a) Binding to different DENV-1 genotypes. To determine whether antibodies recognized different genotypes of DENV-1, we infected Raji-DC-SIGN-R or C6/36 cells (depending on permissiveness) with strains of the five different genotypes of DENV-1. Infected cells were incubated with hybridoma supernatants and analyzed by flow cytometry. All neutralizing MAbs tested efficiently recognized genotypes 1, 2, 4, and 5. However, a few of the MAbs (DENV1-E100, DENV1-E104, and DENV1-E111) showed reduced binding to cells infected with the genotype 3 strain (Table 2). In contrast, other DIII-specific non-neutralizing MAbs (e.g., DENV1-E91) showed reduced binding to several of the heterologous DENV-1 genotypes (Fig 1).

(b) Neutralizing potential of MAbs against different DENV-1 genotypes. Although most MAbs retained binding to cells infected with many of the genotypes, we questioned whether this translated into efficient cross-genotypic neutralization. A recent study of neutralization escape mutants with human MAbs against WNV showed that retention of binding did not necessarily sustain neutralizing activity [38]. To evaluate this, we assessed semi-quantitatively the inhibitory activity of hybridoma supernatants of 15 neutralizing MAbs against all five genotypes by a standard plaque reduction assay with 10² PFU of virus in Vero or BHK21-15 cells, depending on the strain (Table 3). Only 8 of 15 hybridoma supernatants neutralized strains from all five genotypes by greater than 90%, with three MAbs (DENV1-E103, DENV1-E105, and DENV1-E106) showing 100% neutralization of all genotypes. Several MAbs showed reduced neutralizing potential for individual genotypes even at the relatively high (~10 µg/ml) concentration of MAb used in the assay. For example, 9, 12, 12, and 14 MAbs neutralized infection by DENV genotypes 1, 3, 4, and 5, respectively. This was especially surprising for the genotype 1 strain as no appreciable reduction in binding to infected cells was observed (Table 2). As an example, DENV1-E104 showed relatively normal binding to the genotype 1 strain yet showed a 92% loss in neutralization activity. Some MAbs (DENV1-E100 and DENV1-E111), which had decreased binding to genotype 3 infected cells, also showed reduced inhibitory activity. Others (e.g., DENV1-E104) sustained normal inhibitory activity despite attenuated binding to fixed, permeabilized cells. Although more studies are necessary, this could reflect an epitope that is more sensitive to fixation in the context of recognition of specific genotypes.

To more rigorously characterize the neutralizing potency, we purified MAbs and assessed their inhibitory activity against the homologous genotype 2 (16007) strain in cell culture by performing a dose-response curve and determining the concentration of MAb (PRNT50, expressed here as ng/ml of antibody) that blocked plaque formation by 50% (Table 4). For the homologous genotype 2 16007 strain, 8 of 15 MAbs potently neutralized infection with PRNT50 values below 5 ng/ml. This value is significant as it is lower than that observed with our most inhibitory anti-WNV MAb (E16), which functions successfully as a post-exposure therapeutic agent [29,49,50]. Six other MAbs also showed strong inhibitory activity with PRNT50 values against 16007 of between 10 and 70 ng/ml. Only one MAb, E104 showed modest activity with a PRNT50 value of ~600 ng/ml.

Given our findings of genotype variation with respect to single endpoint neutralization using hybridoma supernatants, we repeat-
ed the dose-response curve analysis with a heterologous genotype 4 (West Pac-74) (Table 4). Surprisingly, the neutralizing activity was markedly decreased for all MAbs against the heterologous DENV-1 genotype (e.g., 6 to 9600-fold for DENV1-E100 and DENV1-E113, respectively). Only 2 MAbs, DENV1-E105 and DENV1-E106, retained strong neutralizing activity (≤20 ng/ml) against the West Pac-74 strain. Seven of 15 MAbs neutralized West-Pac 74 poorly with PRNT50 values greater than 1 μg/ml of antibody. Thus, the neutralizing efficiency of several DIII-specific anti-DENV-1 MAbs was significantly altered against strains of a different DENV-1 genotype.

Crystal structure of DENV-1 DIII and analysis of genotypic variation

To begin to understand the disparity in inhibitory potential of the DIII-specific neutralizing MAbs among different genotypes, we determined the X-ray crystal structure of recombinant DIII of the 16007 (genotype 2) strain at 2.25-Å resolution (Fig 2 and

### Table 2. MAb binding to cells infected with different genotypes of DENV-1 virus.

<table>
<thead>
<tr>
<th>MAb</th>
<th>Binding to virus</th>
<th>Genotype 1</th>
<th>Genotype 2</th>
<th>Genotype 3</th>
<th>Genotype 4</th>
<th>Genotype 5</th>
</tr>
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<tr>
<td></td>
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<td>16007</td>
<td>TVP-5175</td>
<td>West Pac-74</td>
<td>3146-SL</td>
<td></td>
</tr>
<tr>
<td>DENV1-E90</td>
<td>93</td>
<td>98</td>
<td>83</td>
<td>95</td>
<td>95</td>
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<tr>
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<td>98</td>
<td>84</td>
<td>96</td>
<td>97</td>
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<td>74</td>
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</table>

*Depending on the strain, Raji-DC-SIGN-R or C6/36 cells were infected with different genotypes of DENV-1 viruses. Fixed and permeabilized infected cells were incubated with the indicated MAbs (10 μg/ml) to determine the binding efficiency by flow cytometry. The data shown are the mean percentage of positive cells and derived from three independent experiments. Values underlined and italicized are statistically different (P < 0.05).

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**Figure 1. Binding of MAbs to cells infected with different genotypes of DENV-1.** C6/36 insect cells were infected with strains of DENV-1 virus corresponding to all five genotypes. After fixation and permeabilization, MAbs were incubated with infected cells and binding was assessed by flow cytometry. The data shown are representative histograms from two independent experiments with a neutralizing (DENV1-E106, upper panels) and non-neutralizing (DENV1-E91, lower panels) MAbs.
doi:10.1371/journal.ppat.1000823.g001
increasing concentrations of purified MAb cells and 10^2 PFU of the indicated DENV-1 genotype. The data was derived from at least two independent assays performed in duplicate. Highlighted, italicized values indicate a genotypic specific reduction in neutralizing potential of a given MAb using neat hybridoma supernatant of greater than 20%.

doi:10.1371/journal.ppat.1000823.t003

Table 3. MAbs neutralization of different DENV-1 genotypes.

<table>
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<tr>
<th>MAb</th>
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<th>Genotype 3</th>
<th>Genotype 4</th>
<th>Genotype 5</th>
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*Neutralizing activity was determined semi-quantitatively by single endpoint plaque reduction assay on BHK21 or Vero cells with neat hybridoma supernatant cells and 10^6 PFU of the indicated DENV-1 genotype. The data was derived from at least two independent assays performed in duplicate. Highlighted, italicized values indicate a genotypic specific reduction in neutralizing potential of a given MAb using neat hybridoma supernatant of greater than 20%.

Table 4. PRNT50 values of MAbs against a homologous and heterologous DENV-1 strain.

<table>
<thead>
<tr>
<th>MAb</th>
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<th>Genotype 4</th>
<th>Fold reduction (WP 74/16007)</th>
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<td>PRNT50 (ng/ml) ± SD</td>
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<td>1.9±1.9</td>
<td>1161±241</td>
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<td>DENVI-E99</td>
<td>11±3.9</td>
<td>803±116</td>
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<td>DENVI-E100</td>
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<td>145±42</td>
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<td>DENVI-E106</td>
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Neutralizing activity was determined by plaque reduction assay on BHK21 with increasing concentrations of purified MAb cells and 10^6 PFU of the indicated DENV-1 genotype. The data was derived from three independent experiments performed in duplicate. PRNT50 values were calculated by non-linear regression analysis and SD indicates the standard deviations. The column on the right was obtained by dividing the PRNT50 values from West Pac-74 by those of 16007 for a given MAb.

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Epitope mapping of DIII neutralizing MAbs

The two most protective MAbs in vivo (see below), DENV1-E105 (type-specific) and DENV1-E106 (sub-complex specific), lost binding when residues on the BC (G328, T329 and D330), DE (K361E and E362K), and FG (K385) loops of the DIII-LR region were altered. Similarly, other protective MAbs (DENV1-E100 and DENV1-E103) also lost binding when residues in the BC or DE loop were altered. Type-specific MAbs (DENV1-E95, DENV1-E101, DENV1-E104, DENV1-E108, DENV1-E111, and DENV1-E112) that inhibited genotype 2 (16007) yet poorly neutralized the genotype 4 (West Pac-74) strain mapped to additional sites in DIII, DENV1-E95, DENV1-E104, DENV1-E108, and DENV1-E112 exhibited reduced binding with mutations in the G-strand (S390, W391, and K393) (Fig 3E) whereas DENV1-E101 was affected by changes in the N-terminal linker (T303) and BC-loop (G328, T329, and D330). Surprisingly, none of the mutations altered DENV-E111 binding, and forward genetic screens with this MAb also failed to identify a loss-of-binding variant (data not shown), DENV1-E104, which showed the weakest neutralizing activity, localized to residues in the A (K310 and E311), F (E375), and G (S390 and W391) β-strands.

Because of analogous studies with DENV-2, we anticipated that sub-complex-specific and cross-reactive MAbs would recognize the A-strand epitope [25–27]. Indeed, mutation of S305, K307, E309, K310, and E311 reduced binding of several sub-complex MAbs (DENV1-E98, DENV1-E99, DENV1-E106, and DENV1-E113) in our panel. For the cross-reactive neutralizing MAb DENV1-E102, its epitope localized to residues in the N-terminal linker region (Y299, V300, and M301) and the BC loop (D330 and P332) (Fig 3F). Although Y299, M301, and P332 are highly conserved among strains of different DENV serotypes, V300 is specific for DENV-1 and D330 is present in DENV-1 and DENV-3; this may explain why DENV1-E102 fails to neutralize DENV-2 and DENV-3 efficiently (S. Sukupolvi-Petty, J. Brien, and M. Diamond, unpublished results).

Despite the extensive epitope mapping data (summarized in Fig 3B and 4), no structural explanation was readily apparent for the decrease in neutralization of the genotype 4 West Pac-74 strain by several antibodies. MAbs that showed markedly depressed neutralization of West Pac-74 localized to residues that were instead conserved among DENV-1 genotypes. To begin to address this, we evaluated whether individual MAbs differentially recognized DIII from 16007 or West Pac-74 strains when expressed on yeast; the DIII of these two strain differ by only two amino acids at positions 339 and 345 in the C strand and C'-loop (Fig 3D). Notably, all neutralizing MAbs equivalently recognized yeast displaying DIII of 16007 or West Pac-74 over a range of concentrations (Fig 5A, and data not shown). Thus, sequences differences in DIII of West Pac-74 and 16007 did not explain the differential patterns of neutralization. Because of this, we hypothesized that sequences variation in other domains of the West Pac-74 E protein could directly alter MAb binding or perhaps influence the display of DIII on the infectious virion. To test this, we performed a virion capture ELISA with 16007 and West Pac-74 viruses and selected MAbs having different neutralization profiles against the two strains (Fig 5B). DENV1-E98, which exhibited a ~50-fold reduction in neutralization showed little difference in binding over several concentrations of antibody. In contrast, DENV1-E111, which had ~4,000-fold less neutralizing activity, exhibited a depressed ability to bind West Pac-74 compared to 16007. Surprisingly, DENV1-E90 and DENV1-E113, which had ~600 to 9,600-fold differences in PRNT50 values with West Pac-74 compared to 16007 showed virtually no variation in binding in the capture ELISA. Thus, differential neutralization of genotypes 2 and 4 of DENV-1 could
Figure 3. Epitope localization of anti-DENV-1 MAbs. A. Flow cytometry histograms of loss-of-function DIII variants (V324I, T329G, D330G, K361E, E362K, and E384K) with individual neutralizing MAbs. Representative histograms are shown for the MAbs WNV E16 (negative control), DENV1-E95, DENV1-101, DENV1-103, and DENV1-106 with the wild type DIII and each of the variants. Data shown are representative of three independent experiments. B. Sequence alignment of different DENV-1 genotypes and mapping of neutralizing MAbs. The sequence and secondary structure of DIII from DENV-1 (strain 16007, genotype 2) E protein is aligned with other DENV-1 genotypes (genotype 1, strain TVP-2130; genotype 3, strain TVP 5175;
be explained by disparate binding to the virion for only a subset of MAbs. For MAbs like DENV1-E90 and DENV1-E113, the profile was similar to that observed with escape variants of a human anti-WNV MAb; in that case, mutations that abolished neutralizing activity did not appear to affect antibody binding to virus [48].

**In vivo protection studies with neutralizing MAbs**

Pre-exposure passive transfer of neutralizing MAbs against WNV, DENV-2, and DENV-4 protects against lethal infection in wild type and immunodeficient mice [24,29,52–56]. To confirm that neutralizing anti-DENV-1 MAbs protect in vivo and begin to explore the possibility for antibody therapy, we evaluated the efficacy of our panel of inhibitory MAbs against West Pac-74, the heterologous genotype 4 DENV-1 strain. The heterologous strain was selected for two reasons: (i) the West Pac-74 strain was the only DENV-1 isolate in our collection that caused 100% lethality in an intraperitoneal challenge model in AG129 mice; and (ii) a possible antibody therapeutic must demonstrate efficacy against DENV-1 strains of different genotypes.

A single dose (500 μg) of neutralizing MAbs against DENV-1 was administered as prophylaxis one day prior to infection with 10^6 PFU of West Pac-74. Two MAbs (DENV1-E105 and DENV1-E106) protected 100% of mice compared to PBS or irrelevant MAb controls (P<0.0001), which had a 0% survival rate (Table 6). Three other MAbs (DENV1-E99, DENV1-E100, and DENV1-E103) exhibited strong yet incomplete protection with 60 to 80% survival rates. However, nine neutralizing MAbs (DENV1-E90, DENV1-E95, DENV1-E98, DENV1-E101, DENV1-E102, DENV1-E108, DENV1-E111, DENV1-E112 and DENV1-E113) protected inefficiently, with an 11 to 38% survival rate. Although the survival rate was relatively low for these MAbs, the mean time to death (MTD) was protracted (23±6.1 to 40±8.6 days) compared to untreated, infected mice (20±3.3 days). One neutralizing MAb, DENV1-E104 showed no protection against lethality although a longer MTD was observed. In general, the protective efficacy in vivo correlated with neutralizing activity against the West Pac-74 genotype 4 strain. As an example, DENV1-E105 and DENV1-E106 had low PRNT50 values (13 to 20 ng/ml) for West Pac-74 and protected against infection whereas DENV1-E104 and DENV1-E112, which protected poorly, had PRNT50 values (18 to 23 μg/ml) that were almost 1,000-fold different.

To begin to define the therapeutic potential of the highly protective MAbs (DENV1-E99, DENV1-E103, DENV1-E105, and DENV1-E106), we administered 5 and 25-fold lower doses (100 μg and 20 μg) one day prior to IP infection of AG129 mice with 10^6 PFU of West Pac-74. The lower doses of DENV1-E99 and DENV1-E103 provided sub-optimal protection against lethal infection [Fig 6A and B], with only a delay in the MTD observed. In comparison, ~50% of mice survived West Pac-74 infection after receiving a single dose of 20 or 100 μg of DENV1-E105 antibody [Fig 6C, P<0.005]. More strikingly, a single 20 or 100 μg injection of DENV1-E106 completely protected DENV-1 infected mice [Fig. 6D, P<0.0001]. These data suggest that DENV1-E106 was the most protective MAb in our panel of neutralizing antibodies against infection by the heterologous strain, DENV-1 West Pac-74.

**Therapeutic studies with neutralizing MAbs**

Antibody-based therapeutics against DENV will need to be administered after infection. To assess the therapeutic efficacy of strongly neutralizing anti-DENV-1 MAbs, mice were infected with 10^6 PFU of West Pac-74 and two days after infection, a single 500 μg MAb dose (DENV1-E99, DENV1-E103, DENV1-E105, or DENV1-E106) was transferred passively by an IP route. Notably, 500 μg of DENV1-E99 or DENV1-E103 provided no protection with animals dying at a rate and time similar to untreated mice (P>0.2). In contrast, DENV1-E105 and DENV1-E106 protected 75 and 82% (P<0.0001) of mice, respectively, when administered two days after infection. When a single dose of DENV1-E105 or DENV1-E106 MAb was given four days after infection, 20 and 40% (P<0.03) of mice, respectively were protected from lethal infection [Fig 7A and B].

Given the potency of DENV1-E105 and DENV1-E106 in protection against the genotype 4 West Pac-74 strain, we performed PRNT50 analysis with strains corresponding to the remaining genotypes to assess potential clinical utility of these MAbs. Both DENV1-E105 and DENV1-E106 strongly neutralized infection of all DENV-1 genotypes [Fig 8A and B], with PRNT50 values ranging from 0.5 to 59.2 ng/ml. Thus, DENV1-E105 and DENV1-E106 protected AG129 immunocompromised mice as a pre and post-exposure treatment from infection by a heterologous DENV-1 genotype and efficiently inhibited all DENV-1 genotypes in cell culture.

**Discussion**

One primary goal of this study was to generate a collection of strongly neutralizing MAbs that would recognize virtually all DENV-1 strains and protect against infection as post-exposure therapy. In an attempt to achieve this, we generated a panel of 79 new MAbs against DENV-1 E protein. Although neutralizing antibodies can be generated against all three domains of the flavivirus E protein [29,32,42,46,52,55,57,58], we mapped the epitopes of the MAbs with the greatest inhibitory activity primarily to epitopes on DIII, analogous to that observed with MAbs against DENV-2 [25–27,41]. One surprising finding that has not been reported previously was the disparate neutralizing activity and protective potential of individual MAbs against different DENV-1 genotypes. In comparative studies with strains from genotype 2 and genotype 4, virtually all MAbs showed reduced (from 6 to 9,600-fold) PRNT50 values against the heterologous genotype. Because of this, few (5 of 15) MAbs protected as pre-exposure prophylaxis against infection by the heterologous DENV-1 genotype in AG129 mice, and only two (DENV1-E105 and DENV1-E106) showed utility as post-exposure therapy.

Although many DENV strains can cause a similar debilitating febrile illness in humans, there is significant genetic variation (25 to 40% amino acid difference for serotypes and up to 3% variation among genotypes within a serotype) and phenotypic difference in virulence among individual strains of specific serotypes and genotype 4, strain Western Pacific-74; genotype 5, strain 3146 Sri Lanka). The secondary structure of DENV-1 E DIII residues 294 to 395 from the strains that had not been crystallized was predicted by DSSP [112] using the 16007 strain coordinates. Black blocks highlight residues of genotypic variation. The results of the yeast surface-display epitope mapping (see Table 5) are denoted underneath in red to indicate the number of neutralizing MAbs in our panel that lose binding when a specific amino acid is changed. Colored boxes correspond to specific neutralizing antibody and structural recognition determinants: N-terminal region, light purple; lateral ridge (BC, DE, and FG loops), dark purple; A-strand, cyan; and F- and G-strand, green. C-F. Localization of neutralizing epitopes on DENV-1 DIII as determined by yeast surface display. Structure of DENV-1 DIII (strain 16007) with amino acid residues marked in blue that significantly affect binding of neutralizing MAbs (C) DENV1-E106, (D) DENV1-E99, (E) DENV1-E95, and (F) DENV1-E102. doi:10.1371/journal.ppat.1000823.g003
**Table 5. Summary of MAb binding to DENV-1 DIII mutants expressed on the surface of yeast.**

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Values shown were achieved by dividing the total fluorescence product (percent positive population × mean linear fluorescence intensity) of a mutant for each individual antibody by the total fluorescence product of the wild type DIII×100. Values in bold indicate reductions in mAb binding of greater than or equal to 80% for a given mutation. Underlined values show a reduction between 50 and 79%. The results are the average of between three and five independent experiments for each mutant and each antibody.

doi:10.1371/journal.ppat.1000823.t005
Figure 4. Summary of neutralizing antibody and structural recognition determinants on DENV-1 DIII. Data from yeast surface display (Table 5) and sequence alignment (Fig 3B) were mapped onto the crystal structure of DENV-1 DIII to visualize the composite epitopes of different neutralizing MAbs. Recognition sites include N-terminal region, light purple; lateral ridge (BC, DE, and FG loops), dark purple; A-strand, cyan; and F- and G-strand, green. doi:10.1371/journal.ppat.1000823.g004

Genotypes [59–63]. Previous studies identified the lateral ridge and A-strand epitopes in DIII as targets of strongly neutralizing type-specific and sub-complex-specific neutralizing MAbs against DENV-2 and DENV-3 [26,27,41,64–67] and the fusion loop in DII as a recognition site for many cross-reactive neutralizing DENV MAbs [58,68,69]. In comparison, the serotype-specific DII as a recognition site for many cross-reactive neutralizing DENV-2 and DENV-3 [26,27,41,64–67] and the fusion loop in specific and sub-complex-specific neutralizing MAbs against A-strand epitopes in DIII as targets of strongly neutralizing type-specific genotypes [59–63].

While our experiments establish that highly neutralizing antibodies against DENV-1 can be generated in vitro and in vivo [86–88]. As such, studies are underway to engineer mutations into the Fc region of a humanized version of DENV1-E106 that abolishes the possibility of enhancement by abrogating binding to Fc-γ receptors.

Amino acid contact residues of neutralizing MAbs that react with DENV-2 or DENV-3 have been defined by analyzing neutralization escape mutants [40], chimeric DENV variants [89], site-specific DENV-2 mutants [68,90], peptide mapping [65,91,92], yeast surface display of variant E proteins [25,26,66], mutant recombinant proteins [27,41,67], and by co-crystallography of recombinant DENV proteins and Fab fragments of neutralizing MAbs [25]. Here, we used genetic strategies to generate mutant DIII of DENV-1 on yeast to map antibody recognition residues. The validity of the yeast surface display mapping for identifying critical contact residues has been confirmed by crystallographic studies that resolved the structural interface between WNV and DENV2 DIII Fab fragments [25,93] as well as DII-fusion loop specific Fab recognition [94].

This is the first study that describes a post-exposure therapeutic effect of a MAb against any DENV strain in any animal model. In particular, DENV1-E105 and DENV1-E106, which neutralized all five DEN1 genotypes showed efficacy when administered two or four days after infection of highly immunocompromised AG129 mice. In contrast, three other neutralizing MAbs (DENV1-E99, DENV1-E100, and DENV1-E103) failed to protect when added a few days after infection even though they functioned as pre-exposure prophylaxis. Although prior studies demonstrated that anti-E MAbs protect against DENV infection in rodents and non-human primates [42,55,56,70,71], none have reported efficacy when added after infection. It is noteworthy that the two MAbs with the most neutralizing PRNT50 values were the ones with greatest therapeutic efficacy, suggesting, at least for strongly neutralizing MAbs of a given class, a correlation between in vitro and in vivo activity. It is unclear why therapeutic anti-DENV MAbs have not been previously described. Several post-exposure therapeutic MAbs or polyclonal antibody preparations against WNV, JEV, VEE, and tick-borne encephalitis virus have been reported [29,30,55,57,72–77], with some entering human clinical trials [43]. One speculation is that because viremia associated with DENV infection is several log greater than WNV [78–80], a condition of viral antigen excess occurs more rapidly in circulation leading to fewer antibody molecules binding to a given DENV virion. As neutralization is determined in part by the stoichiometry of antibody binding [81,82], only MAbs that can block infection at low fractional occupancy may be capable of neutralizing in vivo.

MAb-based therapeutics against DENV could be complicated by antibody-dependent enhancement of infection (ADE). Sub-neutralizing concentrations of antibody augment infection of Fe-γ receptor-expressing cells possibly by enhancing the efficiency of virus attachment or entry [83,84]. Thus, the administration of virus-specific MAbs could adversely impact the outcome of DENV infection. In non-human primates, passive transfer of sub-neutralizing concentrations of monoclonal or polyclonal antibody increased viremia although no change in disease status was observed [85,86]. Based on the possibility of ADE, MAb therapeutics against DENV in humans would appear to have considerable regulatory hurdles. However, recent studies with amino acid substitutions or deletions in the Fc region of recombinant anti-flavivirus antibodies prevented ADE in vitro and in vivo [86–88]. As such, studies are underway to engineer mutations into the Fc region of a humanized version of DENV1-E106 that abolishes the possibility of enhancement by abrogating binding to Fe-γ receptors.
Figure 5. Binding of MAbs to DIII or virions of 16007 and West Pac-74. A. MAb binding to DIII of 16007 or West Pac-74 on yeast. Flow cytometry histograms of DIII of 16007 or West Pac-74 (different at residues 339 and 345) with neutralizing MAbs. Data shown are representative of two independent experiments. B. A capture ELISA was used to detect binding of MAbs to 16007 and West Pac-74 virions. Microtiter plates were coated with the indicated MAbs, incubated with $2 \times 10^5$ PFU of 16007 or West Pac-74 at room temperature, and with biotinylated anti-E MAbs. The data is an average of several separate experiments performed in duplicate, and error bars indicate standard deviation. doi:10.1371/journal.ppat.1000823.g005
multiple DENV serotypes, showed an almost complete loss-of-binding with mutation of residues (Y299, V300, and M301) in the N-terminal linker region. This result is analogous to that described for neutralizing DENV-2 MAbs where the mutation M301G abolished reactivity of five complex-specific and seven serotype-specific MAbs [27,41]. The binding of the N-terminal linker by MAbs against WNV has been speculated to contribute to neutralization by inhibiting the significant rotation of DIII during infection with 10^6 PFU of West Pac-74 by an IP route. Mice were monitored for survival for 60 days after infection. NS, not statistically different from PBS control.

<table>
<thead>
<tr>
<th>MAb</th>
<th>Dose (µg/mouse)</th>
<th>Survival</th>
<th>MTDa ± SD</th>
<th>P valueb</th>
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<td>0</td>
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<td>NS</td>
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<tr>
<td>WNV E16</td>
<td>500</td>
<td>0/5</td>
<td>18 ± 2</td>
<td>NS</td>
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<td>36 ± 11</td>
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<td>40 ± 9</td>
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<td>28 ± 8</td>
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<td>1/8</td>
<td>25 ± 11</td>
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<tr>
<td>DENV1-E113</td>
<td>500</td>
<td>1/8</td>
<td>34 ± 11</td>
<td>0.001</td>
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Mice were administered with 500 µg of indicated MAbs one day before infection with 10^6 PFU of West Pac-74 by an IP route. Mice were monitored for survival for 60 days after infection. NS, not statistically different from PBS control.

Mean time to death (MTD) ± standard deviations (SD) refers to the mean time to death of the animals that succumbed to fatal infection. NA, indicates that no animals died in the presence of this MAb, and thus, the value was not calculated.

aP values were calculated using the log rank test of the Kaplan Meier survival curve by comparing the no antibody treated and antibody treated mice.

doi:10.1371/journal.ppat.1000823.s006

Table 6. In vivo protection of AG129 mice from West Pac-74 (genotype 4) after prophylaxis with neutralizing anti-DENV-1 MAbs.

Although our most strongly neutralizing MAbs localized to DIII of DENV-1, these antibodies were derived from immunodeficient mice, which may not necessarily reflect the neutralizing antibody response in humans. The antibody repertoire against DENV-1 or other serotypes in humans remains unknown, as B cell profiling at the epitope level has not been performed. Nonetheless, recent studies suggest that the humoral response against flaviviruses in humans may be directed away from DIII neutralizing epitopes [35,54,95]. DIII-specific antibodies comprised only a small fraction of the total antibody in DENV immune sera [96,97]; whether these antibodies contribute to DENV neutralization in vivo remains controversial. Because highly neutralizing antibodies against DIII of DENV-1, DENV-2, and DENV-3 map to the lateral ridge and A-strand epitopes [26,27,41,67], DIII-based vaccines [98–101] that skew the humoral response have the potential to elicit highly protective responses.

One intriguing finding was the disparate neutralizing activity of individual MAbs against different DENV-1 genotypes. Infection with one DENV serotype is believed to confer long-term immunity against strains of the homologous but not heterologous DENV serotypes. Based on this, we assumed it would be straightforward to generate DIII-specific therapeutic MAbs that neutralized all five genotypes within the DENV-1 serotype. Indeed, there are limited amino acid changes in DIII among DENV-1 genotypes with a maximum difference of seven amino acids, with genotype 5 the most diverse although the changes are largely conserved and reside in solvent inaccessible regions. Nonetheless, several MAbs in the panel exhibited markedly depressed neutralizing activity against the heterologous West Pac-74 strain. This was perplexing given that the 16007 and West Pac-74 strains differ in DIII by two amino acids, which were not coincident with our epitope mapping data: a T→S change at residue 339 in the C-strand and an A→V change at residue 345 in the C-C’ loop. Indeed, in comparative binding assays with 16007 and West Pac-74 DIII on yeast, no obvious difference in binding at saturating concentrations of MAb was observed. When studies were repeated with selected MAbs in a virus capture ELISA, one MAb (DENV1-E111) with disparate neutralizing potential showed reduced binding to West Pac-74, but others (DENV1-E90 and DENV1-E113) did not. This was corroborated in surface plasmon resonance studies, which showed an ~10-fold decrease in the K_D of binding of DENV1-E111 for West Pac-74 DIII (K. Austin, M. Diamond, D. Fremont, unpublished results). Although further structural studies are warranted, we propose four hypotheses to explain these results:
(a) similar to findings with a recently characterized human anti-WNV MAb [48], mutations that abrogate neutralizing activity do not always reduce measurable antibody binding to the virion; (b) because of sequence variation outside of DIII, the E protein of different DENV-1 genotypes may pack differently on the virion. Some components of an epitope for a given MAb may be differentially exposed on virions of distinct genotype; (c) individual loss-of-function mutations identified by yeast display do not necessarily represent the complete footprint on DIII of bound antibody, as mutation of other residues may have allosteric effects; or (d) neutralizing anti-DENV-1 MAbs in our panel may have additional amino acid contacts outside of DIII that vary among the DENV-1 genotypes. Notably, we did not observe detectable binding of any of the DIII-specific neutralizing MAbs to a DI-DII protein displayed on yeast (data not shown). Structural studies with Fab-E protein or Fab-virion complexes will be required to address these possibilities.

Regardless of the mechanism, our results suggest that antibodies against one DENV genotype may have decreased inhibitory potency against a heterologous genotype within the same serotype.
This has potential implications for assessing the breadth of the protective efficacy of tetravalent DENV vaccines, which are in advanced clinical trials. In addition to evaluating protection against other serotypes, it may be critical to assess whether antibody responses against the vaccine strain of a given serotype neutralize infection of heterologous genotypes equivalently.

**Materials and Methods**

**Cells and viruses**

Vero, BHK21-15 and Raji-DC-SIGN-R cells were cultured in Dulbecco’s Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum (FBS) (Omega Scientific) and antibiotics (penicillin G and streptomycin) at 37°C in a 5% CO₂ incubator.

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**Figure 6. Dose response of protective efficacy MAbs in mice infected with DENV-1.** AG129 mice were passively transferred saline or 20, 100, or 500 µg of (A) DENV1-E99, (B) DENV1-E103, (C) DENV1-E105, and (D) DENV1-E106 MAbs one day before infection with 10⁶ PFU of West Pac-74 (genotype 4) by an IP route. Mice were monitored for survival for 60 days after infection. The survival curves were constructed from data of two independent experiments. The number of animals for each antibody dose ranged from 5 to 10 per group.

doi:10.1371/journal.ppat.1000823.g006

**Figure 7. Therapeutic efficacy of strongly neutralizing antibodies in mice after DENV-1 infection.** Mice were administered saline or a single 500 µg dose of DENV1-E105 or DENV1-E106 MAbs at day (A) 2 or (B) 4 after infection with 10⁶ PFU of West Pac-74 (genotype 4) by an IP route. Mice were monitored for survival for 60 days after infection. The number of animals for each antibody ranged from 10 to 11 per group.

doi:10.1371/journal.ppat.1000823.g007
Generation, purification, and labeling of anti-DENV-1 MAb

MAbs were generated essentially as described [29] after performing several independent splenocyte-myeloma fusions. To generate anti-DENV-1 MAbs, IFN-αβR/−/− C57BL/6 mice were infected with 10^5 PFU of DENV-1 strain 16007 (genotype 2) via an intraperitoneal route and re-challenged two weeks later with the same strain. Mice with serum having the highest neutralizing titer (>1/1500) were immunized with purified DIII (50 μg, strain 16007) in PBS as a final intravenous boost. Three days later splenocytes were fused to P3X63Ag8.33 myeloma cells [102]. MAbs were subcloned by limiting dilution, isotyped (Pierce Rapid ELISA Kit), and purified using protein A affinity chromatography (Invitrogen). For library sorting experiments, MAbs were labeled with Alexa Fluor 647 or Alexa Fluor 488, using a MAb labeling kit (Molecular Probes) according to the manufacturer’s instructions.

In vitro neutralization assay

Plaque reduction neutralization titer (PRNT) assays were performed with the indicated DENV-1 strains with MAbs or serum on BHK21-15 cells as described previously [26,80]. PRNT50 values were determined using non-linear regression analysis (Graph Pad Prism4).

Cloning and expression of DIII of DENV-1 E protein

A cDNA encoding DENV-1 DIII (strain 16007, residues 293 to 400) of the 16007 strain was amplified from viral RNA by reverse transcriptase and high-fidelity Platinum Taq polymerase chain reaction (PCR) according to the manufacturer’s instructions (Invitrogen). The PCR product was cloned into the pET21a bacterial expression plasmid (EMD Biosciences) using flanking NdeI and XhoI restriction sites, sequenced, and then expressed in BL21 Codon Plus (Stratagene) E. coli. Inclusion bodies containing insoluble aggregates were denatured in the presence of 6 M guanidine hydrochloride and 20 mM β-mercaptoethanol and refolded in the presence of 400 mM L-arginine, 100 mM Tris-base (pH 8.0), 2 mM EDTA, 0.2 mM phenylmethylsulfonyl fluoride, and 5 and 0.5 mM reduced and oxidized glutathione, respectively. Refolded protein was separated from aggregates on a Superdex 75 or 200, 16/60 size exclusion column using fast-protein liquid chromatography (GE Healthcare).

X-ray crystallographic structure determination of DV1 DIII

DENV-1 DIII was crystallized by vapor diffusion in hanging drops at 20°C at a concentration of 14 mg/ml. The drop contained equal parts protein and well solution composed of 0.1 M imidazole-HCl at pH 7.5, 0.2 M lithium sulfate, and 30% (w/v) polyethylene glycol 3000. Crystals were cryoprotected after a soak in well solution containing 15% glycerol before rapid cooling in a nitrogen gas stream. Data was collected at ALS beamline 4.2.2 (Lawrence Berkeley Laboratories, Berkeley, CA) at 293 K and at a wavelength of 1.29 Å using a CCD detector. The data were processed and scaled in HKL-3000 [103]. Crystalllographic phasing was obtained by molecular replacement using the program Phaser [104] and the corresponding DIII fragment from DV2 (PDB accession 1OAN) as a search model. The resulting atomic model was iteratively built in O [105] and refined in REFMAC [106]. The final model with one DENV1 DIII monomer per asymmetric unit has been refined to 2.25 Å resolution and contains 105 amino acids (residues 296 to 399 of DIII) and 53 water molecules. The DENV1 DIII domain is similar in structure to that reported for the post-fusion DENV-1 E ectodomain trimer (3G7T) [11] with a root-mean-square difference of 1.6 Å between Cα atom positions for equivalent core residues 296 through 394 [107]. The coordinates and diffraction data have been deposited in the RCSB with accession number 3IRC.

Domain mapping by yeast surface display

The DNA fragments encoding amino acid residues 1 to 293 (DI-DII) and 294 to 409 (DIII) of DENV-1 E protein were amplified from the DENV-1 strain 16007 or West Pac-74 by RT-PCR with BamHI and XhoI sites added at the 5’ and 3’ end, respectively. The PCR products were cloned as downstream fusions to Aga2 and Xpress epitope tag genes in the yeast surface display vector pYDI (Invitrogen), under the control of an
upstream GAL1 promoter. These constructs were transformed into *Saccharomyces cerevisiae* strain EBY100 [108,109] using *E*. coli EasyComp Transformation Kit (Invitrogen) to generate yeast that expressed DENV-1 DI-DII or DIII. Individual yeast colonies were grown to logarithmic phase at 30°C in tryptophan-free yeast media containing 2% glucose. Fusion protein expression was induced on the surface by growing yeast for additional 48 hrs in tryptophan-free media containing 2% galactose at 20°C. Yeast cells were washed with PBS supplemented with BSA (1 mg/ml) and incubated with 50 μl of neat culture supernatant or purified MAbs at a concentration of 25 μg/ml. After a 30 minute incubation on ice, yeast were washed in PBS with BSA and then incubated with a goat anti-mouse IgG secondary antibody conjugated to Alexa Fluor 647 (Molecular Probes). After fixation with 1% paraformaldehyde in PBS, yeast cells were analyzed on a FACSArray flow cytometer (Becton-Dickinson) using FloJo software.

**Yeast library construction and screening**

To generate a library of DENV-1 DIII variants on yeast, mutation was accomplished by error-prone PCR, using a GeneMorph II random mutagenesis kit (Stratagene). The library was ligated into the pYD1 vector and transformed into XL2-Blue ultracompentent cells (Stratagene). The colonies were pooled and transformed into yeast cells as described above. In some instances, additional site-specific mutations were engineered into DENV-1 DIII by a reverse genetic approach using the Quick Change II Mutagenesis Kit (Stratagene).

For individual MAbs, the DENV-1 DIII mutant library was screened according to a previously described protocol [29]. To identify yeast that had selectively lost binding to a given MAb, the library was stained with an individual Alexa Fluor 647 conjugated MAbs for 30 min on ice. To control for surface expression of appropriately folded DIII of DENV-1, yeast cells were subsequently stained for 30 min on ice with an Alexa Fluor 488-conjugated pool of DIII-specific MAbs (DENV1-E90, DENV1-E95, DENV1-E99, DENV1-DENV1-E111, DENV1-E111, and DENV1-E113), and then processed by flow cytometry. The population that was single MAb negative but pool oligoclonal MAbs positive was selected and sorted. After four to five rounds of sorting, yeast were plated and individual colonies were tested for binding to individual MAbs by flow cytometry. For clones that had lost binding to the desired MAb of interest, the plasmid was recovered using a Zymoprep yeast miniprep kit (Zymo Research), and then processed for cloning and sequencing.

**Immunostaining of DENV-infected cells**

For the study of binding of DENV-1 MAbs to different DENV strains, Raji-DC-SIGN-R or C6/36 cells were infected with different DENV strains at a multiplicity of infection (MOI) of 1. Depending on the DENV-1 strain, Raji-DC-SIGN-R cells were harvested at 48 or 96 hours and C6/36 cells were harvested at day 7 after infection. Cells were washed, fixed in PBS with 4% paraformaldehyde, and permeabilized in Hanks’ balanced salt solution (HBSS) supplemented with 10 mM HEPES (pH 7.3), 0.1% (w/v) saponin (Sigma), and 0.02% NaN3. The cells were then incubated with MAbs for 30 minutes on ice, washed and incubated subsequently with an Alexa Fluor 647-conjugated goat anti-mouse IgG (Molecular Probes). After 30 minutes, cells were washed and fixed in PBS with 1% paraformaldehyde and analyzed by flow cytometry. To test whether DENV-1 MAbs cross-reacted with more distantly related flaviviruses, infection and staining experiments were performed with WNV (strain 3000.0259) and Raji-DC-SIGN-R cells as described previously [52].

**DENV-1 virus capture ELISA**

The capture ELISA for DENV-1 was based on a published assay for WNV with modifications [48]. Briefly, anti-DENV-1 MAbs were coated at indicated concentrations on MaxiSorp (Nunc) polystyrene 96-well microtiter plates in a sodium carbonate (pH 9.3) buffer. Plates were washed three times in ELISA wash buffer (PBS with 0.02% Tween 20) and blocked for 1 hour at 37°C with ELISA block buffer (PBS, 2% bovine serum albumin, and 0.02% Tween 20). DENV-1 virions (2.5 to 5.0×10^6 PFU of strain 16007 or West Pac-74) diluted in DMEM with 10% heat-inactivated FBS were captured on plates coated with anti-DENV-1 MAbs for 2 hours at room temperature. Plates were rinsed five times in wash buffer and then incubated with biotinylated 4G2 (1 μg/ml, respectively diluted in ELISA block buffer), which recognizes the fusion loop peptide in DII, for 1 hour at room temperature. Plates were washed again five times and then sequentially incubated with 2 μg/ml of horseradish peroxidase-conjugated streptavidin (Vector Laboratories) and tetramethylbenzidine substrate (Dako). The reaction was stopped with the addition of 2 N H2SO4 to the medium, and emission (450 nm) was read using an iMark microplate reader (Bio-Rad).

**Mouse experiments**

All mouse studies were approved and performed according to the guidelines of the Washington University School of Medicine Animal Safety Committee. IFN-γR−/− × γR−/− mice on the 129 Sv background (AG129 mice) were a gift from Dr. Skip Virgin (Washington University School of Medicine) and bred in a pathogen-free barrier facility. In prophylaxis experiments, AG129 mice were administered a single dose of individual MAbs one day before infection. Subsequently, mice were challenged with West Pac-74 (genotype 4, 10^6 PFU) by an IP route and morbidity and mortality were monitored for 60 days. In post-exposure therapeutic experiments, a single 500 μg dose of MAb dose was administered by IP injection two or four days after infection with 10^6 PFU of West Pac-74.

**Mapping of mutations onto the DENV-1 DIII crystal structure**

Figures were prepared using the atomic coordinates of DENV-1 DII (RCSB accession number 3RC) using the programs CCP4MG [110]. The alignment of DENV-1 DIII from different genotypes was created with the program ALSCRIPT [111].

**Statistical analysis**

All data were analyzed using Prism software (GraphPad software). For survival analysis, Kaplan-Meier survival curves were analyzed by log-rank test. For neutralization assays an unpaired student’s T-test was used to determine significance.

**Supporting Information**

**Table S1** Profile of DENV-1 MAbs

| Found at | doi:10.1371/journal.ppat.1000823.s001 (0.06 MB DOC) |

**Table S2** Summary of Data Collection and Refinement

| Found at | doi:10.1371/journal.ppat.1000823.s002 (0.03 MB DOC) |
Acknowledgments

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