ORIGINAL ARTICLE

Venezuelan Equine Encephalitis Virus V3526 Vaccine RNA-Dependent RNA Polymerase Mutants Increase Vaccine Safety Through Restricted Tissue Tropism in a Mouse Model

Clint A. Haines1, Rafael K. Campos1, Sasha R. Azar2, K. Lane Warmbrod2,a, Tiffany F. Kautz1,b, Naomi L. Forrester2,c,* and Shannan L. Rossi1,2,3,*

Abstract

Background: Venezuelan equine encephalitis virus (VEEV) is an arbovirus endemic to the Americas, for which no vaccines or antiviral agents have been approved. TC-83 and V3526 are the best-characterized vaccine candidates for VEEV. Both are live-attenuated vaccines and have been associated with safety concerns, although fewer concerns exist for V3526. A previous attempt to improve the TC-83 vaccine focused on further attenuating the vaccine by adding mutations that alter the error-incorporation rate of the RNA-dependent RNA polymerase (RdRp).

Methods: The research herein examined the effects of these RdRp mutations in V3526 by cloning the 3X and 4X strains, assessing vaccine efficacy against challenge in adult female CD-1 mice, examining neutralizing-antibody titers, investigating vaccine tissue tropism, and testing the stability of the mutant strains.

Results: The V3526 RdRp mutants exhibited less tissue tropism in the spleen and kidney than the wild-type V3526, while maintaining vaccine efficacy. Illumina sequencing indicated that the RdRp mutations reverted to wild-type V3526 after five passages in murine pup brains.

Conclusions: The observed genotypic reversion is likely to be of limited concern, because wild-type V3526 remains an effective vaccine capable of providing protection. Our results indicate that the V3526 RdRp mutants may be a safer vaccine design than the original V3526.

Key words: Venezuelan equine encephalitis virus, TC-83, V3526, vaccine, fidelity

INTRODUCTION

Venezuelan equine encephalitis virus (VEEV) is a member of the Alphavirus genus in the family Togaviridae with an 11.5 kb positive-sense single-stranded RNA genome [1,2]. Venezuelan equine encephalitis (VEE) commonly causes mild flu-like symptoms, but severe symptoms can occur in approximately 4–14% of cases in humans [3–6]. Severe symptoms include encephalitis,
confusion, coma, photophobia, and seizures [3]. Death as a result of VEE is rare but occurs in approximately 1% of cases, depending on the patient age and the outbreak [7,8].

Multiple VEEV outbreaks have occurred across Central and South America; the most recent outbreak occurred in Peru in 2006 [9–15]. A Central American outbreak between 1969 and 1972 resulted in the deaths of 50,000 equines and 93 humans, and hundreds of additional cases of human disease were reported [13]. The outbreak reached southern Texas in 1971, resulting in 1,500 equine deaths and 110 cases of human disease [12]. Another major outbreak in Venezuela between 1992 and 1995 resulted in 4,000 equine deaths and between 75,000 and 100,000 cases of human disease [14]. The virus tends to recede and emerge in epidemic (outbreak) cycles every 14–20 years and to cause disease in humans and equids [9,14]. Nonetheless, VEEV is believed to cause tens of thousands of human infections every year.

VEEV is considered a biological risk agent, owing to its high aerosol infectivity, numerous documented infections through laboratory exposure, and potential for weaponization [16,17]. Because of the potential for re-emergence coupled with the biological risk factors, a publicly available vaccine for VEE is needed to protect at-risk populations, healthcare providers, biomedical researchers, and emergency responders in the event of an outbreak.

Numerous vaccine candidates for VEE exist, but TC-83 and V3526 are currently the best-characterized candidates [18,19]. TC-83 was previously approved for limited use to protect military personnel and researchers, but V3526 has demonstrated improved protection, safety, and a lower likelihood of reversion or pseudo-reversion to wild type (WT) [19–21]. TC-83 was made by serial passaging of the Trinidad donkey (TRD) strain of VEEV in fetal guinea pig heart cells [19–21]. The development of V3526 involved site-directed mutagenesis of a TRD cDNA clone to remove the PE2 furin-cleavage site and create an E1 protein F253S point mutation [22]. The safety concerns exist for both vaccine constructs. Vaccination with TC-83 can lead to clinical symptoms in 23% of human recipients and lack of neutralizing antibodies in 18% of recipients, and the vaccine can potentially be transmitted by a mosquito vector [20,24]. The safety concerns regarding V3526 include fever and flu-like symptoms in human recipients and lack of neutralizing antibodies in 18% of recipients, and the vaccine can potentially be transmitted by a mosquito vector [20,24]. The safety concerns regarding V3526 include fever and flu-like symptoms in human recipients; the presence of viral antigen in the brains of vaccinated animals, thus indicating possible neurovirulence; and the potential for transmission of the virus by a mosquito vector [24–26].

A previous attempt to improve the TC-83 vaccine candidate focused on the use of mutations altering the error-incorporation rate of the RdRp [27–31]. The mutants included TC-83 3X, which contains the G8R, E31G, and A90T mutations in the RdRp gene nsP4, and TC-83 4X, which contains these nsP4 mutations in addition to C482Y, which was originally discovered in the related alphavirus chikungunya virus (CHIKV) [27,29]. The C482Y substitution has been shown to decrease the RdRp error frequency in CHIKV and thus has been hypothesized to be a high-fidelity variant [29]. Research on TC-83 has suggested that the 3X and 4X mutants have lower virulence than the WT. Our research examined the effects of these 3X and 4X mutations in the V3526 platform, because V3526 has shown better protection and safety than TC-83 in animal studies. Additionally, the furin-cleavage-site deletion should hinder reversion to WT TRD [19,23,32,33]. Our study indicated that V3526 3X and 4X have less tissue tropism than WT V3526, thereby indicating improved vaccine safety without sacrificing immunogenicity.

METHODS

Animals and viruses

The V3526, V3526 3X, and V3526 4X virus strains were cloned, in vitro transcribed, and electroporated to generate viral stocks as previously described for the TC-83 RdRp mutants [27]. Viral stocks were quantified with Vero cell plaque assays before each experiment to ensure consistent inoculation doses. All work with VEEV 3908 was performed in either BSL3 or ABSL3 laboratories, whereas all work with V3526 was performed in BSL2 facilities in accordance with University of Texas Medical Branch (UTMB) regulations and all relevant state and federal laws.

All mice were ordered at 6 weeks of age or as timed-pregnant dams from Charles River, and were housed in the Galveston National Laboratory ABSL2 facilities. CD-1 mice were chosen because they are frequently used in testing for vaccine safety and efficacy, thus facilitating comparisons between this study and previous research on vaccines for VEE [27,28,34,35]. Work was performed after IACUC approval and followed all UTMB regulations, and state and federal laws.

Plaque assays

Plaque assays were performed by seeding Vero (ATCC® CCL-81™) cells at a density of 2 × 10^5 cells/well in a 12-well plate with Dulbecco's modified Eagle's medium (DMEM) supplemented with 1% penicillin and streptomycin, and 10% fetal bovine serum (FBS). The cells were incubated overnight at 37°C with 5% CO₂. Viral samples were serially diluted 10-fold in DMEM supplemented with 1% penicillin and streptomycin, and 2% FBS. The plated cells were infected with the diluted viruses and incubated at 37°C with 5% CO₂ for 1 hour with gentle rocking every 15 minutes. The cells were then overlaid with 0.4% agarose in DMEM supplemented with 1% penicillin and streptomycin, and 2% FBS. The plated cells were incubated with the diluted viruses and incubated at 37°C with 5% CO₂ for 1 hour with gentle rocking every 15 minutes. The cells were then fixed with formalin and stained with 0.25% crystal violet. Plaques were counted and multiplied by the dilution factor to determine the final concentration.

Vaccine efficacy

Adult female CD-1 mice were vaccinated subcutaneously with 10^4 or 10^5 plaque-forming units (PFU) of V3526.
2 × 10^5 cells/well. All plates were treated as standard Vero seeded on a 12-well plate the previous day at a density of an unknown concentration of the virus and incubated for 1 hour. The virus-mixed serum samples were then added to a monolayer of Vero (ATCC® CCL-81™) cells that had been diluted 2-fold in the supplemented DMEM from a range of 1:20 to 1:640. The diluted samples were mixed with a 1% penicillin and streptomycin. The samples were then incubated for 1 hour at 56°C for inactivation before a 10-fold dilution in DMEM supplemented with 2% FBS, in addition to a ball bearing were used to collect the spleen, liver, brain, and kidney samples. A QIAGEN TissueLyser was used to homogenize the samples. Clarification via centrifugation was performed to remove excess tissue and collect virus. Titrations were performed with a Vero cell plaque assay before intracranial injection of the next round of pups until a total of five passages.

RNA isolation was performed on the passage 5 brain homogenate supernatants for V3526, V3526 3X, and V3526 4X with TRIZOL™ LS reagent according to the manufacturer’s instructions. The UTMB Next Generation Sequencing Core performed the Illumina sequencing with a NextSeq 550 system. RT-PCR conversion of RNA into double-stranded cDNA was used to prepare the sequencing library. Fragmentation of the cDNA was performed before ligation of each fragment to an adapter. A glass flow cell was then populated by the adapter-ligated fragments, and template clusters were amplified. Reversible adapter-ligated terminator nucleotides were used to sequence each cluster. A previously described pipeline was used to assemble reads [37]. The starting plasmid sequences for each vaccine were compared against the sequencing results for the identification of major nucleotide variants.

The Illumina sequencing data were analyzed by examination of common SNPs that occurred in at least three of the four RdRp mutants. Only mutations present at ≥ 0.5% of the sequenced population were considered in the analyses. A list of 22 SNPs was created according to these criteria. Each mutation was assessed for the percentage frequency in the population for each biological replicate tested, the gene where the mutation occurred, and the amino acid change encoded.

**RESULTS**

**Vaccine efficacy**

Vaccine efficacy was examined for the V3526 3X and 4X mutants with adult CD-1 outbred mice. CD-1 mice were vaccinated with 10^3 PFU of the V3526 vaccine parent, 3X, or 4X. The post-vaccination survival analysis for each group (Fig 1A) indicated that no animals succumbed after vaccination, as expected. The post-vaccination weights (Fig 1B) indicated that all animals gained weight over the first 14 days, and no significant differences were observed between mutants and the parent strain.

The CD-1 mice were challenged 60 days after vaccination with 10^5 PFU of the epizootic VEEV 3908. All vaccinated mice survived the challenge, whereas unvaccinated (mock) mice all succumbed by day 5 after the challenge (Fig 1C). Furthermore, all vaccinated animals maintained their weights after the challenge, whereas the mock-vaccinated animals steadily lost weight until they met the criteria for euthanasia (Fig 1D). The average weight of the mock-vaccinated animals was significantly lower than that in each of the vaccine test groups on days 2–5 after the challenge, as measured by Tukey’s multiple comparison test. We observed no significant differences in animal survival.
Neutralizing-antibody titers
Neutralizing-antibody levels were measured with PRNTs with serum from mice vaccinated with either $10^5$ PFU (Fig 2A, B) or $10^4$ PFU (Fig 2C, D). PRNT levels in mice vaccinated with $10^5$ PFU of V3526 3X or 4X mutants produced neutralizing-antibody titers similar to those with the parental V3526, and no significant differences were detected, as measured by Sidak’s multiple comparison test. For the $10^4$ PFU dose, no significant differences were observed between the RdRp mutants and the V3526 parent strain. Interestingly, more mice vaccinated with $10^4$ PFU had titers outside the assay’s detectable range (>1:640), thus indicating a potential dose effect. Given that the lower dose might elicit higher neutralizing-antibody titers, this dose was used in subsequent studies.

Vaccine tissue tropism
Vaccine tissue tropism was examined because previous TC-83 RdRp mutant studies indicated that the 3X and 4X mutants have a diminished ability to overcome the host barriers to infection present during tissue dissemination and the establishment of neurovirulence [27]. CD-1 mice were vaccinated with $10^4$ PFU of V3526 parent, 3X, or 4X.

FIGURE 1 | Percentage survival and percentage weight change after vaccination and challenge of CD-1 mice. Adult female CD-1 mice received 10 PFU of V3526 parent, V3526 3X or V3526 4X for the vaccination, and 10% PFU of VEEV 3908 for the challenge. Mice were monitored for A) post-vaccination survival and C) post-challenge survival. Weight charts are represented as B) post-vaccination and D) post-challenge. In the post-challenge survival graph, **** represents a P-value <0.0001 for each test group vs. mock. V3526 3X and 4X are offset from 100% for improved data visualization. In the post-challenge weight graph, * represents a P-value <0.05, and **** represents a P-value <0.0001 vs. mock at each indicated timepoint (2–5 DPC). A log-rank Mantel-Cox test was used for survival analysis, and Tukey’s multiple comparison test was used for weight analysis. Weight-chart error bars represent SEM.

or weight between the mutants and their respective parent strains after the challenge.

Neutralizing-antibody titers
Neutralizing-antibody levels were measured with PRNTs with serum from mice vaccinated with either $10^5$ PFU (Fig 2A, B) or $10^4$ PFU (Fig 2C, D). PRNT levels in mice vaccinated with $10^5$ PFU of V3526 3X or 4X mutants produced neutralizing-antibody titers similar to those with the parental V3526, and no significant differences were detected, as measured by Sidak’s multiple comparison test. For the $10^4$ PFU dose, no significant differences were observed between the RdRp mutants and the V3526 parent strain. Interestingly, more mice vaccinated with $10^4$ PFU had titers outside the assay’s detectable range (>1:640), thus indicating a potential dose effect. Given that the lower dose might elicit higher neutralizing-antibody titers, this dose was used in subsequent studies.

Vaccine tissue tropism
Vaccine tissue tropism was examined because previous TC-83 RdRp mutant studies indicated that the 3X and 4X mutants have a diminished ability to overcome the host barriers to infection present during tissue dissemination and the establishment of neurovirulence [27]. CD-1 mice were vaccinated with $10^4$ PFU of V3526 parent, 3X, or 4X.
Serum, brain, spleen, kidney, and liver samples were collected on days 1, 2, and 7 after vaccination to measure viral load. Mice were perfused with phosphate-buffered saline on the first 2 days to eliminate potential viremia contamination. The weights for all infected animals (Fig S1A) averaged between 95% and 105% of the initial weight over the course of the experiment, similarly to the post-vaccination weights observed for the 105 PFU dose, without signs of disease.

Viral loads were undetectable in the serum (Fig S1B), brain (Fig 3A), or liver (Fig 3D) at all timepoints for each of the V3526 vaccines tested. The viral load in the spleen was detectable for the V3526 parent strain on days 1 and 2 after infection, but the V3526 mutants did not show a detectable viral load at any timepoint (Fig 3B). The V3526 parent strain had a significantly higher viral load than the mutants on the first 2 days after infection, as measured by Sidak’s multiple comparison test. The viral load in the kidney was detectable in one mouse for the V3526 parent strain on the first day after infection, but the viral load in the spleen was undetectable at each timepoint for the V3526 mutants (Fig 3C).

**Sequencing vaccine reversion during neurovirulence testing**

V3526, and the 3X and 4X RdRp mutants were passaged five times in duplicate in neonatal mouse pup brains to assess the safety and stability of the mutant constructs. Mouse pup brains were chosen for this experiment because they are a highly permissive model that allows the virus to replicate to high titers and mutate rapidly in the process [38,39]. Illumina sequencing of passage 5 virus was used to examine changes in the mutant repertoire of V3526 and the RdRp mutants over the course of passaging.
The mutational frequencies for each major nucleotide variant (i.e., >0.5% prevalence) were compiled (Tables S1–S3) and then narrowed (Table 1) to identify SNPs occurring in at least three of the four RdRp mutant samples. Common mutations were found in all genetic regions except for the 5′UTR, capsid, and 6K genes. The mutations C5724G, G5794A, and A5970G correspond to the R8G, G31E, and T90A genetic reversions to the V3526 parent strain genotype in the nsP4 region, respectively. The T7208C mutation corresponds to a silent substitution in the nsP4 protein coding region. The mutation A7147G was present in both replicates of the V3526 4X strain encoding a Y482C genetic reversion in the nsP4 coding region. Each of these substitutions, including the silent mutation, represents a genotypic reversion to the V3526 parent strain from the fidelity variant strains after serial passage in mouse pup brains. All other major nucleotide variants in Table 1 were present in at least one of the V3526 parent strain replicates.

**DISCUSSION**

V3526 and TC-83 are among the best-characterized vaccine candidates for VEE [18,19]. TC-83 is currently the only vaccine candidate approved for limited military use, but V3526 has shown similar or greater protection to that of TC-83 in previous animal studies [19,32,33]. Owing to the presence of a furin-cleavage-site deletion in V3526, reversion to WT TRD should be more difficult than that for the two SNPs associated with the attenuation observed in TC-83 [23]. Neither vaccine candidate has been approved for public use, and researchers and military personnel have limited
TABLE 1 | Common mutations in the V3526 3X and 4X RdRp mutants compared with mutations in parental V3526. The criterion for including a major mutation in this table was presence in at least three of the four sequenced fidelity variants. The nucleotide positions of SNPs are represented as “Position.” Nucleotides present in the starting plasmid are represented as “Reference.” Nucleotides present in Illumina sequencing data are represented as “Mutation.” The percentages of mutations present in each Illumina sequenced population are depicted as “Freq.” followed by the name of the sample. Genes in which mutations occurred are depicted as “Gene.” Substitutions that occurred as a result of the mutation are depicted as “Amino Acid Change.” * in the Position column denotes a mutation that was present in the RdRp mutants but absent in the V3526 parent strain. * in the Amino Acid Change column represents a genotypic reversion to resemble the V3526 parent strain.

| Position | Reference | Mutation | Freq. parent (A) | Freq. parent (B) | Freq. 3X (A) | Freq. 3X (B) | Freq. 4X (A) | Freq. 4X (B) | Gene | Amino acid change |
|----------|-----------|----------|------------------|------------------|--------------|--------------|--------------|--------------|------|------------------|
| 1545     | C         | T        | 98.02%           | 0.00%            | 99.93%       | 99.61%       | 97.82%       | 0.00%        | nsP1 | R501C            |
| 1696     | C         | A        | 99.72%           | 0.00%            | 99.91%       | 99.80%       | 98.10%       | 0.00%        | nsP2 | A16D             |
| 5275     | A         | G        | 99.35%           | 0.00%            | 99.94%       | 99.78%       | 98.00%       | 0.00%        | nsP3 | H415R            |
| 5724*    | C         | G        | 0.00%            | 0.00%            | 100.00%      | 99.81%       | 98.30%       | 0.00%        | nsP4 | R8G*             |
| 5794*    | G         | A        | 0.00%            | 0.00%            | 99.98%       | 99.85%       | 98.25%       | 0.00%        | nsP4 | G31E*            |
| 5970*    | A         | G        | 0.00%            | 0.00%            | 99.97%       | 99.78%       | 97.97%       | 1.85%        | nsP4 | T90A*            |
| 7208*    | T         | C        | 0.00%            | 0.00%            | 99.90%       | 99.70%       | 97.95%       | 0.00%        | nsP4 | Silent            |
| 8549     | G         | A        | 18.68%           | 0.00%            | 19.27%       | 19.76%       | 16.41%       | 0.00%        | E3   | G55R             |
| 8552     | T         | A        | 16.15%           | 0.00%            | 15.56%       | 15.11%       | 14.43%       | 0.00%        | E2   | S1T              |
| 8572     | G         | T        | 99.51%           | 1.36%            | 99.95%       | 99.62%       | 97.58%       | 77.76%       | E2   | K7N              |
| 8804     | C         | T        | 99.70%           | 0.00%            | 99.88%       | 99.70%       | 97.39%       | 0.00%        | E2   | H85Y             |
| 8910     | C         | G        | 99.70%           | 0.00%            | 99.95%       | 99.77%       | 97.77%       | 0.00%        | E2   | T120R            |
| 9061     | A         | G        | 99.73%           | 0.00%            | 99.95%       | 99.70%       | 97.54%       | 0.00%        | E2   | Silent            |
| 9126     | T         | A        | 99.77%           | 0.00%            | 99.94%       | 99.71%       | 97.45%       | 0.00%        | E2   | V192D            |
| 9267     | T         | A        | 99.69%           | 0.00%            | 99.94%       | 99.72%       | 97.80%       | 0.00%        | E2   | I239N            |
| 9438     | C         | T        | 99.76%           | 0.00%            | 99.92%       | 99.76%       | 98.03%       | 0.00%        | E2   | T296I            |
| 9475     | T         | C        | 99.80%           | 0.00%            | 99.95%       | 99.75%       | 97.86%       | 0.00%        | E2   | Silent            |
| 9519     | G         | A        | 99.56%           | 0.00%            | 99.78%       | 99.58%       | 97.30%       | 0.00%        | E2   | G323E            |
| 10469    | T         | A        | 99.71%           | 0.00%            | 99.93%       | 99.71%       | 97.98%       | 0.00%        | E1   | L161I            |
| 10621    | A         | T        | 99.73%           | 0.00%            | 99.94%       | 99.66%       | 97.73%       | 0.00%        | E1   | Silent            |
| 10746    | C         | T        | 99.70%           | 0.00%            | 99.90%       | 99.74%       | 98.01%       | 0.00%        | E1   | S253F            |
| 11373    | C         | T        | 0.95%            | 0.00%            | 0.79%        | 0.78%        | 1.09%        | 0.00%        | 3’UTR | N/A             |

access to TC-83 vaccination, because the only distributor is the Special Immunizations Program [40]. Therefore, improving V3526 vaccine candidate safety is critical. Herein, we accomplished this improvement by adding the 3X and 4X RdRp mutations previously described in TC-83 and CHIKV to develop a vaccine candidate showing evidence of increased safety by decreasing tissue tropism without sacrificing immunogenicity, as measured by PRNTs [27].

Neutralizing-antibody titers are a widely recognized correlate of protection for evaluating alphavirus vaccines [41–43]. Consequently, PRNT₈₀ results after inoculation with 10⁴ PFU indicated that more mice produced titers above the highest dilution of 1:640 than after inoculation with 10⁵ PFU. Because samples above 1:640 were not titrated beyond this cutoff, the titers might have been even higher than indicated in this study. Three mice had titers below the LOD for the PRNT₈₀ after inoculation with 10⁴ PFU, but the PRNT₅₀ data demonstrated that all animals seroconverted. The neutralizing-antibody data indicated that vaccination with the V3526 mutants produced neutralizing-antibody titers equivalent to those of the V3526 parent strain.

Antigens for V3526 have been detected in the brain and olfactory mucosa via immunohistochemistry, and undetectable viremia has been described in multiple animal models [19,25,44,45]. In accordance with prior reports, our study
did not detect viremia in mice vaccinated with \(10^4\) PFU of any of the V3526 vaccines, thus suggesting that the vaccines cannot be transmitted to a mosquito vector [24, 46]. Viremia after TC-83 vaccination might have resulted in unintentional vaccine transmission among mosquito populations in the past, thus supporting the use of the V3526 vaccine rather than the TC-83 vaccine in the future [47]. Low viral titers have been reported in the liver in C3H/HeN mice [48]; consequently, the undetectable viral load in our study was an expected result. Undetectable viral loads in the brain indicate that the incorporated RdRp mutations do not result in neuroinvasion after subcutaneous injection. Decreased tissue tropism for the 3X and 4X mutants in the spleen and kidney on the first 2 days after vaccination may indicate further organ tropism restriction while still maintaining efficacy, thereby resulting in a safer vaccine design than the V3526 parent strain. Some limitations of this study are the lack of data on viral load in additional lymphoid tissues and the absence of descriptions of the histopathological changes in the organs tested. These aspects, in addition to determination of whether mosquitoes can serve as vectors for these vaccines, should be investigated in future studies.

Serial passaging of viruses in the brains of mouse pups allows the viruses to replicate to high titers quickly while acquiring mutations that may occur during an infection [38, 39]. This technique is used to assess vaccine stability and screen for mutations with the potential for reversion or pseudo-reversion to WT VEEV [39]. The Illumina sequencing data from this study indicated a genotypic reversion of the 3X and 4X mutants encoding G8R, E31G, A90T, and C482Y to the V3526 parent strain genotype after five passages in mouse pup brains. However, this genotypic reversion is probably of limited concern, because parental V3526 remains an effective vaccine capable of preventing disease [19]. The genotypic reversions to the parent strain might have occurred because mouse pup brains are a highly permissive model that allows the virus to grow with little selective pressure from a host immune system, and this effect was enhanced by each passage performed before sequencing [38, 39]. The decrease in tissue tropism observed after vaccination with the mutants in the adult CD-1 mouse model suggests that the risk of vaccines genotypically reverting in healthy adults is low. This possibility should be interesting to pursue in future studies.

The Illumina sequencing data from this study also revealed a large difference in the mutations present between the biological replicates of V3526 and V3526 4X. Variations in the mutation profiles of the two virus strains may be explained by a founder effect resulting from the high mutation rate associated with alphaviruses [49]. All three viral strains were rescued from cDNA clones, in an effort to minimize founder effects and start the mouse pup brain passaging from a well-defined stock. However, V3526, and the 3X and 4X RdRp mutants were rescued in cell culture before the experiment began and consequently might have led to genetic diversity between replicates.

Because of VEEV’s status as an agent of biological concern, coupled with the increased risk of re-emergence and the effects of global warming on vector-borne disease, a publicly available vaccine for VEE is important for improving biosafety and biosecurity [50]. The research presented herein improves on the V3526 vaccine candidate through the inclusion of RdRp mutations, which decreased viral tissue tropism while maintaining the efficacy of the parent strain. Future work will focus on increasing the stability of these mutations. These data provide further evidence that RdRp mutants can be used to create safer vaccines against alphavirus-caused diseases.

ACKNOWLEDGEMENTS

The data reported herein were part of CAH’s thesis entitled “Determining the Impact of Fidelity Mutations in the RNA-Dependent RNA Polymerase of V3526 Vaccine on Tissue Dissemination and Intrahost Variation.” This project was supported by NIH R01 grant AI125902.

CONFLICTS OF INTEREST

The authors have no conflicts of interest to declare.

REFERENCES

1. Strauss JH, Strauss EG. The alphaviruses: gene expression, replication, and evolution. Microbiol Rev. 1994;58(3):491-562.
2. Foy NJ, Akhrymuk M, Shustov AV, Frolova EI, Frolov I. Hypervariable domain of nonstructural protein nsP3 of Venezuelan equine encephalitis virus determines cell-specific mode of virus replication. J Virol. 2013;87(13):7569-7584.
3. Lundberg L, Carey B, Keen-Hall K. Venezuelan equine encephalitis virus capsid-the clever caper. Viruses. 2017;9(10):279.
4. Franck PT, Johnson KM. An outbreak of Venezuelan encephalitis in man in the Panama Canal Zone. Am J Trop Med Hyg. 1970;19(5):860-865.
5. Watts DM, Callahan J, Rossi C, Oberste MS, Roehrig JT, Wooster MT, et al. Venezuelan equine encephalitis virus febrile cases among humans in the Peruvian Amazon River region. Am J Trop Med Hyg. 1998;58(1):35-40.
6. Steele KE, Twenhofel NA. REVIEW PAPER: pathology of animal models of alphavirus encephalitis. Vet Pathol. 2010;47(5):790-805.
7. Ehrenkranz N, Ventura A. Venezuelan equine encephalitis virus infection in man. Annu Rev Med. 1974;25(1):9-14.
8. Vilcarromero S, Aguilar PV, Halsey ES, Laguna-Torres VA, Razuri H, Perez J, et al. Venezuelan equine encephalitis and Z human deaths, Peru. Emerg Infect Dis. 2010;16(3):553-556.
9. Wang E, Bowren RA, Medina G, Powers AM, Kang W, Chandler LM, et al. Virulence and viremia characteristics of 1992 epizootic subtype IC Venezuelan equine encephalitis viruses and closely related enzootic subtype ID strains. Am J Trop Med Hyg. 2001;65(1):64-69.
10. Aguilar PV, Estrada-Francisco JC, Navarro-Lopez R, Ferro C, Haddow AD, Weaver SC. Endemic Venezuelan equine encephalitis in the Americas: hidden under the dengue umbrella. Future Virol. 2011;6(6):721-740.
11. Randall R, Mills JW. Fatal encephalitis in man due to the venezuelan virus of equine encephalomyelitis in Trinidad. Science (Washington). 1944;99(2568):225-226.
12. Sudia WD, Newhouse VF, Beadle LD, Miller DL, Johnston JG, Young R, et al. Epidemic Venezuelan encephalitis encephalitis in North America in 1971: vector studies. Am J Epidemiol. 1975;101(1):17-35.
Venezuelan Equine Encephalitis Virus V3526 Vaccine RNA-Dependent RNA Polymerase Mutants Increase Vaccine Safety

13. Estrada-Franco JG, Navarro-Lopez R, Freier JE, Cordova D, Clements T, Moncayo A, et al. Venezuelan equine encephalitis virus, southern Mexico. Emerg Infect Dis. 2004;10(12):2113-2121.

14. Weaver SC, Salas R, Rico-Hesse R, Ludwig GV, Oberste MS, Boshell J, et al. Re-emergence of epidemic Venezuelan equine encephalomyelitis in South America. Lancet. 1996;348(9025):436-440.

15. Morrison AC, Forshey BM, Notyce D, Astete H, Lopez V, Rocha C, et al. Venezuelan equine encephalitis virus in Iquitos, Peru: urban transmission of a compatible strain. PLoS Negl Trop Dis. 2008;2(12):e439.

16. Zacks MA, Paessler S. Encephalopathic alphaviruses. Vet Microbiol. 2010;140(3-4):281-286.

17. Ross SL, Russell-Lodrigue KE, Kileen ZZ, Wang S, Leal G, Bergren NA, et al. IRES-containing VEEV vaccine protects cynomolgus macaques from IE Venezuelan equine encephalitis virus aerosol challenge. PLoS Negl Trop Dis. 2015;9(5):e0003797.

18. Kinney RM, Chang GJ, Tsuchiya KR, Snider J, Roehrig JT, Woodward MT, et al. Attenuation of Venezuelan encephalitis virus strain TC-83 is encoded by the 5'-noncoding region and the E2 envelope glycoprotein. J Virol. 1993;67(3):1269-1277.

19. Hart MK, Caswell-Stephan K, Bakken R, Tammaro R, Pratt W, Davis N, et al. Improved mucosal protection against Venezuelan equine encephalitis virus is induced by the molecularly defined, live-attenuated V3526 vaccine candidate. Vaccine. 2000;18(26):3067-3075.

20. Pittman PR, Makuch RS, Mangiafico JA, Cannon TL, Gibbs PH, Peters CJ. Long-term duration of detectable neutralizing antibodies after administration of live-attenuated VEE vaccine and following booster vaccination with inactivated VEE vaccine. Vaccine. 1996;14(4):337-343.

21. Burke DS, Ramsburg HH, Edelman R. Persistence in humans of antibody to subtypes of Venezuelan equine encephalomyelitis (VEE) virus after immunization with attenuated (TC-83) VEE virus vaccine. J Infect Dis. 1977;136(3):354-359.

22. Berge TO, Banks IS, Tigertt WD. Attenuation of Venezuelan equine encephalitis virus by the molecularly defined, live-attenuated V3526 vaccine candidate. Vaccine. 2001;20(3-4):616-622.

23. Davis NL, Brown KW, Greenwald GF, Zajac AJ, Zacny VL, Smith JF. Improved mucosal protection against Venezuelan equine encephalitis virus delivered by intramuscular vaccination in guinea pig heart cells. Am J Hyg. 1961;73(2):209-218.

24. Davis NL, Brown GW, Greenwald GF, Zajac AJ, Zaney VL, Smith JF, et al. Attenuated mutants of Venezuelan equine encephalitis virus containing lethal mutations in the PE2 cleavage signal virus, southern Mexico. Emerg Infect Dis. 2011;17(10):1603-16043.

25. Coffey LL, Beeharry Y, Borderia AV, Blanc H, Vignuzzi M. Arbovirus high fidelity variant loses fitness in mosquitoes and mice. Proc Natl Acad Sci U S A. 2011;108(38):16038-16043.

26. Pfeiffer JK, Kirkegaard K. A single mutation in poliovirus RNA-dependent RNA polymerase confers resistance to mutagenic nucleotide analogs via increased fidelity. Proc Natl Acad Sci U S A. 2003;100(12):7289-7294.

27. Kautz TF, Jaworski E, Routh A, Forrester NL. A low fidelity virus shows increased recombination during the removal of an alphavirus reporter gene. Viruses. 2020;12(6):660.

28. Hart MK, Lind C, Bakken R, Robertson M, Tammaro R, Ludwig GV. Onset and duration of protective immunity to IA/IB and IE strains of Venezuelan equine encephalitis virus in vaccinated mice. Vaccine. 2001;20(3-4):616-622.

29. Pratt WD, Davis NL, Johnston RE, Smith JF. Genetically engineered, live attenuated vaccines for Venezuelan equine encephalitis: testing in animal models. Vaccine. 2003;21(25-26):3854-3862.

30. Ross SL, Guerbois M, Gorbachov R, Gorachok R, Plante KS, Forrester NL, Weaver SC. IRES-based Venezuelan equine encephalitis virus candidate elicits protective immunity in mice. Virology. 2013;437(2):81-88.

31. Bernad KA, Klimstra W, Johnston RE. Mutations in the E2 glycoprotein of Venezuelan equine encephalitis virus confer heparan sulfate interaction, low morbidity, and rapid clearance from blood of mice. Virology. 2000;276(1):93-103.

32. Kimney RM, Chang GJ, Tsuchiya KR, Snider J, Roehrig JT, Woodward MT, et al. Attenuation of Venezuelan encephalitis virus strain TC-83 is encoded by the 5'-noncoding region and the E2 envelope glycoprotein. J Virol. 1993;67(3):1269-1277.

33. Pratt WD, Davis NL, Johnston RE, Smith JF. Genetically engineered, live attenuated vaccines for Venezuelan equine encephalitis. testing in animal models. Vaccine. 2003;21(25-26):3854-3862.

34. Ross SL, Guerbois M, Gorbachov R, Gorachok R, Plante KS, Forrester NL, Weaver SC. IRES-based Venezuelan equine encephalitis virus candidate elicits protective immunity in mice. Virology. 2013;437(2):81-88.

35. Bernard KA, Klimstra W, Johnston RE. Mutations in the E2 glycoprotein of Venezuelan equine encephalitis virus confer heparan sulfate interaction, low morbidity, and rapid clearance from blood of mice. Virology. 2000;276(1):93-103.

36. Ross SL, Comer JE, Wang E, Azar SR, Lawrence WS, Plante JA, et al. Immunogenicity and efficacy of a measles virus-vectorized chikungunya vaccine in nonhuman primates. J Infect Dis. 2019;200(5):735-742.

37. Patterson EL, Khanirov K, Rosjas MM, Kautz TF, Rockx-Brouwer D, Golovko G, et al. Mosquito bottlenecks alter viral mutant swarm in a tissue and time-dependent manner with contraction and expansion of variant positions and diversity. Virus Evol. 2018;4(1):vey001.

38. Li XF, Deng Y-Q, Yang H-Y, Zhao H, Jiang T, Xu Y-D, et al. A chimeric dengue virus vaccine using Japanese encephalitis virus vaccine strain SA14-14-2 as backbone is immunogenic and protective against either parental virus in mice and nonhuman primates. J Virol. 2013;87(24):13694-13705.

39. Yang D, Li X-F, Ye Q, Wang H-J, Deng Y-Q, Zhu S-Y, et al. Characterization of live-attenuated Japanese encephalitis vaccine virus SA14-14-2. Vaccine. 2014;32(23):2675-2681.

40. National Research Council. Protecting the Frontline in Biodefense Research: The Special Immunizations Program. Washington, DC: The National Academies Press; 2011.

41. Milligan GN, Schnierle BS, McAuley AJ, Beasley DWC. Defining a correlate of protection for chikungunya virus vaccines. Vaccine. 2019;37(50):2675-2681.

42. Repellent JW, Freier JE, Cordova D, Clements T, Moncayo A, et al. Venezuelan equine encephalitis virus, southern Mexico. Emerg Infect Dis. 2011;17(10):1603-16043.

43. Dupuy LC, Richards MJ, Ellefsen B, Chau L, Luxembourg C, et al. Venezuelan equine encephalitis virus in Iquitos, Peru: urban transmission of a sylvatic strain. PLoS Negl Trop Dis. 2015;9(5):e1007610.

44. Reed DS, Lind CM, Lackemeyer MG, Sullivan LJ, Pratt WD, Parker MD. Genetically engineered, live attenuated vaccines for viral diseases: a correlate of protection for chikungunya virus vaccines. Vaccine. 2019;37(50):7427-7436.

45. Porta J, Jose J, Roehrig JT, Blair CD, Kuhn RJ, Rossmann MG. Locking and blocking the viral landscape of an alphavirus with neutralizing antibodies. J Virol. 2014;88(17):9616-9623.

46. Toogardnaida. In Fenner's Veterinary Virology. 5th edition. Edited by Maclachlan NJ, Dubovi, EJ. Elsevier; 2017.
47. Pedersen Jr CE, Robinson DM, Cole Jr FE. Isolation of the vaccine strain of Venezuelan equine encephalomyelitis virus from mosquitoes in Louisiana. Am J Epidemiol. 1972;95(5):490-496.

48. Julander JG, Skirpustunas R, Siddharthan V, Shafer K, Hoopes JD, Smee DF, et al. C3H/HeN mouse model for the evaluation of antiviral agents for the treatment of Venezuelan equine encephalitis virus infection. Antiviral Res. 2008;78(3):230-241.

49. Sanjuán R, Nebot MR, Chirico N, Mansky LM, Belshaw R. Viral mutation rates. J Virol. 2010;84(19):9733-9748.

50. Rocklöv J, Dubrow R. Climate change: an enduring challenge for vector-borne disease prevention and control. Nat Immunol. 2020;21(5):479-483.