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Flexibility of NS5 Methyltransferase-Polymerase Linker Region Is Essential for Dengue Virus Replication

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We examined the function of the conserved Val/Ile residue within the dengue virus NS5 interdomain linker (residues 263 to 272) by site-directed mutagenesis. Gly substitution or Gly/Pro insertion after the conserved residue increased the linker flexibility and created slightly attenuated viruses. In contrast, Pro substitution abolished virus replication by imposing rigidity in the linker and restricting NS5’s conformational plasticity. Our biochemical and reverse genetics experiments demonstrate that NS5 utilizes conformational regulation to achieve optimum viral replication.

Nonstructural protein 5 (NS5) is a multifunctional protein essential for dengue virus (DENV) replication. NS5 consists of an N-terminal S-adenosyl-L-methionine (SAM)-dependent methyltransferase (MTase) domain (1) and a C-terminal RNA-dependent RNA polymerase (RdRp) domain (2–5). The MTase domain catalyzes the formation of type I RNA cap, which is critical for efficient translation and subverting the host immune surveillance (1, 6–8). The MTase domain may also be responsible for guanylyltransferase activity (9, 10). The RdRp domain (NS5 RdRp) synthesizes both negative-strand RNA from the input genomic RNA (gRNA) and the progeny plus-strand gRNA (5, 11).

Previous structural studies on DENV NS5 individual domains revealed electron density covering residues 6 to 262 (for the MTase domain) (PDB code 3P97) (12), and residues 273 to 882 (for the RdRp) (PDB code 2J7U) (5). Limited proteolysis of full-length NS5 (NS5 FL) in combination with mass determination suggested that the residues 263 to 272 (5) form the interdomain linker, and sequence comparison across various flaviviruses showed that this region is poorly conserved (Fig. 1). Small-angle X-ray scattering (SAXS) studies suggested that NS5 could adopt different conformations permitted by a flexible linker (13). Interestingly, an N-terminally extended RdRp spanning residues from 265 to 900 improved thermostability and RdRp activity compared with a shorter RdRp spanning residues 273 to 900 (14). More recently, the structures of the full-length NS5 protein from DENV3 (15) and Japanese encephalitis virus (JEV) full-length NS5 (PDB code 4K6M) (16) have been resolved. Extensive comparisons between the two structures have been reported (15). Notably, unlike JEV NS5, the DENV NS5 structure revealed a hydrophilic interdomain interface and a linker region composed of a 3_10-helix (amino acids aa 263 to 266) followed by a short loop (aa 267 to 272) (Fig. 1A and B). In DENV3 full-length NS5, the 3_10-helix linker adopts a compact conformation compared to JEV full-length NS5 or DENV2 MTase (1 to 296) (PDB code 1L9K) (Fig. 1C). Functionally, the MTase domain stimulates both de novo initiation and elongation activities of the RdRp domain, which implies a critical role for an interdomain linker in controlling NS5 RNA polymerization activities (17). Despite the various conformations adopted by NS5 in solution, position 264 (in DENV3 NS5) is found to be exclusively Val in flaviviruses, except for a homologous substitution of Ile (position 265) in DENV2 (Fig. 1B). In the three-dimensional (3D) structure of DENV3 NS5FL, the side chain of Val packs against side chains of R262 and E267, forming a pocket (Fig. 1A). We therefore hypothesized that this strictly conserved Val or Ile residue plays a functional role in regulating the enzymatic coupling between the NS5 MTase and NS5 RdRp domains of NS5 and also plays a role in regulating virus replication.

To characterize the enzymatic function of the linker mutants, the recombinant DENV3 NS5 and its V264G, V264P, VGN (G insertion after V264), and VPN (P insertion after V264) mutants were expressed, purified to >90% homogeneity (Fig. 2A), and assessed for their enzymatic activities as previously described (15). Interestingly, the four mutant NS5 proteins displayed dramatic differences in the coupled de novo initiation/elongation activity, even though their elongation activities were comparable (Fig. 2B and C). The V264G and V264P mutants showed only 25% and 15% de novo polymerase activities, respectively, compared to the wild type (WT). The VGN insertion mutant showed de novo activity similar to that of the WT, while the VPN mutant displayed a higher de novo polymerase activity. Both the WT and the four mutants displayed N7 MTase activities comparable to that of the WT protein (Fig. 2D). The V264G mutant showed a 2-fold-higher
FIG 1  (A) Crystal structure of DENV3 NS5 is displayed as a cartoon (PDB code 4V0R). The MTase domain is colored in yellow, the RdRp domain is in cyan, and linker residues 263 to 266 are in red. The inset shows a closeup view of the linker region. The KDKE catalytic tetrad of MTase is shown as magenta sticks and labeled; the GDD active site is in green, and the priming loop is in blue and labeled. (B) Sequence alignment of the linker regions between the MTase and RdRp domains of NS5 from DENV1 to -4 and various flaviviruses showing the secondary structures observed in DENV3 NS5. WNV, West Nile virus; YFV, yellow fever virus; TBEV, tick-borne encephalitis virus. (C) Superposition of the MTase domain of the flaviviral NS5 structures with structural information for the linker region. The distance between Ca’s of the first and fourth linker residues was measured. DENV3 NS5, PDB code 4V0R; DENV2 MTase, PDB code 1L9K; JEV NS5, PDB code 4K6M.
The activity in the VPN mutant was 70% of that of the WT (Fig. 2E). Together, these data suggest that structural perturbation of the linker α-helix can have differential effects on the enzymatic activities of NS5, presumably through altered conformational plasticity between the two enzymatic domains and their specific interaction with viral RNA.

To examine the functional role of the conserved residue in the context of the virus life cycle, the same mutations as listed above were introduced into a DENV2 infectious cDNA clone (18). The viral RNA synthesis and infectious virus production capabilities of the sequence-confirmed clones and the WT were examined over the course of 5 days posttransfection by reverse transcription quantitative PCR (qPCR) and confirmed by immunofluorescence assay (IFA) staining of double-stranded RNA (dsRNA) and NS5 protein with specific antibodies (Fig. 3). Of the four analogous mutants in DENV2 (the I265G, I265P, IGG, and IPG mutants), only the I265P mutant (replacement of I265 with Pro) failed to show recovery of any viable viruses by plaque assay, similarly to the negative-control K330A mutant (18). Also, the I265P virus displayed significantly lower infectivity (<5%) than that of the WT (50 to 60%) on day 3, as indicated by the IFA staining of dsRNA and NS5. By comparison, the other three mutant viruses resulted in slightly attenuated viruses with slower growth and reduced infectivity (Fig. 3).

Our findings support the hypothesis that cross talk between MTase and RdRp domains of NS5 is essential for virus replication and that the linker region between the two domains has evolved to...
FIG 4 All atom root mean square deviations (RMSD) from molecular dynamics simulations of DENV NS5 structure generated using 4V0R (15) and 4HDG (23) and a schematic model depicting the dynamics of NS5 regulated by the interdomain linker. (A) Molecular dynamics simulations carried out with Gromacs-5.0.5 (www.gromacs.org) show that the V264P mutation exhibits a destabilizing effect on NS5 structure, and large conformational changes are observed in two independent simulations, while the V264G and V264I mutations have a minor effect on the structure and dynamics of NS5 compared to the wild-type protein. V264 is conserved and forms van der Waals interactions with side chains of residues R262 and E267. Molecular dynamics simulations suggest that I265 in DENV2 may adopt a similar interaction. (B) Schematic model showing that NS5 multiple enzymatic functions may require a flexible linker that permits the protein to adopt a greater variety of conformations (and thus yields viable viruses), as opposed to the V264P mutation, which abolishes 310-helix formation for the compact conformation of NS5 (suggested by molecular dynamics simulations), resulting in loss of some of the functions and abolished replication.
reach an optimal flexibility through the “greasy finger” made by residue V264/I265, which plays an important role in allowing the two domains to adopt functional orientations (17).

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REFERENCES


