Optimized P2A for reporter gene insertion into Nipah virus results in efficient ribosomal skipping and wild-type lethality

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Incorporation of reporter genes within virus genomes is an indispensable tool for interrogation of virus biology and pathogenesis. In previous work, we incorporated a fluorophore into a viral ORF by attaching it to the viral gene via a P2A ribosomal skipping sequence. This recombinant Nipah virus, however, was attenuated in vitro relative to WT virus. In this work, we determined that inefficient ribosomal skipping was a major contributing factor to this attenuation. Inserting a GSG linker before the P2A sequence resulted in essentially complete skipping, significantly improved growth in vitro, and WT lethality in vivo. To the best of our knowledge, this represents the first time a recombinant virus of Mononegavirales with integration of a reporter into a viral ORF has been compared with the WT virus in vivo. Incorporating the GSG linker for improved skipping efficiency whenever functionally important is a critical consideration for recombinant virus design.

The insertion of reporter genes into recombinant viruses is an important tool not only for the study of virus biology and pathogenesis, but also for the development of faster screening assays for the evaluation of antivirals. For the henipaviruses Nipah virus (NiV) and Hendra virus (HeV) (genus Henipavirus), emerging and zoonotic paramyxoviruses (family Paramyxoviridae, order Mononegavirales) with negative-sense, ssRNA genomes, reporter genes have been inserted either as independent ORFs or as part of existing viral ORFs (Lo et al., 2012; Marsh et al., 2013; Yoneda et al., 2006; Yun et al., 2015). In the former strategy, conserved gene start and stop signals present within virus intergenic sequences are used to drive reporter mRNA expression; however, insertion of additional intergenic sequences can disturb the polar transcriptional gradient of the virus (Conzelmann, 1998; Falzarano et al., 2014). As an alternative, we have used a ribosomal skipping sequence to incorporate the reporter gene into an existing viral ORF, thus avoiding the use of additional intergenic sequences (Yun et al., 2015). While this strategy indeed did not affect the natural transcriptional gradient of NiV, the recombinant reporter virus was significantly attenuated for in vitro growth as compared with the parental NiV (Yun et al., 2015).

There are several commonly used ‘2A’ ribosomal skipping sequences, derived from porcine teschovirus-1 (P2A), foot-and-mouth disease virus (F2A), Thosea asigna virus (T2A) and equine rhinitis A virus (E2A). All translate to short 18–22 aa peptides that mediate ribosomal skipping between a C-terminal glycine and proline, thus resulting in separate polypeptides (Donnelly et al., 2001). For our recombinant NiV (based on the Malaysia prototype strain), we previously appended the mCherry fluorophore to the N-terminal end of the NiV matrix gene via a P2A sequence (Fig. 1 and Yun et al., 2015), which appears to be the most efficient of the skipping sequences in widely used human cell lines (Kim et al., 2011). Even so, any inefficiency in skipping would result in a fusion product, which
might inhibit the function of the fused viral protein. A large
N-terminal fusion is known to impede the budding function
of NiV matrix (Wang et al., 2010). Therefore, we considered
whether any inefficiency of P2A skipping in our recombi-
nant NiV was a factor in its attenuation relative to WT NiV.

We infected human umbilical vein endothelial cells
(HUVECs) with our recombinant NiV incorporating
mCherry at the N terminus of the matrix (M) gene via a
P2A sequence (henceforth labelled rNiV-mChM). Western
blotting for NiV-M revealed that P2A ribosomal skipping
was indeed inefficient, with about a third of the matrix pre-
sent as a mCherry fusion protein (Fig. 2a, see lane 2 at vari-
ous time points). As the efficiency of 2A skipping is known
to be dependent on the amino acid context (Minskaia &
Ryan, 2013), it appears that the amino acid sequence adja-
cent to the P2A peptide in our recombinant NiV is not
conducive to efficient skipping. It is known that addition
of a GSG linker immediately upstream of the skipping
sequence improves skipping efficiency (Holst et al., 2006;
Szymczak et al., 2004), presumably by allowing the 2A pep-
tide to favour the conformation that induces ribosomal
skipping. We therefore added this linker to our reverse
 genetics construct (Fig. 1a), rescued the modified virus
(rNiV-mChM-opt) as previously described (Yun et al.,
2015), and compared skipping efficiencies. Addition of the
GSG linker resulted in essentially complete ribosomal skip-
ning (Fig. 2a, compare lanes 2 and 3 at various time points).

We previously determined that rNiV-mChM had slower
replication kinetics relative to WT NiV in permissive cell
lines such as Vero (Yun et al., 2015) and HeLa (unpub-
lished data) as well as primary human cells such as
human neural stem cell derived neurons/astrocytes and
HUVECs (Yun et al., 2015). The defect appeared most pro-
nounced in HUVECs. We therefore infected HUVECs with
WT NiV, rNiV-mChM and rNiV-mChM-opt and found
that rNiV-mChM-opt infection resulted in significantly
higher released virus titres relative to rNiV-mChM at 12 h
post-infection (p.i.) (Fig. 2b). rNiV-mChM-opt titres
remained similar to those of WT NiV until 24 h p.i., peak-
ing at about 0.5 log lower titres (Fig. 2b).

We then determined whether the improved growth kinetics
of rNiV-mChM-opt relative to rNiV-mChM would translate
to in vivo lethality more similar to WT NiV. Using a widely
used small animal model for NiV pathogenesis, we inocu-
lated Syrian golden hamsters (10 3- to 8-week-old females

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**Fig. 1.** Schematic of recombinant NiV genome with the mCherry reporter expressed in the same transcriptional unit as the
matrix (M) gene (rNiV-mChM). (a) mCherry expression is driven by the gene start (GStart) and gene stop (GStop) signals that
flank the M ORF. mCherry and M are expressed as individual proteins via the P2A ribosomal skipping sequence (blue letters).
Arrowhead (blue) indicates the ‘cleavage’ site between the glycine (G) and proline (P) residues. The M protein thus retains
an additional N-terminal proline residue. For rNiV-mChM-opt, a GSG linker was inserted preceding the P2A sequence, with
an additional glycine to preserve the rule of six for paramyxovirus genomes. (b) Human umbilical vein endothelial cells
(HUVECs) were infected with rNiV-mChM and imaged by confocal microscopy. Left panel, mCherry can be seen in multi-
nucleated syncytia caused by NiV-induced cell–cell fusion. Right panel, same field stained with phalloidin to detect F-actin
for cell demarcation.

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optimized P2A for reporter gene insertion into NiV per condition, intraperitoneal route) with 10^3 or 10^4 p.f.u. of WT NiV, rNiV-mChM or rNiV-mChM-opt. As suggested by its attenuated growth in vitro, rNiV-mChM was significantly attenuated in vivo relative to WT NiV at the higher dose (P=0.037, log-rank Mantel–Cox test) (Fig. 3a, right panel). At the lower dose, there was a clear difference in survival (although just beyond statistical significance, P=0.067 for rNiV-mChM vs WT NiV), with only 4/10 animals infected with rNiV-mChM succumbing by 25 days p.i. vs 7/10 for rNiV-mChM-opt and 8/10 for WT NiV (Fig. 3a, left panel). In contrast, rNiV-mChM-opt had no significant difference from WT NiV at either dose (P>0.05). Ex vivo mCherry imaging of tissues from hamsters inoculated with 10^3 p.f.u. rNiV-mChM-opt confirmed virus replication and spread, with predominant replication in the lungs but also in the kidneys, spleen and liver, and the beginnings of detectable brain infection at the olfactory bulb by day 7 p.i. (Fig. 3b). Immunohistochemistry with anti-NiV-M on lung and brain tissues from WT NiV- vs rNiV-mChM-opt-inoculated hamsters showed similar detection of viral antigen in blood vessel endothelial cells, a hallmark of henipavirus pathogenesis (Fig. 3c).

In conclusion, we found that incorporation of a GSG linker preceding the P2A sequence resulted in essentially complete ribosomal skipping (Fig. 2a), which in turn significantly improved the replication kinetics as compared with the original rNiV-mChM (Fig. 2b). As might be expected from this improvement, the optimized virus also had in vivo lethality more similar to WT, with no statistical difference between the two viruses at two different doses of infection (Fig. 3). Although the use of a GSG linker immediately preceding the 2A sequence to promote efficient skipping has been known for some time (Holst et al., 2006; Szymczak et al., 2004), many research groups in virology are not yet aware of this simple improvement. We hope this work draws further attention to the GSG linker and the importance of verifying efficient skipping whenever 2A sequences are used.

Consistent with our findings, another group has shown that a recombinant NiV with similar insertion of GFP upstream of the matrix gene via a P2A sequence had similar replication kinetics to WT NiV in Vero cells (Lo et al., 2014). To maintain the rule of six (by which paramyxovirus genome lengths are exact multiples of six), Lo et al. (2014) had inserted a single glycine residue between GFP and the P2A, which may have had the advantage of serving as a linker to provide more efficient ribosomal skipping.

In previous work, we showed that insertion of a reporter gene in between the nucleoprotein (N) and phosphoprotein (P) genes as a separate ORF did not affect either the polar transcriptional gradient or the in vitro growth of the virus (Yun et al., 2015). It appears that for NiV, the first two intergenic regions (N to P, and P to M) do not result in attenuation of transcript levels, while the intergenic regions following the matrix gene result in progressive
several-fold reductions in relative mRNA levels (Yun et al., 2015). Insertion of a foreign ORF between two paramyxovirus genes is typically accomplished by duplication of the respective intergenic region. Therefore, one might expect that for NiV, insertion of a foreign ORF between N and P, or between P and M, would not result in disturbance of the transcriptional gradient due to the non-attenuating nature of these intergenic regions, consistent with our previous results (Yun et al., 2015). However, intergenic regions may have regulatory functions beyond mRNA transcriptional regulation, and it may thus be preferable to simply insert the foreign ORF within an existing viral ORF. Further, as the complexity of our modifications to paramyxovirus genomes increases, even encompassing combinations of

**Fig. 3.** Improved ribosomal skipping results in lethality more similar to WT NiV in vivo. (a) WT NiV and recombinant mCherry reporter viruses without (rNiV-mCh\textsuperscript{M}) or with (rNiV-mCh\textsuperscript{M}-opt) the GSG linker for optimal P2A skipping were used to inoculate groups of Syrian hamsters (n=10 per group for each virus and dose combination, intraperitoneal route) at 10\textsuperscript{3} p.f.u. or 10\textsuperscript{4} p.f.u. per animal. Kaplan–Meier survival curves show no significant differences between WT NiV (○) and rNiV-mCh\textsuperscript{M}-opt (▲), whereas rNiV-mCh\textsuperscript{M} (▼) exhibited significant attenuation relative to WT NiV that was most apparent at the higher inoculum used (P=0.037, log-rank Mantel–Cox test). (b) Two hamsters were inoculated with rNiV-mCh\textsuperscript{M}-opt (10\textsuperscript{4} p.f.u., intraperitoneal route), and tissues were imaged ex vivo for mCherry fluorescence at 6 and 7 days p.i. using an IVIS Spectrum imaging platform. Data are displayed as radiant efficiency on a colour scale from 2×10\textsuperscript{7} (dark red) to 4.35×10\textsuperscript{7} (yellow). Gb, Gallbladder. White arrow indicates fluorescence in olfactory bulb. (c) Immunohistochemistry with anti-NiV-M was performed on lung and brain tissues from similarly infected hamsters. Arrows indicate examples of positive antigen staining. PA, Pulmonary artery; BR, bronchiole.
reporters and exogenous factors within a single genome, making use of both insertion strategies may become increasingly valuable.

As an alternative to using a 2A ribosomal skipping sequence, an internal ribosome entry site (IRES)-like sequence that allows mRNA cap-independent initiation of translation and thus bicistronic expression has been used for Sendai virus (genus Respirovirus within the Paramyxoviridae) to incorporate a luciferase reporter within the N gene ORF (Touzelet et al., 2009). This recombinant virus was not attenuated in vivo, although how it compares with the WT virus in vivo has not been evaluated. Further, the strategies differ in that expression of the IRES-dependent gene relative to the cap-dependent gene is highly variable, usually significantly lower than the cap-dependent gene (Mizuguchi et al., 2000), whereas 2A skipping is co-translational and therefore results in similar expression of linked genes. Thus, for high reporter expression, or reporter expression more indicative of virus protein expression, it may be more advantageous to use a 2A-based strategy. As a final consideration, if expression of the reporter is in any way disadvantageous for virus fitness, mutation and loss of reporter expression would be more likely with an IRES-based strategy or insertion of the reporter as an independent ORF, whereas in the P2A insertion strategy, the expression of the downstream virus protein is dependent on continued translation of the upstream reporter. In our case, optimizing the efficient ribosomal skipping of our P2A-based reporter insertion strategy resulted in a recombinant Nipah virus that reflected WT lethality in the currently most widely used small animal model.

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