Regulation of influenza a virus mRNA splicing by CLK1

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ABSTRACT

Influenza A virus carries eight negative single-stranded RNAs and uses spliced mRNAs to increase the number of proteins produced from them. Several genome-wide screens for essential host factors for influenza A virus replication revealed a necessity for splicing and splicing-related factors, including Cdc-like kinase 1 (CLK1). This CLK family kinase plays a role in alternative splicing regulation through phosphorylation of serine-arginine rich (SR) proteins. To examine the influence that modulation of splicing regulation has on influenza infection, we analyzed the effect of CLK1 knockdown and inhibition. CLK1 knockdown in A549 cells reduced influenza A/WSN/33 virus replication and increased the level of splicing of segment 7, which encodes the viral M1 and M2 proteins. CLK1 \textsuperscript{−/−} mice infected with influenza A/England/195/2009 (H1N1pdm09) virus supported lower levels of virus replication than wild-type mice. Screening of newly developed CLK inhibitors revealed several compounds that have an effect on the level of splicing of influenza A gene segment M in different models and decrease influenza A/WSN/33 virus replication in A549 cells. The promising inhibitor KH-CB19, an indole-based enaminoanitrile with unique binding mode for CLK1, and its even more selective analogue NIH39 showed high specificity towards CLK1 and had a similar effect on influenza mRNA splicing regulation. Taken together, our findings indicate that targeting host factors that regulate splicing of influenza mRNAs may represent a novel therapeutic approach.

1. Introduction

The process of alternative splicing diversifies gene expression, with 75\% of human genes having at least two alternatively spliced isoforms. Splicing is highly regulated via recognition of sites by different proteins and synergistic effects of multiple weak binary-interactions (Schellenberg et al., 2008; Wahl et al., 2009). Several viruses also employ alternative splicing to code for diverse proteins from their small genomes (Fukuhara et al., 2006; Hryckiewicz et al., 2011; Johansson and Schwartz, 2013; Ortì́n, 1998). Influenza A virus (IAV) makes use of this process to generate several of its proteins (Lamb and Lai, 1980; Lamb et al., 1981; Wise et al., 2012). It belongs to the family of Orthomyxoviridae and carries a genome consisting of eight negative single-stranded viral RNAs (vRNAs). According to current knowledge, the HA,
Human lung epithelial cells (A549, CCL-185, ATCC-LGC) were cultured in Dulbecco's modified Eagle's medium (DMEM, Gibco) supplemented with 10% fetal calf serum (FCS, Biochrome), 4 mM L-glutamine and 4 mM sodium pyruvate at 37 °C and 5% CO₂. Madin–Darby canine kidney cells (MDCK, CCL-34, ATCC-LGC) were grown in DMEM supplemented with 10% fetal calf serum, 4 mM L-glutamine and 100 UI/ml penicillin/streptomycin at 37 °C and 5% CO₂. Influenza virus A/WSN/33 and A/England/195/2009 virus was propagated in allantoic fluid of eleven-day-old embryonated chicken eggs as previously described (Szretter et al., 2006). The recombinant wild-type virus A/Victoria/3/75 (H3N2) was generated by reverse genetics, as described previously (Ellemann and Barclay, 2004; Neumann et al., 1999; Roberts et al., 2011). The titer of virus stocks was determined by plaque assay on MDCK cells using agar overlay medium (Szretter et al., 2006).

2.2. Chemical inhibitor treatment in eukaryotic cells

Chemical inhibitor was diluted to the specified concentration in culture medium, added to A549 cells and incubated at 37 °C with 5% CO₂ for 2 h. DMSO diluted in culture medium at the same volume as the inhibitor served as control. After 2 h, cells were infected with influenza virus A/WSN/33 diluted in infection buffer at the specified MOI and incubated at room temperature for 1 h. Virus was then removed, replaced with infection medium containing the chemical inhibitor or DMSO at the specified concentration and incubated at 37 °C with 5% CO₂. TG003 was purchased from Sigma.

2.3. CRISPR/Cas9-mediated CLK1 knockout cells

A549 cells lacking a functional CLK1 gene were generated as described (Karlas et al., 2016). Briefly, Cas9-expressing A549 cells were generated by transducing with lentiviruses based on the plasmid lentiCas9-Blast (Addgene number 52962), followed by selection with blasticidin. Cells were then transfected with lentivirus derived from the plasmid lentiguide-Puro44 (Addgene number 52963), which leads to the expression of CLK1-specific gRNAs.

2.4. SC35 subnuclear distribution detection upon CLK overexpression and inhibitor treatment

A549 cells were transfected with plasmid expressing GFP-tagged mCLK1, mCLK2, mCLK3 and mCLK4 using Lipofectamine LTX (Invitrogen) according to manufacturer’s instruction. The plasmids expressing GFP-tagged mCLKs were a kind gift from Alan Cochrane (University of Toronto, Canada). At 16 h post-transfection, cells were treated with 50 μM TG003, 12.5 μM NIH39 or 50 μM hCB19 for 6 h, washed once with PBS and fixed with 4% paraformaldehyde. Cells were permeabilized with 1% Triton X-100, followed by blocking in 1xPBS containing 1% BSA/0.5% gelatine. Subnuclear distribution of SC35 was detected by labelling with mouse anti-SC35 antibody (BD Science) followed by Cy3-labelled anti-mouse IgG (Jackson Immuno Research Lab) and Hoechst, as described above. Images were captured using a Leica DMR microscope.

2.5. Luciferase splicing assay

To quantify influenza segment M splicing, a cell-based influenza-driven splicing assay that monitors expression of the three mRNAs produced from the M gene (M1, M2 and M3) was used (Moncorgé O. and Barclay W., in preparation). Briefly, plasmids that generate in situ viral-like RNAs that can be amplified and expressed by influenza virus polymerase are transfected in 293T cells 24 h prior to viral infection.
The viral-like RNAs are based on segment M sequence (A/England/195/2009, H1N1pdm09) and retain all the documented control regions potentially involved in splicing (Lamb and Lai, 1982; Moss et al., 2011, 2012; Shih and Krug, 1996). Instead of encoding the authentic virus products, the reporter RNAs encode luciferase proteins in frame with the M1 (unspliced), M2 (spliced) or M3 (spliced) mRNA open reading frames. This allows quantification of expression of proteins that arise from the various alternative splicing routes by a dual luciferase assay on lysates of infected cells. 24 h post-infection (MOI 1), cells are lysed using 5x passive lysis buffer (Promega) and luciferase activity is measured.

2.6. LabChip kinase screening

Enzymatic kinase screening was carried out using the Caliper mobility shift assay, which is based on the difference in capillary electrophoresis mobility of a fluorescently tagged peptide as a result of the addition of a phosphate moiety by the studied kinase. The consensus peptide for CLK1 (AFREWSPGKEAKK) was solubilized at 10mM in addition of a phosphatemoiety by the studied kinase. The consensus peptide and ATP at concentrations set to the KM for CLK1 at 19.2μM. After incubation for 120 min at 20 °C 50 μl stop solution was added (100mM HEPES [pH 7.5], 5% DMSO, 0.1% coating reagent [Caliper Lifescience] 10 mM EDTA [pH 8.0], 0.015% BRIJ35) and reactions analyzed in a LC3000 reader (Caliper Life Sciences) using the following settings: DS -600, US -2300, base pressure – 0.5, screen pressure – 1.8, plate cycles 1, end of plate delay 60, final delay 30, sample time 0.2, post sample buffer time 35, dye time 0.2, post-dye buffer time 40. Validation of dosage-dependent inhibitory activity was carried out by IC₅₀ determinations in serial 1:1 dilutions from 50μM to 50 nM in ten steps and in duplicate. For automated data analysis, the LabChip files are converted to a standardized output format (in-house developed software) and fed into statistical analysis by the open source software R and KNIME to generate exact curve fittings and IC₅₀ calculations.

2.7. Animal experiments

Animals were housed and bred under pathogen-free conditions, in a BSL 2 laboratory according to the German Animal Protection Law (Tierschutzgesetz TierSchG). Animal testing was approved by the local authorities (Landesamt für Gesundheit und Soziales Berlin) under license G0206/12. C57BL/6/J and CLK1−/− mice were obtained from Charles River and the European Conditional Mouse Mutagenesis Program (EUCCOMM) Consortium, respectively, and further bred in-house. C57BL/6 mice aged 11–16 weeks and weighing 20.9–25.6 g and CLK1−/− mice aged 7 weeks and weighing 20.4–24.0 g were intranasally infected with 9 × 10⁶ PFU of influenza A/England/195/2009 virus in 30 μl infection buffer. Two days later, lungs of infected animals were isolated and homogenized in PBS, followed by centrifugation at 800 × g for 8 min at 4 °C. The amount of infectious virus was then quantified using plaque assay.

3. Results

3.1. CLK1 knockdown reduces influenza A virus replication and regulates the splicing of viral mRNA

CLK1 was identified as an essential host factor for influenza A virus infection in two previous screens (Karlas et al., 2010; König et al., 2010). To verify the result, we performed knockdown experiments in A549 cells to silence kinases that regulate splicing, including the CLK and SRPK family kinases and the dual specificity tyrosine phosphor-ylation-regulated kinase 1 (DYRK1A), followed by infection with influenza A/WSN/33 at MOI 0.01 for 36 h. The titer of infectious viral particles in the supernatant was measured using indirect immunofluorescence staining (shown are mean values of three independent experiments ± SEM). *p-value < 0.05, **p-value < 0.01, ***p-value < 0.001, one-way ANOVA. (B) Cells isolated from the lungs of either C57BL/6 wild-type or CLK1−/− mice were infected with influenza A/WSN/33 at MOI 0.01 for 72 h. Production of infectious viral progeny was measured using indirect immunofluorescence staining. *p-value < 0.05, two-tailed unpaired t-test. (C) C57BL/6 wild-type or CLK1−/− mice (n = 6) were intranasally infected with 9 × 10⁶ PFU of influenza A/England/195/2009 (H1N1pdm09). At 48 h after infection, infectious viral particles within the lungs were quantified using plaque assay. *p-value < 0.05, two-tailed unpaired t-test. (D) Validation of CLK1 as relevant cellular factor. Amount of virus produced in A549 cells depleted for CLK1 by CRISPR/Cas9 and infected with A/WSN/33 at MOI 0.001 for 24 h. Virus titer was quantified by plaque assay (shown are mean values of three independent experiments ± SEM).

Fig. 1. CLK1 is an essential host factor for influenza A virus replication. (A) Replication assay was carried out by infection of A549 cells 48 h post siRNA transfection with influenza A/WSN/33 at MOI of 0.01 for 36 h. The titer of infectious viral particles in the supernatant was measured using indirect immunofluorescence staining (shown are mean values of three independent experiments ± SEM). *p-value < 0.05, **p-value < 0.01, ***p-value < 0.001, one-way ANOVA. (B) Cells isolated from the lungs of either C57BL/6 wild-type or CLK1−/− mice were infected with influenza A/WSN/33 at MOI 0.01 for 72 h. Production of infectious viral progeny was measured using indirect immunofluorescence staining. *p-value < 0.05, two-tailed unpaired t-test. (C) C57BL/6 wild-type or CLK1−/− mice (n = 6) were intranasally infected with 9 × 10⁶ PFU of influenza A/England/195/2009 (H1N1pdm09). At 48 h after infection, infectious viral particles within the lungs were quantified using plaque assay. *p-value < 0.05, two-tailed unpaired t-test. (D) Validation of CLK1 as relevant cellular factor. Amount of virus produced in A549 cells depleted for CLK1 by CRISPR/Cas9 and infected with A/WSN/33 at MOI 0.001 for 24 h. Virus titer was quantified by plaque assay (shown are mean values of three independent experiments ± SEM).
not feasible.

To further verify the importance of CLK1 in influenza A virus replication, we isolated cells from the lungs of CLK1−/− and C57BL/6 mice. Equal numbers of isolated cells were infected with influenza A/WSN/33 at MOI 0.01 for 72 h. Viral replication was significantly reduced when compared to control cells isolated from wild-type C57BL/6 mice (Fig. 1B), despite the fact that even in the CLK1−/− cells a slight expression of CLK1 was detectable (Fig. S1C). To confirm this effect in vivo, intranasal infection of C57BL/6 and CLK1−/− mice was performed with influenza A/England/195/2009 for two days. Determination of virus titer in the lungs harvested at 2 days post-infection showed that the number of infectious viral particles obtained from CLK1−/− mice was significantly reduced (Fig. 1C). Similarly, A549 cells lacking CLK1 expression after CRISPR/cas9-mediated knockout replicated influenza viruses less efficiently than controls (Fig. 1D).

As CLK1 is known to regulate mRNA splicing, we next investigated whether knockdown has any effect on splicing of influenza mRNAs. qRT-PCR quantification of spliced and unspliced viral mRNAs upon infection with A/WSN/33 at MOI 4 for 5 h showed an increased ratio of spliced to unspliced M mRNA in CLK1 knockdown A549 cells, but no significant effect on NS mRNA splicing was observed compared to the negative control Allstars (Fig. 2A). Western blot analysis also showed that expression of the unspliced viral M1 and NS1 proteins was reduced upon CLK1 knockdown, but little or no effect on the level of the spliced M2 protein was observed (Fig. 2B).

3.2. Screening of CLK inhibitors identifies new compounds that inhibit influenza virus replication

We previously observed that cells treated with the CLK inhibitor TG003 showed reduced influenza A/WSN/33 virus replication (Karlas et al., 2010). This prompted us to screen 60 new compounds (structurally related to KH-CB19, previously published as a CLK1 inhibitor (Fedorov et al., 2011)) targeting CLK family kinases in an IAV replication assay. Several of these compounds inhibited influenza replication to a greater extent than the commercially available TG003 (Fig. 3A), without significantly affecting cell viability at 48 h post-treatment (Fig. 3B). Two of these were selected for further experiments - NIH39 and KH-CB19, which had IC50 values of 6.6 μM and 13.6 μM for antiviral activity, respectively (Fig. 3B and C). Treatment of A549 cells with NIH39 at 6.25 μM or 12.5 μM upon infection with A/WSN/33 at MOI 4 for 5 h resulted in an increase of the spliced to unspliced viral M mRNA ratio (Fig. 4A, Fig. S3A). Unexpectedly, however, qRT-PCR analysis showed that the viral NS mRNA splicing ratio was significantly reduced when cells were treated with 12.5 μM NIH39 (Fig. 4A, Fig. S3B). Viral M1, M2 and NS1 protein levels were all found to be markedly reduced when analyzed by Western blot (Fig. 4B, Fig. S3F).

In contrast to the effects observed with NIH39 treatment, A549 cells treated with KH-CB19 at 50 μM or 100 μM did not show any effect on the spliced to unspliced ratio of viral M and NS mRNAs (Fig. 4C, Figs. S3C–D), although the levels of all three viral proteins were also reduced (Fig. 4D, Fig. S3F).

It has been previously reported that overexpression of CLK family kinases alters the subnuclear distribution of the SR protein by altering its phosphorylation state (Wong et al., 2011, 2013). The observed differential effects of the various CLK inhibitors on influenza mRNA splicing raised the question whether they affected the four CLK isoforms differently. Therefore, we next tested the specificity of the inhibitors by analysing the nuclear speckle pattern of SC35 (SRSF2) labelling upon mClk overexpression (Wong et al., 2011). In accordance with the previous reports, CLK overexpression altered the subnuclear distribution of SC35 from a speckled to a diffuse pattern (Fig. 5A). Treatment of cells with TG003 inhibited nuclear speckle disruption by CLK1, 2 and 4 (Fig. 5B). This confirms reports that TG003 inhibits CLK1, CLK4 and to a lesser extent CLK2 (Muraki et al., 2004; Wong et al., 2011). NIH39 treatment blocked the disruption of nuclear speckles by CLK1 and 4 (Fig. 5C, Fig. S6), while KH-CB19 only inhibited the disruption by CLK4 (Fig. 5D, Fig. S6).

3.3. Identification of the essential SR protein in influenza A virus replication and its effect on viral mRNA splicing

To identify the downstream targets of CLK1 in influenza infection, knockdown of SR proteins was performed in A549 cells, followed by influenza virus replication assay and cell viability analysis. Knockdown of SRSF3 with each of two siRNAs significantly impaired influenza virus replication, while the other SRSFs had a less pronounced effect or showed strong reduction only with one siRNA (Fig. 6A). Host cell viability at 48 h after siRNA transfection was not significantly impaired upon knockdown of any of SRSF proteins (Fig. S4A) and all siRNAs achieved efficient knockdown (Fig. S4B).

Next, we further analyzed viral mRNA splicing upon SRSF3 knockdown (Fig. S4C). Quantification of spliced and unspliced viral mRNAs was performed in A549 cells after knockdown, followed by infection with influenza A/WSN/33 at MOI 4 for 5 h. The result shows that in the absence of SRSF3 there is an increase in the viral M and NS mRNA splicing ratios (Fig. 6B, Figs. S4D–E). Remarkably, in-depth analysis of viral M and NS mRNA sequences using ESEFinder and SFmap showed different binding sites for several SR proteins between the M and NS mRNA including binding sites for SRSF3 (Fig. S7). On the protein level, SRSF3 knockdown slightly reduced the levels of viral M1 and NS1 proteins, as we observed with CLK1, and slightly increased the level of the spliced M2 protein (Fig. 6C, Fig. S4F). Based on these results, SRSF3 seems to be the main actor influencing the levels of spliced viral RNAs upon removal or inhibition of CLK1.

3.4. Improved CLK1 inhibitors

The CLK1 inhibitors that performed best in our assays, NIH39 and KH-CB19, had antiviral IC50 values of 6.6 μM and 13.6 μM, respectively. In the search for a therapeutic intervention based on splicing inhibition, we decided to further improve the compound efficacy. We started a rational drug development program supported by (i) virtual screening of inhibitor libraries, (ii) enzymatic screening using luciferase- and LabChip-based assay systems and (iii) screening of selected inhibitors regarding antiviral efficacy and cell viability.

We designed a library of 580 compounds by docking based on the molecular structure of the hits and by docking of putative inhibitors into the active site of the published CLK1 crystal structure (PDB-code...
Fig. 3. Screening of CLK inhibitors affecting influenza virus replication (A) A549 cells were treated with eight serial dilutions of the inhibitor dissolved in DMSO. Two h later, cells were infected with A/WSN/33 at MOI of 0.0095 for 40 h. Infectious viral particles produced in the presence of the inhibitor were quantified using indirect immunofluorescence staining and calculated as normalized percentage of infection from three independent experiments. (B,C) IC₅₀ curve of NIH39 (B) and KH-CB19 (C) activity on influenza virus replication, as well as the effect of inhibitor treatment on A549 cell viability (red lines). Data represent mean ± SEM of at least three independent experiments. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)
2VAG) (Fedorov et al., 2011). For docking simulations, the Schrödinger Suite (https://www.schrodinger.com) was used. The compounds were tested against CLK1 in a luciferase-based assay using recombinant CLK1 expressed in E. coli, and 56 compounds were found to be effective (Supplementary Table 3). These results were further validated using a capillary electrophoresis LabChip-based enzyme activity/phosphorylation assay capable of determining the IC50 concentration of each substance (Supplementary Table 3). Selected compounds with IC50 values < 1 μM were then analyzed by virus replication assay in A549 cells to determine antiviral efficacy. We identified two compounds, VCC080174 and VCC463764, which efficiently inhibited influenza virus replication at very low concentrations (< 1 μM) and revealed a promising therapeutic index (Fig. 7A and B).

VCC463764 and VCC080174 were then characterized by crystallography to enable further optimization of the chemical structure for maximum effectiveness against CLK1. Solving the crystal structures of CLK1 in complex with VCC080174 to the resolutions of 2.03 Å confirms that the inhibitor is localized within the ATP binding pocket, giving it high efficiency against CLK1 (Fig. 7C). VCC463764 was also found to bind CLK1 at the same binding pocket (data not shown). VCC080174 interacts with CLK1 at the active site by means of several hydrogen bonds (Fig. 7D). The amino group connecting both six-membered rings...
of the inhibitor forms a hydrogen bond with the backbone oxygen atom of Leu 244, whereas the nitrogen acceptor atom in the pyrimidine ring is in close contact to the backbone nitrogen. Further, the thiazole amino group is involved in a hydrogen bond to the Asp 325 carboxyl group. This finding differs from other CLK1 complex structures such as the one with KH-CB19 (PDB code 2vag) showing a different side chain conformation of Asp325 that enables a hydrogen bond between the carboxylic group of Asp325 and Gly327 nitrogen. Similarly, in the isoforms CLK2, CLK3 and CLK4, hydrogen bonds between the corresponding Asp and Gly exist (PDB codes 6fyi, 6fyp, 6fyv). A superposition of the isoform structures suggests that VCC080174 may show a similar hydrogen bond pattern in complexes with other members of the CLK family. In CLK1, Leu 246 is located close to the VCC080174 benzene ring, while in CLK3 this residue corresponds to Lys 241 (PDB code 6fyi). There is no change in CLK2 and CLK4. Further, Val 324 corresponds to Ala 319 in CLK3 whereas there is no substitution in CLK2 and CLK4. Thus, hydrophobic interactions with the thiazole group might be different in CLK3 (Kallen et al., 2018). The similarity of the CLK binding pockets and the identity of key residues, however, suggest that it is difficult to obtain selective inhibitors binding to this site, in particular for CLK1, CLK2 and CLK4.

Substitutions and extensions of the inhibitor structure may enable the targeting of residues that vary between different CLK isoforms. For example, the side chain of Ser 247 is located close to the inhibitor VCC080174 in the CLK1 complex structure. This residue corresponds to Asn 242 in CLK3. Further, Asp 250, corresponding to Glu 245 of CLK3, is located at a suitable distance from the inhibitor. Differential targeting of such isoform-specific key residues may be utilized to optimize inhibitor selectivity during lead optimization.

We then used a cell-based IAV-driven splicing assay that monitors splicing from a viral-like mRNA derived from the M segment to analyze the ratio of viral M1 to M2 mRNA after treatment of HEK293 cells with the two CLK1 inhibitors, using the H3N2 (A/Victoria/3/75) seasonal influenza virus strain. VCC080174 increased the ratio of spliced to unspliced viral M mRNA (Fig. 7E), similar to the effect observed after inhibition of CLK1 by siRNAs (see Fig. 2A). VCC463764, however, reduced the ratio of spliced to unspliced viral mRNA (Fig. 7D), as was observed with the other chemical inhibitors (see Fig. 4A, C). Despite this, VCC463764 nevertheless impaired virus replication, which suggests that changes in the splicing ratio per se are detrimental to the virus.

4. Discussion

Splicing factors are one of the enriched essential host factors for influenza virus replication identified in several genome-wide screens (Karlaset al., 2010; König et al., 2010; Watanabe et al., 2010). In the screens performed in our lab (Karlaset al., 2016) and by König et al. (2010) CLK1 (Colwill et al., 1996; Prasad et al., 1999), but no other kinases known to regulate splicing, was identified as an essential host factor. Here, we confirm that CLK1 is required for successful IAV replication in vitro and in vivo, while the other CLK isoforms are not.

We previously found that the CLK inhibitor TG003 inhibits the replication of IAV (Karlaset al., 2010). Based on this initial result, newly developed CLK inhibitors were screened for their effectiveness against IAV replication. Two of the most effective ones, NIH39 and KH-CB19, were further assessed for their effect on influenza mRNA splicing. Only NIH39 enhanced splicing, while KH-CB19 appeared to inhibit splicing. In addition, viral M and NS mRNAs were affected differently. Regulation of alternative splicing is influenced by CLK-mediated phosphorylation of SR proteins. To date, it remains unknown which of the 9 SR proteins are phosphorylated by which of the 4 CLK proteins. Thus, CLK1 might affect the splicing of M and NS mRNA via different phosphorylation status of several SR proteins. We made the same observation when testing two further compounds with enhanced effectiveness against CLK1. Previous reports have shown differential effects of CLK inhibitors towards different CLK isoforms (Muraki et al., 2004; Wong et al., 2011), although the differential role of each isoform remains
unclear. Using the subnuclear distribution of SRSF2/SC35 as a read-out, TG003, which effectively inhibits IAV replication, was shown to reverse the effect of CLK1, 2 and 4 overexpression on SC35 subnuclear distribution (Wong et al., 2011, 2013). Here we observed that KH-CB19 was only able to reverse the effect of CLK4 overexpression, while NIH39 showed specificity towards CLK1 and 4. This may explain why NIH39 increases the ratio of spliced to unspliced influenza mRNA in a similar manner to CLK1 knockdown, while KH-CB19 does not. It has been reported before that thermal shift assay experiments with KH-CB19 using different kinases showed the highest temperature shift for CLK4, followed by CLK1 (Fedorov et al., 2011). Meanwhile, the same experiment performed for NIH39 showed the highest temperature shift for CLK1, followed by CLK2 and CLK4 (personal communication). The differences of inhibitor specificity, determined either by using CLK proteins in the thermal shift assay or by using cell based assays as shown in Fig. 5, might be the reason for the different effects on influenza mRNA splicing. These data also suggest that a specific inhibition of CLK1 is required to alter influenza M mRNA splicing. At the same time, CLK inhibitors with a lower affinity to CLK1, but specific for the other CLK isoforms, strongly reduced viral protein expression from both spliced and unspliced mRNA, thus indicating an additional effect on viral mRNA export or translation, most likely via downstream effects on SR proteins, which also play a role in mRNA export. Several SR proteins, e.g. SRSF1, SRSF7 and SRSF3, can also shuttle between nucleus and cytoplasm and interact with the export factor NXF1 (Caceres et al., 1998; Huang et al., 2004). Remarkably, the biological functions of SR are mainly regulated by distinct phosphorylation states (Botti et al., 2017). Thereby, hyperphosphorylation of SR proteins by CLKs leads to recruitment to transcription sites and spliceosome assembly, whereas the PP1/2A phosphatases-mediated dephosphorylation during splicing causes the release of the splicing machinery and supports the recruitment of NXF1 and thus the export of mature mRNAs (Zhou and Fu, 2013).

Knocking down SR proteins revealed that SRSF3, and to a lesser degree SRSF2 and SRSF5, are essential for influenza infection. The effects of SRSF3 knockdown on IAV mRNA splicing resembled those of CLK1 knockdown. None of these factors have been reported to be involved in influenza infection before, except for co-localization of SRSF2 with the NS1 protein of influenza B virus (Schneider et al., 2009). Interestingly, SRSF1 (SF2/ASF) knockdown only caused a minor reduction of IAV replication, despite the fact that SRSF1 has been shown to bind M mRNA at the 3’ exon and regulate its splicing (Shih and Krug,
Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.antiviral.2019.06.003.

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Conflicts of interest

LO and GK are owners of Vichem Chemie Ltd; DE, IS and ZH are employees of Vichem Chemie Ltd.

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