Moonlighting glycolytic enzyme glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is required for efficient hepatitis C virus and dengue virus infections in human Huh-7.5.1 cells

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Abstract

Hijacking of cellular biosynthetic pathways by human enveloped viruses is a shared molecular event essential for the viral lifecycle. In this study, the accumulating evidence of the importance of human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in the host secretory pathway led us to hypothesize that this moonlighting enzyme could play a key role in the lifecycle steps of two important Flaviviridae members, hepatitis C virus (HCV) and dengue virus (DENV). We used short interfering RNA (siRNA)-mediated knockdown of human GAPDH in Huh-7.5.1 cells – both pre- and post-HCV infection – to demonstrate that GAPDH is a host factor for HCV infection. siRNA-induced GAPDH knockdown performed pre-HCV infection inhibits HCV core production in infected cells and leads to a decrease in infectivity of the HCV-infected cell supernatants. siRNA-induced GAPDH knockdown performed post-HCV infection does not have an effect on HCV core abundance in infected cells, but does lead to a decrease in infectivity of the HCV-infected cell supernatants. Exogenous expression of V5-tagged human GAPDH, pre- and post-infection, increases the infectivity of HCV-infected cell supernatants, suggesting a role for GAPDH during HCV post-replication steps. Interestingly, siRNA-induced GAPDH knockdown in HCV replicon-harbouring cells had no effect on viral RNA replication. Importantly, we confirmed the important role of GAPDH in the HCV lifecycle using Huh-7-derived stable GAPDH-knockdown clones. Finally, siRNA-induced GAPDH knockdown inhibits intracellular DENV-2 E glycoprotein production in infected cells. Collectively, our findings suggest that the moonlighting enzyme, GAPDH, is an important host factor for HCV infection, and they support its potential role in the DENV lifecycle.

INTRODUCTION

It is now well established that the hijacking and manipulation of host cell biosynthetic pathways by human enveloped viruses are shared molecular events essential for the viral lifecycle [1–3]. For example, lipid metabolism and associated host-cell pathways are manipulated by Flaviviridae members such as hepatitis C virus (HCV) and dengue virus (DENV) to enhance viral production [1, 4]. In addition, mounting evidence implicates the manipulation by HCV and DENV of cellular functions associated with the host secretory pathway in the viral entry and virus maturation steps of the viral lifecycle [5, 6].

An important step towards understanding Flaviviridae biology and host–virus interactions is to further characterize how Flaviviridae members HCV and DENV are able to successfully exploit specific pathway components and associated proteins in these and other host pathways. Moreover, uncovering the molecular players involved during viral hijacking may unearth a common Achilles’ heel in the Flaviviridae lifecycle, leading to the identification of potential broad-spectrum therapeutic targets [6].

HCV, a hepacivirus member of the Flaviviridae family, is a single-stranded, positive-sense RNA virus [7]. The positive-strand RNA genome of HCV is directly translated by the host machinery into a single viral polyprotein, which is cleaved by host- and virus-encoded proteases to release the individual structural (core, E1 and E2) proteins and non-structural (NS) proteins (p7, NS2, NS3, NS4A, NS4B, NS5A...
and NS5B) [7]. HCV is a globally important human pathogen afflicting more than 170 million people worldwide [8].

The four DENV serotypes (DENV-1–4) are members of the Flavivirus genus of the Flaviviridae family, with single-stranded positive-sense RNA genomes encoding three structural [capsid (C), precursor membrane (prM), and envelope (E)] proteins and seven nonstructural (NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5) proteins [9]. DENV represents a significant threat to global public health, with 50–100 million cases annually and about 2.5 billion people living in endemic countries [9].

Because of increasing evidence of the importance of human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in host secretory pathway functions [10], we hypothesized that this multifunctional enzyme could contribute to multiple steps in the viral lifecycles of HCV and DENV. GAPDH plays an integral role in glycolysis [11], but it is also now associated with an important number of non-glycolytic functions such as intracellular membrane trafficking [12], endocytosis [13], receptor-mediated cell signalling [14, 15] and translational control of gene expression [16–18], all important biological processes for HCV and DENV lifecycles. Interestingly, GAPDH has been shown to interact with the genomes of several viruses, suggesting that GAPDH could be involved in the regulation of viral replication [19–22]. For HCV, GAPDH binds to the untranslated region of the 3′ end of viral RNA, but its function is uncertain [23]. Together, these results underline the ‘moonlighting’ nature of GAPDH (i.e. an enzyme with additional functional activities [24, 25]), but the contributions of these moonlighting activities to host–Flaviviridae interactions remain poorly understood.

In this study, we investigated whether the multifunctional GAPDH is a host factor that regulates the lifecycle steps of HCV and DENV in human hepatoma Huh-7.5.1 cells. First, we demonstrated that siRNA-mediated GAPDH silencing in naïve Huh-7.5.1 cells not only inhibits primary HCV infection, but also inhibits the production and/or release of infectious HCV particles in HCV-infected Huh-7.5.1 cell supernatants. Second, we demonstrated that GAPDH also plays an important role during the post-replication steps of the HCV lifecycle because siRNA-mediated GAPDH silencing in HCV-infected Huh-7.5.1 cells results in a significant decrease in infectivity of the HCV-infected cell supernatants. Importantly, siRNA-mediated GAPDH suppression in HCV replicon-harbouring cells has no effect on HCV RNA replication. Third, we demonstrated that exogenous expression of V5-tagged human GAPDH pre- and post-infection increases the viral infectivity of HCV-infected Huh-7.5.1 cell supernatants, suggesting a predominant role of GAPDH during the post-replication steps of the HCV lifecycle.

Finally, we validated the important role of GAPDH in the HCV lifecycle by generating two Huh-7-derived stable GAPDH-knockdown (kd) clones (67D2 and 67B3), which show a robust reduction in intracellular GAPDH mRNA levels and GAPDH protein abundance, with a concomitant reduction in GAPDH enzymatic activity. Analysis of the GAPDH-kd clone’s susceptibility to HCV (JFH-1) infection showed a reduction in intracellular HCV core abundance and a significant decrease in viral infectivity of the HCV-infected GAPDH-kd clone supernatants. Interestingly, our preliminary results with DENV have shown that siRNA-mediated GAPDH suppression in naïve human Huh-7.5.1 cells robustly inhibits primary DENV-2 infection.

Collectively, the results of our studies demonstrate that the moonlighting enzyme, human GAPDH, is an important host factor for HCV infection in human Huh-7.5.1 cells, and they support its potential role in the DENV-2 lifecycle.

RESULTS AND DISCUSSION

siRNA-mediated GAPDH mRNA silencing in naïve human Huh-7.5.1 cells dramatically decreases GAPDH protein abundance

We first optimized the experimental conditions needed to obtain a robust transient knockdown of GAPDH by RNA interference. Cultured Huh-7.5.1 cells were initially transfected with a siRNA pool targeting human GAPDH (siGAPDH) or a non-targeting siRNA pool (siCTRL) with 15 nM of each respective siRNA pool. Seventy-two hours post-transfection, cell lysates were prepared for Western blot analysis (Fig. 1, upper panel). A 14.3-fold decrease in GAPDH abundance was observed for cells treated with 15 nM of siGAPDH relative to control cells (siCTRL) (Fig. 1, lower panel). These results confirmed that a robust transient knockdown of GAPDH is achieved by using 15 nM of the GAPDH siRNA pool in Huh-7.5.1 cells for up to 72 h, the duration of the HCV infection examined in this study. Importantly, no significant effect on cell density was detected in siRNA-treated Huh-7.5.1 cells using the siGAPDH compared to siCTRL at a concentration of 15 nM and up to 5 days post-transfection (p.t.; Fig. S1, available in the online Supplementary Material).

siRNA-mediated GAPDH knockdown in naïve human Huh-7.5.1 cells decreases host-cell susceptibility to primary and secondary HCV infections

First, to examine the effect of siRNA-mediated GAPDH suppression on primary HCV infection of naïve Huh-7.5.1 cells, cells were transfected with siGAPDH or siCTRL for 24 h. Forty-eight hours p.t., treated cells were infected with HCV at an m.o.i. of 0.1. Seventy-two hours post-viral-infection (p.i.), HCV-infected Huh-7.5.1 cells were fixed for in-cell Western (ICW) analysis (Fig. 2a). A 2.3-fold reduction of HCV core abundance was measured for siGAPDH-treated cells during the primary infection compared to siCTRL (Fig. 2a: lower panel). Thus, siRNA-mediated GAPDH silencing in naïve Huh-7.5.1 cells robustly inhibits primary HCV infection.

Next, to examine the effect of siRNA-mediated GAPDH suppression on HCV infectious virus particle production and its spread to naïve cells, we performed an ICW assay involving HCV secondary infection. Briefly, Huh-7.5.1 cells
were treated as described for the primary infection with the exception that at 72 h p.i., the HCV-infected Huh-7.5.1 cell supernatants were collected and used to perform a secondary infection on naïve Huh-7.5.1 cells. After the secondary infection had proceeded for 72 h, the HCV-infected Huh-7.5.1 cells were fixed for ICW assays. A 3.9-fold reduction of HCV core abundance was measured for siGAPDH-treated cells during the secondary infection compared to siCTRL (Fig. 2d) and cells were fixed for ICW analysis (Fig. 2c).

We found that GAPDH suppression in Huh-7.5.1 cells when HCV infection has already been established does not have an effect on intracellular HCV core abundance during the primary infection (Fig. 2c). However, the relative abundance of HCV core associated with the secondary infection is reduced 2.5-fold compared to siCTRL-treated cells (Fig. 2d). This suggests that GAPDH also plays an important role during the post-replication steps of the virus lifecycle because siRNA-mediated GAPDH silencing in HCV-infected Huh-7.5.1 cells caused a significant decrease in viral infectivity of the HCV-infected cell supernatants.

In addition to its potential roles early in the HCV lifecycle, GAPDH is an important component of the Rab2-Src-aPKC-i-GAPDH microtubule-bound complex, which is vital to endoplasmic reticulum–Golgi trafficking in the secretory pathway [12]. Since HCV hijacks this pathway to promote the formation and egress of lipoviroparticles, it seems that the assembly and budding of infectious virions could be inhibited as a result of siRNA-mediated GAPDH silencing. Thus, silencing GAPDH may significantly impact the pre- and post-replication steps of the HCV lifecycle, underlining the multifunctional roles of GAPDH in intracellular membrane trafficking [25], an important molecular event for the biogenesis of organelles in the secretory pathway, siRNA-mediated suppression of GAPDH may impact essential cellular biological processes that HCV requires for maturation in the host secretory pathway, including the formation of lipoviroparticles and their release from the infected cells [4].

**GAPDH knockdown in HCV-infected Huh-7.5.1 cells leads to a decrease in viral infectivity of the HCV-infected cell supernatants**

To test the effect of siRNA-mediated GAPDH silencing in established infections, Huh-7.5.1 cells were first infected with HCV for 24 h to allow uninterrupted HCV replication and establishment of infection. At the end of this time, Huh-7.5.1 cells were transfected with siGAPDH or siCTRL and incubated for an additional 72 h (Fig. 2c, d). The HCV-infected Huh-7.5.1 cell supernatants were collected to perform a secondary infection on naïve Huh-7.5.1 cells (Fig. 2d) and cells were fixed for ICW analysis (Fig. 2c).

Interestingly, the secondary infection of naïve Huh-7.5.1 cells with the HCV-infected cell supernatants collected from the primary infection resulted in an even further decrease in intracellular HCV core abundance. These results are consistent with a compromised host-cell susceptibility to HCV infection observed during the primary infection of siGAPDH-treated cells, but they also imply that key maturation and trafficking steps leading to the production of infectious virus particles and release are also compromised. Because of the multifunctional roles of GAPDH in intracellular membrane trafficking [25], an important molecular event for the biogenesis of organelles in the secretory pathway, siRNA-mediated suppression of GAPDH may impact essential cellular biological processes that HCV requires for maturation in the host secretory pathway, including the formation of lipoviroparticles and their release from the infected cells [4].
Fig. 2. siRNA-mediated GAPDH knockdown in human Huh-7.5.1 cells leads to decreased infectivity of HCV-infected cell supernatants. (a, b) siRNA-mediated GAPDH suppression in naive human Huh-7.5.1 cells decreases host-cell susceptibility to primary and secondary HCV infections. (a) Primary infection. Huh-7.5.1 cells were transfected with an siRNA pool targeting human GAPDH (siGAPDH, 15 nM) or with a non-targeting siRNA pool (siCTRL, 15 nM) for 24 h. 48 h p.t., treated cells were infected with HCV (m.o.i. of 0.1); 24 h p.i., cell supernatants were replaced with fresh medium for secondary infection. 72 h p.i., HCV-infected supernatants were collected for a secondary infection in naive Huh-7.5.1 cells (b), and HCV-infected Huh-7.5.1 cells were fixed for ICW analysis (a) as described in Methods. (b) Secondary infection. HCV-infected Huh-7.5.1 cell supernatants collected in (a) were used to infect naive Huh-7.5.1 cells for 72 h, then fixed for ICW assays (b). (c, d) siRNA-mediated GAPDH suppression in HCV-infected Huh-7.5.1 cells leads to decreased viral infectivity of the HCV-infected cell supernatants. (c) Primary infection. Huh-7.5.1 cells were infected with HCV (m.o.i. of 0.1) for 24 h. HCV-infected Huh-7.5.1 cells were then transfected with an siRNA pool targeting GAPDH (siGAPDH, 15 nM) or with a non-targeting siRNA pool (siCTRL, 15 nM). 24 h p.t., cell supernatants were replaced with fresh medium for secondary infection. 72 h p.t., cell supernatants
the varied and numerous functions performed by this moonlighting enzyme [24, 27, 28].

**GAPDH knockdown in HCV replicon-harbouring cells has no effect on HCV replication**

To determine if the host-cell susceptibility to primary and secondary HCV infections observed in siGAPDH-treated cells is due to reduced viral RNA replication, we examined the impact of siRNA-mediated GAPDH suppression on viral RNA replication using HCV subgenomic replicons [29, 30].

Human hepatoma cells harbouring stable HCV replicons encoding wild-type NS5A (Huh.8 cells: Fig. 3a) or NS5A with an adaptive mutation (Huh.2 cells: Fig. 3b) were transfected for 72 h with siGAPDH or siCTRL. Total RNA was harvested and the levels of HCV and GAPDH RNA were quantified using qRT-PCR analysis (Fig. 3a, b). Although a robust knockdown of GAPDH was observed in Huh.8 cells (16.7-fold decrease) and Huh.2 cells (25-fold decrease), no significant differences in HCV RNA levels were observed between siGAPDH and siCTRL (Fig. 3a, b). In contrast, Huh.8 cells treated with the positive control, BILN2061, a viral protease inhibitor that inhibits HCV replication [31], resulted in a 33.3-fold decrease in HCV RNA compared to DMSO (Fig. 3a (right panel)). These findings strongly suggest that the robust reduction in HCV core abundance observed during primary and secondary HCV infections in siGAPDH-treated cells (Fig. 2a, b) is not due to a defect in HCV RNA replication. In addition, since we have not observed any significant differences in HCV RNA replication between siGAPDH (>95 % kd) and siCTRL in both Huh.8 and Huh.2 replicon-harbouring cells, our results support the apparent lack of cytotoxic effects associated with GADH-kd in human hepatoma cells under our experimental conditions.

Interestingly, GAPDH has been shown to interact directly with 3′-UTRs, in the context of cellular mRNAs including angiotensin II type 1 receptor and endothelin-1 [16, 17] as well as the genomes of several RNA viruses, including hepatitis A virus and Japanese encephalitis virus [19, 22]. These interactions generally have the effect of destabilizing the mRNA or preventing translation by other means. Despite this, it seems
that any ability GAPDH may have to interact with HCV RNA [23] does not confer an inhibitory or stimulatory effect on HCV replication. Thus, it appears that the role of GAPDH in the HCV lifecycle is limited to pre- and post-replication steps while RNA replication itself is GAPDH-independent.

**Exogenous expression of V5-tagged human GAPDH increases the viral infectivity of HCV-infected Huh-7.5.1 cell supernatants**

Next, we wanted to test whether over-expression of human GAPDH in Huh-7.5.1 cells would increase host-cell susceptibility to primary and secondary HCV infections. This was accomplished by first producing a plasmid encoding the V5-tagged full-length human GAPDH (pcDNA3.1-GAPDH-V5, abbreviated GAPDH-V5) (Fig. 4a). This construct was then transfected in Huh-7.5.1 cells for 72 h. WB analysis of GAPDH-V5-transfected cellular lysates using anti-GAPDH antibody (Fig. 4b, left side) and anti-V5 antibody (Fig. 4b, right side) demonstrated the successful over-expression of the GAPDH-V5 recombinant protein, associated with a 1.9-fold increase in GAPDH intracellular enzymatic activity in GAPDH-V5-transfected cells versus control cells (CTRL) (Fig. 4c).

To determine whether exogenous expression of GAPDH-V5 can increase primary and secondary HCV infection in Huh-7.5.1 cells, we examined the effect of over-expressing GAPDH-V5 on HCV core abundance pre- (Fig. 5a, b) and post-establishment (Fig. 5c, d) of viral infection in Huh-7.5.1 cells. First, Huh-7.5.1 cells were transfected with pcDNA3.1-GAPDH-V5 (GAPDH-V5) or pcDNA3.1 (CTRL) for 24 h. Treated cells were infected with HCV (m.o.i. of 0.1). Seventy-two hours p.i., the HCV-infected Huh-7.5.1 cell supernatants were collected to perform a secondary infection on naïve Huh-7.5.1 cells (Fig. 5b) and cells were fixed for ICW analysis (Fig. 5a). Results showed that transfection of Huh-7.5.1 naïve cells with GAPDH-V5 prior to infection with HCV does not have an effect on the level of intracellular HCV core protein in primary infected cells (Fig. 5a), but it increases the level of HCV core protein 1.7-fold in secondary infected cells (Fig. 5b). Since HCV core abundance is an indicator of viral load in the host cells, this shows that the over-expression of GAPDH and the concomitant boost in GAPDH enzymatic activity pre-establishment of HCV infection lead to an increase in the viral infectivity of HCV-infected Huh-7.5.1 cell supernatants while cell susceptibility remains unaffected.
Fig. 5. Over-expression of human GAPDH-V5 increases the viral infectivity of HCV-infected Huh-7.5.1 cell supernatants. (a, b) Effect of GAPDH-V5 on host-cell susceptibility to HCV infection when expressed before establishing viral infection in Huh-7.5.1 cells. (a) Primary infection. Huh-7.5.1 cells were transfected with pcDNA3.1-GAPDH-V5 (GAPDH-V5) or pcDNA3.1 (CTRL) for 24 h. Treated cells were infected with HCV (m.o.i. of 0.1). 24 h p.i., cell supernatants were replaced with fresh medium for secondary infection. 72 h p.i., the HCV-infected Huh-7.5.1 cell supernatants were collected for secondary infection in naïve Huh-7.5.1 cells (b) and fixed for ICW analysis (a). (b) Secondary infection. HCV-infected Huh-7.5.1 cell supernatants from (a) were used to infect naïve Huh-7.5.1 cells for 72 h, then
To test the effect of GAPDH-V5 over-expression in established infections, Huh-7.5.1 cells were first infected with HCV for 24 h. HCV-infected Huh-7.5.1 cells were transfected with pcDNA3.1-GAPDH-V5 (GAPDH-V5) or pcDNA3.1 (CTRL); 72 h p.t., the HCV-infected Huh-7.5.1 cell supernatants were collected to perform a secondary infection on naïve Huh-7.5.1 cells (Fig. 5d), and cells were fixed for ICW analysis (Fig. 5c). This resulted in a 1.6-fold increase in HCV core abundance only during secondary infection (Fig. 5d), not primary infection of Huh-7.5.1 cells (Fig. 5c). Thus, over-expression of GAPDH enzymatic activity post-establishment of HCV infection again increases the viral infectivity of HCV-infected Huh-7.5.1 cell supernatants but does not affect cell susceptibility.

Collectively, these results suggest a novel and important role of GAPDH during the post-replication steps of the HCV lifecycle, since over-expression of enzymatically active GAPDH molecules pre- or post-establishment of infection triggers an equivalent ~twofold increase in viral infectivity of HCV-infected Huh-7.5.1 cell supernatants. However, it remains to be determined if GAPDH enzymatic activity is required to increase HCV infectivity in human Huh-7.5.1 cells. Importantly, the role of GAPDH in intracellular membrane trafficking and the implications of silencing it for the secretory pathway may have indirect as well as direct repercussions for HCV’s post-replication steps.

**Huh-7-derived stable GAPDH-kd clones 67D2 and 67B3 show a robust reduction in intracellular GAPDH protein abundance and GAPDH mRNA levels, with a concomitant reduction in GAPDH enzymatic activity**

In order to validate our results obtained using the siRNA-mediated GAPDH mRNA silencing approach in naïve human Huh-7.5.1, we worked to generate Huh-7-derived stable GAPDH-kd clones using a lentiviral vector-based short-hairpin RNA (shRNA) system targeting human GAPDH (Methods; Fig. S2). Two Huh-7-derived stable GAPDH-kd clones (67D2 and 67B3) were successfully established using our lentivirus-based system (Fig. S2). The biochemical results demonstrating robust reduction in GAPDH protein abundance, enzymatic activity, and mRNA levels for 67D2 and 67B3 Huh-7-derived clones are presented in Fig. 6(a–d).

First, WB analysis (Fig. 6a; upper panel) of 67D2 and 67B3 cell lysates revealed a robust knockdown of GAPDH protein abundance [20-fold decrease (67D2) and 12.5-fold decrease (67B3), respectively] compared to control Huh-7 cells (CTRL). Second, consistent with the WB results, the ICW analysis of GAPDH intracellular abundance in GAPDH-kd clones demonstrated a 16.7-fold decrease (67D2) and a 4.8-fold decrease (67B3) in intracellular GAPDH abundance compared to control Huh-7 cells (CTRL) (Fig. 6b). Third, using a fluorescence-based GAPDH enzymatic assay, we demonstrated that the reduction in GAPDH protein abundance (Fig. 6a–b) is associated with a concomitant reduction in intracellular GAPDH enzymatic activity [12.5-fold decrease (67D2) and fivefold decrease (67B3)] compared to control Huh-7 cells (CTRL) (Fig. 6c). Fourth, using qRT-PCR, we demonstrated that GAPDH mRNA levels in 67D2 and 67B3 Huh-7-derived clones are also robustly reduced, with an 11-fold (67D2) and a ninefold (67B3) decrease compared to control Huh-7 cells (CTRL) (Fig. 6d). Finally, the reduction in GAPDH mRNA levels determined for 67D2 and 67B3 provides evidence that the stable GAPDH knockdown observed for our two Huh-7-derived clones occurred through an shRNA-mediated degradation mechanism of human GAPDH mRNAs. In addition, the specificity of the lentiviral vector-based GAPDH shRNA approach used in this study is underlined by the lack of statistically significant differences in the results between the parental Huh-7 cells and CTRL (Fig. 6a–d).

**Huh-7-derived stable GAPDH-kd clones 67D2 and 67B3 show a reduced susceptibility to HCV infection**

Next, the GAPDH-kd clones were tested for their susceptibility to HCV infection (Fig. 7a, b). Cultured parental Huh-7 cells, control Huh-7 cells (CTRL), and GAPDH-kd clones (67D2 and 67B3) were infected with HCV (m.o.i. of 0.5) for 24 h to allow uninterrupted HCV replication and establishment of infection. Seventy-two hours post-infection, medium was replaced with fresh medium to allow accumulation of extracellular infectious virus. On day 5 p.i., the HCV-infected GAPDH-kd clone supernatants were collected for a re-infection assay (secondary infection) using naïve Huh-7.5.1 cells (Fig. 7b). At the same time, the HCV-infected cells from the primary infection were fixed for ICW analysis (Fig. 7a).

The upper panel in Fig. 7(a) shows representative ICW wells scanned using the Odyssey infrared imaging system from the primary infection experiments. Cells were probed with HCV anti-core antibody (green) and stained with dyes for...
Fig. 6. The Huh-7-derived stable GAPDH-kd clones 67D2 and 67B3 show a robust reduction in intracellular GAPDH protein abundance, GAPDH enzymatic activity, and GAPDH mRNA levels. (a) GAPDH protein abundance determined by WB for Huh-7-derived GAPDH-kd clones 67D2 and 67B3. Cell lysates were harvested from parental Huh-7 cells (Parental), control Huh-7 cells (CTRL), and Huh-7-derived stable GAPDH-kd clones (67D2 and 67B3) for WB analysis and probed with human GAPDH antibody (green) and β-tubulin antibody (red) (see Methods). Upper panel: a representative WB. Lower panel: protein abundance was quantified as described in Methods, averaged across WB bands and expressed relative to protein abundance in CTRL. Results: mean±SEM of three independent WB analyses. Significance is based on Student’s t-test (***, P<0.0001). (b) GAPDH protein abundance determined by ICW for Huh-7-derived stable GAPDH-kd
CD normalization (red). HCV core was quantified and expressed relative to protein abundance in control Huh-7 cells (CTRL) (Fig. 7a; lower panel). A significant reduction in HCV core abundance was measured for GAPDH-kd clones [4-fold decrease (67D2) and 8.3-fold decrease (67B3)] during the primary infection compared to CTRL (Fig. 7a; lower panel).

Next, supernatants from the HCV-infected GAPDH-kd clones were collected and used to perform a secondary infection in naïve Huh-7.5.1 cells. After the secondary infection procedure for 72 h, these supernatant-infected Huh-7.5.1 cells were fixed for ICW analysis and expressed relative to GAPDH protein abundance in CTRL. Results: mean±SEM of four independent ICW experiments, each in triplicate. Significance is based on Student’s t-test (***, P<0.0001). (c) GAPDH enzymatic activity determined for Huh-7-derived stable GAPDH-kd clones 67D2 and 67B3. Parental, CTRL, and 67D2 and 67B3 cells were seeded in a 96-well plate. 24 h post-seeding, cell lysates were prepared to detect intracellular GAPDH enzymatic activity as described in Methods. Values are plotted relative to GAPDH enzymatic activity detected in CTRL. Results: mean±SEM of four independent experiments, each in triplicate. Significance is based on Student’s t-test (***, P<0.0001). (d) GAPDH mRNA levels determined for 67D2 and 67B3. Total RNA was harvested from parental, CTRL, 67D2 and 67B3 cells. GAPDH mRNA levels, normalized to ß-actin mRNA levels, were relatively quantified by QPCR as described in Methods. Values are plotted as relative GAPDH mRNA levels in comparison to CTRL. Results: mean±SEM of two independent experiments in triplicate. Significance is based on Student’s t-test (***, P<0.0001).

GAPDH knockdown in naïve human Huh-7.5.1 cells decreases host-cell susceptibility to primary DENV-2 infection

Finally, to investigate whether GAPDH is an important host factor for other Flaviviridae members, we determined the effect of siRNA-mediated GAPDH silencing in naïve human Huh-7.5.1 cells on DENV-2 infection. Huh-7.5.1 cells were transfected with siGAPDH or siCTRL. Forty-eight hours post-transfection, treated cells were infected with DENV-2 (m.o.i. of 0.005); 72 h p.i., the DENV-2-infected Huh-7.5.1 cells were fixed for ICW analysis (Fig. 8). A 1.7-fold reduction of intracellular DENV-2 E protein abundance was measured for the siGAPDH-treated cells during the primary infection compared to the siCTRL-treated cells (Fig. 8; lower panel). Thus, siRNA-mediated GAPDH suppression in naïve human Huh-7.5.1 cells significantly inhibits DENV-2 infection, although the specific lifecycle steps compromised in these GAPDH-kd cells remain to be determined. Interestingly, Allonso et al. [33] recently identified GAPDH as a binding partner interacting with intracellular DENV NS1. Both DENV infection and DENV NS1 over-expression increased GAPDH glycolytic activity. Those authors hypothesized that DENV NS1 is responsible for modulating the host metabolism by increasing GAPDH glycolytic activity during the early steps of infection. Together, these results suggest that GAPDH is a host factor required to enhance glycolysis and, consequently, energy production during the DENV lifecycle [33].

Conclusion

Uncovering the molecular players involved during viral hijacking may unearth a common Achilles' heel in the lifecycle of important human pathogens such as HCV and DENV, thus leading to a better understanding of host–virus interactions and to identifying potential broad-spectrum therapeutic targets [34]. The results of our studies underlined the important contributions of GAPDH's 'moonlighting' activities to host–Flaviviridae interactions, and they uncovered novel complex molecular interplays between human GAPDH and the Flaviviridae lifecycle steps. Importantly, in this study, we established unique Huh-7-derived stable GAPDH-kd clonal cell lines that are valuable tools not only for further investigations of GAPDH’s function in DENV infection but also for unravelling the functional role of GAPDH.

clones 67D2 and 67B3. Equal numbers of parental, CTRL and 67D2 and 67B3 cells were seeded in a 96-well plate. 24 h post-seeding, cells were fixed for ICW analysis (b) as described in Methods. Upper panel: representative ICW wells probed with anti-GAPDH antibody (green) and stained with two dyes to determine CD (red) for normalization. Lower panel: protein abundance was quantified as described in Methods, averaged across triplicate wells and expressed relative to GAPDH protein abundance in CTRL. Results: mean±SEM of four independent ICW experiments, each in triplicate. Significance is based on Student’s t-test (***, P<0.0001). (c) GAPDH enzymatic activity determined for Huh-7-derived stable GAPDH-kd clones 67D2 and 67B3. Parental, CTRL, and 67D2 and 67B3 cells were seeded in a 96-well plate. 24 h post-seeding, cell lysates were prepared to detect intracellular GAPDH enzymatic activity as described in Methods. Values are plotted relative to GAPDH enzymatic activity detected in CTRL. Results: mean±SEM of four independent experiments, each in triplicate. Significance is based on Student’s t-test (***, P<0.0001). (d) GAPDH mRNA levels determined for 67D2 and 67B3. Total RNA was harvested from parental, CTRL, 67D2 and 67B3 cells. GAPDH mRNA levels, normalized to ß-actin mRNA levels, were relatively quantified by QPCR as described in Methods. Values are plotted as relative GAPDH mRNA levels in comparison to CTRL. Results: mean±SEM of two independent experiments in triplicate. Significance is based on Student’s t-test (***, P<0.0001).
of GAPDH during viral infection of other emerging flaviviruses such as Zika virus [35].

**METHODS**

**Cell culture and reagents**

Human hepatoma Huh-7.5.1 cells were kindly provided by Dr Francis Chisari (Scripps Research Institute) [36, 37]. Huh-7 cells, Huh.8 (Con1/SG-Neo) cells supporting the HCV genotype 1b subgenomic replicon, and Huh.2 (Con1/SG-Neo: S2197P) cells supporting the same replicon with an NS5A adaptive mutation were provided by Dr Charles Rice (The Rockefeller University and Apath, LLC, St Louis, USA) [29, 30]. BILN2061 was kindly provided by Dr Peter W. White (Boehringer Ingelheim, Canada). Vero cells (ATCC CCL-81) were obtained from ATCC [38]. Cells were cultured and maintained as described previously [6, 39, 40].

**Antibodies and dyes**

Two anti-GAPDH antibodies were employed for detecting human GAPDH in cultured cells: a mouse anti-GAPDH monoclonal antibody (1:1000 for WB) and a rabbit anti-GAPDH monoclonal antibody (1:1000 for WB or ICW assay). A mouse anti-core monoclonal antibody (1:1000,
Abcam) was employed for detecting HCV infection by ICW assay. A mouse anti-envelope (E) monoclonal antibody (1 : 35, Abcam) was employed for detecting DENV-2 infection by ICW assay. Intracellular human β-tubulin was detected by WB using a rabbit anti-β-tubulin polyclonal antibody (1 : 1000, Abcam). A rabbit anti-V5 antibody was employed for detecting recombinant V5-tagged human GAPDH (1 : 1000, Abcam). Secondary antibodies for WB (1 : 10 000) and ICW (1 : 200 (red channel) or 1 : 800 (green channel)) included IRDye 800-conjugated (green channel) or 680-conjugated (red channel) raised against mouse or rabbit antibodies (LI-COR Biosciences). Dyes used included DRAQ5 stain (1 : 10 000, Biostatus) and Sapphire700 stain (1 : 1000, LI-COR Biosciences).

**Viral stock production and titre determination**

The plasmid pUClvJFH-1 (a generous gift from Dr Takaji Wakita, National Institute of Infectious Diseases, Japan) was used for generating HCV RNA and infectious HCV stocks as described previously [37, 41]. HCV stocks were produced and titres determined as described previously [6, 40]. DENV serotype-2 (DENV-2; New Guinea C) was kindly provided by Dr Mike Drebot from the National Microbiology Laboratory (Canada). DENV-2 stocks were generated and titres determined as described elsewhere [42].

**Viral infections**

Human hepatoma cells were either infected with HCV (m.o.i. of 0.1 or 0.5) or DENV-2 (m.o.i of 0.005). Twenty-four hours p.i., medium was removed and fresh complete medium added. Thereafter, the cells were incubated for the indicated number of days p.i. (see Figs 2, 5, 7 and 8) and cells fixed for ICW assay. Alternatively, cell supernatants were collected at various time-points p.i. for performing secondary infection of naive Huh-7.5.1 cells and determining viral protein abundance (HCV core; DENV-2 E-glycoprotein) using ICW assay.

**RNA isolation**

Total RNA was isolated using a miniRNAeasy kit (Qiagen) according to the manufacturer’s instructions. The concentration and purity of RNA were determined by a NanoDrop ND-1000 Spectrophotometer (Thermo Scientific) as described previously [6, 43, 44].

**Quantitative real-time (qRT) PCR**

Purified total RNA (15 ng) was reverse transcribed to cDNA using the qScript cDNA synthesis kit (Quanta Biosciences) according to the manufacturer’s instructions. qRT-PCR was carried out using PerfeCTa Multiplex qPCR SuperMix (Quanta Biosciences) according to the manufacturer’s instructions on an MX3005P QPCR system (Stratagene) as described previously [43, 44].

PrimerQuest [Integrated DNA Technologies (IDT)] was used to design qRT-PCR assays for detecting (i) HCV genomic abundance [probe: (5'-CAGTACCACAAAGGCTTTGCACTC-3'); forward primer (5'-CAAGACTGCTAGGCGGAGT-3'); reverse primer (5'-ACTCGCAAAGCCCGCTATC-3')]; (ii) GAPDH RNA levels [probe: (5'-GCTCCTGGAAGATGGTGATGGTG-3'); forward primer (5'-AGAAGGGGAAGCTTTCGTAATC-3'); reverse primer (5'-GATCGCCCCACTTGAGT-3')]; and (iii) human β-actin (ACTB) RNA levels [probe: (5'-ACTCCATGCCAGAAAGGACGGC-3'); forward primer (5'-GGCCGTGAGGCACCTGCT-3'); reverse primer (5'-GGATATCCACTGCTGATATC-3')].

HCV RNA levels were relatively quantified across samples and normalized to β-actin RNA levels (5’ Cy5 fluorophore and 3’ Iowa Black RQ quencher) using 300 nM primers and 150 nM double-quenched probes (5’ FAM fluorophore and
siRNA-mediated GAPDH silencing in hepatoma cells

Huh-7.5.1 cells were transfected according to the manufacturer’s instructions with a pool of non-targeting control siRNAs (siCTRL: D-001910-02-05, D-001910-03-05 and D-001910-04-05) or a pool of siRNAs targeting GAPDH (siGAPDH: D-001930-10-20) obtained from Dharmacon (Thermo Scientific). Briefly, human hepatoma cells were treated with 15 nM of the Accell GAPDH siRNA pool and 15 nM of a non-targeting siRNA pool using DharmaFECT 4 transfection reagent (Dharmacon, Thermo Scientific).

V5-tagged human GAPDH construct

Total RNA isolated from human Huh-7 cells (PureLink RNA Mini Kit, Ambion) was reverse transcribed to cDNA (TaqMan Reverse Transcription Reagents, Applied Biosystems) using manufacturer-supplied oligo d(T)16 primers. KOD Hot Start DNA Polymerase (Toyobo, EMD Biosciences) was used to amplify the cDNA corresponding to the coding region of human GAPDH (hGAPDH) using reverse transcription mix with primer sets 5'-ATGGGAAGG TGAAGGTCCGG-3' and 5'-TTACTCCTGGAGGCCATG TGGGC-3' (forward) and 5'-GGAGGGTTAGGGATAGGCTTACCGAATTCCGGAT-3' (reverse) (IDT). The purified hGAPDH PCR fragment (PCR purification kit, Invitrogen) was cloned into a pGEM-t vector (Promega). Briefly, the cloning method of the V5-tagged hGAPDH construct entails the introduction of KpnI and EcoRI restriction cloning sites on the 5' end and the 3' end of the hGAPDH PCR fragment, respectively, along with the elimination of a stop codon using primer sets 5'-GCTTGG TACCATG GGAAGGTGAAAGGTGTC-3' (forward) and 5'-TGGGCGATTTCCCTCCTGGAGGGCATTGT-3' (reverse) (IDT). The double-digested PCR fragment was then cloned into the mammalian expression vector pcDNA3.1+ (Invitrogen). A duplex sequence of V5-tag was designed with restriction sites EcoRI at the 5' end and XhoI at the 3' end (5'-TAGGGCTCGAGTTTACGTGAAATCGAGACCAGGAGAGGGTTAGGGATAGGCTTACCGAATTCCGGAT-3' (IDT)). The duplex was double-digested with EcoRI (NEB) and XhoI (NEB), and it was introduced into a GAPDH-containing pcDNA3.1+ vector to generate the hGAPDH-V5 construct (pcDNA3.1-GAPDH-V5). The final construct was verified by sequencing.

Transfection of Huh-7 cells with the hGAPDH-V5 construct

Huh-7.5.1 cells were transfected with the pcDNA3.1-GAPDH-V5 construct using the transfection reagent, TransIT-LT1 (Mirus) according to the manufacturer’s instructions. The relative level of abundance of intracellular GAPDH-V5 under the experimental conditions described in Figs 4 and 5 was determined using WB or ICW assays.

ICW assays and WBs

ICW assays were performed using black flat-bottom 96-well plates (BD Biosciences). Cells were seeded onto 96-well plates for 24 h, and were then transfected and/or infected as described in the figure legends. Cells were fixed in 4% v/v formaldehyde in PBS for 45 min, then permeabilized and blocked in PBS containing 0.1% Triton-X 100 (permeabilization buffer) and PBS diluted 1:1 with Odyssey blocking buffer for 1.5 h. Primary and secondary antibodies were diluted in Odyssey blocking buffer containing 0.02% Tween 20; proteins were detected by probing with the appropriate primary antibodies overnight at 4 °C followed by the addition of the secondary antibodies for 1 h. For normalization, the fixed cells were stained with two dyes [Sapphire 700 (LI-COR Biosciences) and a DNA interactive stain, DRAQ5 (BioStatus)], for the purpose of determining CD. The fixed cells were scanned at a wavelength of 700 nm for detecting IRDye 680 labelled antibodies and at a wavelength of 800 nm for detecting IRDye 800CW conjugated antibodies. Signal intensities were quantified by means of Odyssey software version 2.0. Western blots were performed on whole cell lysate as described previously and intracellular β-tubulin was used as a loading internal control for normalization of the GAPDH abundance in each sample [6].

GAPDH enzymatic assays

GAPDH enzymatic activity was measured using the KDalert GAPDH assay kit according to the manufacturer’s instructions (Invitrogen Life Technologies). The fluorescence signal was detected using a Gemini EM fluorescence microplate reader ( Molecular Devices).

Huh-7-derived GAPDH-kd clones (67D2 and 67B3)

The human GAPDH MISSION short-hairpin RNA (hGAPDH-shRNA) sequence [Seq: CCGGGTGAGATTG TTGCCCATACTCGAGATGTAGGCAAACATCGA CTTTTT, MISSION TRC shRNA target (TRCN0000025867)] was custom-designed using GAPDH RefSeq: NM_002046.2. The hGAPDH-shRNA targeted the 5’ region of the hGAPDH mRNA (see Fig. S2a, b), MISSION pLKO.1-puro control (SHC001V-lentiviral vector empty of shRNA) was used as control (CTRL). Huh-7-cells (5 × 10^4) cells were infected with hGAPDH-shRNA encoding lentiviral transduction particles (Sigma Aldrich) at an m.o.i. of 1 in the presence of 2.5 μM hexamethine bismide (Sigma Aldrich) for 24 h. Seventy-two hours p.i., transduced cells were selected and maintained in medium containing 7.35 μM puromycin and supplemented with 10 mM sodium pyruvate to compensate for GAPDH activity. Over the next 5–10 days p.i., selection medium was replaced when excessive cell death was observed. Upon repopulation (10–20 days) of transduced cells, single-cell Huh-7-derived cell clones 67D2 and 67B3 were isolated by serially diluting transduced cells in a 96-well plate. Thereafter, these Huh-7-derived cell clones were characterized for stable GAPDH knockdown.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

References


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