

Influenza A virus and p53: Can the Two Walk Together? A Commentary on “p53 and the Viral Connection: Back into the Future”

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Abstract

Influenza A is a very common cause for respiratory infections, which constitutes a major public health concern due to high rates of morbidity and mortality in high-risk population. In our previous publication, ‘p53 and the Viral Connection: Back Into the Future’, we discussed the involvement of the p53 tumor suppressor in the response to non-tumorigenic viruses, among which is the Influenza virus. In the current comment, we focus on the interplay between p53 and the influenza viral cycle. We discuss recent publications that provide evidence for the potential antiviral and pro-viral roles of p53 and its isoforms towards influenza, both in the host cell, as well as in the immune system. On the other side of the coin, we also discuss how the influenza virus may manipulate p53 to promote its own replication and spreading. An understanding of the interplay between p53 and the virus may lead to the development of a host-based influenza virus therapy.

Influenza A virus (IAV) is one of the most common sources of human respiratory infections, causing morbidity and death in high-risk population and constituting a major public health and economic concern. Up to 20% of the world population may be affected by an IAV infection, and up to 250,000-500,000 deaths are reported each year¹. As a preventive strategy, prophylactic vaccination is offered to high-risk population. However, as IAV possesses high rates of genetic drift and genetic shift, new IAV strains continuously arise, making previously prepared vaccines and acquired immunity less relevant². Thus, annual development of new vaccines is compulsory. Consequently, efforts are made to develop a broad universal vaccine³. Similarly, more and more resistant strains of IAV arise against the M2 and the NA inhibitors, the two classes of FDA approved anti-IAV drugs, pointing to the urgent need for the development of new therapies⁴. These efforts are based on targeting conserved domains of the viral protein or, alternatively, targeting host factors that are involved in the viral life cycle.

In our recently published review “p53 and the viral connection: Back into the future”⁵, we highlighted the roles of the tumor suppressor p53, known as “the guardian of the genome”, in tumor virology. In a historical perspective view of 40 years of research, we describe the different strategies by which tumor-promoting viruses manipulate wild-type p53 (Wtp53) functions in ways that may seed the onset of cancer development. Alongside, through the understanding of the tactics by which various viruses hijack Wtp53 functions to their own benefit, came the appreciation of the roles of Wtp53 also in the life cycle of non-oncogenic viruses, such as the

IAV, the poxvirus (smallpox and vaccinia viruses)^{6,7}, the flavivirus (Zika and West Nile)^{8,9}, Japanese encephalitis virus¹⁰, Human Immunodeficiency virus (HIV) type I^{11,12}, Human herpes simplex virus 1^{13,14} and more.

One of the hallmarks of IAV infection is the modulation in WTp53 levels and activity. Indeed, various studies reported different mechanisms by which IAV infection modulates WTp53 activity, resulting in different biological outcomes, of which most launch antiviral effects¹⁵⁻¹⁸, while some favor IAV replication^{19,20}. Terrier et al. reported a biphasic modulation of p53 transcriptional activity during IAV infection, with a high activity at initial time points, followed by a marked reduction during the advanced stages²¹. Moreover, global transcriptome analyses by microarray showed that p53 is implicated in the response to IAV infection, both *in vitro*^{20,22}, as well as *in vivo*¹⁸.

WTp53 does not play an active role in initial virus entry. However, as infection proceeds and cell stress increases, apoptosis is induced and type I interferon pathways are activated, leading to enhanced innate and adaptive immune responses as an outcome of WTp53 activity^{15,16,18}. Indeed, Shen et al.²³ reported on a biphasic pattern of WTp53 elevation, where the first elevation in p53 levels occurs upon IAV adsorption, prior to the onset of virus replication, whereas the second elevation occurs at the middle-late phase of IAV replication. Of note, this elevation in p53 level does not necessarily correlate with p53 activity, as it was shown that some p53 target genes were actually downregulated at late time points, an effect which was mediated by the viral protein NS1²¹. It is possible, however, that some genes, such as immune modulating genes, are upregulated, while another subset of p53 target genes is downregulated. Aside from p53-induced immune response, p53-mediated apoptosis may also be regarded as a host defense mechanism against the virus¹⁷. Altogether, these actions are aimed at reducing infectivity. However, it should be noted that appropriately timed apoptosis benefits IAV and has been reported to be central for viral replication and spreading²⁴. Consistently with this finding, Wang et al. reported that expression of pro-apoptotic molecules, including p53, was associated with increased viral titers in lung cells upon IAV H1N1 infection¹⁹. Thus, the conflicting role of p53 in either facilitating or attenuating IAV replication may stem from the opposed roles reported for apoptosis for IAV infection. Interestingly, Wang et al.²⁰ report contrasting biological effects of different p53 forms. p53 was shown to down-regulate, independently of its transcriptional activity, the antiviral host factors interferon-induced transmembrane family members IFITM1, IFITM2 and IFITM3, which are known to restrict IAV infectivity, thus extending the time window of efficient infection and promoting infectivity²⁰. In their study, the authors used specific CRISPR/Cas9

knockout (KO) in the influenza host cells, which caused either the entire loss of p53 protein, or the loss of the p53 full-length protein, while retaining the expression of the $\Delta 40$ p53 isoform. Interestingly, the entire p53 KO caused a marked decrease in the efficiency of influenza viral replication, while retaining the expression of the $\Delta 40$ isoform caused a significant increase, compared to WT host cells, in viral replication efficiency. These effects were mediated by affecting the expression levels of antiviral host factors interferon-induced transmembrane family members IFITM1, IFITM2 and IFITM3, which were upregulated upon entire p53 KO, but reduced upon retention of the $\Delta 40$ isoform. In all, these results suggest that while full-length WTp53 limits influenza replication, the $\Delta 40$ isoform seems to promote it, at least in part by modulating the host cell antiviral response. Intriguingly, another report suggested that the NS1 protein of the influenza virus manipulates the host splicing machinery, leading to increased expression of p53 β and γ isoforms and to increased viral replication²⁵. In addition to modulating p53 isoform expression, viral proteins may also modulate p53 stability and protein accumulation via interacting with p53 itself. For example, the viral nucleoprotein (NP) associates with p53²⁶, thus impairing the binding of p53 to Mdm2, the major factor that regulates p53 ubiquitination and degradation²⁷. In turn, this inhibition of p53-Mdm2 interaction by NP contributes to p53 accumulation, stabilization and to an increase in its transcriptional activity²⁶. It seems therefore, that p53 transcriptional activity is modulated during the course of infection, with a significant increase at early stages due to the presence of NP, and a significant decrease during the late stages of infection, where the levels of NS1 rise. Altogether, these findings imply an ongoing "arms race" between the host p53 and the influenza virus, in which p53, in all, aims to limit viral replication, while the virus aims to modulate p53 activity, in part by modulating the expression of p53 isoforms, or by modulating p53 stability and activity.

Aside from the role of WTp53 in the host cell, another aspect that is worth considering regarding the effect of WTp53 on IAV infectivity is the known role of WTp53 in the immune system^{28,29}. Indeed, p53 KO mice exhibited impaired function of immune cells, including dendritic cells, monocytes and cytotoxic T-cells, as well as attenuated induction of cytokines, which led to increased IAV replication and, consequently, to increased mortality¹⁵. Interestingly, not only that p53 induces the expression of target genes in the immune system³⁰, but the interferon pathway, which comprises some p53 target genes, regulates the transcription of p53 itself³¹, thus suggesting the existence of a positive feedback loop. Consistently with the aforementioned studies, it was shown that mice harboring an extra p53 copy ('super p53' mice) were more resistant to viral infection than their WT counterparts³².

Thus, it is not only p53 cell-autonomous functions that exert an antiviral response, but p53 non-cell autonomous functions in the immune system are crucial for the host's antiviral response as well.

Taken together, it is intriguing to hope that a broader understanding of the interplay between p53 and IAV may open new horizons for the use of p53-based therapies (developed for cancer diseases) as general antiviral agents. A potential advantage of p53-based therapies to IAV may be the activity of p53 both at the prime site of IAV infection, at the epithelial cells, as well as in the immune cell subset involved in the antiviral response, resulting in a dual additive antiviral response. However, one must bear in mind the potential toxic adverse effects of p53 stabilization on normal cells, and perhaps try to ameliorate them by targeting or delivering the p53-based therapies specifically to virus-infected cells. Moreover, the use of natural products that were shown to inactivate IAV through p53 activation may be beneficial³³.

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Conflicts of Interest

The authors declare no conflict of interest.

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