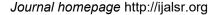


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Review Article

The Role of microRNA-155 in Viral Diseases of Humans

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Abstract

MicroRNAs, as key regulators of gene expression, have garnered significant attention in recent antiviral research due to their potential to modulate viral pathogenesis and host immune responses. On account of their potential to regulate gene expression, microRNAs are currently the focus of modern antiviral research. miR-155 is a multifunctional microRNA that plays a significant role in the regulation of the host immune system. Predictably, it also has a profound role in the pathogenesis of numerous viruses. Increasing research has revealed the involvement of miR-155 in various aspects of the host-viral interface. Studies have also shown that miR-155 or its inhibitor could be used as a potential tool in viral therapeutics and diagnostics. The current review aims to highlight viral diseases that have been significantly modulated by miR-155. This was achieved by searching several globally recognised and distinguished scientific databases, followed by data extraction and analysis. This work is particularly important, as exogenous molecular control of miR-155 expression could open new avenues for limiting viral proliferation.

Keywords: Hepatitis; microRNA; microRNA-155; Viral Disease; Viruses

Introduction

MicroRNAs are small (19 to 24 nucleotides), single-stranded, non-coding RNAs that are primarily synthesised from the introns (Ying, Chang & Lin, 2018; Anglicheau, Muthukumar & Suthanthiran, 2010). Due to their ability to bind to and silence DNA post-transcriptionally, facilitated by complementarity in their sequences, they have been widely utilised in research and therapeutic applications (Ying, Chang & Lin, 2018; Segert, Gissel Brecht & Bulyk, 2021; Tiwari, Mukherjee & Dixit, 2018; Ganju et al., 2017; Rupaimoole & Slack, 2017; Bernardo et al., 2015). Almost all living organisms synthesise microRNAs, with a total of 10,000 human microRNAs identified (Friedländer et al., 2014). These small entities have tremendous potential to modulate various gene expressions. Studies have predicted that they can potentially target and regulate the expression of at least 30% of the entire mammalian genome (Li et al., 2009; Xiong & Zhang, 2023). However, they exhibit distinct expression profiles in response to specific conditions in human body. For example, immune-related microRNAs such as miR-1, miR-9, miR-21, miR-121, miR-144, miR-155, miR-145, miR-181, and miR-146 (Chandan, Gupta & Sarwat, 2020) are increased when a pathogen invades body (Shang et al., 2023). On the other hand, miR-17-92 cluster levels, miR-21, miR-590, and others are elevated during cancer (Peng & Croce, 2016; Hill et al., 2025). Among them, microRNA-155 has been extensively studied as a typical multifunctional microRNA. Existing studies indicate that miR-155 controls various pathological and physiological

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processes, such as cardiovascular diseases, immunity, haematopoiesis, inflammation, and cancer (Faraoni *et al.*, 2009). Increasing research has also shown that miR-155 plays a role in several viral infections, such as neuroviruses, circulating viruses, respiratory viruses, etc. (Dickey *et al.*, 2017). However, its mode of functioning varies in different viruses (Jafarzadeh *et al.*, 2021). The current review aims to compile all the information regarding the functioning of miR-155 in different viral infections in humans.

Biogenesis of microRNAs

MicroRNAs are tiny, non-coding RNA fragments that were first identified in *C. elegans* (Ying, Chang and Lin, 2018; Friedländer *et al.*, 2014; Dickey *et al.*, 2017). It has now been established that they regulate gene-expression profiles in numerous animal species at the post-transcriptional level (Friedländer *et al.*, 2014; Dickey *et al.*, 2017).

RNA Polymerase II transcribes the miRNAs, primarily from the intron regions of the genome, into primary miRNAs (pri-miRNAs) (Kim & Kim, 2007). These are then cleaved by RNA Pol-III, the Drosha, and DGCR8 complex into shorter, 70-nucleotide long, precursor miRNAs (pre-miRNAs) (Ying, Chang & Lin, 2018; Kim & Kim, 2007; Sarkar & Chakravarty, 2015). The pre-miRNAs then leave the nucleus and are transported by Exportin-5 into the cytoplasm, where the enzyme Dicer undergoes further processing, resulting in the formation of even shorter double-stranded RNA fragments (Bofill-De Ros & Vang Ørom, 2023). These miRNAs (22 nucleotides long) then bind with Argonaute and other enzymes to generate the RNA-induced silencing complex (RISC) (Hou *et al.*, 2024). The RISC approaches the target mRNA, and one of the two strands in the miRNA binds with it at its 3' UTR (untranslated region), while the other strand is degraded (Hart *et al.*, 2024). The binding of miRNA to the target mRNA represses its expression either by blocking the initiation of translation or by degrading the target mRNA (Ying, Chang & Lin, 2018).

MicroRNA-155

The miR-155 is produced from an exon present in a non-coding RNA that is transcribed from BIC (B cell integration cluster) on chromosome 21 (Lagos-Quintana *et al.*, 2002). It was initially recognised in chicken lymphomas as an oncogene. However, subsequent work revealed that it is a multifunctional microRNA and is associated with several biological processes, including haematopoiesis, cancer, immunity, inflammation, cardiovascular diseases, contraction of vascular smooth muscle, mediating renal function, and viral infections (Faraoni *et al.*, 2009; Mahesh & Biswas, 2019).

The role of MicroRNA-155 in regulating immune responses is manifold. It works in association with diverse types of immune cells, such as definite T cell populations, B cells, macrophages, dendritic cells, NK cells, etc. (Haasch *et al.*, 2002; O'Connell *et al.*, 2007) and regulates the production of cytokines and chemokines by them. The expression of miR-155 can alter the production of IFN- γ and IL-2 by T cells (Banerjee *et al.*, 2010; Das *et al.*, 2012; Gracias *et al.*, 2013). It has been reported to facilitate the IFN- γ -dependent T cell (both CD4+ helper T cells and CD8+ cytotoxic T cells) responses to tumours (Huffaker *et al.*, 2012). It also enhances the maturation of T regulatory cells [21, 22], and alters the CD8+ memory T cell: effector T cell ratio (Kohlhaas *et al.*, 2009; Almanza *et al.*, 2010). miR-155 targets and represses a variety of immunoregulatory proteins, signalling molecules, and transcription factors such as SOCS1, Jarid2, Ets1, PU.1, Fosl2, CEBP β , etc. (Wang *et al.*, 2010; Jiang *et al.*, 2019; Escobar *et al.*, 2014; Xie *et al.*, 2018; Elton *et al.*, 2013).

As increasing studies have proven the indissoluble association between miR-155 and immune-related genes/proteins, it is not surprising that it plays an important role in microbial infection (Zhou, Li & Wu, 2018) (including viral infections), as host immunity is a major player in such infections (Chandan, Gupta & Sarwat, 2020). Strikingly, there are indeed several reports that have recognised the vital role of miR-155 in host responses to numerous viral diseases (Peng *et al.*, 2023). This review explores how miR-155 is associated with viruses belonging to diverse families and the infections they cause.

Material and Methods

Globally accepted and distinguished scientific databases comprising PubMed, Scopus, Google Scholar, Springer, ScienceDirect, and Wiley Online Library were used to search literature by focusing on specific terms such as "microRNA-155", "virus", "pathways", "treatment", and "biomarker". Only those studies that showed sufficient evidence of the involvement of miR-155 in host responses to viruses were considered. West Nile Virus, Ebola, etc., were excluded from the study due to limited reports. Only literature written in the English language was considered due to language barriers. This has used the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines as illustrated in Figure 1 (Page et al., 2021).

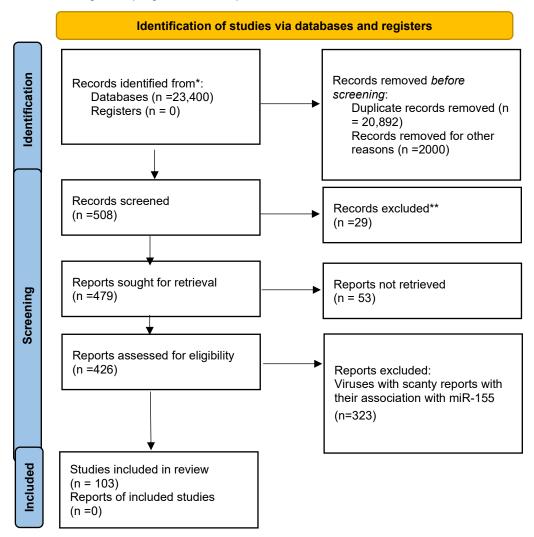


Figure 1: PRISMA Fow Diagram Depicting the Systematic Selection Process of Databases for Viral Diseases Associated with microRNA 155

DNA Viruses:

- Herpesviridae
- Herpes Simplex Virus:

Herpes Simplex Virus (HSV) causes lesions in the skin, mucosa, eyes, etc., during its primary infection. It also invades the nervous system and establishes a lifelong latent infection there (Zhu & Viejo-Borbolla, 2021). Intermittently, such latent infections might be reactivated (probably due to fever, stress, exposure to UV light, etc.) and can even invade the brain, causing Herpes Simplex Encephalitis (HSE) (Roizman & Whitley, 2013; Whitley et al., 1952). Infection in the brain in adults is generally caused by

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HSV-1, which affects the temporal lobe of the brain, causing focal haemorrhagic necrosis with fatal consequences (Whitley *et al.*, 2006). These lesions in the brain are a result of both the infection by the virus and the immune responses of the host (Wang *et al.*, 2007). MicroRNA-155 (miR-155) plays a major role in this regard. Studies show that miR-155 knock-out mice were more susceptible to HSV infection than wild-type mice. This includes both zosteriform infection (affecting the brain) and ocular infection (affecting the eyes) (Zingale, Gugliandolo & Mazzon, 2021). The host responses (such as astrocytosis and CD8+ T cell responses) were also found to be more pronounced in the wild-type mice than in those where miR-155 was knocked out (Bhela *et al.*, 2014). Reduction of CD8+ T cell responses in the miR-155 knockout host consequently also reduced cytokines such as TNF-α and/or IFN-γ (Bhela *et al.*, 2014).

A recent study proposed that during ocular infection caused by HSV-1, accumulation of CD4+ helper T cells (mainly in corneas) was diminished in microRNA-155 KO hosts than wild type6 (Bhela *et al.*, 2015). Low frequency of Th1 and Th17 cells were also noted in HSV-infected microRNA-155 KO lesions and lymphoid organs. When treated with Local antagomir-155, host cells also exhibited a reduction in neutrophil infiltration to corneas and decreased the expression of IL-16, IL-1β, IFN-γ, and IL-6 (Bhela *et al.*, 2015). The wild types are more autoimmune than the miR-155 KO host (Thompson *et al.*, 2023). Overexpression of microRNA-155 targeted and reduced SOCS1 in the microglial cell, which elevated the levels of NO and cytokines. HSV reactivation has been highly associated with stress. Interestingly, the levels of glucocorticoids increase in stress which triggers the decrease of miR-155. Hence miR155 might play an inhibitory role against HSV (Zheng *et al.*, 2012; Mulik *et al.*, 2012).

A contrasting study by Wang *et al.* stated that HSV-1 infection elevated the levels of miR-155-5p, and this consequentially facilitated HSV-1 replication (Wang *et al.*, 2019). They proposed that miR-155-5p elevated the synthesis of the SRSF2 gene, which aids in the duplication of viruses. In the brain, HSV infection has been shown to increase the expression of miR155 and different inflammatory cells (Zingale, Gugliandolo & Mazzon, 2021). All these studies together indicate that miR155 has a profound role in regulating the HSV infection-related immune responses (Table 1).

Epstein Bar Virus

Epstein-Barr Virus (EBV) is transmitted primarily through body fluids like saliva, blood, etc. It infects epithelial cells of the oropharynx and parotid gland, then infects B cells and becomes latent in the body (Damania, Kenney & Raab-Traub, 2022). However, it might cause Burkitt's Lymphoma, Nasopharyngeal carcinoma, and other lymphoproliferative diseases in immune-compromised individuals (Shannon-Lowe, Rickinson & Bell, 2017).

Several studies indicated that EBV-positive B cell malignancies cause up-regulation of miR-155 (Wood *et al.*, 2018; Lu *et al.*, 2008; Wang *et al.*, 1991). EBV carries two genes, LMP1 (Latency membrane protein 1) and EBNA2 (EBV nuclear antigen 2), which enhance the expression of miR-155 (Wood *et al.*, 2018; Lu *et al.*, 2008). Studies show that viral EBNA2 and a B cell transcription factor called Interferon Regulatory Factor 4 (IRF4) activate host genes that encode miR-155. EBNA2 also promotes the transcription of IRF-4 (L. Wang *et al.*, 2011a). Thus, EBNA2 stimulates the synthesis of miR-155 both directly and indirectly via IRF-4 (Wang *et al.*, 2011b). Studies have established that this upregulation is mediated by specific enhancers dependent on the Notch signalling transcription factor RBPJ (Wood *et al.*, 2018). The viral LMP-1 protein is a potential activator of NF-κB, which is essential for EBV-mediated immortalisation of the B cells (Awasthi *et al.*, 2022). Interestingly, miR-155 enhances NF-κB by targeting IKKB. Lu *et al.* showed that inhibition of miR-155 could resist EBV-mediated carcinogenesis in B cells by deactivation of NF-κB (Lu *et al.*, 2008). The multiple roles of miR-155 in EBV infection have been summarised in Table 1.

Table 1: A Summary of the Modulation of Host Mir-155 By Different Viruses and the Associated Changes in the Host Immune Pathways

SI. No.	Virus	Cells affected by the virus	Effect of Virus on miR- 155 and corresponding effect on body	Potential use of miR155	Ref
1.	Herpes Simplex Virus (DNA Virus)	Cells of skin, mucosa, eyes. Cells of nervous system.	 miR155 KO renders cell more susceptible to HSV. Invasion of HSV elevates miR155. Activation of host cell immune Responses (CD8+ Tcells, CD4+ T cells, TNF-α, IFN-γ, IL-1β, IL-6, IFN-γ, 1L-16 and neutrophil infiltration as an aftermath of miR155 induction. Suppression of miR155 reduces inflammation in corneas. 	Studies propose that use of antagomiRs against miR-155 reduces lesions in eyes. However targeting miR155 for HSV therapy has not yet been acknowledged.	Kim and Kim (2007) Kohlhaas et al. (2009) Mulik et al. (2012) Bhela et al. (2015) Wang et al. (2011a) Whitley et al. (1982) Whitley (2006)
2.	Epstein Bar Virus (DNA Virus)	Epithelial cells of the oropharynx and parotid gland and B cells	 Up regulation of miR-155 (promoted by viral EBNA2 protein) NF-KB activated by viral LMP-1 protein and miR155 Promotion of carcinogenesis. 	miR-155 silencing resists EBV mediated carcinogenesis.	Shannon-Lowe, Rickinson & Bell (2017) Lu et al. (2008) Momen-Heravi et al. (2014) Wang et al. (2011b) Wang et al. (1991) Wood et al. (2018) Xu et al. (2008)
3.	Hepatitis C Virus (RNA virus)	Hepatocytes	 Virus Up-regulates miR-155 via the NF-KB and p300 pathway (in HCV genotypes, 1,2 and 3) Inhibition of Apoptosis and promotion of cell proliferation by Wnt signaling pathway. Up-regulation of Inflammatory cytokines like TNF-α, IL-10, IFN-γ, IL-12. 	MiR155 knock out diminishes HCV viral load and HCV associated acute lymphoid Leukemia in vitro	Cheng <i>et al.</i> (2015) Zeisel <i>et al.</i> (2009) Zhang <i>et al.</i> (2021) Zhou <i>et al.</i> (2021)
4.	Japanese Encephalitis Virus (RNA Virus)	Neuronal cells	 Activation of miR-155 Activation of inflammation in neuronal cells by targeting SHIP-1. Upregulation of TNF-α, IL-6. IL-10, MCP-1, IFN-γ 	Overexpression of miR155 can reduce JEV in microglial cells.	Bhela et al. (2014) Campbell et al. (2011) Filgueira & Lannes (2019) Pareek et al. (2014) Rastogi and Singh (2020) Thounaojam et al. (2014) Yun and Lee (2013)

5.	SARS-CoV-2 (RNA Virus)	Alveolar cells	 Activation of miR-155 in acute and post-acute phases. Activation of IL-1 signaling pathway. MiR-155 has a role in the synthesis of ACE2 (Receptor of SARS-CoV-2) Repression of miR-155 could inhibit cytokine storm in the lungs. 	Can serve as a potential Biomarker to detect disease severity of and death. AntagomiR-155 can serve as a treatment strategy.	Arghiani et al. (2021) Donyavi et al. (2021) Ganju et al. (2021) Hu et al. (2021) Kassif-Lerner et al. (2022) Kooshkaki et al. (2020) Widiasta et al. (2020) Soni et al. (2020) Singhal et al. (2020) Hosseini et al. (2020)
6.	Influenza A Virus (RNA)	Epithelial cells of respiratory tract	 Activates miR-155 Enhancement of CD8+ T cell responses and antibody responses. Overexpression of miR-155 increases the amount of IL-6, IFN-β by targeted inhibition of SOCS-1. 	miR-155 gene incorporated in the IAV vaccine exhibits enhanced immunogenicity against the Virus.	Izzard <i>et al.</i> (2014) Shen <i>et al</i> . (2020)
7.	Hepatitis B Virus (Reverse Transcribing Viruses)	Hepatocytes	 Inhibition of miR-155 mediated through down-regulation of TLR7 miR-155 silencing impairs NK cell responses in chronic HBV patients. Over-expression of miR-155 can decrease viral load by targeted inhibition of CEBP-β and activating immune responses through JAK-STAT pathway. 	Ectopic expression of miR-155 could decrease the HBV viral load in vitro.	Chen et al. (2020) Nguyen et al. (2020) Sarkar and Chakravarty (2015) Sarkar et al. (2015) Tang et al. (2018) Yu et al. (2016)
8.	Human Immunodefici ency Virus (Reverse Transcribing Viruses)	CD4 T cells	Activation of miR-155 Activation of T cells and host immunity miR-155 can diminish HIV infection by targeting HIV-1 dependency factors	MiR155 can be used as a biomarker to detect immune Responses against HIV infection	Jin et al. (2016) Campbell-Yesufu and Gandhi (2011) (German Advisory Committee Blood, 2016) Cheng, Lin & Cheng, (2021) Dey et al. (2016) Ruelas et al. (2015) Swaminathan et al. (2012) Zhang et al. (2021)

RNA VIRUSES

- > Flaviviridae
- Hepatitis C Virus

The Hepatitis C virus (HCV) infects hepatocytes causing chronic liver inflammation, and is transmitted either vertically from pregnant mother to child or horizontally through contaminated blood and semen (Cacoub & Comarmond, 2017; Ganta *et. al.*, 2018).

Numerous studies have found that miR-155 levels are upregulated during HCV infection, primarily mediated by NF-kB (Bala *et. al.*, 2012; Zhang *et. al.*, 2012). Zhang *et al.*, 2021 reported that this NF-KB mediated up-regulation of miR-155 was increased by p300 (Zhang *et. al.*, 2012). A rise in miR-155

levels resulted in the accumulation of β-catenin and an increase in the levels of c-myc and survivin, and this consequently inhibited apoptosis and promoted proliferation of the cells via the Wnt signalling pathway (Zhang et. al., 2012). On the other hand, inhibition of miR-155 triggered G0/G1 arrest (Zhang et. al., 2012). In another study from Egypt, Hassan et. al., 2020 showed that knock out of miR-155 in vitro diminishes HCV viral load in HCV associated acute lymphoid leukemia (Hassan et. al., 2020). In addition, Bala et al. (2012) demonstrated that increased miR-155 levels in HCV-infected cells augmented inflammation by up-regulation of the cytokine TNF-α and resulted in Inflammation mediated hepatocyte damage Zhou et al. (2021) also reported a similar rise in TNF-α corresponding to higher levels of miR-155 in CD14+ monocytes from HCV-infected patients They reported increased expression of the JNK, IL-10 and IL-12, and Tim 3 genes Cheng et al. (2015) after a few years, found that Tim-3 is overexpressed in HCV infected natural killer (NK) cells where miR-155 was down-regulated, but reconstitution of miR-155 enhanced IFN-Y productionvia phosphorylation of signal transducer and activator of transcription 5 (STAT-5). All these together indicate that miR155 facilitates the progression of disease during HCV infection (Table 1). Interestingly, El-Ekiaby et al. (2012) reported a HCV genotype dependent differential modulation of miR-155. Precisely, they found that miR-155 levels were down-regulated in peripheral blood mononuclear cells (PBMCs) infected with particularly HCV genotype 4 (GT4) (in contrast to infection with HCV genotypes 1, 2, and 3 where miR155b was up-regulated).

Japanese encephalitis virus (JEV)

Japanese encephalitis (JE) is a kind of viral disease in which the flavivirus is transmitted by mosquitoes and infects neuronal cells (Yun & Lee, 2013) It invades the central nervous system resulting in the inflammation of the brain and might lead to serious conditions like encephalitis (Filgueira & Lannes, 2019). Campbell *et al.* (2011) reported that fatality in JEV-infected individuals can soar up to 30% (Campbell *et.al.*, 2011).

Thounaojam *et al.* (2014) found that miR155 levels were increased during JE infectionThey also proved that thisincrease in miR-155 levels triggers Inflammation in neuronal cells by blocking its target SHIP (Src Homology 2 containing inositol Phosphatase-1) and enhancing the synthesis of inflammatory cytokines (IL-6,TNF- α , MCP-1) and interferon- β through activation of TBK-1 (Tank Binding Kinase-1). They proposed that modulation of miR-155 could be used as a therapeutic option in managing JE (Campbell & Gandhi, 2011). Additionally, Pareek *et al.* (2014) affirmed that over-expression of mir155 in microglia is associated with the reduction of JEV reproduction and elevation of IFN- β , TNF- α , IL-10, and other interferon-stimulated genes. They proposed that induction of miR-155 may be beneficial in limiting the virus). Another independent report by Rastogi reveals that JEV-mediated up-regulation of miR-155 inhibits the non-canonical NF-kB pathway via TRAF-3 and PELI-I in human microglial cells (Rastogi & Singh, 2020).

> Coronaviridae:

SARS-CoV 2:

The novel SARS CoV-2 infection caused a severe pandemic and almost crippled the world since 2019 when it was first detected. It is a type of Corona Virus that has been found to affect the respiratory systems in humans and bears a history of zoonotic transfer from bats. The manifestations in the host are largely dependent on the host's immune responses post-infection. This ranges from low or moderate infection causing fever, cough, loss of smell and taste, etc., but may even lead to pneumonia-like symptoms and death (Hu *et al.*, 2021). The severity of this infection is generally caused by a cytokine storm that takes place as an aftermath (Singhal, 2020; Kooshkaki *et al.*, 2020).

Donyavi et al. (2021) established that the levels of miR-155-5p were significantly high in the Peripheral Blood Mononuclear cells (PBMCs) from COVID-19 patients in acute and post-acute phases than in healthy controls. He proposed that it could be used as a potential circulating biomarker to detect the severity of the disease Several other independent studies also had similar findings. They proposed that the up-regulation of miR-155 is in coordination with the heightened Inflammation among acute and post-acute patients (Xiao et. al., 2019; Han, Li & Jiang, 2016). The increased levels of miR-155 ininfected patients could indicate body inflammation and cardiac myocyte-specific damage. Kassif-Lerner et al.

(2022) showed that miR-155 could be used as a prospective biomarker for predicting death in SARS-CoV-2 infected patients. Arghiani, Nissan and Matin (2021); demonstrated that the upregulated miR155 levels trigger the IL-1 signaling pathway, and therefore, its appropriate management could limit the Inflammation caused by the virus. Interestingly, Soni *et al.* (2020) validated that the repression of miR-155 could decrease the lung cytokine storm induced by covid-19Strikingly, in addition to this, Widiasta *et al* (2020).; proved that miR-155 had a role in the synthesis of ACE2 (angiotensin-converting enzyme 2) which happens to be a receptor for SARS-Cov 2 and facilitates its entry into host cells. Thus, antagomiRs against miR-155 could be used as a treatment strategy to combat Sars-CoV2 infection.

> Orthomyxoviridae:

• Influenza A Virus:

The Influenza A Virus (IAV) is one of the four influenza viruses that affects the epithelial cells of the respiratory tract (Shen *et al.*, 2020). Though rarely may also lead to acute respiratory distress syndrome (ARDS) and death. miR155 has been extensively studied in the context of IAV. Infection with IAV elevates mir155 (Shen *et al.*, 2020). It enhances CD8+ T cell responses and specific antibody responses inpatients infected with IAV (Izzard *et al.* 2014). Izzard *et al.* (2014) proposed that overexpression of miR-155 in IAV infected cells consequentially facilitated the amount of IL-6 and IFN-β in the human body system by targeted inhibition of SOCS1. Shen *et al.* (2020) showed that miR155 enhances inflammatory responses against IAV by targeting S1PR1 (sphingosine-1-phosphate receptor 1 In two independent studies, Rodriguez and Thai *et al.* revealed that the miR-155 KO host could not create a proper humoral defence against IAV infection. On the other hand, Gracias *et al.* (2013) found that miR155 enhances influenza-specific CD8+T responses cells in transgenic mice. Izzard *et al.* (2014) designed a vaccine where he integrated the miR-155 gene with the IAV genome and showed enhanced immunogenicity against the virus.

Reverse Transcribing Viruses

> Hepadnaviridae:

Hepatitis B virus:

The hepatitis B virus (HBV) is a DNA virus with a genome that is partially double-stranded. It infects the liver cells (hepatocytes) that may lead to fatal liver diseases like Liver Cirrhosis and Hepatocellular carcinoma (Nguyen *et al.*, 2020). The outcome of this infection is highly dependent on the host's immune responses, so miR155 plays a major role in it (Nguyen *et al.*, 2020; Tang *et al.*, 2018).

Several studies independently showed that HBV suppresses miR155 in Peripheral Blood mononuclear cells (PBMCs) and liver cells (Yu et. al. 2016; Ge et. al., 2017). They have proposed that the virus paralyses the host immune system and inflammatory responses to establish itself since various cytokines and Interferons were also found to be down-regulated during infection (Yu et. al. 2016; Ge et. al., 2017; Su et al., 2011). Sarkar et al (2015) proposed that this down-regulation of miR155 resulted as an aftermath of TLR7 inhibition by HBV (2015). Ge et al. showed that reduced expression of miR155 impairs Natural Killer cell responses in chronic HBV patients (2017), whereas Chen et al. 2020 showed that microRNA-155 regulates HBV replication by contributing to autophagy induced by SOCS1 signalling (Chen et. al., 2020).

Su *et al.* overexpressed miR155 ectopically in hepatoblastoma cell lines and found that it mildly inhibits HBV by activating innate immune responses mediated through the JAK-STAT pathway. Likewise, Sarkar *et al.* also found that overexpression of miR155 suppresses HBV replication through targeted inhibition of the transcription factor- CEBP-β (Sarkar *et al.*, 2015).

Reoviridae:

Human Immunodeficiency Virus:

Human Immunodeficiency Virus (HIV) is communicated through body fluids like blood, semen etc. and infects the CD4+ T cells in the blood, thereby reducing their count. This results in severe immune deficiency leaving the body susceptible to secondary infection (German Advisory Committee Blood,

2016). When the CD4+ T cell count drops below 200 per mm3 of blood, the condition is termed Acquired Immunodeficiency Syndrome (AIDS) (Battistini *et. al.*, 2022).

Jin et al. (2016) suggested that the levels of miR-155 are up-regulated in the PBMCs of HIV-1 positive patients and that this could be associated with the activation of T cells. Zhang et al. (2021) also reconfirmed this finding, stating that higher miR-155 levels could be an indicator of immune activation (Zhang et al., 2021). Jin et al. (2016) further proposed that miR-155 could be used as a biomarker to detect immune responses against HIV-1 infection. Another independent study established that miR-155 has the potential to reinforce latency in HIV patients who had a sudden reactivation of infection following latency (Ruelas et al., 2015). Swaminathan et al. (2012) showed that miR-155 could diminish HIV-1 infection by targeting numerous HIV-1 dependency factors. In another study from the Indian Subcontinent, Dey et al. (2016) established that the levels of miR-155, along with miR-382-5p, were significantly higher in HIV patients with regular disease progression compared to long-term non-progressors, and these miRNAs could be used as an indicator to distinguish the two groups.

Discussion

The outcome of viral infections is largely dependent on the host. Evidently, host factors, if managed properly, can be effectively used to curb viral pathogenesis. Because of their potential to regulate gene expression, microRNAs are currently the focus of modern antiviral research. These small RNAs and their inhibitors can be efficiently delivered to the host via exosomes and liposomes (Momen-Heravi *et al.*, 2014). In this respect, miR-155 has been profoundly studied in several viral infections (Table 1). Its capacity to trigger numerous inflammatory cytokines and antiviral interferons is manifold. It can effectively stimulate the humoral (specific antibodies) and cell-mediated (CD4+ and CD8+ T cells) arms of adaptive immunity (Haasch *et al.*, 2002; O'Connell *et al.*, 2007). Though it is highly likely that miR-155 could favour the host in the process of viral elimination, there are a number of viruses (HSV, EBV, HCV, SARS) where it increases the chances of amplified inflammation and carcinogenesis. Antagonists against miR-155 have proven to have promising results in limiting EBV and HCV-mediated carcinogenesis and also cytokine storms during SARS-CoV-2 infection (Lu *et al.*, 2008; Widiasta *et al.*, 2020). Appropriate testing through human clinical trials could open up new treatment options.

After reviewing several literatures available online, this could not find any correlation between the mechanisms of miR-155 mediated viral clearance and the type of cells that harbour the virus. Of the studied viruses, some affect the neuronal cells, some affect the immune cells, some paralyse the cells of the respiratory tract, and others affect hepatocytes. Interestingly, the level of miR-155 is elevated in all of these cells upon viral invasion, with the exception of HBV in hepatocytes, where miR-155 is down-regulated. Obviously, the viral nucleic acids trigger the expression of Toll-like receptors (TLR3, 4, 7, 8), which eventually activate miR-155 through the downstream TRIF-MyD88 signalling pathway (Jafarzadeh *et al.*, 2021). However, HBV suppresses TLR7 and thus represses miR-155 (Sarkar *et al.*, 2015).

miR-155 has potential in viral clearance in the case of both HBV and HIV. Interestingly, both of these viruses have shared means of transmission, and about 10-20% of HIV-positive patients across the globe are co-infected with HBV (Cheng, Lin & Cheng, 2021). Activation of miR-155 could be a novel treatment option in such cases, as miR-155 imparts both anti-HBV and anti-HIV effects by targeting key HIV and HBV dependency factors (Swaminathan *et al.*, 2012; Sarkar *et al.*, 2015).

A very significant finding in this regard is that the incorporation of miR-155 in the IAV vaccine enhances its immunogenicity. Thus, the use of miR-155 as an adjuvant while designing vaccines or immune therapy could also be tested in other viral infections.

Owing to its vital role in the mediation of inflammation, miR-155 could also serve as a biomarker to trace disease progression. Excess miR-155 levels are suggestive of severe damage to the host, as has been proved in the case of HIV (Jin *et al.*, 2016). In SARS-CoV-2 infection, it could even predict death (Donyavi *et al.*, 2021; Soni *et al.*, 2020).

Conclusion

MicroRNA-155 exhibits a multifaceted role during viral infections, whereby in the case of certain viruses, it supports viral pathogenesis, while in others it prevents it. Nevertheless, it can also be used as a biomarker. Appropriate studies in animal models and clinical trials could offer promising insights. This is particularly important as the exogenous control of miR-155 expression might provide a new alternative to confine viral proliferation.

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Abbreviations: HSV-Herpes Simplex Virus, EBV-Epstein Bar Virus, JEV-Japanese Encephalitis Virus, HBV-Hepatitis B Virus, HCV-Hepatitis C Virus, HIV- Human Immunodeficiency Virus, SARS-CoV 2-Severe Acute Respiratory syndrome corona virus 2.

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