# Exhibit 436

## Report 16: MicroRNA, the Hidden RNA in the Pfizer Vaccine

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# Report 16: Daily Clout Report: MicroRNA, the Hidden RNA in the Pfizer Vaccine

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**DailyClout 5/12/22 Report:** MicroRNA, the Hidden RNA in the Pfizer mRNA Vaccine

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## Introduction

MicroRNAs (miRNAs) are a class of non-coding RNAs that play a role in a multitude of cellular processes. The first miRNA was discovered in 1993 in a nematode (O'Brien et al., 2018; Lee et al., 1993). The first viral miRNA was only identified in 2004 (Pfeffer et al., 2004). Thus, the history of miRNAs is short, and therefore, limited scientific data has been gathered on this special class of RNA.

On average mature miRNAs are just 19-22 nucleotides in length (O'Brien et al., 2018; Mallick et al., 2009). By comparison with messenger RNA (mRNA), a coding RNA, the average mature mammalian mRNA is typically 2,200 nucleotides long. The full-length mature SARS-CoV-2 mRNA is about 29,900 nucleotides long while the Pfizer vaccine spike protein mRNA is 4,284 nucleotides long (Nance et al., 2021; Kim et al., 2020).

MicroRNAs are highly stable molecules, contrary to mRNA molecules (O'Brien et al., 2018). The SARS-CoV-2 spike protein mRNA is unstable (Pallesen et al., 2017), which is why Pfizer made modifications to stabilize it and prevent it's degradation in the body.

Although miRNAs are small, they are abundant and critical for normal animal development. They function in gene expression, mRNA stability and degradation, regulation of translation (protein production), and wound healing. They can act as chemical messengers to mediate cell-cell communication and can be released into the extracellular fluids and delivered to other cells and organs, thus exhibiting hormone-like activities. It is estimated that 60% of mammalian genes are influenced by miRNAs which affect regulatory pathways including cancer, apoptosis (cell death), metabolism and development. MicroRNAs have been detected in plasma and serum, cerebrospinal fluid, saliva, breast milk, urine, tears and seminal fluid (Marchi et al., 2021; Abedi et al., 2021; Khan et al., 2020; O'Brien et al., 2018).

There is a delicate balance within the miRNA regulatory system. There is an interaction of miRNAs with their target genes, mRNA molecules, other endogenous miRNAs as well as exogenous miRNA and other nucleic acids (viral and bacterial). It is a highly dynamic system that is dependent on many factors including miRNAs' relative abundance. O'Brien et al. (2018) point out that alterations in host miRNA levels would interfere with specific cellular processes crucial for host biology. In fact, evidence indicates that miRNA expression and dysregulation are associated with the development of pathological processes and chronic diseases, including viral infections and the diseases caused by viral infections (Marchi et al., 2021; Zhang et al., 2021; Giardi et al., 2008).

It has been shown that miRNAs play a crucial role in host antiviral responses and viral pathogenesis of various viruses. MicroRNAs can modulate innate and adaptive immunity by affecting protein levels. Viral genomes can express their own

miRNAs and can "hijack human miRNAs to the repertoire of the infected cells" (Abedi et al., 2021). MicroRNAs are known to play a role in the pathogenesis of other coronaviruses, such as SARS-CoV and the Middle East Respiratory Syndrome coronavirus (MERS-CoV) that caused epidemic outbreaks in 2003 and 2012, respectively (Mallick et al., 2009; Hasan et al., 2014). The SARS-CoV-2 genome, including the spike protein mRNA, have been shown to encode their own miRNAs, some of which interact with human miRNAs (Liu et al., 2020).

SARS-CoV-2 encoded miRNAs can target different organ-specific cellular functions including insulin signaling and heart development related pathways which might lead to diabetes and consequences similar to viral myocarditis, respectively. These viral encoded miRNAs might also target genes associated with brain development which might provide a clue about neurological signs like headaches, vomiting and nausea (Khan et al., 2020).

Viral miRNAs encoded by the SARS-CoV-2 genome can target several host genes. One study predicted that 3,377 human genes were potential targets of 170 miRNAs produced from the SARS-CoV-2 genome. Also, 10 human miRNAs were identified that possess binding sites across the SARS-CoV-2 genome. Said another way, there are human miRNAs binding to the SARS-CoV-2 mRNA and there are SARS-CoV-2 encoded miRNAs binding within the human genome (Abedi et al., 2021). Using prediction analysis (theoretical), Sacar Demirci et al. (2020) identified 67 human miRNAs with potential targets in the SARS-CoV-2 spike protein region. If human miRNAs are binding to regions within the spike protein mRNA, then what does a spike protein mRNA vaccine do to the delicate balance within the miRNA regulatory system that O'Brien et al. (2018) described?

"Manipulating the level of host miRNAs could have unintended consequences because the physiological functions of the miRNAs might be altered or viral pathology might be enhanced" (Mallick et al., 2009).

It is clear that viruses encode their own miRNAs that can interact with host DNA, mRNA and miRNAs thereby altering the delicate balance of the miRNA regulatory system. Mishra et al. (2021) proposed that the SARS-CoV-2 spike protein itself is able to modify the host exosomal cargo (with two human miRNAs, miR-148a and miR-590) that get transported to distant uninfected tissues and organs to "initiate a catastrophic immune cascade within the central nervous system" (Mishra et al., 2021). In other words, miRNAs encoded within the SARS-CoV-2 spike protein mRNA cause the infected host cells to package human miRNAs, miR-148a and miR-590,

into exosomes (vesicles that release cellular molecules into the extracellular fluid) for export out of the cell to the central nervous system where they initiate pathogenesis.

When a vaccine receives a Pfizer BNT162b2 mRNA vaccine, they not only receive the vaccine's mRNA, they also receive an unknown number of miRNAs, hidden within the sequence of the vaccine mRNA. How do the miRNAs introduced by the Pfizer vaccine disrupt the balance of the host miRNA system? What pathogenesis do they cause? What are the long-term toxicity, carcinogenicity and pharmacological concerns? None of this was studied by Pfizer. In fact, there is no mention of miRNAs in the Pfizer document 2.4 NONCLINICAL OVERVIEW ( https://phmpt.org/wp-content/uploads/2022/03/125742_S1_M2_24_nonclinical-overview.pdf (https://phmpt.org/wp-content/uploads/2022/03/125742_S1_M2_24_nonclinical-overview.pdf) ).

Good science demands answers to these important questions, and the answers should have been obtained before injecting hundreds of millions of people globally (billions of doses) with such an experimental substance.

In summary, miRNAs are being recognized as an enormously important component of gene expression and regulation and are associated with many diseases as well as host immunity (Zhang et al., 2021; O'Brien et al., 2018). It has been demonstrated that SARS-CoV-2 encoded miRNAs, including miRNAs from the spike protein region, bind to the host genome and that host miRNAs bind within the SARS-CoV-2 genome. But there is a delicate balance within the host miRNA regulatory system and it has been shown that these exogenous miRNAs, as well as exogenous mRNA encoding them, alter this delicate balance with potential deleterious consequences (O'Brien et al., 2018). This undeniably important biomolecule was not mentioned by Pfizer.

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## 1 reply added

Dr. Eleanor Hall June 7, 2022 Reply

Great article, complex as it may be but provokes further research and understanding of the role of miRNA. Of note, please look at the following paragraph because I think the intent should be: “When an individual (or person) receives a Pfizer….?”
“When a vaccine receives a Pfizer BNT162b2 mRNA vaccine, they not only receive the vaccine’s mRNA, they also receive an unknown number of miRNAs, hidden within the sequence of the vaccine mRNA. How do the miRNAs introduced by the Pfizer vaccine disrupt the balance of the host miRNA system? What pathogenesis do they cause? What are the long-term toxicity, carcinogenicity and pharmacological concerns? None of this was