

# The Genetics of the Influenza Virus

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## Abstract

The purpose of this project is to study the genetics of the influenza virus. This is an important subject because this virus is well known and has a history of causing global sickness and death. For my research, I utilized academic resources to discover the structure of the influenza virus and its methodology of infiltrating and infecting the human body.

## Introduction

Influenza is a virus that is most common in the fall and winter of each year, but can be detected year-round. Activity usually begins in October, peaks between December and February, and can last as late as May [2]. In humans, it affects the respiratory system causing symptoms that include:

Fever	Cough	Sore throat
Rhinorrhea	Myalgias	Headaches
Fatigue	Vomiting	Diarrhea

It is important to study the influenza virus for several reasons, the most important being prevention of disease and possible death.

In 1918, the “Spanish influenza,” caused by the H1N1 influenza virus, caused a major global impact where an estimated 40 million people died in less than a year. [5]

Last year, the CDC estimates the influenza virus is associated with 35.5 million illnesses, more than 16.5 million medical visits, 490,600 hospitalizations, and 34,200 deaths in the US alone. [2]

## Discussion

### Structure of Virus

The genetic information of influenza virus is 8 segments of single-stranded RNA, which allows the virus to exchange genetic information with other influenza viruses. [1] Each RNA segment codes for a specific protein. The exact arrangement of the strands of RNA is unknown, but are listed below in order from largest to smallest for simplicity. See Figure 1.

1. PB2 (basic polymerase 2), located on segment 1, controls the recognition of host-cell RNA.
2. PB1 (basic polymerase 1), on segment 2, catalyzes nucleotide addition.
3. PA, an acidic protein on segment 3, is thought to possess transcriptase protease activity.
4. HA (haemagglutinin), on segment 4, is responsible for binding to sialic-acid receptors and entry into host cells. This is divided into two domains (or subunits) HA1 and HA2.
5. NP (nucleoprotein) is encoded by a single segment of segment 5, which binds to the viral RNA.
6. Neuraminidase (NA), on segment 6, is involved in budding of new virions from infected cells.
7. The seventh segment (M) encodes two proteins that share a short overlapping region: the matrix protein M1 encodes the main component of the viral capsid, and M2 is a membrane protein and functions as an ion channel.
8. Segment 8, (NS) is the smallest segment that encodes NS1 and NS2. NS1 (non-structural protein) controls cellular RNA transport, splicing and translation. NS2 is an overlapping reading frame and minor component of the virus, whose function is unknown. [4]

### How does the virus work?

Once the influenza virus enters the human body, it attaches to cells in the respiratory tract. As seen in Figure 2, the haemagglutinin (HA) surface proteins of the virus bind to sialic acid receptors of our cells, and essentially unlock the cell. This allows the virus to invade the cell and take over. Once inside the cell, the virus releases its RNA into the host cell's nucleus and uses host cell to create duplicate copies of the virus. Newly formed virions emerge out of the infected cell, where the neuraminidase (NA) cuts the virion's attachment to the cell. [3]

The influenza virus undergoes continuous mutations in the genes that code for antibody binding sites. These changes occur at the HA and NA surface glycoproteins. [6] These mutations allow the virus to evade the host's defenses.

Fig 1: Structure of Flu Virus [4], shown in order from left to right.

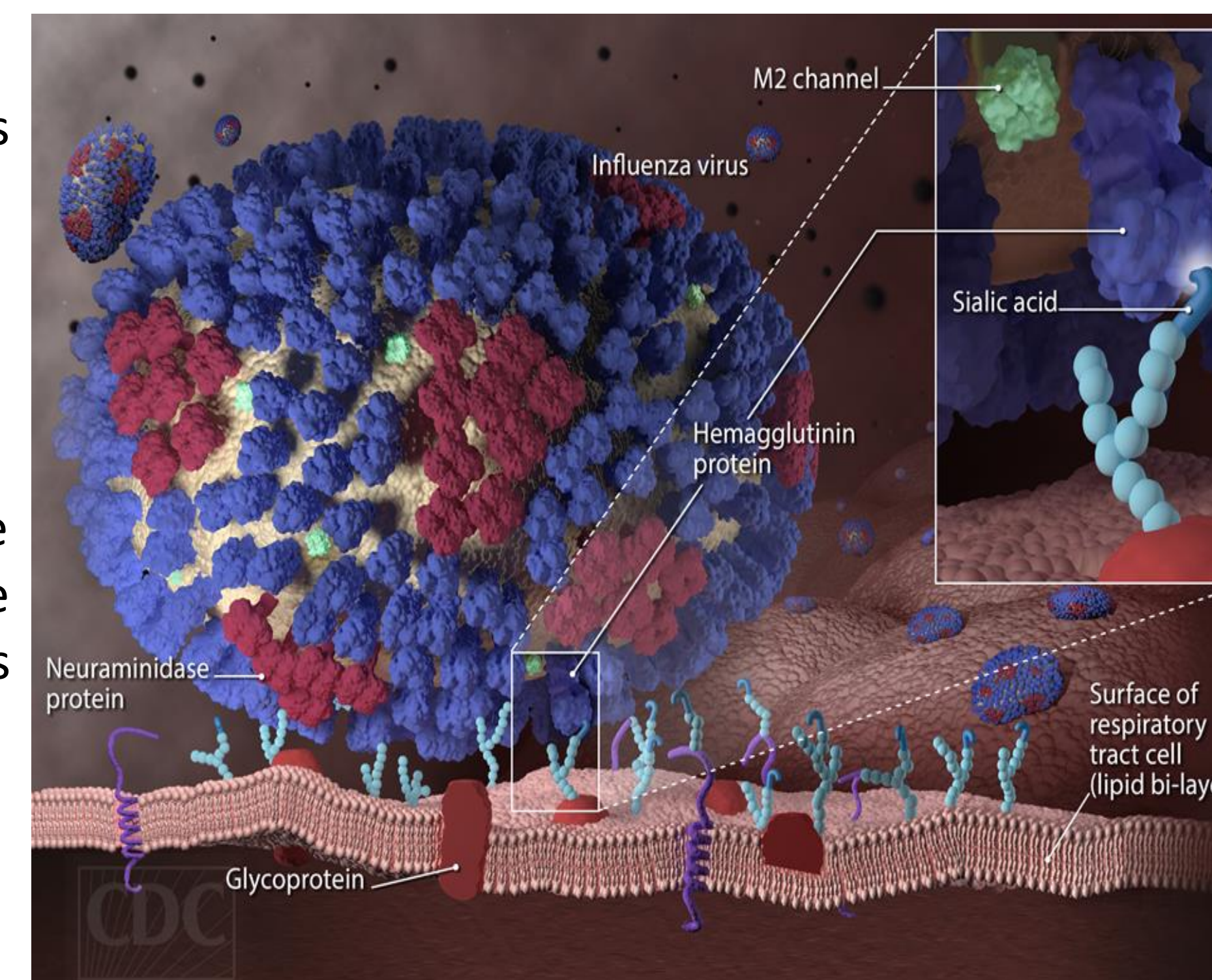
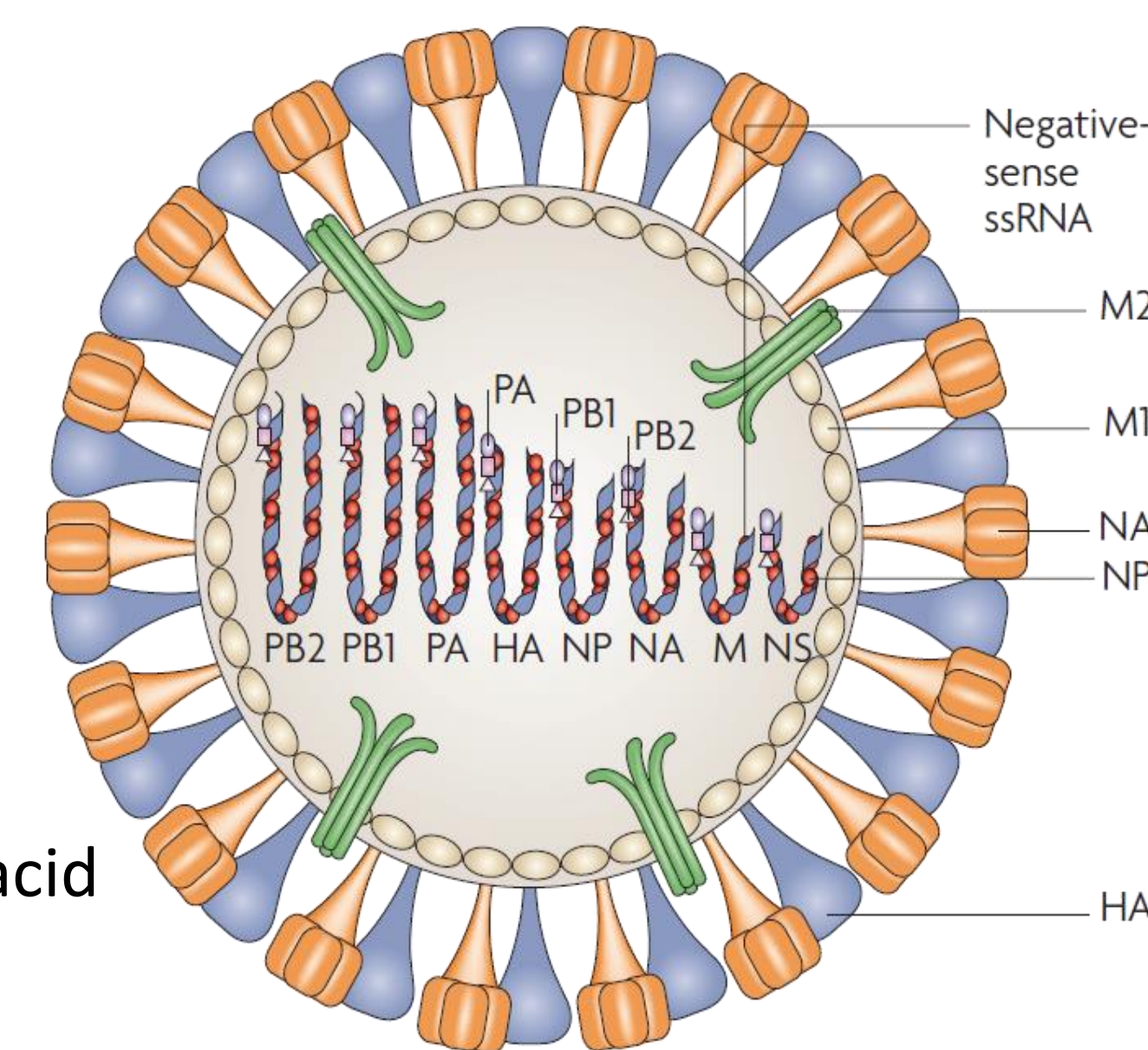


Fig 2: An Influenza Virus Binds to a Respiratory Tract Cell [2]

## Conclusion

The influenza virus is composed of 8 segments of single-stranded RNA. The virus continuously mutates its surface proteins to evade host defenses. Once inside the body, it attaches to cells in our respiratory tract, causing a wide range of symptoms. In some cases, it has even been known to cause widespread epidemics and death.

History reveals several instances where possessing more information about the influenza virus would have been beneficial. Therefore, it is important that we continue to study the influenza virus and develop new protocols, treatments, and preventative measures. By understanding the genetics of the influenza virus, we are better prepared to face the challenges the virus poses as it continues to mutate and evolve.

## References

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