CRISPR Cas9 as a Possible Mechanism to Modify Influenza Viral Mutation

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Influenza virus is a single-stranded negative RNA virus, divided into three types, A, B, and C (Shao, Li, Goraya, Wang, & Chen, 2017). This research focused on influenza type A, which mainly affects humans, and its mutations occur primarily through the HA and NA proteins (Shao, Li, Goraya, Wang, & Chen, 2017). CRISPR Cas9 is a gene-editing tool that can be used to modify or remove genes (Redman, King, Watson, & King, 2016). The purpose of this research was to determine how CRISPR Cas9 could be a viable option in preventing a mutation in Influenza type A virus. To perform this research, information was gathered from scientific articles and databases on the Influenza virus, its mutations, and CRISPR Cas9. Additionally, the changes in genetic sequences of the HA and NA segments of five different Influenza A subtypes were aligned and studied. To determine which subtypes were going to be studied, a table was made that includes the different Influenza A subtypes. Two additional tables were created with the different types of CRISPR mechanisms, divided by class and type. Finally, the last results are the genetic sequences of 5 different Influenza A subtypes aligned, presenting the conservation. The GeneDoc results were key in determining where the CRISPR Cas9 be implemented since it displays the location of the mutations that occurred in the genome segments as new subtypes appeared.

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