



**CALIFORNIA STATE SCIENCE FAIR  
2010 PROJECT SUMMARY**

<b>Name(s)</b> <b>Jnaneshwar T. Weibel</b>	<b>Project Number</b> <b>J0425</b>
<b>Project Title</b> <b>Comparison of Antigenic Drift and Shift in Influenza Virus Strains</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives/Goals</b> The objectives are to determine whether the 2009 H1N1 swine flu evolved by antigenic shift or antigenic drift and to explore the data and tools provided by the National Center for Biotechnology Information (NCBI). The hypothesis is that the nucleotide base pair (bp) sequence of the hemagglutinin protein (HA) gene of the 2009 H1N1 swine flu virus will have significantly more differences than the HA gene of the H1N1 viruses used in the composition of flu vaccines over the past ten years.</p> <p><b>Methods/Materials</b> The composition of the influenza vaccine recommended by the World Health Organization (WHO) over the past ten years was researched. The genetic sequence of the HA gene for the H1N1 subtypes were queried from the Influenza Virus Sequence database and BLAST from NCBI and compared using the Multiple Alignment tools. The number of nucleotide base pairs that differed from the consensus sequence were identified.</p> <p><b>Results</b> The HA gene segment is 1782 nucleotide base pairs (bp) in length. The four H1N1 virus strains prior to 2009 ranged from 8 to 43 nucleotide bp differences from the consensus, while the 2009 H1N1 virus gene had 382 bp differences. The 2009 H1N1 virus HA gene had from 9 to 47 times more bp differences than the previous H1N1 viruses studied.</p> <p><b>Conclusions/Discussion</b> These results support the hypothesis that the 2009 H1N1 swine flu virus evolved via antigenic shift due to the significantly higher number of bp differences in the genetic sequence. Antigenic shift occurs when a virus abruptly changes genetically when viruses from two different animal species infect the same host cell and the genes mix. Antigenic drift occurs when a virus slowly evolves over time and is represented by less change in the genetic sequence. NCBI provides access to a large database of information with tools useful for analyzing trends in virus evolution which can assist in determining vaccines and fighting influenza.</p>	
<b>Summary Statement</b> The project is about comparing the genetic sequences of the 2009 H1N1 Swine Flu to historical H1N1 influenza vaccine strains.	
<b>Help Received</b> My parents criticized my writing. Dr. Jacob Varkey and Dr. Jianmin Zhong of Humboldt State University answered questions.	