Vaccine Design Using in silico Tools: Novel Influenza Vaccines with Genetic Adjuvant

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Worldwide, Influenza kills more than 250,000 yearly. Despite this, the approach to flu vaccination has not changed in several decades. One novel technique in vaccine development is the use of a DNA vaccine. DNA vaccines require less time and resources to produce, as well as allowing for recombinant techniques to increase multivalency. One drawback of DNA vaccines is the ineffectiveness of traditional adjuvants however, the use of an alternative aggregation-based genetic adjuvant has been shown to be effective. This project aims to use in silico tools to design more effective Influenza vaccines and adjuvants. Using VioliNet databases and search tools, a chimeric DNA plasmid protecting against pandemic strains of the flu was designed. This plasmid would produce two proteins that elicit protective antibodies against the five most pathogenic strains. In the process of designing of this plasmid, a program for identifying splice sites was created. Additionally, a program for creating vaccines to respond to geographically centered epidemics was created. It is based on a prediction algorithm for genetic drift that determines likely paths of mutation. As a genetic adjuvant, a 21 nucleotide aggregation domain was designed using the PASTA aggregation prediction program. The resulting sequence was constructed using a gene synthesis kit and incorporated in E.Coli. Aggregation in the isolated protein solution was verified using a spectrophotometer. The process and tools used and created in this project can be expanded for the design of vaccines for other highly variable diseases, such as Hepatitis C and HIV.