CALIFORNIA STATE SCIENCE FAIR
2015 PROJECT SUMMARY

Name(s)

Min Jean Cho

Project Number

35358

Project Title

Identification of Pathogen and Anti-Ebola Drug Targets Using Bayes' Theorem and Information Entropy

Abstract

Objectives/Goals

The objective is to predict anti-Ebola virus drug targets and to design RNAi-based small RNA drugs and mimotope-based peptide vaccines.

Methods/Materials

A total of 262 RNA/protein sequences of Ebola virus RNA-dependent RNA polymerase (RdRp) and glycoprotein (GP) were downloaded from the public database of viral pathogens (ViPR database). Conserved sequence region was searched using information entropy because this low information region could indicate highly conserved region across all known strains of Ebola virus. For antisense miRNA drugs, binding strength of antisense miRNA to its complementary target sequence was determined from GC% of predicted miRNA sequence. For the effective binding of anti-Ebola ligand and anti-Ebola antibody, its target region (ligand-binding site or epitope for antibody binding) should be located at the surface of Ebola viral proteins, thus the hydrophobicity of protein regions was determined according to the method of Kyte and Doolittle.

Results

Anti-Ebola drug targets were identified from the genome sequences of Ebola virus using information entropy. A total of 15 anti-Ebola miRNA targets were identified from three low entropy regions of Ebola virus RdRp RNA sequences, and three miRNA drugs were designed. Also, among highly conserved regions of RdRp protein sequences, one region was identified as a candidate target for ligand-based drugs. For preventing Ebola infection, three mimotope-based peptide vaccines were designed from the protein sequences of Ebola virus glycoprotein. The target sites of these anti-Ebola peptide vaccines were conserved in all known subtypes of Ebola virus and was predicted to be surface-exposed regions.

Conclusions/Discussion

Along with Bayesian sequence identification method, the entropy-based method for predicting drug targets and designing miRNA drugs and peptide vaccines will be a valuable tool for improving public health and for developing effective drugs against life-threatening pathogens such as Ebola virus.

Summary Statement

I used Information Entropy to design anti-Ebola miRNA drugs and mimotope-based vaccines, and to predict ligand binding sites.

Help Received