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Computational methods for assessing host specificity/ pathogenicity in Ebolavirus strains

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Ebolavirus causes an extremely deadly form of hemorrhagic fever in humans and primates, with mortality rates exceeding 90 percent in some outbreaks. As BSL-4 agents, these RNA viruses are both expensive and difficult to work with in the laboratory. Of the five known strains, only Reston ebolavirus appears to be asymptomatic in humans, while remaining fatal in primates. Ebolaviruses are highly mutable and exhibit hundreds of SNPs across their 14 kb genome among various strains. This study examined the genome and proteome of all known strains of Ebolavirus to identify possible locations that might explain the decreased pathogenicity of the Reston strain in humans. SNPs were identified with 100 percent correlation to all isolates of Reston ebolavirus but complete absence in any other non-Reston isolate. These SNPs were correlated with corresponding amino acid changes determined to be either synonymous or non-synonymous changes. As a surrogate for structural change, hydrophobicity plots were made for each of the viral protein sequences in all strains, and this data was transformed using a continuous wavelet transformation. The composite wavelets were correlated between Reston and non-Reston isolates to identify areas of low correlation which may indicate structural variation between isolates. These regions of potential structural change were then correlated back to the amino acid and SNP substitutions. From this analysis several key SNPs were identified which may correspond to host specificity. Gaining an understanding of these differences may lead to safer experimentation using the Reston strain and may aid in the development of novel treatments.

Biography

Dr. Campbell is a currently a Principal Molecular Biologist with Noblis and has a decade of professional experience in bioinformatics. Her research has focused on the analysis of population based experiments designed to study both human disease and animal models of disease. Projects have involved in silico identification of medical countermeasures and pathogen identification and informatics research for a wide variety of complex neurological disorders. Her research work has encompassed both laboratory experiments and statistical and bioinformatics analysis of several important diseases including Ebola, plague, Gaucher's disease, multiple sclerosis, chronic fatigue syndrome, and neurofibromatosis.