
SEQUENCING AND CHARACTERIZATION OF CANINE VIRAL GENOMES

Stephen Torna, Rocky Mountain College, Billings, MT. 59102

Josiah Hamilton, Rocky Mountain College, Billings, MT. 59102

Dr. Holly Basta, Rocky Mountain College, Billings, MT. 59102

Some viruses, like canine parvoviruses, are known to infect both human and canine hosts. Currently there is a significant lack of information about canine viruses, as a result there is no conclusive way to evaluate whether a virus is capable of cross species infection. Another problem that stems from this lack of information is that screening for viruses in sick canines is rarely practiced and instead antibiotics are almost exclusively the choice remedy. Improper use of antibiotics will not stop viral infection and may create antibiotic resistance as well as cause further discomfort to sick dogs. The goal of this research project is to isolate and sequence viral strains, to drastically improve the genome databases for other scientists to use, and conduct phylogenetic analysis to characterize found viruses. To accomplish these goals, fecal samples will be taken from sick and healthy canines noting in detail any symptoms the dog is exhibiting. The viral DNA/RNA is extracted and purified using a specially designed kit. After extraction the viral DNA/RNA is amplified and the products are sequenced.

The newly sequenced viruses will be compared to each other as well as known strains to aid in characterizing their type. Using the information that corresponds to each sample, characterized viruses will be correlated to symptoms found in canines. By expanding the known information about viruses, it may be used later to determine more viruses that infect both human and canine hosts as well as a way to better diagnose sick dogs.