Detecting Novel Strains of Lassa Virus via an Interdisciplinary Modernization Based on Genomic Sequencing

Park, Matthew

The rapid evolution of viral species complicates the management of chronic infections and the control of emerging infectious agents. Especially for pathogens that are highly fatal upon infection and difficult to control, a modernized understanding of their epidemiology is necessary for appropriate responses to epidemics. To combat a vastly branched network of polymorphic strains, developing variegated and target-specific anti-viral therapies and vaccines is critical to both public and military health. The Lassa virus (LASV), endemic to West Africa, causes highly fatal hemorrhagic fever like that of Ebola fever. The majority of humans infections result from zoonotic transmission. The LASV genome is very diverse with three major lineages associated with distinct geographic locations. In this project, RT-PCR and resequencing DNA microarrays were used to detect and sequence LASV in 41 of 214 samples taken from rodents captured at 8 locations in Sierra Leone. Phylogenetic analysis of partial sequences of the NP, GPC, and L genes revealed 5 separate clades within lineage IV of LASV present in Sierra Leone. The sequence diversity was found to be higher than previously observed with a mean diversity of 7.01% for the NP gene at the nucleotide level. These results have significant implications for understanding the pathogenic behavior of the spread of LASV and designing diagnostic and therapeutic drugs for LASV infections.

Awards Won: