

MA Thesis – Human Skeletal Biology Track, Physical Anthropology - New York
University (2014)

CROSS HOST EVOLUTION AND RELATIVE DIVERGENCE TIMES OF MIDDLE EAST
RESPIRATORY SYNDROME CORONAVIRUS (MERS-CoV) VARIANTS

LaShanda R. Williams

Abstract

Whole genome sequencing and phylogenetic analysis of human MERS-CoV has provided insight into the spread and evolution of the virus since 2012. In this paper, human-, camel-, bat-, and hedgehog-derived MERS and MERS-like coronaviruses are incorporated in a meta-phylogenetic analysis to reconstruct the degree of relatedness and relative times of divergence between genomes. Phylogenetic trees using neighbor joining, maximum likelihood, and maximum parsimony allow for the inference of the evolutionary history of the MERS-CoV genome and S protein. Results depict the close relationship between bat and human and camel and human MERS-CoV S gene and complete genomes. S gene analysis suggests differential divergence times between the S protein coding gene of MERS-CoV human and bat variants.