**African horsesickness virus proteins associated with virus virulence and disease pathogenesis.**

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African horsesickness (AHS) is one of the most lethal of equine diseases, and endemic to southern Africa. It causes four distinct clinical forms, with the most severe form having a 95% mortality rate. Most of the pathological changes are related to fluid imbalances that correlate to membrane permeability changes in endothelial cells of affected organs. AHS is caused by African horsesickness virus (AHSV), which is transmitted by biting midges. There are nine serotypes of the virus, however the disease phenotype and virulence profile of a specific virus strain does not relate to its serotype. We are interested in identifying viral genes and proteins that are involved in viral virulence and disease pathogenesis. AHSV has a segmented dsRNA genome, with each viral segment encoding at least one viral protein. Three candidate genes have been identified that are possible virulence or pathogenesis determinants. These genes code for two of the viral capsid proteins, VP2 and VP5, that are involved in host cell attachment and penetration of the cytoplasm respectively, and a non-structural viral protein NS3 that is involved in transport and release of mature viral particles. This paper will give an overview of the variation profile of these genes within AHSV and between related viruses, possible virulence markers, structural motifs in the proteins, amino acid domains that confer specific phenotypic characteristics to the proteins, and qualities of individual proteins that correspond to pathological features of African horsesickness disease.