

Virus-Host Co-evolution: Determining the Origin of Human Cytomegalovirus US27 and US28

G protein-coupled receptors (GPCR) are the largest family of cell surface proteins, found in organisms from yeast to humans. Human cytomegalovirus (HCMV) is a widespread pathogen that is particularly skilled at evading immune detection and defense mechanisms, largely due to extensive co-evolution with its host's immune system. One aspect of this co-evolution involves the acquisition of four virally encoded GPCR homologs: US27, US28, UL33 and UL78. In this research, phylogenetic analysis was used to investigate the origins of the US27 and US28 genes, which are adjacent in the viral genome. The results indicate that both US27 and US28 share the same common ancestor, human chemokine receptor CX3CR1, suggesting that a single human gene was captured and a viral gene duplication event occurred. While the evolutionary purpose of the gene duplication event remains unclear, experimental evidence indicates that each gene has evolved distinct, important functions during virus infection.