

Oral presentation

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Gene expression patterns in human blood cells exposed to common flu-like viruses and arenavirus

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Viral infections are the main cause of disease in the world, with the respiratory diseases being the main cause of morbidity. The arenaviruses are zoonotic pathogens transmitted from rodents to humans, and are the cause of flu-like disease that can rapidly develop into fatal hemorrhagic fevers. The respiratory diseases and in particular those produced by arenaviruses, have similar prodromal phases. For this reason it is important to look for differences in gene expression during the early stages of disease and identify specific patterns that diagnose exposure to a specific pathogen. The common flu-like viruses we studied were flu A, PI3, rhinovirus 15, and RSV A2; and LCMV-Arm, LCMV-WE, Mop, Mop29). We compared the effects of different viral infections on gene expression in human PBMC. RNA from these cultures was isolated at 4, 8, and 24 hours after exposure to virus, and cDNAs were hybridized to custom microarrays bearing 9000 human genes. Gene responses that were altered included the immune, cell adhesion, inflammatory, apoptotic, and antiviral pathways. Correlation of these genes with *in vivo* exposure provides the opportunity to identify diagnostic and therapeutic markers that may provide early indications of impending severe illness.