

Invited speaker presentation

Host genome influences on susceptibility to HIV-1

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In vitro and *in vivo* analyses identified a significant component of heritability in cellular or host susceptibility to HIV-1. The bases for susceptibility can be traced to genetic differences (inter-species) resulting from evolutionary adaptation to exogenous (and endogenous) retroviral infections, and to intra-species and inter-individual (human) differences associated with genetic variation. We have completed large scale evolutionary analysis of genes involved in HIV life cycle and pathogenesis, as well as participating and conducting genome-wide association studies, linkage analysis, and transcriptome analysis. These studies allowed a better understanding of the influence of common human variants in HIV-1 susceptibility and define a number of experimental challenges in the field: understanding of the role of rare and private mutations in susceptibility, and the development of better tools for the integration of data from large-scale studies.