

## Abstract of Presentation

Host genomics and evolutionary genetics in infectious diseases

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### Abstract :

Pathogens have been a constant force in the evolution of humans. Selective pressures have modeled the human genome contributing to genetic variation, which in turn, may contribute to modern diversity on susceptibility to infection.

The laboratory studies the basis of differences in human susceptibility to HIV. Humans display great differences in susceptibility to infection (eg, individuals that are not infected despite of exposure), and in disease progression (eg, some individuals are infected but will never develop AIDS). We have participated in the first two genome-wide analysis of genomic determinants of susceptibility to AIDS, and are currently working on meta-analysis of gene-wide association studies of larger populations. In parallel, the laboratory is studying the expression pattern in CD4 T cells from individuals for whom genome-wide genotype exists.

The patterns of enrichment for low  $P$  values (association signals) across the genome are placed in the context of the localization of signals of positive selection across the genome and in the exome. The hypothesis tested is that long-term exposure of primate genomes to retroelements (including retroviruses) have resulted in polymorphic regions that determine modern susceptibility to HIV.