

## Probing the Complexity of HIV-AIDS Pathogenesis Through Genetics

**“No gene is an island, entire of itself, every gene is a piece of the interactive genome and epigenome”**

adapted from Meditation XVII (No man is an island...) by John Donne

There has been immense interest in harnessing the power of genetic association studies for the elucidation of host factors that influence susceptibility to a variety of diseases, including HIV-AIDS. No doubt significant advances have been made in this regards, and I will review some of these as they pertain to our work in defining the host genetic determinants that influence HIV-AIDS and how this information may have translational utility to improve the clinical care of HIV-positive patients. However, I will also describe some of the complexities of the “interactive genome” that we will have to embrace in our quest to decode the genetic determinants of HIV-AIDS susceptibility and possibly other diseases. In addition to this, I will show that we may need to embrace the burgeoning field of *epigenetic epidemiology* to understand fully the determinants that influence disease susceptibility.

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