Host Pathogen Co-evolution: Viruses and the Adaptive Immune System

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The human immune system needs to protect its host from multiple pathogens that are constantly evolving. While there are numerous examples of mechanisms that pathogens have evolved to evade or counteract the host immune response, little is known about the evolution of the human immune system itself to optimize its ability to detect pathogens. In this talk I will describe a computational approach to study host pathogen co-evolution of humans and viruses.

Heat map distribution of allele efficiencies for human viruses and human proteins (x axis) by HLA supertype families (y axis). A matrix of efficiency scores computed for each of the 95 HLA alleles studied for 52 human viruses and a set of human proteins. Each entry in this efficiency matrix represents the efficiency score of a specific HLA allele (y axis) for a specific viral proteome. HLA alleles were grouped by supertypes, and human viruses were grouped by viral families and by Baltimore classification. Average efficiency scores over a large set of human proteins are presented in the bar to the left of the matrix. Distinct patterns of targeting efficiency can be observed for both HLA alleles (grouped by supertype or loci) and for different viral groups and families. UC, unclassified alleles that have not been assigned to supertypes; HSV-1, herpes simplex virus type 1; EBV, Epstein-Barr virus; CMV, cytomegalovirus; KSHV, Kaposi's sarcoma-associated herpesvirus; SARs-CoV, severe acute respiratory syndrome coronavirus; HTLV-1, human T-cell leukemia virus type 1; ssRNA, single-stranded RNA; RT, reverse transcriptase.