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Application of neutralization fingerprints in delineating antibody recognition in HIV-1 sera and antibody epitope prediction

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Antibody neutralization assays, which measure the reduction of viral infectivity mediated by the antibody, are often performed as one of the first steps in the characterization of an antibody to determine its breadth and potency. The neutralization potency against different viral strains ("neutralization fingerprint") is a unique signature of an antibody, and it can be used to classify antibodies targeting the same virus based on their epitope specificity. For HIV-1 where multiple major antibody epitope-sites of vulnerability have been identified on the envelope spike, the prevalence of different classes of antibodies in an HIV-1 serum can be elucidated by comparing the serum neutralization fingerprint to the prototypic neutralization fingerprint of each antibody class. This information can assist the understanding of antibody development in HIV-1 infected patients and the isolation of new broadly neutralizing antibodies. In additional to sera analysis, by quantifying the mutual information between antibody neutralization fingerprint and "amino acid fingerprint" (the amino acid type for each viral strain) at each antigen residue position, the antibody epitope can be predicted at the residue level with neutralization data and viral sequence alignment as input. The identified antibody epitope residues can provide clues about functional vulnerabilities and mechanisms of resistance, and can provide the basis for epitope-based vaccine design.

Biography

Gwo-Yu Chuang has earned his Bachelor's degree in Electrical Engineering from National Taiwan University and PhD in Biomedical Engineering from Boston University. He is currently a Research Fellow at the Vaccine Research Center of National Institutes of Health (NIH). He has published 19 peer reviewed journal articles, including 8 first/co-first authorship publications in prestigious journals such as PNAS and Journal of Virology. His research interest lies in utilizing computational tools to design therapeutic antibodies, vaccines, and small molecule drugs targeting various pathogens such as HIV-1, RSV, and influenza virus.

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