Computational Analysis of Human Antibody Repertoires To Inform Design of HIV-1 Vaccines

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The Human Immunodeficiency Virus (HIV-1) is a globally prevalent virus that attacks CD4 cells in the human immune system, decreasing the quality and length of life for those affected. The most effective way to combat HIV-1 is through development of a vaccine that elicits antibodies able to recognize, bind to, and neutralize the virus. To accelerate vaccine development, this research aims to score and rank precursor antibodies by their likelihood of binding to the HIV-1 envelope glycoprotein. The consensus CSV files representing the data from approximately 3 billion antibody sequences from human antibody repertoires were downloaded from The Great Repertoire Project (https://github.com/briney/grp_paper). An algorithm was developed in Java that scores the antibodies according to their exhibition of characteristics previous research suggests make an antibody prone to an HIV-1 binding event. These properties include a viable diversity (D)-gene, a long heavy-chain complementarity determining region 3 (HCDR3), the presence of a sulfation motif on the HCDR3, and placement of the sulfation motif that encourages sulfation. The algorithm determines a total score from 0.00-1.00, a weighted sum of each of these properties, for each potential antibody precursor then ranks the antibodies from greatest to least score. Validation of the results found that the algorithm accurately prioritized antibodies likely to bind to the HIV-1 envelope glycoprotein. This algorithm accelerates the rate at which viable antibodies can be selected for in vivo experimentation with vaccine antigens and therefore the development of an effective HIV-1 vaccine.

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