493. Defining background shared antibody sequences between unrelated healthy individuals (public clonotypes) to support future studies on specific infectious disease related conditions.

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Background. Public clonotypes, antibodies against specific antigens in unrelated individuals that have genetic similarities, have been shown in a variety of infections, including SARS-CoV-2 and HIV. Likely, there are shared antibody responses between individuals for many infections. To explore antibody responses that would coincide with specific infectious diseases that may set off chronic illnesses, such as Multiple Sclerosis or Alzheimer’s disease, defining the background shared clonotypes is needed to differentiate disease from normal background public clonotype responses.

Methods. Heavy chain variable sequences were retrieved from public biorepositories (Bioproject PRJNA486667) composed of 43 healthy persons, and two groups of HIV infected persons; 114 with broadly neutralizing antibodies and 91 without broadly neutralizing antibodies. We utilized the Immcantation package of software run on our SUNY Buffalo computational cluster. After PRESTo annotation, duplicate sequences were collapsed and sequences of only single counts were removed. Clonal groups were determined using ChangeO requiring IGHV, IGHJ, and CDR3 amino acid sequence to be perfectly matched. Figures and statistics were generated with immcantation, excel, and graphpad prism 8.

Results. 244850 heavy chain sequences from 43 healthy controls were compared for exact matches to predicted germline variable segment and CDR3 amino acid sequence and identified 0.23% as public clonotypes. Comparison to 205 HIV + individuals (a total of 1.4 million comparative sequences) showed that 2.35% of heavy chain sequences were seen in more than one individual. Generally, public clonotypes had shorter CDR3s (peak of 9 amino acids). VH 3-9, 3-30 and 4-34 were the most commonly used variable segments in public clonotypes. Common exact match CDR3 sequences using a variety of variable sequences, including an 11 amino acid CDR3 sequence motif, were also discovered.

Conclusion. This early work has identified several public clonotypes that are shared among subjects who are HIV positive and otherwise healthy people. Defining the sequences commonly seen between individuals can assist in specifying antibody responses specific to disease states from larger sequence databases.

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