Deep mutational scanning of an H3 hemagglutinin can inform evolutionary forecasting of human H3N2 influenza virus

Juhye M. Lee[1,4,5,†]   John Huddleston[2,6,†]   Michael B. Doud[1,4,5]

Kathryn A. Hooper[1,6]   Trevor Bedford,[2,3]

Jesse D. Bloom[1,3,4*]

[1]Basic Sciences Division, [2]Vaccine and Infectious Diseases Division, and [3]Computational Biology Program,
Fred Hutchinson Cancer Research Center, Seattle, WA, USA

[4]Department of Genome Sciences, [5]Medical Scientist Training Program, and [6]Molecular and Cellular Biology Program,
University of Washington, Seattle, WA, USA

[†]These authors contributed equally

[*]Correspondence: jbloom@fredhutch.org

Abstract

Abstract text.

INTRODUCTION

RESULTS

Strategy for deep mutational scanning of an H3 hemagglutinin

H3 site-specific amino-acid preferences

Estimating mutational effects from an H3N2 phylogeny

Comparing H1 and H3 preferences

DISCUSSION

METHODS

HA numbering

Generation of HA codon mutant plasmid libraries

Generation and passaging of mutant viruses

Barcoded subamplicon sequencing

Analysis of deep sequencing data

Quantification of mutational effects and sequence preferences from an H3N2 phylogeny

Data availability and source code

Deep sequencing data are available from the Sequence Read Archive under BioSample accession [*add accession*].