THERAPEUTIC, TOOL

Barcoded influenza genome for deep mutational scanning

Brief Technology Description

Methods to insert nucleotide barcodes into the influenza virus genome which significantly improves the performance and cost associated with deep mutational scanning analyses

BUSINESS OPPORTUNITY

Exclusive licence
Non-exclusive license
Sponsored research

TECHNOLOGY TYPE

Therapeutic
Tool

STAGE OF DEVELOPMENT

Preclinical *in vitro*

PATENT INFORMATION

Patent Pending

INVESTIGATOR OVERVIEW

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Technology Overview

Mutagenesis screens, which involve individually altering amino acids at different positions, are a powerful way to study the structure and function of proteins. Deep mutational scanning refers to the process of generating hundreds of thousands of mutants from a single protein, including screens where every amino acid position is mutated with all possible amino acid replacements. These techniques are important when characterizing viral entry proteins, which often evolve and mutate over time and can allow viruses to escape recognition by the immune system and therapeutic antibodies. One major challenge to analyzing data generated from deep mutational scanning is the deep sequencing required "read" the mutant proteins. Current sequencing methods have a high error rate, are expensive to analyze, or lack the throughput required to characterize diverse libraries. "Barcoding", or associating variants with unique nucleotide sequences, is inexpensive and allows for mutants to be sequenced with standard sequencing. Unfortunately, barcoding hasn't been successful in the past with many viruses without disrupting their functionality due to the compactness of the viral genome. Hutch researchers have discovered a method to create mutant libraries of the influenza virions, each containing a specific nucleotide barcode. By sequencing these individual barcodes, the full sequence of the viral gene can be identified, which significantly improves the process of finding mutations that affect viral growth and immune recognition during deep mutational scans, eliminating previous bottlenecks. Therefore, this innovation could be used to better understand and predict viral evolution, an important factor when selecting influenza vaccine strains.

Applications

- Influenza viral evolution and vaccine development

Potential Advantages

- Greatly decreased cost and increased accuracy of deep mutational scanning

Market Overview: The global influenza vaccine market is estimated to grow from $3.96 billion in 2018 to $6.20 billion by 2026, registering a CAGR of 5.9%