

A new approach to study flu drug resistance

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Researchers have created a new approach for studying resistance to Neuraminidase Inhibitors (NI) in influenza. The study, published December 7 in *PLoS Computational Biology*, combines data from influenza infections of human volunteers with a mathematical model which estimates the expected number of newly generated resistant infections. This new approach provides a more meaningful assessment of the danger of drug resistance emergence, compared to the current way of reporting the fraction/number of resistant cases.

Neuraminidase Inhibitors are currently the most effective drugs against influenza. However, recent cases of resistance to NI have caused some concern. A number of studies have reported that resistant mutants could be isolated from a fraction of patients treated with Neuraminidase Inhibitors. While this provides some qualitative insights, it is even more important to know how likely an infected, treated patient will generate resistance to NI and will cause infections with the resistant strain in others.

A team from Emory University, the Fred Hutchinson Cancer Research Center, and the University of Washington set out to determine this likelihood. Since the epidemiological data that is customarily used to estimate parameters of this type is not available for NI resistant influenza, the team, led by Dr. Andreas Handel, used an alternative approach. The team took data from volunteers infected with the flu and combined it with a mathematical framework to obtain a more quantitative assessment of the danger of resistance.

This result could predict models of resistance emergence and spread. The study additionally shows that the results depend strongly on the role the immune response plays; this is an issue that will be important to address in future studies.

Citation: Handel A, Longini IM Jr, Antia R (2007) Neuraminidase inhibitor resistance in influenza: Assessing the danger of its generation and spread. PLoS Comput Biol 3(12): e240.
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