1048-92-204   **Katia Koelle*** (`katia.koelle@duke.edu`), Duke Biology, Box 90338, Durham, NC 27708, and **Meredith Kamradt**. *A simple mathematical model to understand influenza's complex evolutionary dynamics.*

Seasonal influenza epidemics in humans are caused almost exclusively by three viral variants: influenza A (H3N2), influenza A (H1N1), and influenza B. Despite sharing a common route of aerosol transmission, these variants differ significantly from one another in both ecological and evolutionary dynamics. In this session, we will present a mathematical model to explain these dynamical differences. Applying the model first to H3N2, we show that a combination of punctuated and gradual antigenic evolution is required to capture H3N2's ecological dynamics and the evolutionary dynamics of its hemagglutinin protein. After taking into consideration the differences between influenza A and B's mutation rates, we then show that differences in the basic reproductive number alone are sufficient to account for these variants' distinct ecological and phylogenetic patterns. (Received February 08, 2009)