

COLLABORATIVE RESEARCH CENTER | SFB 680

Molecular Basis of Evolutionary Innovations

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The global circulation of seasonal influenza viruses

Recent studies have shown that human influenza A (H3N2) viruses circulate continuously in East and Southeast (E-SE) Asia via a network of temporally overlapping epidemics and that epidemics in the rest of the world are seeded from this network each year. A new analysis of complimentary influenza B virus data shows that influenza B viruses circulate in substantially more complex patterns than those identified for influenza A. Key among these patterns is that influenza B viruses circulating in E-SE Asia are a poor indicator of which viruses will cause epidemics in the rest of the world. Rates of evolution and age profiles of infection are likely to play important roles in determining differences in global migration patterns.

December 19, 14:15

**Institute for Genetics, Zülpicher Str. 47a,
New Seminar Room 0.46, Ground Floor**

Host: Michael Lässig

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