

CONFÉRENCE

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Genomic signatures of selection, transmission and host adaptation in Lassa virus.

Lassa is an arenavirus endemic to West Africa. It is thought to replicate mostly in a rodent reservoir, occasionally infecting humans and causing a deadly hemorrhagic fever. In this talk, I will describe a long-term Lassa surveillance program conducted in collaboration with colleagues from Harvard, Sierra Leone and Nigeria. We sequenced 95 full length Lassa genomes, mostly from infected human hosts, but also a few rodents. Based on population genetic analysis of mutations identified in these genomes, I will present evidence that (1) Lassa may be better adapted for replication in humans than previously thought, (2) the spread of Lassa from Nigeria into Sierra Leone was accompanied by increased adaptation, possibly due to improved translational efficiency, and (3) Lassa faces an evolutionary tradeoff between immune evasion and replication within a host and efficient transmission to the next host. I will conclude with a discussion of how this 'population genomic' approach can be applied to other viruses and bacteria.

Vendredi 15 février 2013 à 11 h 30
Pavillon Claire McNicoll, salle Z-260

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