

Evaluation of the zoonotic potential of H18N11 virus variant tested in the ferret model

Inhalt

Influenza A viruses (IAV) are important zoonotic pathogens that cause epidemic outbreaks in birds, swine and other mammals. In 2012 and 2013 two influenza A-like virus genomes were found in little yellow-shouldered fruit bats (*Sturnira lilium*) in Guatemala and flat-faced fruit bats (*Artibeus planirostris*) in Peru, provisionally designated as H17N10 and H18N11. Conventional IAV hemagglutinins (HAs) bind canonical sialic acid-containing receptors. In contrast, biochemical and structural studies indicated that influenza A-like H17 does not. In fact, H17 and H18 HAs are unable to bind and hemagglutinate red blood cells, and are therefore atypical HAs. Whether or not these viruses are able to infect further mammalian species including the model species for human influenza pathogenesis: the ferret is currently unknown. By reverse genetic techniques a H18N11 virus was generated. Passaging in vitro (canine cell culture) selected an H18N11 variant virus (rP11) with two mutations within the HA (K170R and N250S) and a stop codon in NA (G107X) protein. Ferrets were experimentally inoculated to check for the zoonotic potential of the variant virus. Viral genome was detected in the upper respiratory tract, lung and brain but transmission to ferrets in direct contact was excluded. All inoculated ferrets euthanized 7 days post infection or later seroconverted. Therefore, we assume, the variant virus is poorly adapted to ferrets and does have a low zoonotic potential, since low level of replication was obviously demonstrated.

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