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Adaptation of influenza A(H1N1)pdm09 virus in experimental mouse models

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Highlights

- BALB/c, C57BL/6z and CD1 mouse-adapted influenza A(H1N1)pdm09 variants were produced.
- Influenza A(H1N1)pdm09 virus can easily adapt to mammals and cause 100% lethality.
- There were identical aa substitutions in all of the mouse-adapted variants: in PB2 (K251R), PB1 (V652A), NP (I353V), NA (I106V, N248D) and in NS1 (G159E).

Abstract

In the present study, three mouse-adapted variants of influenza A(H1N1)pdm09 virus were obtained by lung-to-lung passages of BALB/c, C57BL/6z and CD1 mice. The significantly increased virulence and pathogenicity of all of the mouse-adapted variants induced 100% mortality in the adapted mice. Genetic analysis indicated that the increased virulence of all of the mouse-adapted variants reflected the incremental acquisition of several mutations in PB2, PB1, HA, NP, NA, and NS2 proteins. Identical amino acid substitutions were also detected in all of the mouse-adapted variants of A(H1N1)pdm09 virus, including PB2 (K251R), PB1 (V652A), NP (I353V), NA (I106V, N248D) and NS1 (G159E). Apparently, influenza A(H1N1)pdm09 virus easily adapted to the host after serial passages in the lungs, inducing 100% lethality in the last experimental group. However, cross-challenge revealed that not all adapted variants are pathogenic for different laboratory mice. Such important results should be considered when using the influenza mice model.