

Large scale multiple sequence alignment of intraspecies samples: conserved sequence analysis of influenza A virus HA segment and its application in rapid typing

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Abstract

Background The high mutation rate of influenza A virus hemagglutinin segment brings great challenges to its long-term effective testing and subtyping. **Method** We analyzed the conserved sequences of hemagglutinin subtype H1-H9 by breadth first, and designed primers for HA subtyping based on conserved sequences. **Results** Our conserved sequence searching method get high specificity conserved sequences on H1-H9 subtypes respectively. And PCR experiments show that primers based on conserved sequences can be used in influenza A virus HA subtyping. **Conclusions** Conserved sequences based primers are expected to be the long-term effective influenza A virus HA subtyping tools.

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