

Transmission Dynamics and Spatiotemporal Evolution of H1N1pdm09 in Anhui Province, China, 2009–2023

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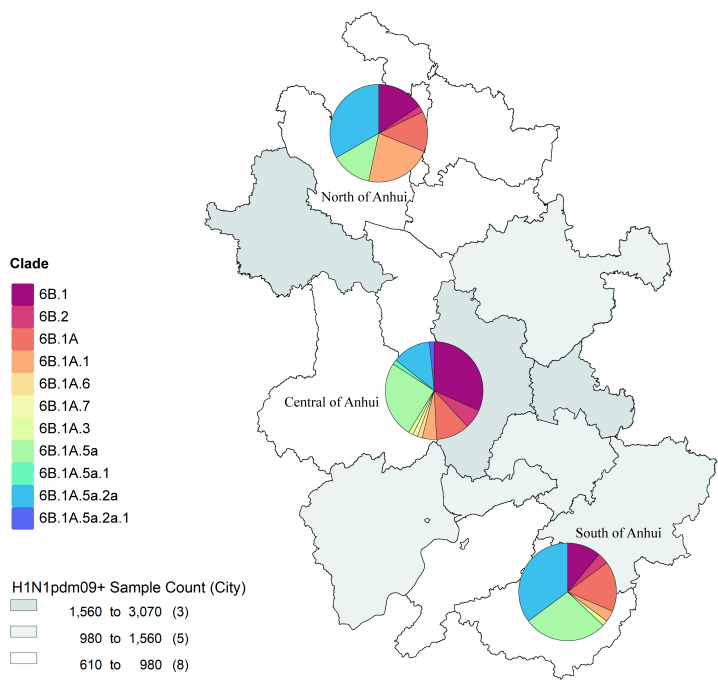
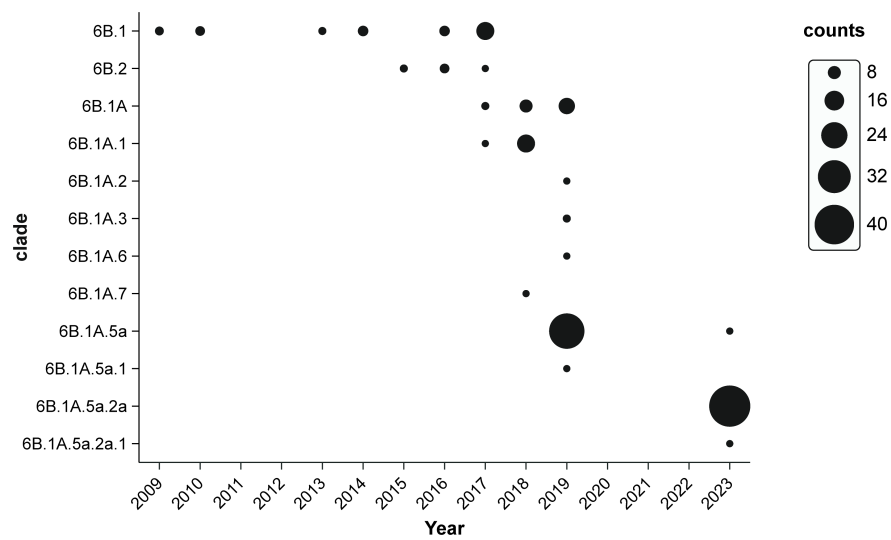
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Abstract

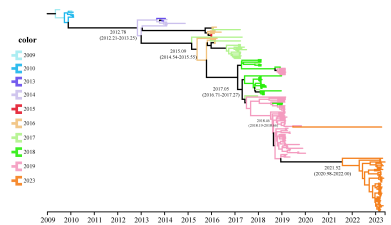
Background: No studies have deeply examined the transmission patterns of H1N1pdm09 in Anhui Province, China. **Methods:** We conducted a genome-wide analysis of 162 historical epidemic strains in Anhui Province, China to understand the transmission patterns, incoming and outgoing events, and evolutionary dynamics of the strains. **Results:** Our study showed that the number of recent infections was higher in 2018–2023 compared to previous years. Compared to the global strain sequences, the clade production times were all delayed in Anhui Province, China, suggesting that Anhui is an introduced region in the global transmission chain. The NA fragments had higher dN/dS values than the HA fragments. The circulation pattern of the strain in Anhui Province, China was mainly from central to northern, followed by northern to central and central to southern. Central Anhui was the transmission center of H1N1pdm09 in Anhui Province, China. Calculation of transmission events for the whole country showed that the main source of the epidemic strain in Anhui Province was East China, but the national epidemic of the H1N1pdm09 strain in 2023 appeared to originate from Anhui Province, China. **Conclusion:** The above results emphasize the focus of influenza prevention and control in Anhui Province, China, as well as the importance of sharing information about epidemics between different provinces.

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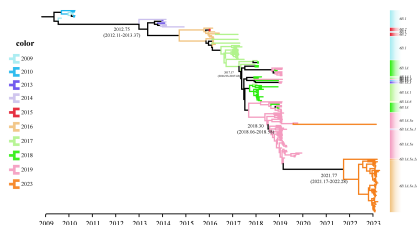
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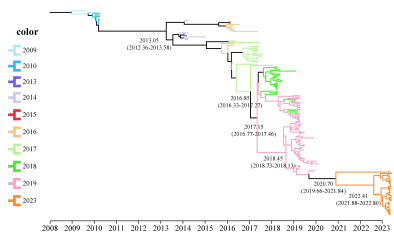
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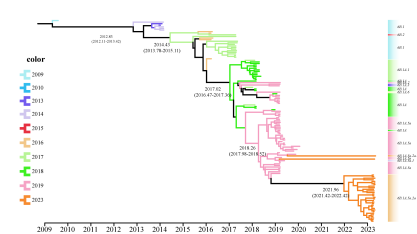
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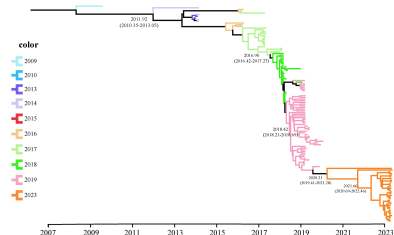
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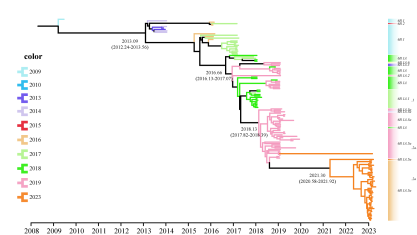
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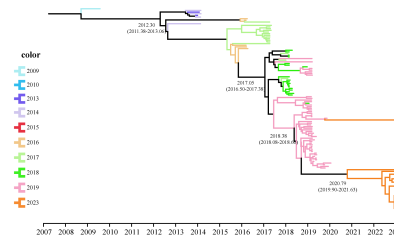
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PA



PB1



PB2

