**Virologica Sinica**

**Supplementary Data**

**The evolution, pathogenicity and transmissibility of quadruple reassortant H1N2 swine influenza virus in China: A potential threat to public health**

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**Supplementary Data**

**Supplementary figure 1**. Phylogenetic trees of *PB2*, *PB1*, *PA*, *NP*, *NS* and *M* genes for swine influenza viruses. The red color indicates human influenza viruses. The red circles indicate the H1N2 isolates in this study.

**Supplementary Table S1. Marginal likelihoods of different combinations of clock model and tree prior.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Segment** | **Molecular clock model** | **Coalescent tree prior** | **Path sampling Marginal L Estimate** | **Stepping-stone Marginal L Estimate** |
| HA | Strict clock | Bayesian skyline | -8385.0063 | -8378.1075 |
| Strict clock | Exponential growth | -8443.4378 | -8438.5175 |
| Strict clock | Constant size | -8565.2833 | -8558.4150 |
| Uncorrelated lognormal relaxed clock | Bayesian skyline | -8328.4687 | -8319.0472 |
| **Uncorrelated lognormal Relaxed clock** | **Exponential growth** | **-8325.4048** | **-8319.0471** |
| Uncorrelated lognormal Relaxed clock | Constant size | -8331.3091 | -8321.3308 |

The best-fitting tree prior and molecular clock model are indicated in bold font.

**Supplementary Table S2. Nucleotide and amino acid homology of five strains.**

**Supplementary Table S2a. Nucleotide and amino acid homology of *HA* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 91.98 | 96.28 | 95.92 | 96.27 |
| SW/198/20 | 92.48 | - | 94.12 | 93.40 | 93.43 |
| SW/209/20 | 96.11 | 93.63 | - | 99.11 | 99.64 |
| SW/510/21 | 96.00 | 93.36 | 99.65 | - | 99.47 |
| SW/700/21 | 96.06 | 93.53 | 99.82 | 99.82 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2b. Nucleotide and amino acid homology of *NA* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 100.00 | 96.66 | 96.68 | 96.49 |
| SW/198/20 | 100.00 | - | 96.65 | 96.88 | 96.70 |
| SW/209/21 | 96.88 | 97.30 | - | 100.00 | 100.00 |
| SW/510/21 | 96.95 | 97.38 | 99.92 | - | 100.00 |
| SW/700/20 | 96.88 | 97.30 | 100.00 | 99.93 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2c. Nucleotide and amino acid homology of *PB2* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 99.47 | 99.07 | 99.07 | 99.20 |
| SW/198/20 | 98.94 | - | 98.82 | 98.82 | 98.95 |
| SW/209/21 | 97.41 | 97.41 | - | 100.00 | 99.87 |
| SW/510/21 | 97.95 | 97.50 | 99.91 | - | 99.87 |
| SW/700/20 | 98.14 | 97.63 | 99.52 | 99.60 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2d. Nucleotide and amino acid homology of *PB1* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 98.28 | 98.94 | 98.55 | 98.68 |
| SW/198/20 | 97.01 | - | 98.81 | 98.42 | 98.55 |
| SW/209/21 | 97.98 | 98.46 | - | 99.08 | 99.21 |
| SW/510/21 | 97.19 | 97.63 | 98.59 | - | 99.87 |
| SW/700/20 | 97.19 | 97.63 | 98.55 | 99.96 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2e. Nucleotide and amino acid homology of *NP* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 100.00 | 94.29 | 94.47 | 94.36 |
| SW/198/20 | 100.00 | - | 94.25 | 94.44 | 94.36 |
| SW/209/21 | 97.30 | 97.56 | - | 99.80 | 99.79 |
| SW/510/21 | 97.36 | 97.62 | 99.93 | - | 100.00 |
| SW/700/20 | 97.26 | 97.53 | 99.87 | 99.93 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2f. Nucleotide and amino acid homology of *PA* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 99.30 | 98.74 | 98.88 | 98.88 |
| SW/198/20 | 97.95 | - | 98.33 | 98.47 | 98.47 |
| SW/209/21 | 97.63 | 96.79 | - | 99.86 | 99.86 |
| SW/510/21 | 97.72 | 96.89 | 99.91 | - | 100.00 |
| SW/700/20 | 97.72 | 96.89 | 99.81 | 99.81 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2g. Nucleotide and amino acid homology of *NS* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 100.00 | 97.49 | 97.85 | 97.49 |
| SW/198/20 | 100.00 | - | 97.49 | 97.85 | 97.49 |
| SW/209/21 | 97.49 | 98.21 | - | 99.64 | 100.00 |
| SW/510/21 | 97.61 | 98.33 | 99.88 | - | 99.64 |
| SW/700/20 | 97.49 | 98.21 | 100 | 99.88 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S2h. Nucleotide and amino acid homology of *M* gene of five strains**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain name** | **Sequence identities with strains isolated in this study** | | | | |
|  | SW/188/20 | SW/198/20 | SW/209/20 | SW/510/21 | SW/700/21 |
| SW/188/20 | - | 100.00 | 99.07 | 97.83 | 98.45 |
| SW/198/20 | 99.69 | - | 99.08 | 97.87 | 98.47 |
| SW/209/21 | 97.96 | 97.26 | - | 98.78 | 99.39 |
| SW/510/21 | 97.04 | 96.44 | 98.88 | - | 99.39 |
| SW/700/20 | 97.14 | 96.53 | 98.98 | 99.70 | - |

The gray shadow part is amino acid homology.

**Supplementary Table S3.** **Genes of the five isolates with the closest nucleotide homology sequence in GenBank.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Strain Name** | **Gene** | **Closest Virus** | **Homology (%)** |
| SW/188/20 | HA | A/swine/Liaoning/PJ89/2014(H1N1) | 97.59% |
|  | NA | A/Guangdong/YueFang277/2017(H3N2) | 99.79% |
|  | PB2 | A/Guangdong/YueFang277/2017(H3N2) | 99.29% |
|  | PB1 | A/swine/Liaoning/CY102/2014(H1N1) | 97.98% |
|  | PA | A/swine/Liaoning/PJ43/2014(H1N1) | 99.21% |
|  | NP | A/Guangdong/YueFang277/2017(H3N2) | 99.94% |
|  | NS | A/Guangdong/YueFang277/2017(H3N2) | 99.40% |
|  | M | A/swine/Hong Kong/2403/2012(H1N1) | 98.47% |
| SW/198/20 | HA | A/swine/Guangdong/3747/2011(H1N1) | 97.00% |
|  | NA | A/Guangdong/YueFang277/2017(H3N2) | 99.36% |
|  | PB2 | A/Guangdong/YueFang277/2017(H3N2) | 99.47% |
|  | PB1 | A/Guangdong/YueFang277/2017(H3N2) | 99.96% |
|  | PA | A/swine/Hong Kong/4893/2012(H3N2) | 98.65% |
|  | NP | A/Guangdong/YueFang277/2017(H3N2) | 99.54% |
|  | NS | A/swine/Liaoning/PJ89/2014(H1N1) | 99.40% |
|  | M | A/swine/Hong Kong/2403/2012(H1N1) | 97.86% |
| SW/209/20 | HA | A/swine/Liaoning/PJ89/2014(H1N1) | 98.05% |
|  | NA | A/swine/Hong Kong/NS3335/2014(H3N2) | 98.30% |
|  | PB2 | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.29% |
|  | PB1 | A/swine/Liaoning/CY102/2014(H1N1) | 100% |
|  | PA | A/swine/Liaoning/PJ43/2014(H1N1) | 98.23% |
|  | NP | A/swine/Guangxi/BB1/2013(H1N1) | 98.68% |
|  | NS | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.69% |
|  | M | A/Jiangsu/ALS1/2011(H1N1) | 99.81% |
| SW/510/21 | HA | A/swine/Liaoning/PJ89/2014(H1N1) | 97.94% |
|  | NA | A/swine/Guangdong/2863/2012(H3N2) | 98.37% |
|  | PB2 | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.38% |
|  | PB1 | A/swine/Liaoning/CY102/2014(H1N1) | 98.59% |
|  | PA | A/swine/Liaoning/PJ43/2014(H1N1) | 98.33% |
|  | NP | A/swine/Guangxi/BB1/2013(H1N1) | 98.75% |
|  | NS | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.81% |
|  | M | A/swine/Liaoning/CY102/2014(H1N1) | 99.39% |
| SW/700/21 | HA | A/swine/Liaoning/PJ89/2014(H1N1) | 98.00% |
|  | NA | A/swine/Hong Kong/NS3335/2014(H3N2) | 98.30% |
|  | PB2 | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.77% |
|  | PB1 | A/swine/Liaoning/CY102/2014(H1N1) | 98.59% |
|  | PA | A/swine/Liaoning/PJ43/2014(H1N1) | 98.33% |
|  | NP | A/swine/Liaoning/PJ89/2014(H1N1) | 98.73% |
|  | NS | A/swine/Guangxi/NNXD2023/2013(H1N1) | 98.69% |
|  | M | A/swine/Liaoning/FS487/2015(H1N1) | 99.59% |

Note: Strains marked in red color indicate human influenza viruses.