

# Swine Influenza in Sri Lanka

## Technical Appendix 1

### Methods

The HA sequences were aligned with other sequences from animal and human influenza A viruses available in the GenBank. Maximum-likelihood (ML) tree was estimated using the general time-reversible with invariant sites and 4 gamma distributed heterogeneous substitution rates) in PhyML version 3.0 (1). To evaluate the robustness of the tree topology, a set of 500 pseudo-replicates of the sequences was generated and used in bootstrap analysis. The ML tree topology was also confirmed by using Bayesian analysis in MrBayes version 3.2 (2).

### References

1. Guindon S, Gascuel O. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol.* 2003;52:696–704. [PubMed](#)  
<http://dx.doi.org/10.1080/10635150390235520>
2. Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol.* 2012;61:539–42. [PubMed](#) <http://dx.doi.org/10.1093/sysbio/sys029>