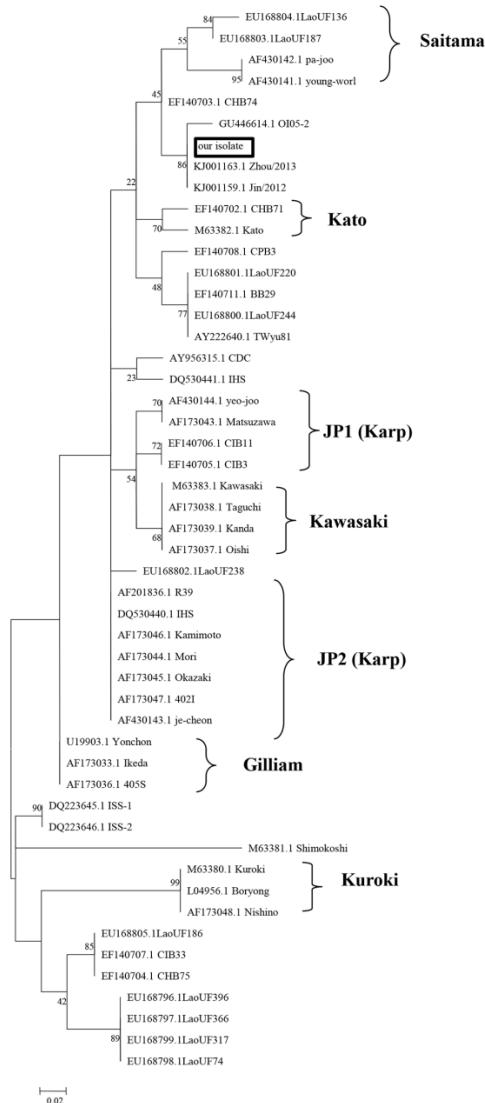


Orientia tsutsugamushi in Lung of Patient with Acute Respiratory Distress Syndrome, France, 2013

Technical Appendix



Online Technical Appendix Figure. Phylogenetic tree constructed by using the neighbor-joining method and MEGA software (<http://megasoftware.net/>) for *Orientia tsutsugamushi* 56-kDa protein-encoding gene sequences obtained from GenBank, as previously described (1). The

isolate from this study is indicated by a box labeled “our isolate.” Sequences are identified by GenBank accession number. Numbers at nodes represent bootstrap values based on 100 replicates. Scale bar represents 2% nucleotide sequence divergence. JP, Japan

Reference

1. Fournier PE, Siritantikorn S, Rolain JM, Suputtamongkol Y, Hoontrakul S, Charoenwat S, et al. Detection of new genotypes of *Orientia tsutsugamushi* infecting humans in Thailand. Clin Microbiol Infect. 2008;14:168–73. [PubMed http://dx.doi.org/10.1111/j.1469-0691.2007.01889.x](http://dx.doi.org/10.1111/j.1469-0691.2007.01889.x)