# Epidemiology and Infection.

*Ralstonia* Infection in Cystic Fibrosis.

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Supplementary Material.



Supplementary Figure S1: Dendrogram showing comparison of an 800 bp section corresponding to nt16-815 of GenBank accession number JQ914279 of the *gyrB* gene from clinical isolates of *Ralstonia* spp. compared with type and reference strains of this genus. *gyrB* sequences for type and/or reference strains of *R. solanacearum* and *R. syzgii subsp. indonesiensis* are not shown as these were <800 bp in length. Sequence data for the type strain of *R. pseudosolanacearum* was likewise not included.The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 0.187 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. Evolutionary analyses were conducted in MEGA6 [4].

[1] Saitou N. and Nei M.The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 1987; **4**:406-425.

[2] Felsenstein J. Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 1985; **39**:783-791.

[3]Tamura K., Nei M., and Kumar S. Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)* 2004; **101**:11030-11035.

[4]Tamura K. *et al.* (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 2013; **30**: 2725-2729.