

Supplementary Table S1 Probabilities of the Shimodaira-Hasegawa (SH) test of maximum likelihood tree topologies based on the alignments of seven housekeeping genes sequences and the concatenated data set. Values in bold ($P>0.05$) indicate that the tree topologies are congruent

Phylogenetic tree	<i>atpD</i>	<i>dnaK</i>	<i>Efp</i>	<i>fyuA</i>	<i>glnA</i>	<i>gyrB</i>	<i>rpoD</i>	Concatenated dataset
<i>atpD</i>	*	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<i>dnaK</i>	0.000	*	0.256	0.000	0.000	0.000	0.001	0.000
<i>efp</i>	0.000	0.000	*	0.000	0.000	0.000	0.000	0.000
<i>fyuA</i>	0.000	0.000	0.007	*	0.000	0.000	0.000	0.000
<i>glnA</i>	0.000	0.000	0.004	0.000	*	0.000	0.000	0.000
<i>gyrB</i>	0.000	0.000	0.000	0.000	0.000	*	0.000	0.000
<i>rpoD</i>	0.000	0.000	0.000	0.000	0.000	0.000	*	0.000
Concatenated dataset	0.288	0.552	0.440	0.115	0.011	0.333	0.038	*