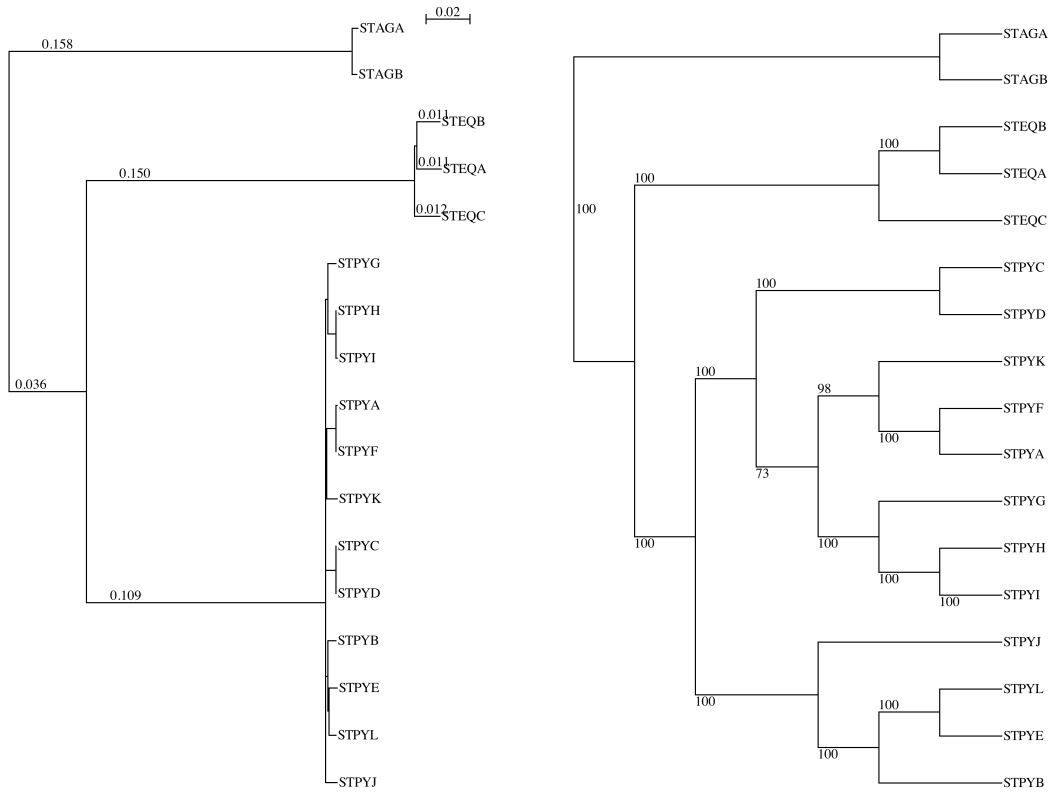
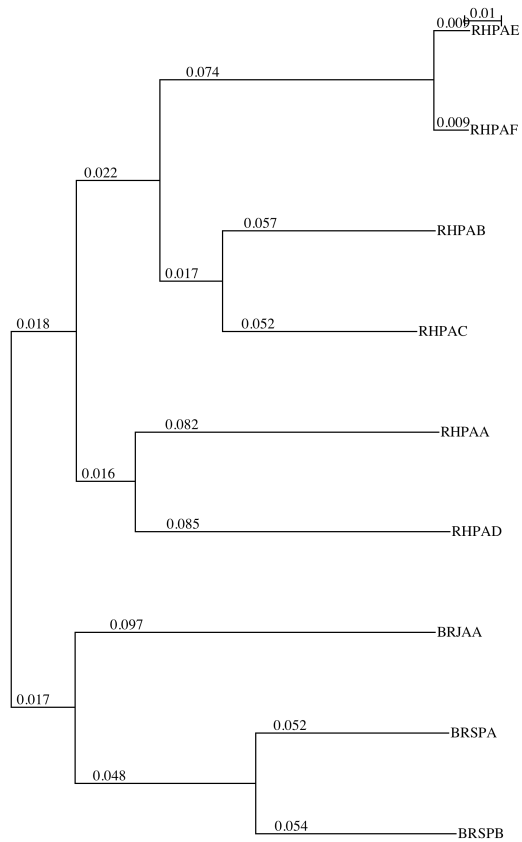


ENTEROBACTERIACEAE PHYLOGENY RECONSTRUCTED FROM THE ALIGNMENT OF THE 1405 CORE GENOME GENES. The values in blue above the branches represent branch length. The region highlighted with a vertical black bar is the only one containing a node less than 100% bootstrap support.



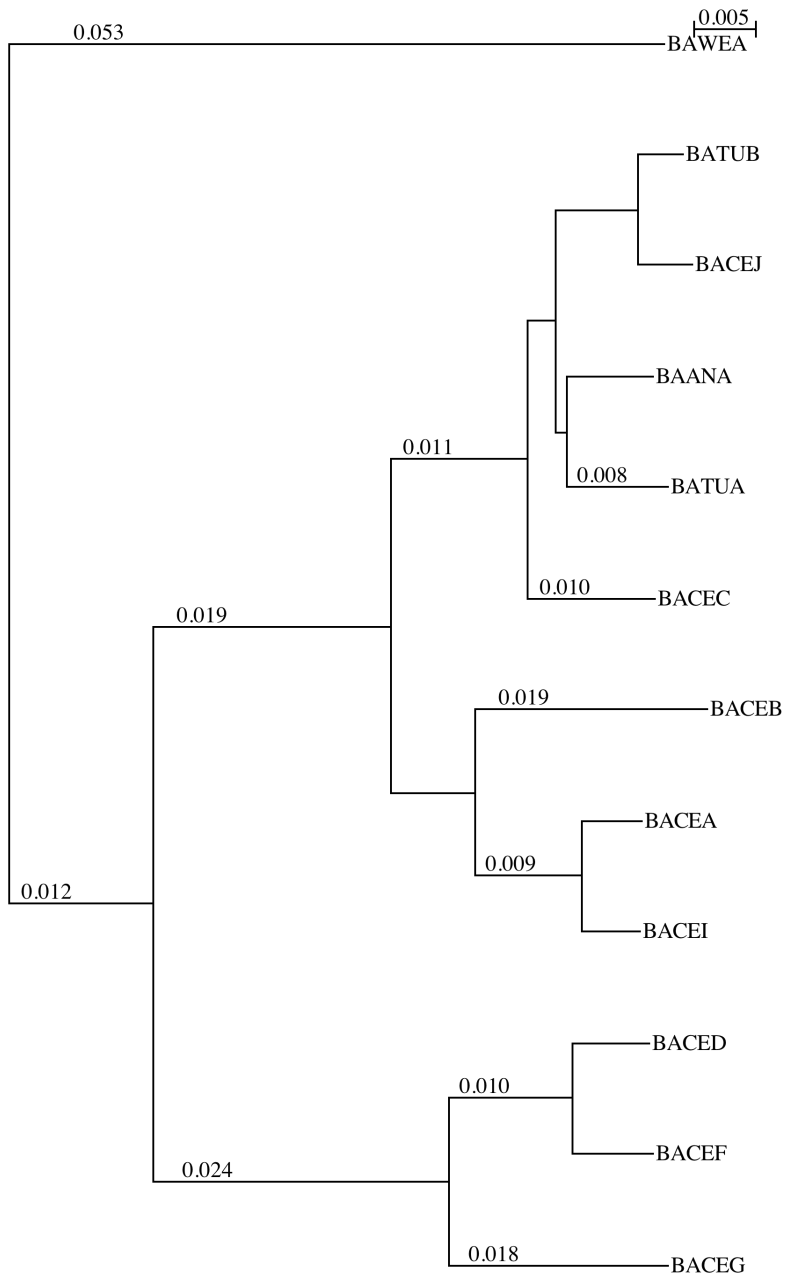
*STREPTOCOCCUS* PHYLOGENY RECONSTRUCTED FROM THE 518 CORE GENOME GENES.

The values above the branches represent their length. Nearly all branches showed high bootstrap support.



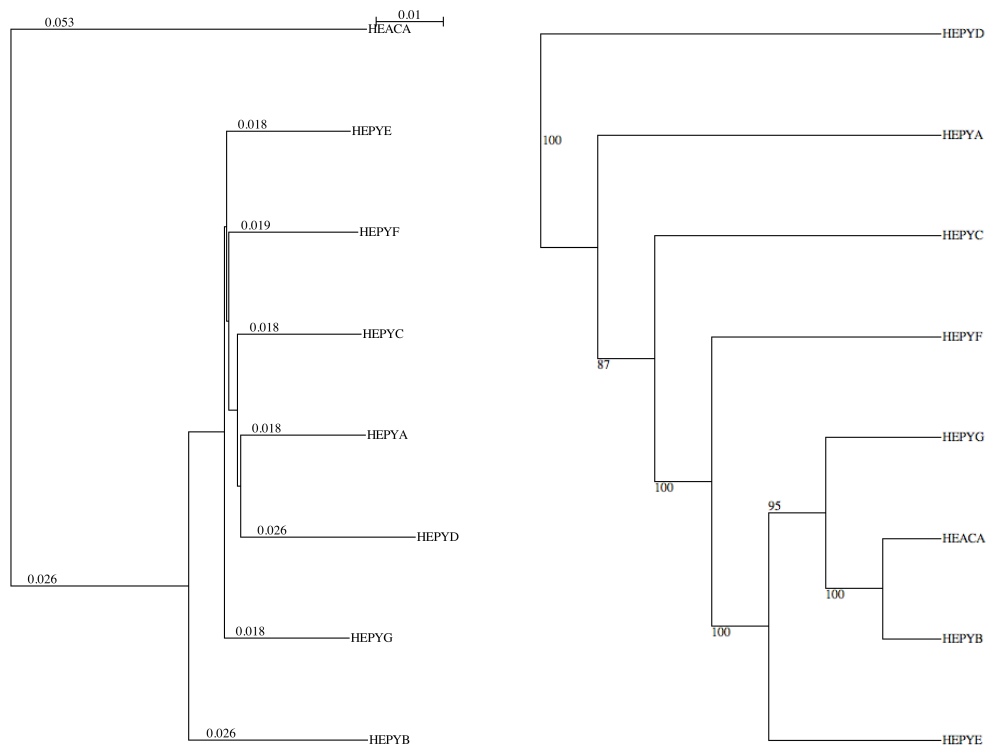
**BIONJ TREE FROM MAXIMUM LIKELIHOOD (ML) DISTANCES OF 9 BRADYRHIZOBIACEAE STRAINS RECONSTRUCTED FROM THE 1186 CORE GENOME GENES.**

The values above the branches in blue represent their length. All branches have maximal bootstrap support of 100.

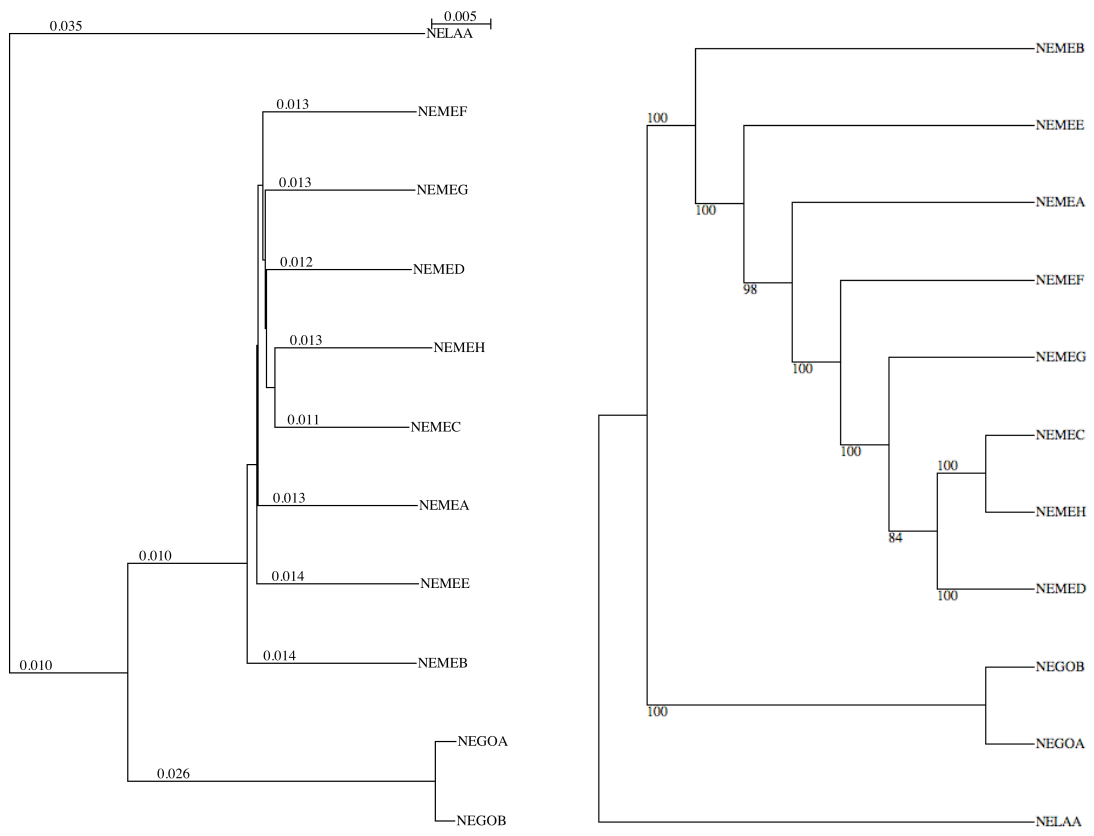


BACILLUS PHYLOGENY RECONSTRUCTED FROM THE 2933 CORE GENOME GENES.

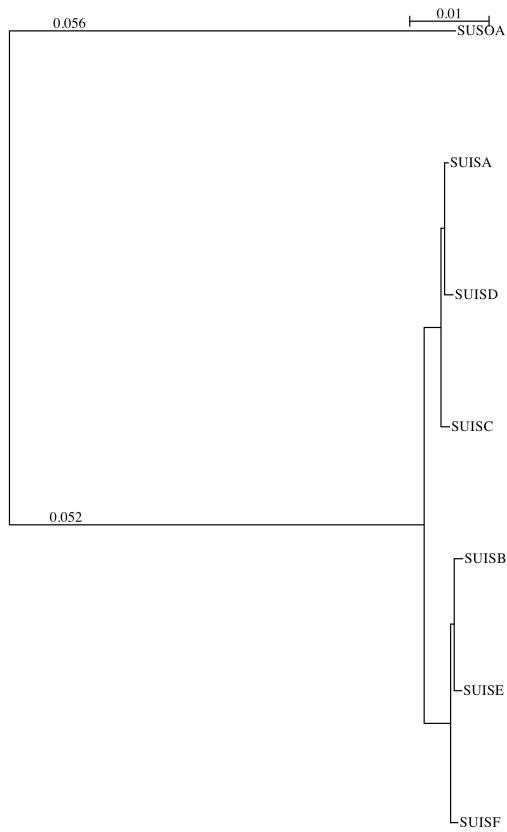
All branches have maximal bootstrap support of 100.



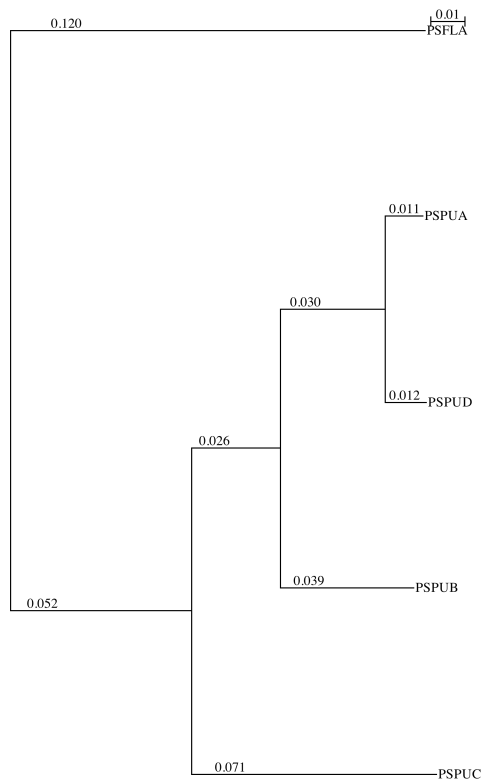
HELICOBACTER PHYLOGENY RECONSTRUCTED FROM THE 1030 CORE GENOME GENES.



*NEISSERIA* PHYLOGENY RECONSTRUCTED FROM THE 739 CORE GENOME GENES



*SULFOLOBUS* PHYLOGENY RECONSTRUCTED FROM THE 1751 CORE GENOME GENES.  
All branches have maximal bootstrap support of 100.



*PSEUDOMONAS* PHYLOGENY RECONSTRUCTED FROM THE **2963** CORE GENOME GENES.

All branches have maximal bootstrap support of 100.