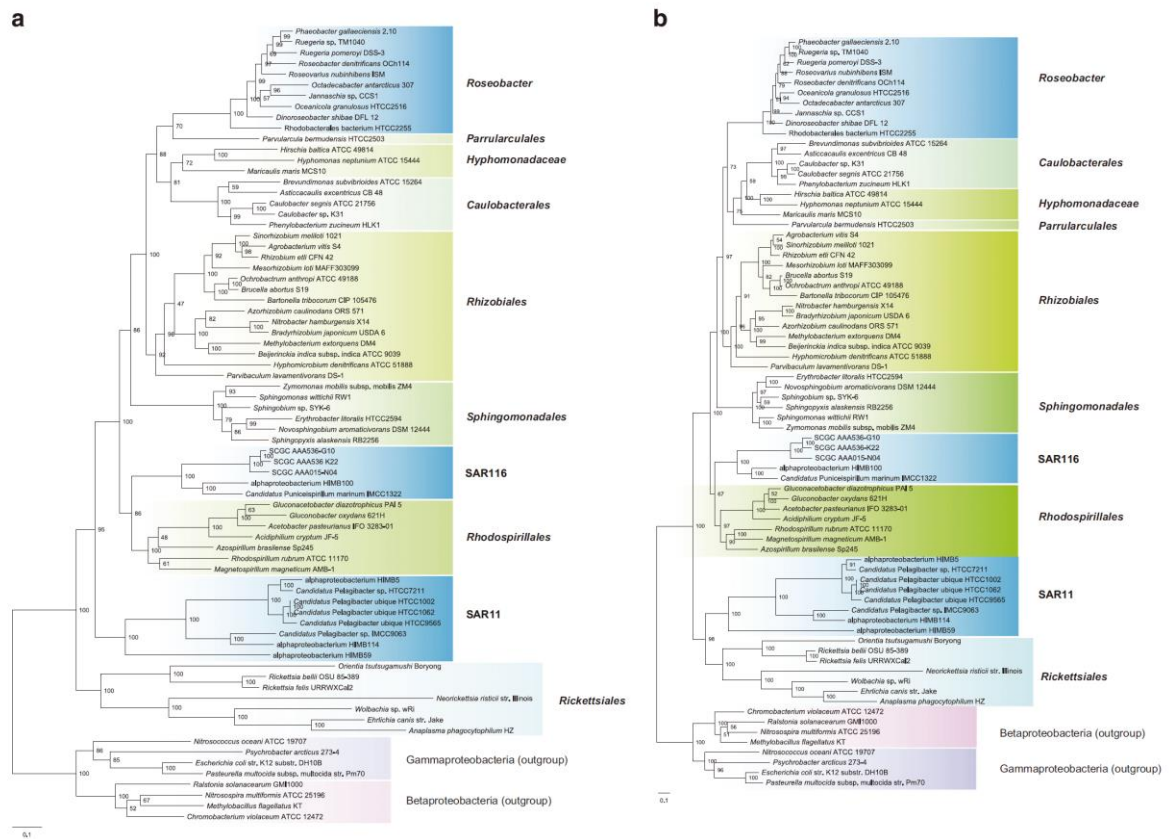


The phylogenetic position of the globally dominant ocean SAR11 bacteria has been highly controversial in the Alphaproteobacteria tree. Prof. Haiwei Luo has recently provided substantial phylogenomic evidence showing that the previous clustering of this planktonic lineage and the obligate endosymbiotic *Rickettsiales* is an artifact due to the consistently low genomic G+C content shared by these bacteria. Further statistical phylogenetic analyses allow him to identify a highly confident evolutionary position of SAR11. This new phylogeny has significant implications for the evolutionary path to genome streamlining of the SAR11 clade.



Maximum likelihood phylogeny of Alphaproteobacteria using RAxML. (A) Tree based on a concatenation of the 28 composition-homogeneous proteins, in which 19 are ribosomal proteins. Note that SAR11 and *Rickettsiales* are disassociated. (B) Tree based on a concatenation of the 24 composition-heterogeneous ribosomal proteins, in which SAR11 and *Rickettsiales* comprise a monophyletic clade due to a compositional artifact.

Link: <http://www.nature.com/ismej/journal/vaop/ncurrent/abs/ismej2014227a.html>