



Fig. 2- figure supplement 2. Tree of ochrophyte glycyl-tRNA synthetase sequences.

This tree shows the consensus unrooted Bayesian topology for a 95 taxa x 487 aa alignment of glycyl tRNA synthetase sequences. The font colour of each sequences corresponds to the taxonomic origin (see legend below for details) and are labelled with the taxonomic identifiers previously defined in Table S1. Sequences labelled with chl_ possess apparent plastid targeting sequences recognisable by CASH lineage plastids. The ancestral ochrophyte plastidic isoform, of apparent chlamydiobacterial origin, is labelled with a blue ellipse. Black circles at each node denote posterior probabilities of 1.0 in Bayesian inferences with three different substitution matrices (GTR, Jones, and WAG), and grey circles indicate posterior probabilities of 0.8 with at least two of these matrices. Support values for all remaining nodes, using both Bayesian and RAxML analysis, is provided in the form

MrBayes posterior probabilities: GTR/Jones/WAG
RAxML best tree likelihoods: GTR/ JTT/ WAG

- Taxonomic key**
- Prokaryotes
 - Red algae
 - Green algae
 - Aplastidic stramenopiles
 - Haptophytes
 - Cryptomonads
 - Alveolates
 - Chlorarachniophytes/ Euglenids
 - Ochrophytes- Chrysista
 - Ochrophytes- Hypogyrstea
 - Ochrophytes- Diatoms
 - Other eukaryotes

