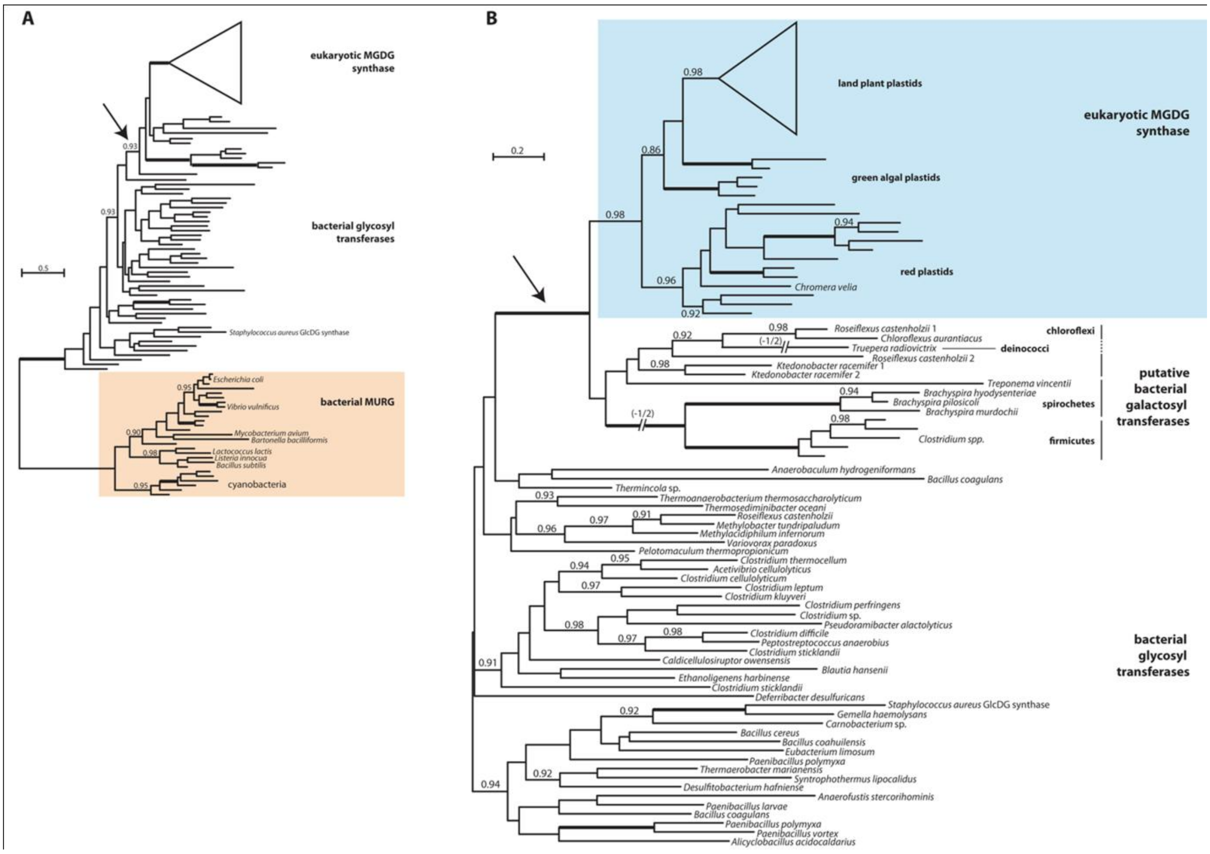

Figure S4: Global phylogeny of MGDG synthases and related glycosyltransferases.

Eukaryotic MGDG synthases are related to diverse bacterial glycosyltransferases and distantly related to bacterial MURG protein family (A). Removal of MURG sequences reveals strong association (arrow) between eukaryotic MGDG synthases and a subgroup of bacterial glycosyltransferases, which may constitute a previously uncharacterized galactosyl transferase family (B). Maximum likelihood trees (PhyML) display aLRT branch supports. Thick lines represent branch supports ≥ 0.99. These phylogenies provide rationale for rooting the eukaryotic MGDG synthase phylogeny, analysed in detail in Figure 8A.