

## **Electronic Supplementary Material**

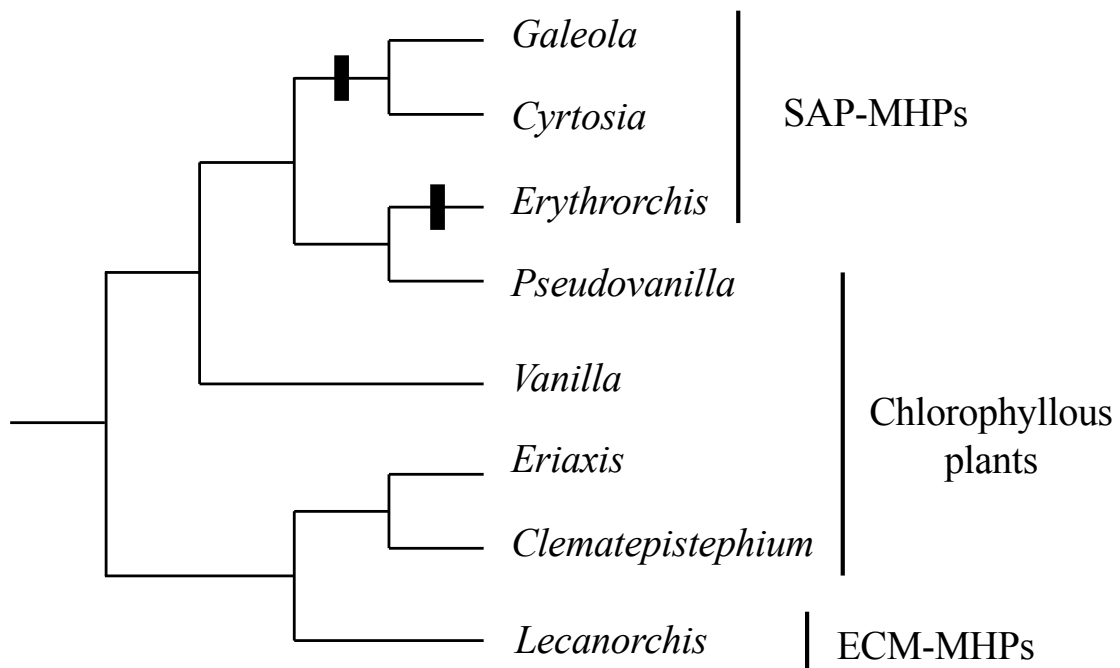
Evolutionary histories and mycorrhizal associations of mycoheterotrophic plants dependent on saprotrophic fungi

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**Fig. S1** Evolutionary course of saprophytic fungi-associated mycoheterotrophic plants (SAP-MHPs) in subfamily Vanilloideae, Orchidaceae. Bars show points where SAP-MHPs likely evolved. The phylogram of Vanilloideae is summarized from Cameron et al. (2009) and Cameron (2011).

**Fig. S2** Phylogenetic placements of saprophytic fungi-associated mycoheterotrophic plants (SAP-MHPs) within Marasmiaceae and Omphalotaceae as inferred from maximum likelihood (ML) analysis based on ribosomal DNA internal transcribed spacer sequences. After multiple alignment of 34 SAP-MHP sequences with 204 published sequences of Omphalotaceae and Marasmiaceae using MAFFT7 (Kato and Standley 2013), ML analysis was conducted using the IQ-TREE web server (Trifinopoulos et al. 2016) with SH-like-aLRT branch support and a best fit GTR+F+R5 evolutionary model as selected by ModelFinder (Kalyaanamoorthy et al. 2017). Clade name assignment for Marasmiaceae and Omphalotaceae was in accordance with Antonín et al. (2019), Oliveira et al. (2019), and Sandoval-Leiva et al. (2016). Mycobionts of SAP-MHPs are indicated in bold and clades without SAP-MHPs mycobionts are collapsed. SH-aLRT values  $\geq 75\%$  are shown below the branches.

