Supplementary Information Files

Table S1. Accession numbers or references of the nuclear and mitochondrial sequences used for the phylogenetic analysis of Balanophoraceae.

Figure S1. Maximum Likelihood phylogenetic analysis of Balanophoraceae based on a concatenated alignment of nuclear (rDNA operon) and mitochondrial (*matR*) sequences. Alignments were prepared with MAFFT v7.407 (parameters: -localpair -maxiterate 1000), unaligned blocks were removed with BMGE v1.12 (parameters: -t DNA -m DNAPAM150:2), and the phylogenetic analysis was performed with RAxML v.8.2.11 (parameters: -f a -m GTRGAMMA -N 1000). Bootstrap support values >50% are shown above each branch. The scale bar corresponds to substitutions per site.

Note S1. List of species and accession numbers of taxa mentioned in Table 1.

cpDNAs available in public databases:

Balanophoraceae: Balanophora fungosa MN414176, B. harlandii MN414177 (Chen et al. 2019), B. laxiflora KX784265, B. reflexa KX784266 (Su et al. 2018), B. yakushimensis MT901289 (unpublished), Lophophytum pyramidale MT834848, Ombrophytum subterraneum MT834847 (Ceriotti et al. 2021), Rhopalocnemis phalloides MK036331 (Schelkunov et al. 2019), Sarcophyte sanguinea OQ810027- OQ810028, Thonningia sanguinea OQ810029-OQ810031 (Kim et al. 2023).

Hydnoraceae: Hydnora abissinica NC065049, H. africana NC065136, H. arabica NC065211, H. esculenta NC065050, H. longicollis NC065051, H. triceps NC065052 (Jost et al 2022), H. visseri NC029358 (Nauman et al. 2016), Prosopanche bonacinae NC065053, P. panguanensis NC065054 (Jost et al. 2022).

Cynomoriaceae: Cynomorium coccineum KX270752 (Bellot et al. 2016).

Rafflesiaceae lacks a cpDNA (Molina et al. 2014, Cai et al. 2021).

Cytiniaceae: Cytinus hypocistis NC031150 (Roquet et al. 2016).

Mitrastemonaceae: Mitrastemon kanehirai MF372930, M. yamamotoi MZ317931 (unpublished).

Apodanthaceae: Pilostyles aethiopica KT981956, P. hamiltonii KT981955 (Bellot & Renner 2016).
Lennoaceae: Lennoa madreporoides NC039720, Pholisma arenarium NC039719 (Schneider et al. 2018).
Cuscuta: C. reflexa NC009766, C. gronovii NC009765 (Funk et al 2007), C. approximata NC052871, C. pedicellata NC052872, C. africana NC052870, C. nitida NC052869 (Banajeree 2020), C. carnosa NC043868, C. mexicana NC_043869, C. chapalana NC043870, C. strobilacea NC043775, C. bonafortunae NC_043871, C. costaricense NC042956, C. boldinghii NC042949, C. erosa NC042948, C. pentagona NC_039759, C. obtusiflora NC_009949 (Banerjee 2019), C. japonica NC060789 (Feng and Lin 2022), C. exaltata NC009963 (McNeal 2007), C. chinensis MH780079 (Park and Moon 2018), C. australis NC045885 (Wang et al. 2020), C. campestris BK059222 (Anderson et al. 2021), C. epithymum NC_070194 (unpublished), C. europaea NC_070193 (unpublished), C. pacifica OP263625, C. micrantha OP356701, C. nevadensis OP390286, C. haughtii OP402844, C. volcanica OP402844, C. macrocephala OP414597, C. chinensis OPP414596, C. corymbosa var. stylosa OP414598, C. polyanthemos OP441382, C. indecora OP414599, C. vandervenderii OP414600 (Banerjee & Stefanovic 2023). Cuscuta subgenus Grammica section Subulatae lost or drastically reduced the plastome (Banerjee & Stefanovic 2023).
Orobanchaceae: Aeginetia indica MW851293; MN529629 (Choi & Park 2021; Chen et al. 2020), Aphyllon californicum NC025651 (Wicke et al. 2013), A. epigalium MH050785, A. fasciculatum NC039679, A. purpureum MH499250, A. uniflorum MH580290 (Schneider et al. 2018), Boschniakia himalaica NC068836 (unpublished), Boulardia latisquama NC025641 (Wicke et al. 2013), Christisonia kwangtungensis OL362208 (Zhang et al. 2022), Cistanche deserticola NC_021111 (Li et al. 2013), C. phelypaea NC_025642 (Wicke et al. 2013), C. salsa MN614128 (Liu et al. 2020), C. sinensis MK386641; MN614129 (Liu et al. 2020), C. tubulosa MK386642.1 (Liu et al. 2020), Conopholis americana NC023131 (Wicke et al. 2013), Diphelypaea coccinea NC043877 (Gruzdev et al. 2019), Epifagus virginiana NC001568 (Wolfe et al. 1992), Lathraea squamaria NC027838 (Samigullin et al. 2016), Orobanche austrohispanica NC031441, O. densiflora NC031442, O. pancicii NC031443, O. rapum-genistae NC_031444 (Cusimano & Wicke, 2016), O. cernua KT387722 (Wicke et al. 2013), O. coerulescens NC068242 (unpublished), O. crenata NC024845, O. gracilis NC023464 (Wicke et al. 2013),

Phacellanthus tubiflorus NC068243 (unpublished), Phelipanche purpurea NC023132, P. ramosa NC023465 (Wicke et al. 2013), P aegyptiaca KU212370 (Wicke et al. 2016).

Complete and draft mitochondrial genome assemblies available in public databases:

Balanophoraceae: Complete mtDNAs of Lophophytum mirabile KU992322-KU992380, KX792461 (Sanchez-Puerta et al. 2017), Ombrophytum subterraneum MT076267-MT076320 (Roulet et al. 2020), Rhopalocnemis phalloides MZ269392–MZ269412 (Yu et al. 2022).

Hydnoraceae: Draft mtDNAs of Hydnora visseri OP649464.1- OP649479.1 and Prosopanche americana: OP649480.1 - OP649522.1 (Yu et al. 2023).

Cynomoriaceae: Complete mtDNAs of Cynomorium coccineum KX270753.1-KX270801.1 (Bellot et al. 2016).

Rafflesiaceae: Draft mtDNAs of Sapria himalayana SRR629601, SRR629606, Rafflesia cantleyi SRR629613, and Rafflesia tuan-mudae SRR629600 (Xi et al. 2013; assembled contigs not available), Rafflesia lagascae SRR1120517, SRR1121763 (Molina et al. 2014; assembled contigs not available), Rafflesia leonardi KJ154961-KJ155011 (Nickrent et al. unpublished).

Cuscuta: Complete mtDNAs of C. australis (8 contigs) BK059197-BK059204, C. campestris BK016277 (Anderson et al. 2021), C. epilinum BK059237, C. europea BK059238, C. japonica NC_060804 (Lin et al. 2022).

Orobanchaceae:

Complete mtDNAs of Aeginetia indica NC_069194; MW851294; MW582538 (Zhong et al. 2022; Choi & Park, 2021), Boschniakia himalaica OP019634-OP019648, B. rossica OP019631-OP019633 (Zhang et al. 2023), Christisonia kwangtungensis OM219025-OM219027 (Zhang et al. 2022), Cistanche spp. ON890398 - ON890419 (Miao et al. 2022).

Draft mtDNAs of Aphyllon epigalion MG987142, MH129026 (Schneider et al. 2018) and Orobanche spp. KT366929 - KT366933, KT366957-KT366958 KT366955; KT367291-KT367292; KT367470, KT367476, KT367509-KT367510, KT367489 (Fan et al. 2016).

Table S1. Accession numbers or references of the nuclear and mitochondrial sequences used for the phylogenetic analysis of Balanophoraceae.

Species	**18S**	**26S**	**ITS1 - 5.8S - ITS2**	***matR***
Balanophora fungosa	JN392868	KP263238	JN392881	JQ613244
Balanophora laxiflora	JN392870	KP263239	JN392888	JQ613245
Corynaea crassa	L24400	KP263242	OM471919	KP263265
Helosis cayennensis	L25682	-	KT709670	KP263268
Langsdorffia hypogaea	L25683	-	KT709672	MG234111
Lophophytum mirabile	Ceriotti *et al.* 2021 -	Ceriotti *et al.* 2021 -	SRX1630042	KU992322
Lophophytum pyramidale	KP263283	KP263249	KT709674	KP263270
Ombrophytum subterraneum	L24406	KP263254	-	EU281127
Rhopalocnemis phalloides	Ceriotti *et al.* 2021 -	Ceriotti *et al.* 2021 -	SRX4826442	-
Sarcophyte sanguinea	KP263286	-	-	KP263277
Scybalium jamaicense	U59933	-	-	-
Thonningia sanguinea	KP263289	-	KT763386	KP263280
Spinacia oleracea (outgroup)	L24420	HQ843464	-	NC_035618

Note: the available sequence of the rDNA operon of *Lathrophytum* is too short for meaningful phylogenetic analysis.

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