



Symbiosis triggers the functioning of selected *PKS* genes in the lichenized fungus
Xanthoparmelia taractica

Mycological progress

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Fig. S1

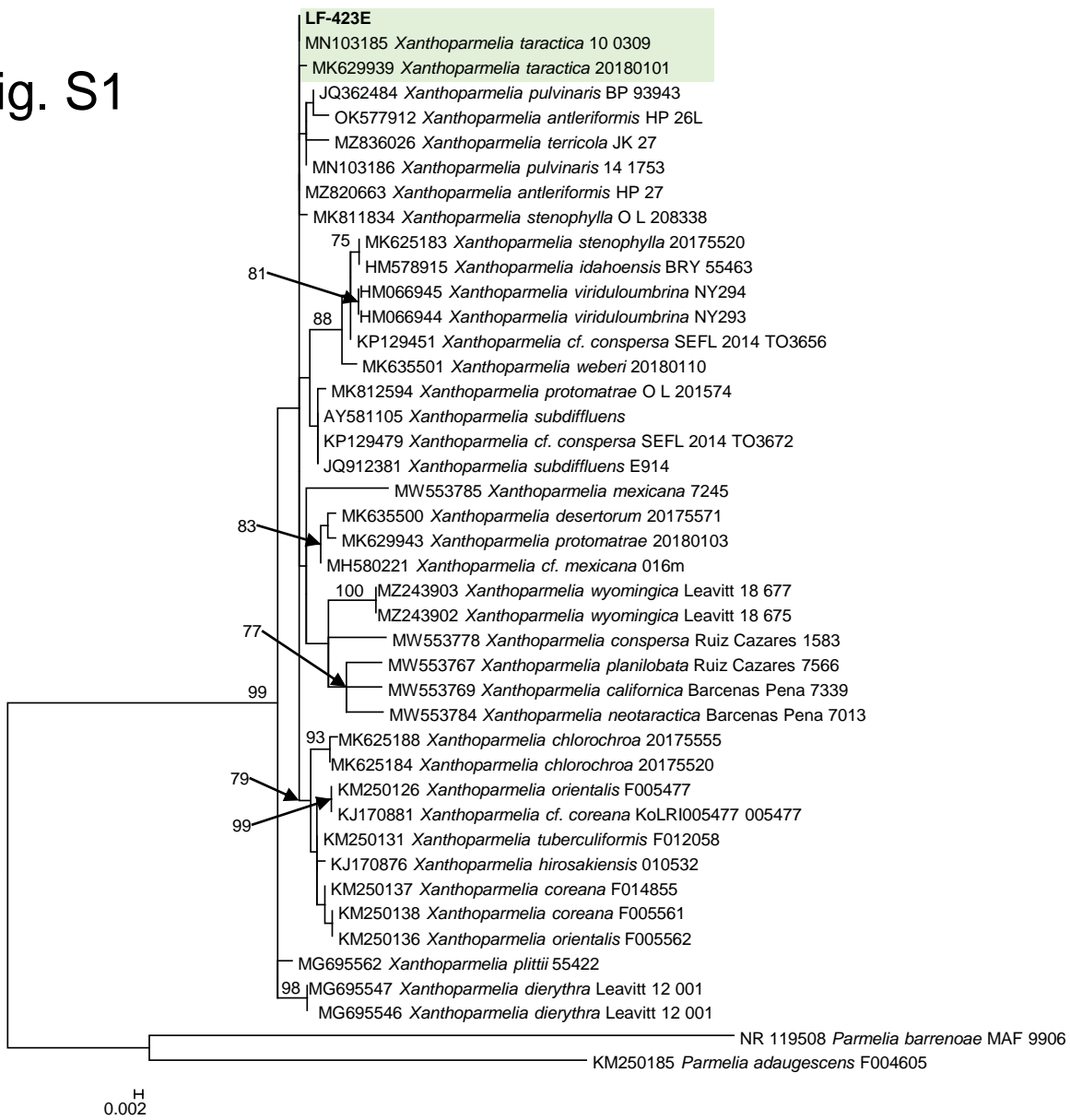


Fig. S2

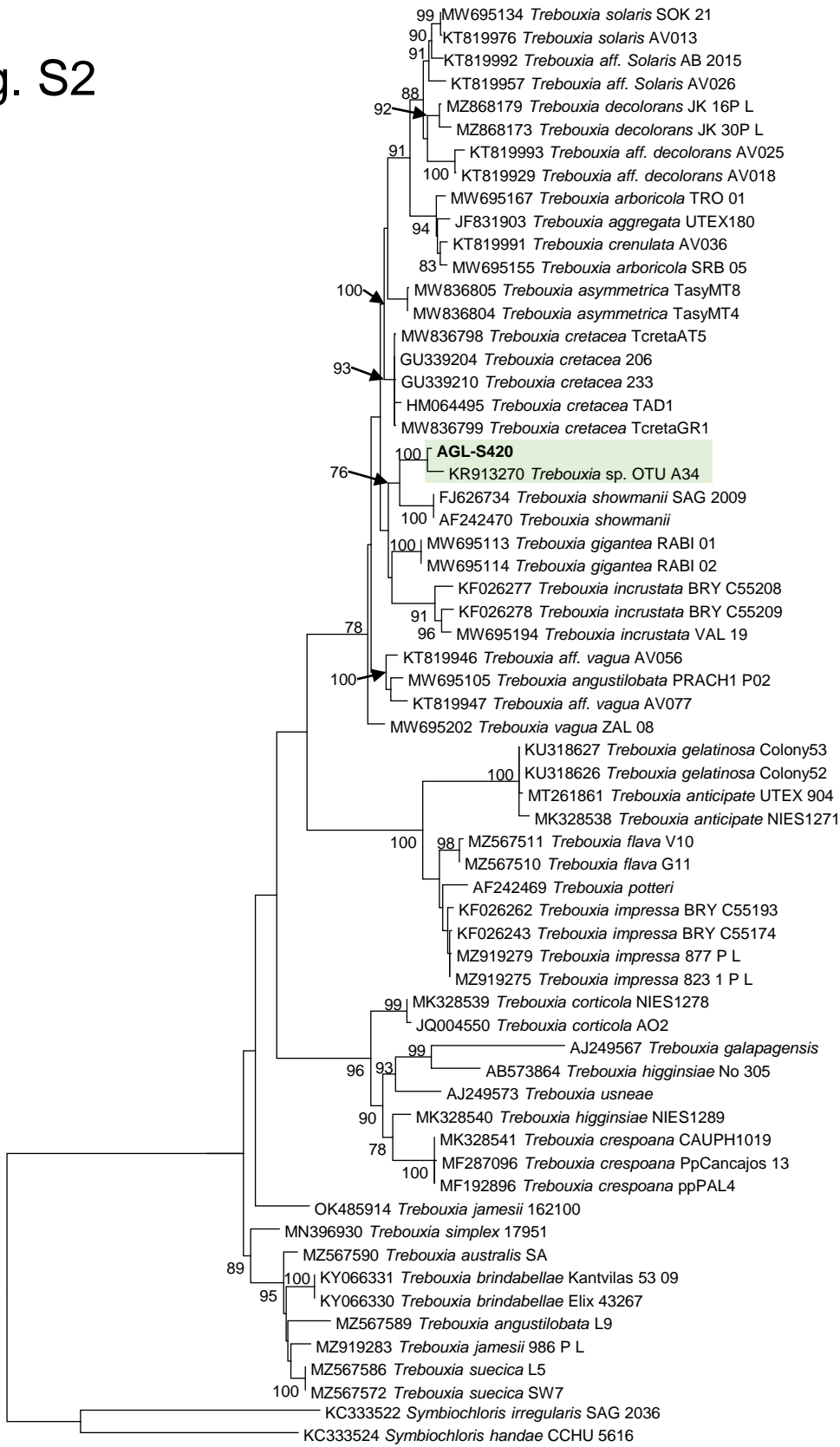


Fig. S3

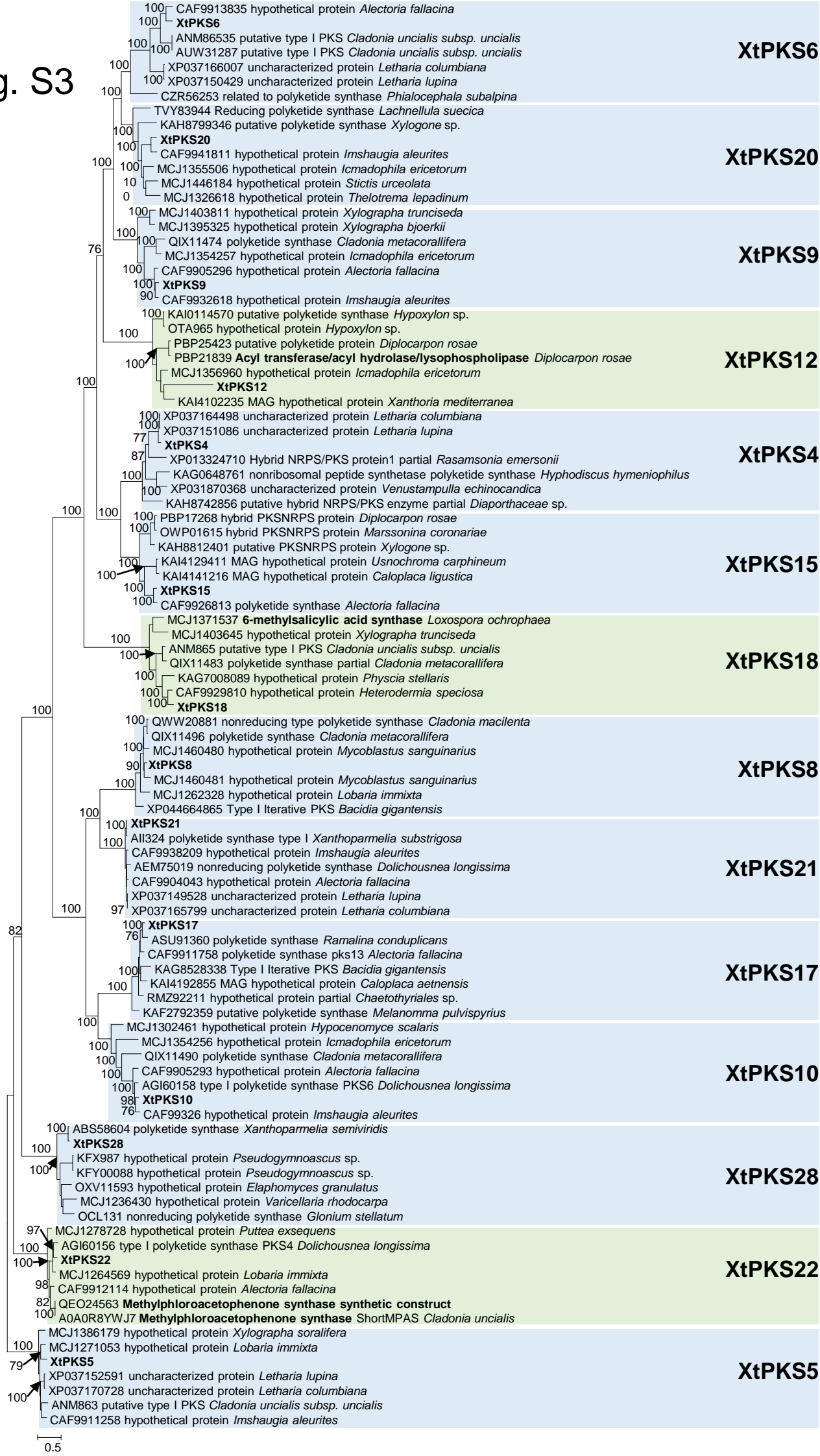


Table S1 GenBank accession numbers of complete ITS sequences of *Xanthoparmelia* species used for the maximum likelihood phylogenetic analysis. Two species of *Parmelia* served as the outgroup taxa.

Taxa	Isolate numbers	Accession numbers
<i>Xanthoparmelia antleriformis</i>	HP-26L	OK577912
<i>X. antleriformis</i>	HP-27	MZ820663
<i>X. californica</i>	Barcnas-Pena 7339	MW553769
<i>X. chlorochroa</i>	20175520	MK625184
<i>X. chlorochroa</i>	20175555	MK625188
<i>X. conspersa</i>	Ruiz-Cazares 1583	MW553778
<i>X. cf. conspersa</i>	TO3656_Cryptogamia	KP129451
<i>X. cf. conspersa</i>	TO3672_Cryptogamia	KP129479
<i>X. coreana</i>	KoLRI005561	KM250138
<i>X. coreana</i>	KoLRI014855	KM250137
<i>X. cf. coreana</i>	005477	KJ170881
<i>X. desertorum</i>	20175571	MK635500
<i>X. dierythra</i>	Leavitt 12-001illumina	MG695546
<i>X. dierythra</i>	Leavitt 12-001sanger	MG695547
<i>X. hirosakiensis</i>	010532	KJ170876
<i>X. idahoensis</i>	BRY-55463	HM578915
<i>X. mexicana</i>	Barcnas-Pena 7245	MW553785
<i>X. cf. mexicana</i>	016m	MH580221
<i>X. neotaractica</i>	Barcnas-Pena 7013	MW553784
<i>X. orientalis</i>	KoLRI00547	KM250126
<i>X. orientalis</i>	KoLRI005562	KM250136
<i>X. planilobata</i>	Ruiz-Cazares 7566	MW553767
<i>X. plittii</i>	55422	MG695562
<i>X. protomatrae</i>	20180103	MK629943
<i>X. protomatrae</i>	O-L-201574	MK812594
<i>X. pulvinaris</i>	BP-93943	JQ362484
<i>X. pulvinaris</i>	14-1753	MN103186
<i>X. stenophylla</i>	O-L-208338	MK811834
<i>X. stenophylla</i>	20175520	MK625183
<i>X. subdiffluens</i>	E914	JQ912381
<i>X. subdiffluens</i>	MAF 9910	AY581105
<i>X. taractica</i>	20180101	MK629939
<i>X. taractica</i>	10-0309	MN103185
<i>X. taractica</i>	LF-423E	OP279582
<i>X. terricola</i>	JK-27	MZ836026
<i>X. tuberculiformis</i>	KoLRI012058	KM250131
<i>X. viriduloumbrina</i>	NY293	HM066944
<i>X. viriduloumbrina</i>	NY294	HM066945
<i>X. weberi</i>	20180110	MK635501
<i>X. wyomingica</i>	Leavitt 18-675	MZ243902
<i>X. wyomingica</i>	Leavitt 18-677	MZ243903
<i>Parmelia adaugescens</i>	KoLRI004605	KM250185
<i>P. barrenoae</i>	MAF 9906	NR 119508

Table S2 GenBank accession numbers of complete ITS sequences of *Trebouxia* species used for the maximum likelihood phylogenetic analysis. Two species of *Symbiochloris* served as the outgroup taxa.

Taxa	Isolate numbers	Accession numbers
<i>Trebouxia aggregata</i>	UTEX180	JF831903
<i>T. angustilobata</i>	PRACH1-P02	MW695105
<i>T. angustilobata</i>	L9	MZ567589
<i>T. anticipata</i>	UTEX 904	MT261861
<i>T. anticipata</i>	NIES1271	MK328538
<i>T. arboricola</i>	TRO-01	MW695167
<i>T. arboricola</i>	SRB-05	MW695155
<i>T. asymmetrica</i>	TasyMT8	MW836805
<i>T. asymmetrica</i>	TasyMT4	MW836804
<i>T. australis</i>	SA	MZ567590
<i>T. brindabellae</i>	Kantvilas 53/09	KY066331
<i>T. brindabellae</i>	Elix 43267	KY066330
<i>T. corticola</i>	NIES1278	MK328539
<i>T. corticola</i>	AO2	JQ004550
<i>T. crenulata</i>	AV036	KT819991
<i>T. crespoana</i>	ppPAL4	MF192896
<i>T. crespoana</i>	CAUPH1019	MK328541
<i>T. aff. crespoana</i>	PpCancajos_13	MF287096
<i>T. cretacea</i>	TcretaAT5	MW836798
<i>T. cretacea</i>	TcretaGR1	MW836799
<i>T. decolorans</i>	JK-16P/L	MZ868179
<i>T. decolorans</i>	JK-30P/L	MZ868173
<i>T. aff. decolorans</i>	AV025	KT819993
<i>T. aff. decolorans</i>	AV018	KT819929
<i>T. flava</i>	G11	MZ567510
<i>T. flava</i>	V10	MZ567511
<i>T. galapagensis</i>	UTEX 2230	AJ249567
<i>T. gelatinosa</i>	Colony52	KU318626
<i>T. gelatinosa</i>	Colony53	KU318627
<i>T. gigantea</i>	RABI-01	MW695113
<i>T. gigantea</i>	RABI-02	MW695114
<i>T. higginsiae</i>	NIES1289	MK328540
<i>T. higginsiae</i>		AB573864
<i>T. impressa</i>	823-1-P/L	MZ919275
<i>T. impressa</i>	877-P/L	MZ919279
<i>T. aff. impressa</i>	BRY-C55174	KF026243
<i>T. aff. impressa</i>	BRY-C55193	KF026262
<i>T. incrustata</i>	VAL 19	MW695194
<i>T. aff. incrustata</i>	BRY C55209	KF026278
<i>T. aff. incrustata</i>	BRY C55208	KF026277
<i>T. jamesii</i>	986-P/L	MZ919283
<i>T. potteri</i>	UTEX 900	AF242469
<i>T. showmanii</i>	SAG 2009	FJ626734
<i>T. showmanii</i>	UTEX 2234	AF242470
<i>T. simplex</i>	17951	MN396930
<i>T. solaris</i>	SOK-21	MW695134
<i>T. solaris</i>	AV013	KT819976
<i>T. aff. solaris</i>	AV026	KT819957
<i>T. aff. solaris</i>	AV044	KT819992
<i>T. suecica</i>	L5	MZ567586
<i>T. suecica</i>	SW7	MZ567572
<i>T. usneae</i>	UTEX 2235	AJ249573

<i>T. vaga</i>	ZAL-08	MW695202
<i>T. aff. vaga</i>	AV056	KT819946
<i>T. aff. vaga</i>	AV077	KT819947
<i>T. jamesii</i>	162100	OK485914
<i>Trebouxia</i> sp.	OTU A34	KR913270
<i>Trebouxia</i> sp.	233	GU339210
<i>Trebouxia</i> sp.	TAD1	HM064495
<i>Trebouxia</i> sp.	206	GU339204
<i>Trebouxia</i> sp.	AGL-S420	OP279583
<i>Symbiochloris handae</i>	CCHU 5616	KC333524
<i>S. irregularis</i>	SAG 2036	KC333522

Table S3 RT-qPCR primers designed in this study for the expression analysis of selected *PKS* genes. Forward and reverse primers are denoted by the letters F and R in the primer name.

Gene regions	Primers	Primer sequence (5'→3')
<i>β-tubulin</i>	β-tubulin F4	GGCATCCTGGTACTGCTGGT
	β-tubulin R4	GCGACCAGTTCACTGCCATG
<i>XTPKS12</i>	xtpks12F	GCGTTTCATCACTTCTCAC
	xtpks12R	GTCCGGTCCTCGTAATCTG
<i>XTPKS18</i>	xtpks18F	TGCGACAACCGTGAAAAGT
	xtpks18R	TTGTTGCGATTGAGGACAG
<i>XTPKS22</i>	xtpks22F	GATCTCTACCGCTTGAC
	xtpks22R	TCATACCGGCAGAACTCAT

Table S4 Summary of BUSCO statistics for the *Xanthoparmelia taractica* genome.

Property	Number	Percent (%)
Complete BUSCOs	286	98.60%
Complete and single-copy BUSCOs	286	98.60%
Complete and duplicated BUSCOs	0	0.00%
Fragmented BUSCOs	0	0.00%
Missing BUSCOs	4	1.40%
Total BUSCO groups searched	290	100%

Table S5 List of repeats identified from the genome of *Xanthoparmelia taractica*.

Repeat contents	Number of elements	Length occupied	Percentage of sequence
Short interspersed elements (SINEs)	0	0 bp	0.00%
ALUs	0	0 bp	0.00%
MIRs	0	0 bp	0.00%
Long interspersed nuclear elements (LINEs)	12	828 bp	0.00%
LINE1	0	0 bp	0.00%
LINE2	0	0 bp	0.00%
L3/CR1	0	0 bp	0.00%
Long terminal repeat (LTR)	3724	3503293 bp	8.19%
ERVL	0	0 bp	0.00%
ERVL-MaLRs	0	0 bp	0.00%
ERV_classI	0	0 bp	0.00%
ERV_classII	0	0 bp	0.00%
DNA elements	1346	1150524 bp	2.69%
hAT-Charlie	0	0 bp	0.00%
TcMar-Tigger	19	1948 bp	0.00%
Unclassified	10891	4880186 bp	11.41%
Total interspersed repeats		9534831 bp	22.29%
Small RNA	0	0 bp	0.00%
Satellites	76	20853 bp	0.05%
Simple repeats	38	12900 bp	0.03%
Low complexity	0	0 bp	0.00%

Table S6 Non-coding RNA identified from the genome of *Xanthoparmelia taractica*.

Type	Copy	Avg. Length (bp)	Total Length (bp)	% of Genome
ncRNA	25	145.12	3628	0.0084
5S rRNA	8	115.5	924	0.0021
5.8S rRNA	1	152	152	0.0003
18S rRNA	2	900.5	1801	0.0041
28S rRNA	1	3686	3686	0.0085
tRNA	61	90.4262	5516	0.0127

Table S7 A summary of the functional annotations of the *Xanthoparmelia taractica* genome.

Databases	No. Of Genes	Percentage %
NCBI-nr database	8883	82.79
EggNOg	8278	77.15
Kyoto Encyclopedia of Genes and Genomes	3585	33.41
SwissProt	6452	60.13
Gene Ontology	6127	57.10
P450	10480	97.67
Transporter Classification Database	1364	12.71
Protein Families database	6876	64.08
Pathogen Host Interactions database	2314	21.57