

Supplementary material

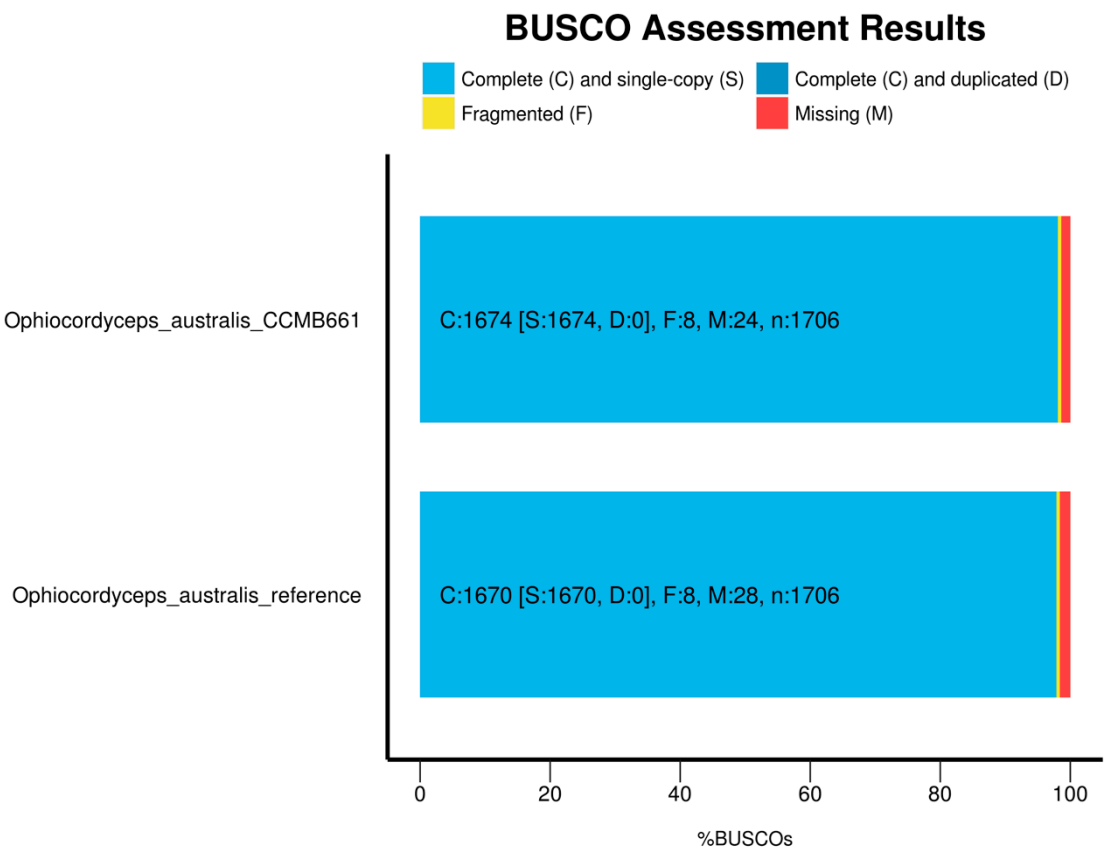


Figure S1: BUSCO quality assessment results for the genome of *Ophiocordyceps australis* CCMB661 and Map64.

Table S1: Sequences of *Ophiocordyceps* species from NCBI-GenBank databases used in phylogenetic analyses and their associated metadata.

Species	ID Isolate	GenBank Accession Number			Host order	Reference
		LSU	ITS	TEF		
<i>Metacordyceps taii</i>	ARSEF 5714	AF543787	-	AF543775	Lepidoptera	[120]
<i>Metacordyceps taii</i>	ARSEF 5714	-	JN049829	-	Lepidoptera	[53]
<i>Ophiocordyceps arborescens</i>	NBRC 105891	AB968414	AB968398	AB968572	Lepidoptera	[121]
<i>Ophiocordyceps arborescens</i>	NBRC 105890	AB968415	AB968399	AB968573	Lepidoptera	[121]
<i>Ophiocordyceps australis</i>	Ophaus 1780	KC610762	KP200888	KC610732	Hymenoptera	[17]
<i>Ophiocordyceps australis</i>	Ophaus 774	KC610764	n/a	KC610734	Hymenoptera	[17]
<i>Ophiocordyceps australis</i>	Ophaus 926	KC610765	n/a	KC610735	Hymenoptera	[17]
<i>Ophiocordyceps australis</i>	HUATSF 774a	MF416562	n/a	MF416510	Hymenoptera	[122]
<i>Ophiocordyceps coccidiicola</i>	NBRC 100682	AB968419	AB968404	AB968583	Hemiptera	[121]
<i>Ophiocordyceps coenomyia</i>	NBRC 108993	AB968412	AB968396	AB968570	Diptera	[121]
<i>Ophiocordyceps coenomyia</i>	NBRC 106964	AB968413	AB968397	AB968571	Diptera	[121]
<i>Ophiocordyceps evansii</i>	Ophsp 858	KC610770	KP200889	KC610736	Hymenoptera	[17]
<i>Ophiocordyceps evansii</i>	Ophsp 912	KC610771	KP200890	KC610737	Hymenoptera	[17]
<i>Ophiocordyceps gracilis</i>	EFCC 8572	EF468811	-	EF468751	Lepidoptera	[18]
<i>Ophiocordyceps gracilis</i>	EFCC 8572	-	JN049851	-	Lepidoptera	[53]
<i>Ophiocordyceps heteropoda</i>	EFCC 10125	EF468812	-	EF468752	Hemiptera	[18]
<i>Ophiocordyceps heteropoda</i>	EFCC 10125	-	JN049852	-	Hemiptera	[53]
<i>Ophiocordyceps irangiensis</i>	OSC 128577	DQ518760	JN049823	DQ522329	Hymenoptera	[123]
<i>Ophiocordyceps irangiensis</i>	OSC 128578	DQ518770	JN049833	DQ522345	Hymenoptera	[123]
<i>Ophiocordyceps longissima</i>	NBRC 106965	AB968420	AB968406	AB968584	Hemiptera	[121]
<i>Ophiocordyceps macroacicularis</i>	NBRC 100685	AB968416	AB968400	AB968574	Lepidoptera	[121]
<i>Ophiocordyceps macroacicularis</i>	NBRC 105888	AB968417	AB968401	AB968575	Lepidoptera	[121]
<i>Ophiocordyceps myrmecophila</i>	BCC 82796	MH028153	MH028150	MH028187	Hymenoptera	[124]
<i>Ophiocordyceps myrmecophila</i>	BCC 82985	MH028155	MH028149	MH028189	Hymenoptera	[124]
<i>Ophiocordyceps myrmecophila</i>	BCC 82258	MH028159	MH028147	MH028190	Hymenoptera	[124]
<i>Ophiocordyceps myrmecophila</i>	BCC 82984	MH028162	MH028148	MH028192	Hymenoptera	[124]
<i>Ophiocordyceps nutans</i>	NBRC 101749	JN941429	-	-	Hemiptera	Okane, I., 2011 (Unpublished)
<i>Ophiocordyceps nutans</i>	NBRC 101749	-	AB968408	AB968589	Hemiptera	[121]
<i>Ophiocordyceps rhizoidea</i>	NHJ 12522	EF468825	JN049857	EF468764	Blattodea (Termite)	[18]
<i>Ophiocordyceps sinensis</i>	EFCC 7287	EF468827	-	EF468767	Lepidoptera (pupae)	[18]
<i>Ophiocordyceps sinensis</i>	EFCC 7287	-	JN049854	-	Lepidoptera (pupae)	[53]
<i>Ophiocordyceps sobolifera</i>	NBRC 106967	AB968422	AB968409	AB968590	Hemiptera	[121]

<i>Ophiocordyceps stylophora</i>	OSC 111000	DQ518766	-	DQ522337	Coleoptera	[123]
<i>Ophiocordyceps stylophora</i>	OSC 111000	-	JN049828	-	Coleoptera	[53]
<i>Ophiocordyceps stylophora</i>	NBRC 100947	JN941447	JN943352	-	Coleoptera (larvae)	[125]
<i>Ophiocordyceps stylophora</i>	NBRC 100947	-	-	AB968579	Coleoptera (larvae)	[121]
<i>Ophiocordyceps thanathonensis</i>	MFLU 162908	MF362990	MF362991	MF372760	Hymenoptera	[126]
<i>Ophiocordyceps thanathonensis</i>	MFLU 162909	MF850378	MF850376	MF872613	Hymenoptera	[126]
<i>Ophiocordyceps thanathonensis</i>	MFLU 162910	MF850377	MF850375	MF872614	Hymenoptera	[126]
<i>Ophiocordyceps tricentri</i>	NBRC 106968	AB968423	AB968410	AB968593	Hemiptera	[121]

References Supplementary material (Table S1)*

120. Currie, C. R., Wong, B., Stuart, A. E., Schultz, T. R., Rehner, S. A., Mueller, U. G., Soung, G. H., Spatafora, J. W. & Straus, N. A. Ancient tripartite coevolution in the attine ant-microbe symbiosis. *Science*. 2003, 299, 5605, 386-388.
121. Ban, S., Sakane, T., & Nakagiri, A. Three new species of *Ophiocordyceps* and overview of anamorph types in the genus and the family Ophiocordyceptaceae. *Mycological progress*. 2015, 14, 1, 1017.
122. Kepler, R. M., Luangsa-Ard, J. J., Hywel-Jones, N. L., Quandt, C. A., Sung, G. H., Rehner, S. A., Aime, M. C., Henkel, T. W., Sanjuan, T., Zare, R., Chen, M., Li, Z., Rossman, A. Y., Spatafora, J. W. & Shrestha, B. A phylogenetically-based nomenclature for Cordycipitaceae (Hypocreales). *IMA fungus*. 2017. 8, 2, 335-353.
123. Spatafora, J. W., Sung, G. H., Sung, J. M., Hywel-Jones, N. L., & White Jr, J. F. Phylogenetic evidence for an animal pathogen origin of ergot and the grass endophytes. *Molecular ecology*. 2007, 16, 8, 1701-1711.
124. Khonsanit, A., Luangsa-ard, J. J., Thanakitpipattana, D., Kobmoo, N., & Piasai, O. Cryptic species within *Ophiocordyceps myrmecophila* complex on formicine ants from Thailand. *Mycological progress*. 2019, 18 (1-2), 147-161.
125. Schoch, C. L., Seifert, K. A., Huhndorf, S., Robert, V., Spouge, J. L., Levesque, C. A., Chen, W. & Fungal Barcoding Consortium. (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences*, 109(16), 6241-6246.
126. Xiao, Y. P., Wen, T. C., Hongsan, S., Sun, J. Z., & Hyde, K. D. (2017). Introducing *Ophiocordyceps thanathonensis*, a new species of entomogenous fungi on ants, and a reference specimen for *O. pseudolloydii*. *Phytotaxa*, 328(2), 115-126.

*Other citations are listed in the manuscript.

Table S2: Proteases and related domains.

Protein ID	Domain	Clan	Biological process	Molecular function	Cellular component	Feature	Gene
NODE_311_length_27694	Subtilase family	n/a	proteolysis	serine-type endopeptidase activity	cytoplasm	n/a	CDD81_3328
NODE_70_length_116917					extracellular space	signal peptide	CDD81_7855
NODE_112_length_83290					extracellular space	n/a	CDD81_3718
NODE_133_length_71514					cytoplasm	n/a	CDD81_648
NODE_149_length_66206	Subtilase family; Peptidase inhibitor I9	n/a; Protease propeptides/inhibitors	proteolysis	serine-type endopeptidase activity	extracellular space	signal peptide	CDD81_2218
NODE_243_length_37519					extracellular space	signal peptide	CDD81_253
NODE_67_length_121081					cytoplasm	n/a	CDD82_1444
NODE_94_length_88402	Subtilase family; Peptidase inhibitor I9; Chitin recognition protein	n/a; Protease propeptides/inhibitors; n/a	proteolysis	serine-type endopeptidase activity; chitin binding	nucleus	n/a	CDD81_3985
NODE_70_length_116917	Subtilase family; Proprotein convertase P-domain	n/a; Galactose-binding domain-like superfamily	proteolysis	serine-type endopeptidase activity	integral component of membrane; plasma membrane	transmembrane alpha helix	CDD81_7829
NODE_235_length_39940	Peptidase family C54	Peptidase clan CA	protein transport; autophagy	cysteine-type peptidase activity	nucleus; cytoplasm	n/a	CDD82_1507
NODE_52_length_140965	Peptidase family M28; PA domain	Peptidase clan MH/MC/MF; LeuD/IlvD-like	n/a	metal ion binding; aminopeptidase activity	extracellular space	signal peptide	CDD81_229
NODE_84_length_99438	Dipeptidyl peptidase IV (DPP IV) N-terminal region; Prolyl oligopeptidase family	Beta propeller; Alpha/Beta hydrolase fold	proteolysis	serine-type peptidase activity	cytoplasm	n/a	CDD81_6047
NODE_149_length_66206	Dipeptidyl peptidase IV (DPP IV) N-terminal region; Prolyl oligopeptidase family; Alpha/beta hydrolase family	Beta propeller; Alpha/Beta hydrolase fold	proteolysis	serine-type peptidase activity	extracellular space	signal peptide	CDD81_2227
NODE_42_length_162368	ERAP1-like C-terminal domain; Peptidase family M1 domain; Peptidase M1 N-terminal domain	Ig-like fold superfamily (E-set); Peptidase clan MA; Baculovirus p35 protein superfamily	n/a	aminopeptidase activity; metallopeptidase activity; zinc ion binding	cytoplasm	n/a	CDD81_2826
NODE_347_length_22686							CDD81_3652
NODE_103_length_85904	Metallopeptidase family M24	n/a	protein initiator methionine removal	metal ion binding; metalloaminopeptidase activity	cytoplasm; extracellular space	n/a	CDD81_6391
NODE_25_length_195320	Metallopeptidase family M24; Aminopeptidase P, N-terminal domain	n/a; Creatinase/prolidase N-terminal domain superfamily	n/a	aminopeptidase activity; manganese ion binding	mitochondrion	mitochondrial transit peptide	CDD81_1315
NODE_128_length_73625					cytoplasm	n/a	CDD81_746
NODE_243_length_37519					mitochondrion	n/a	CDD81_258

NODE_29_length_188585	Metallopeptidase family M24; zf-MYND-like zinc finger, mRNA-binding; MYND finger	n/a; TRASH superfamily	protein initiator methionine removal	metal ion binding; metalloaminopeptidase activity	cytoplasm	n/a	CDD81_3215
NODE_448_length_10035	Metallopeptidase family M24; Creatinase/Prolidase N-terminal domain; C-terminal region of peptidase M24	n/a; Creatinase/prolidase N-terminal domain superfamily	n/a	metal ion binding; metalloaminopeptidase activity; hydrolase activity	mitochondrion	n/a	CDD81_5383
NODE_73_length_110288	Aminopeptidase I zinc metalloprotease (M18)	Peptidase clan MH/MC/MF	proteolysis	aminopeptidase activity; metallopeptidase activity; zinc ion binding	cytoplasm	n/a	CDD81_1040
NODE_168_length_57686	Aminopeptidase I zinc metalloprotease (M18); M42 glutamyl aminopeptidase	Peptidase clan MH/MC/MF	proteolysis	aminopeptidase activity; metallopeptidase activity; zinc ion binding	extracellular space	n/a	CDD81_1337
NODE_147_length_67131	LysM domain	LysM-like domain	n/a	n/a	nucleus	n/a	CDD81_780
NODE_135_length_70958	Glycosyl hydrolase family 61	Ig-like fold superfamily (E-set)	n/a	chitin binding	extracellular space	signal peptide	CDD81_5862

Table S3: Predicted phospholipase domains for the entomopathogenic fungus *O. australis* CCMB661.

Protein ID	Domain	Clan	Biological process	Molecular function	Cellular component	Feature	Gene
NODE_347_length_22686	Patatin-like phospholipase; Domain of unknown function	Patatin/FabD/lysophospholipase-like superfamily; n/a	lipid metabolic process	triglyceride lipase activity	organelle membrane	transmembrane alpha helix	CDD82_222
NODE_169_length_56692					endomembrane system	transmembrane alpha helix	CDD81_1349
NODE_47_length_145112	Patatin-like phospholipase; Cyclic nucleotide-binding domain	Patatin/FabD/lysophospholipase-like superfamily; Cupin fold	lipid metabolic process	lysophospholipase activity; phosphatidyl phospholipase B activity	endomembrane system	transmembrane alpha helix	CDD81_4216
NODE_39_length_172552	Phosphatidylinositol-specific phospholipase C, X domain; Phosphatidylinositol-specific phospholipase C, Y domain	PLC-like phosphodiesterases	lipid metabolic process; signal transduction; intracellular signal transduction	phosphatidylinositol phospholipase C activity	nucleus	n/a	CDD81_4134
NODE_105_length_84742					nucleus	n/a	CDD81_5878
NODE_527_length_5624					mitochondrion	mitochondrial transit peptide	CDD81_1859
NODE_6_length_286604					mitochondrion	n/a	CDD81_3072
NODE_383_length_17045	Phospholipase D Active site motif	Phospholipase D superfamily	inositol lipid-mediated signaling; lipid catabolic process; phosphatidic acid biosynthetic process	catalytic activity; N-acylphosphatidylethanolamine-specific phospholipase D activity; phospholipase D activity	cytoplasm	n/a	CDD81_7299
NODE_7_length_267218	Phospholipase D Active site motif; Phospholipase D Active site motif				endomembrane system	transmembrane alpha helix	CDD81_1994
NODE_149_length_66206	Prokaryotic phospholipase A2	Phospholipase A2 superfamily	arachidonic acid secretion; phospholipid metabolic process	phospholipase A2 activity	extracellular space	signal peptide	CDD82_2377

NODE_420_length_13204	Platelet-activating factor acetylhydrolase, isoform II	Alpha/Beta hydrolase fold	lipid catabolic process	1-alkyl-2-acetylgllycerophosphocholine esterase activity	cytoplasm	n/a	CDD81_6623
NODE_378_length_17628	Lysophospholipase catalytic domain	Patatin/FabD/lysophospholipase-like superfamily	phospholipid catabolic process	phospholipase activity	mitochondrion	mitochondrial transit peptide	CDD81_7307
NODE_105_length_84742					anchored component of plasma membrane	signal peptide, lipidation GPI-anchor	CDD81_6239

Table S4: Protein tyrosine phosphatase – PTP domains.

Protein ID	Domain	Clan	Biological process	Molecular function	Cellular component	Feature	Gene	Pfam predicted active site
NODE_3_length_322389	Dual specificity phosphatase, catalytic domain	Phosphatase	dephosphorylation	protein tyrosine/serine/threonine phosphatase activity	cytoplasm	n/a	CDD81_7917	Similarity to A0A0V0X9Z7 (A0A0V0X9Z7_9BILA)
NODE_1_length_491455					mitochondrion	n/a	CDD81_5603	Similarity to A0A0V0X9Z7 (A0A0V0X9Z7_9BILA)
NODE_111_length_83425					mitochondrion	n/a	CDD81_1320	Similarity to Q93096 (TP4A1_HUMAN)
NODE_486_length_7628	Dual specificity phosphatase, catalytic domain; Dual specificity protein phosphatase, N-terminal half; Protein-tyrosine phosphatase	Phosphatase	dephosphorylation; protein dephosphorylation; regulation of exit from mitosis	protein tyrosine/serine/threonine phosphatase activity; protein tyrosine phosphatase activity	organelle membrane	transmembrane alpha helix	CDD81_4327	Similarity to A0A0V0X9Z7 (A0A0V0X9Z7_9BILA)
NODE_88_length_94299	Dual specificity phosphatase, catalytic domain; Alpha/beta hydrolase family; Alpha/beta hydrolase fold; Serine aminopeptidase, S33; Thioesterase domain	Phosphatase; Alpha/Beta hydrolase fold	dephosphorylation; biosynthetic process	protein tyrosine phosphatase activity; protein tyrosine/serine/threonine phosphatase activity; hydrolase activity, acting on ester bonds	cytoplasm	n/a	CDD81_5141	Similarity to A1CLZ0 (CCSE_ASPL); A0A0V0X9Z7 (A0A0V0X9Z7_9BILA)
NODE_371_length_19466	Low molecular weight phosphotyrosine protein phosphatase	Phosphatase	protein dephosphorylation	acid phosphatase activity; non-membrane spanning protein tyrosine phosphatase activity	extracellular space	n/a	CDD81_6384	Similarity to P11064 (PPAC_BOVIN)
NODE_2_length_336043	Myotubularin-like phosphatase domain	Phosphatase	dephosphorylation	protein tyrosine phosphatase activity	cytoplasm	n/a	CDD81_6925	Similarity to Q9Z2C9 (MTMR7_MOUSE)
NODE_92_length_90100	Protein-tyrosine phosphatase	Phosphatase	protein dephosphorylation	protein tyrosine phosphatase activity	endomembrane system	transmembrane alpha helix	CDD81_4528	Similarity to A0A287D394 (A0A287D394 ICTTR)
NODE_143_length_68526	Rhodanese-like domain	Phosphatase	positive regulation of cell cycle G2/M phase transition	protein tyrosine phosphatase activity	nucleus	n/a	CDD81_4305	Similarity to A0A0H5C8P2 (A0A0H5C8P2_CYBJN)
NODE_42_length_162368	Rhodanese-like domain; Protein-tyrosine phosphatase	Phosphatase	protein dephosphorylation	protein tyrosine phosphatase activity	cytoplasm	n/a	CDD81_1533	Similarity to A0A287D394 (A0A287D394 ICTTR); A0A0Q3SZT0 (A0A0Q3SZT0_AMAAE)

NODE_19_length_209599	Tyrosine phosphatase family; Tyrosine phosphatase family	Phosphatase	dephosphorylation	protein tyrosine phosphatase activity	cytoplasm; integral component of membrane	n/a	CDD81_3541	Similarity to Q4P7L6 (OCA1_USTMA)
NODE_82_length_100911	Uncharacterized protein	Uncharacterized protein	protein dephosphorylation; dephosphorylation	protein tyrosine phosphatase activity; protein tyrosine/serine/threonine phosphatase activity	mitochondrion	mitochondrial transit peptide	CDD81_2497	n/a