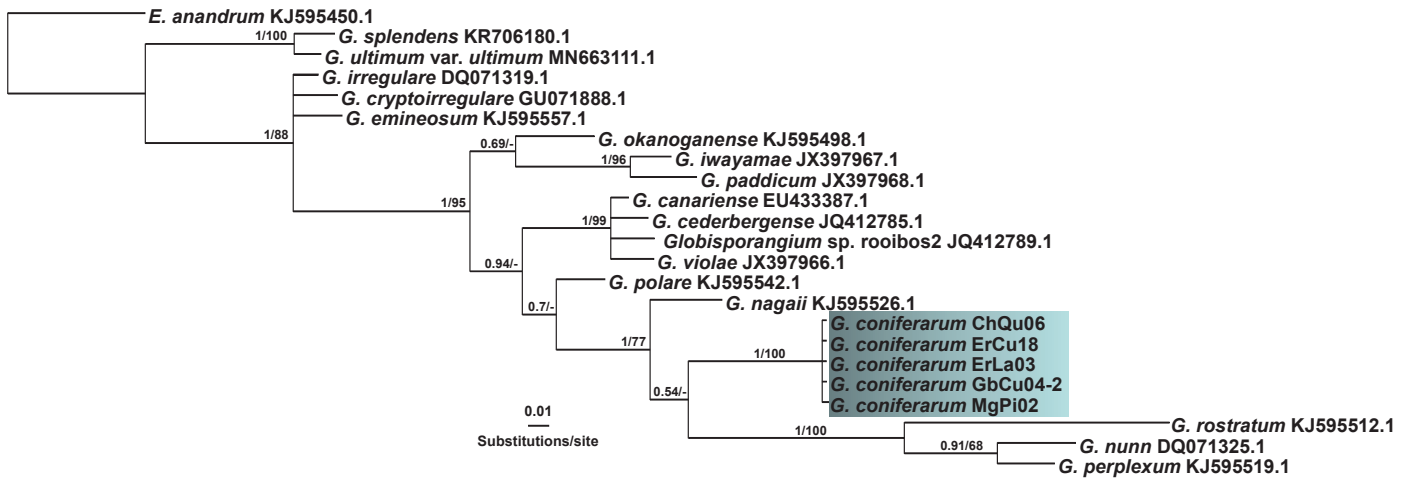


**Fig. S1**



**Fig. S1.** Phylogenetic relationships of *Globisporangium* spp. from conifers and *Quercus* sp. (Shiraz County, Iran) among 17 *Globisporangium* species based on Bayesian analysis of *βtub* sequences. Numbers on branches represent posterior probability based on Bayesian analysis and the bootstrap support based on maximum likelihood analysis, respectively.

Fig. S2

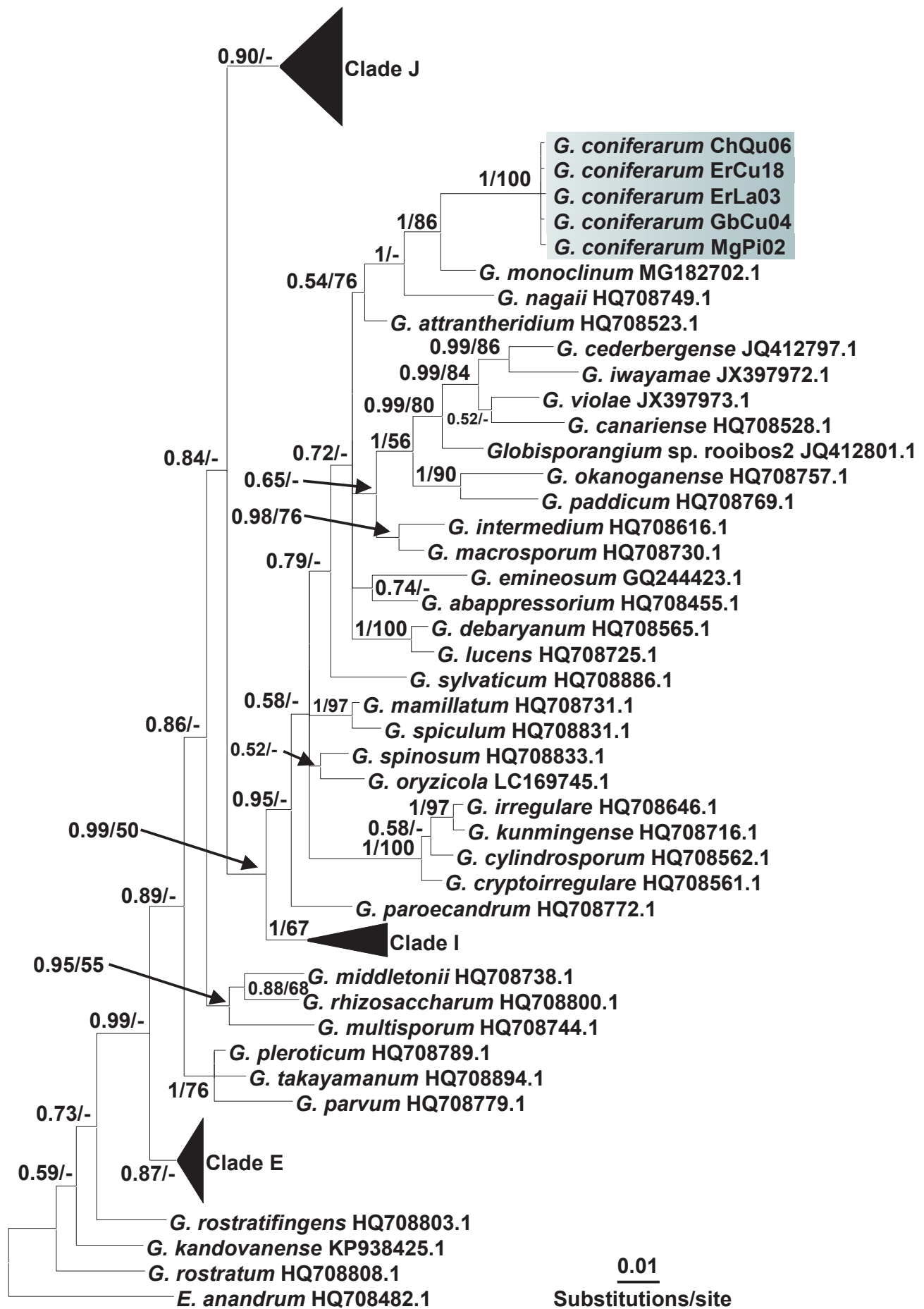


Fig. S2. Phylogenetic relationships of *Globisporangium* spp. from conifers and *Quercus* sp. (Shiraz County, Iran) among 16 *Globisporangium* species based on Bayesian analysis of *cox1* sequences. Numbers on branches represent posterior probability based on Bayesian analysis and the bootstrap support based on maximum likelihood analysis, respectively.

Fig. S3

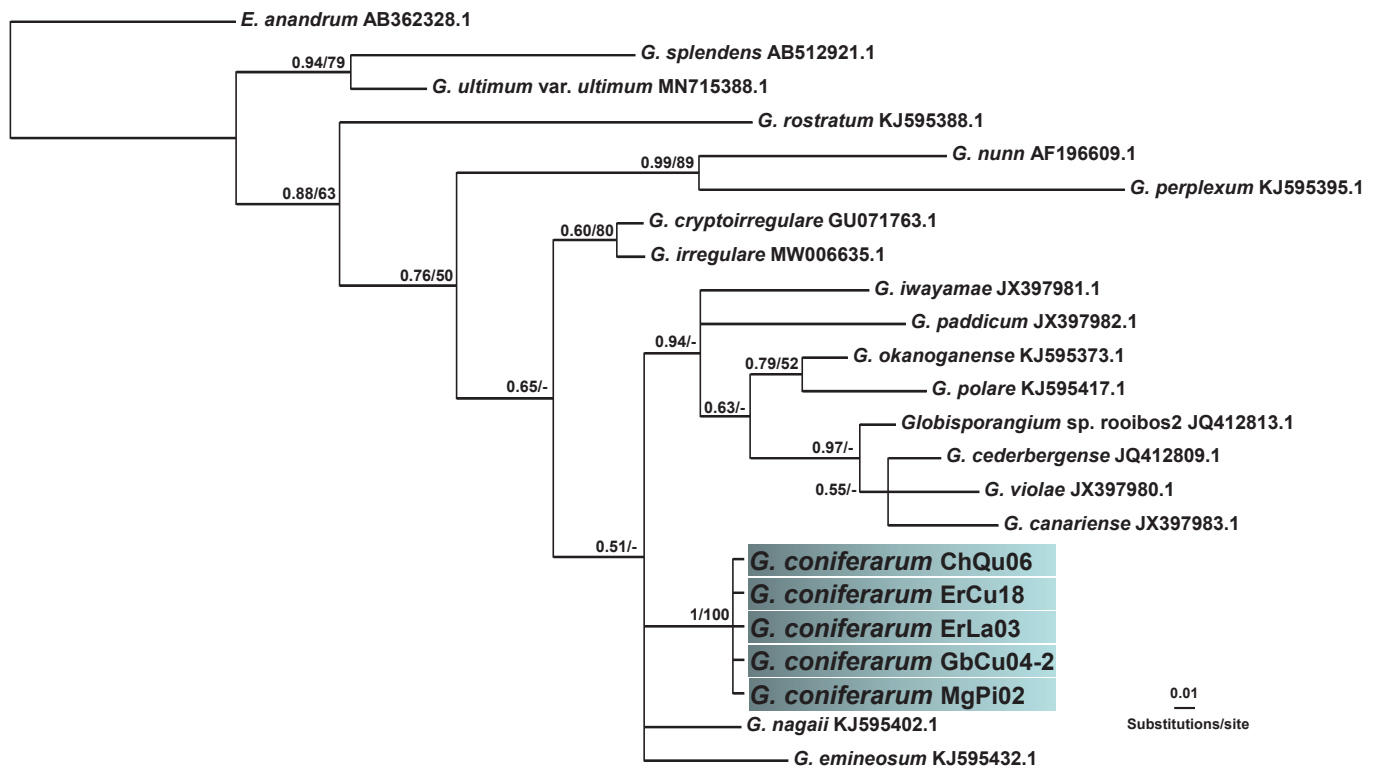


Fig. S3. Phylogenetic relationships of *Globisporangium* spp. from conifers and *Quercus* sp. (Shiraz County, Iran) among 17 *Globisporangium* species based on Bayesian analysis of *cox2* sequences. Numbers on branches represent posterior probability based on Bayesian analysis and the bootstrap support based on maximum likelihood analysis, respectively.

Fig. S4

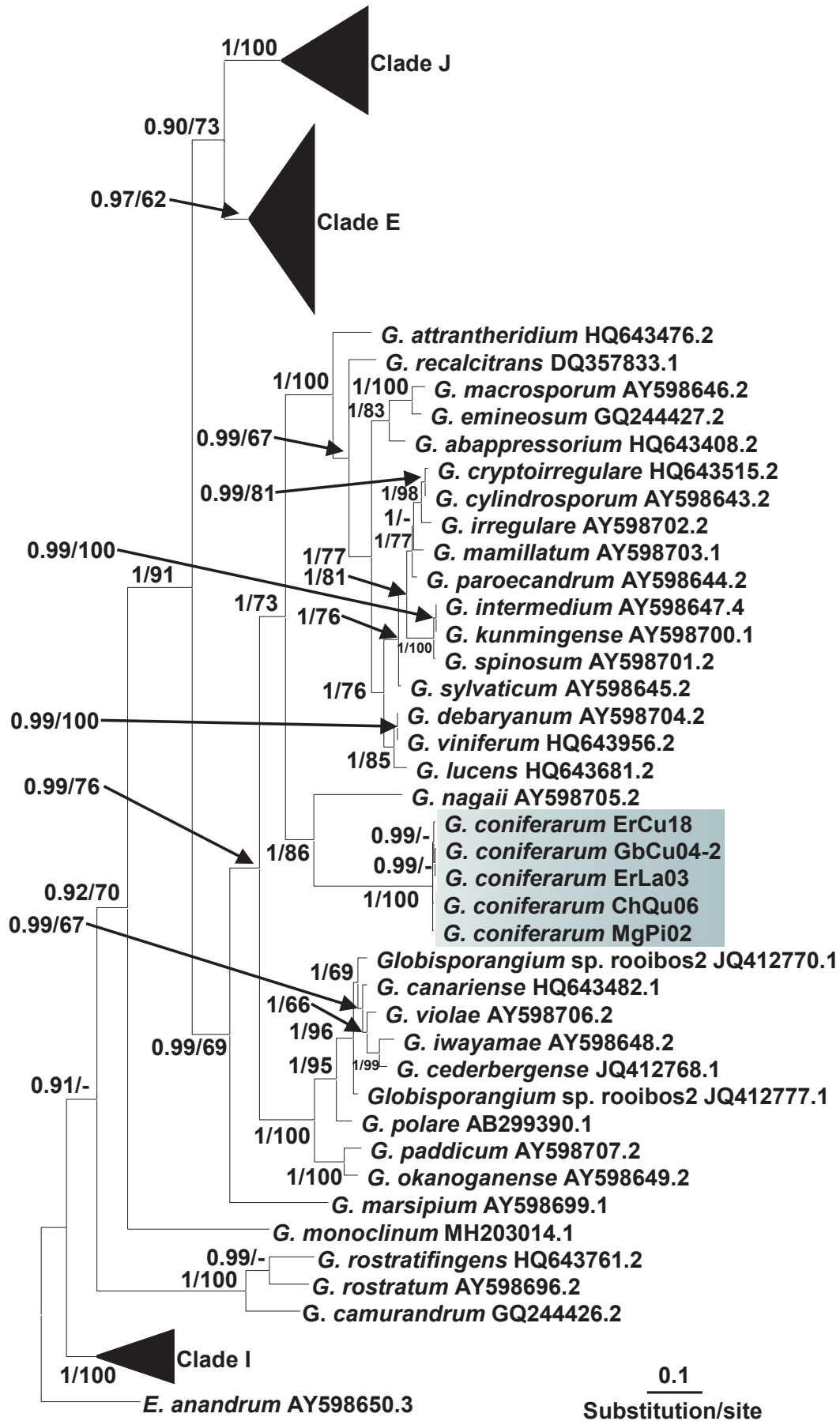


Fig. S4. Phylogenetic relationships of *Globisporangium* spp. from conifers and *Quercus* sp. (Shiraz County, Iran) among 33 *Globisporangium* species based on Bayesian analysis of Internal transcribed spacer (ITS) sequences. Numbers on branches represent posterior probability based on Bayesian analysis and the bootstrap support based on maximum likelihood analysis, respectively. Table S1. Information of all the *Globisporangium* isolates used in the phylogenetic analyses, including local, international, and alternative isolate identifications. GenBank accession numbers for sequences obtained in present study are shown in bold.

## Table S1

**Table S1.** List of primers used in this study.

Target DNA	Primer name	Primer sequence (5'→3')	Reference
ITS <sup>a</sup>	ITS4	TCCTCCGCTTATTGATATGC	White <i>et al.</i> (1990)
	ITS6	GAAGGTGAAGTCGTAACAAGG	Cooke <i>et al.</i> (2000)
	LR0	GCTTAAGTTCAGCGGGT	Mancalvo <i>et al.</i> (1995)
	DC6	GAGGGACTTTTGGGTAATCA	Bonants <i>et al.</i> (1997)
<i>βtub</i> <sup>b</sup>	BT5	GTATCATGTGCACGTACTCGG	Villa <i>et al.</i> (2006)
	BT6	CAAGAAAGCCTTACGACGGA	Villa <i>et al.</i> (2006)
<i>cox1</i> <sup>c</sup>	OomCoxI-Levup	TCAWCW/MGATGGCTTTTTTCAAC	Robideau <i>et al.</i> (2011)
	OomCoxI-Levo	CYTCHGGRTGWCCRAAAAACCAAA	Robideau <i>et al.</i> (2011)
	FM58mod	RRHWACKTGACTDATRATACAAA	Robideau <i>et al.</i> (2011)
<i>cox2</i> <sup>d</sup>	FM66	TAGGATTTCAAGATCCTGC	Villa <i>et al.</i> (2006)
	FM58	CCACAAATTTCACTACATTGA	Villa <i>et al.</i> (2006)

<sup>a</sup>Internal transcribed spacers 1, 2 and 5.8S gene of rDNA. <sup>b</sup>β-tubulin. <sup>c</sup>cytochrome c oxidase subunit I. <sup>d</sup>cytochrome c oxidase subunit II.

## Table S2

**Table S2.** Polymerase chain reaction conditions for primers used in this study.

Gene	Initial desaturation	Number of cycles	Desaturation	Annealing	Expansion	Final extension
ITS <sup>a</sup>	95 (120) <sup>e</sup>	30	95 (20)	55 (25)	72 (50)	72 (600)
<i>βtub</i> <sup>b</sup>	95 (120)	30	95 (20)	63 (25)	72 (50)	72 (600)
<i>cox1</i> <sup>c</sup>	95 (120)	35	95 (60)	55 (60)	72 (60)	72 (600)
<i>cox2</i> <sup>d</sup>	95 (120)	30	95 (20)	52 (25)	72 (50)	72 (600)

<sup>a</sup>Internal transcribed spacers 1, 2 and 5.8S gene of rDNA. <sup>b</sup>β-tubulin. <sup>c</sup>cytochrome c oxidase subunit I. <sup>d</sup>cytochrome c oxidase subunit II. <sup>e</sup>Temperature °C (time s').

## Table S3

**Table S3.** Information of all the *Globisporangium* spp. isolates used in the phylogenetic analyses, including local, international, and alternative isolate identifications. GenBank accession numbers for sequences obtained in present study are shown in bold.

Clade	Species	Isolate Identification	GenBank Accession Number			
			ITS	<i>βtub</i>	<i>cox1</i>	<i>cox2</i>
E	<i>G. rostratum</i>	CBS 533.74	AY598696	KJ595512	HQ708808	KJ595388
E	<i>G. rostratifingens</i>	CBS 115464	HQ643761	KJ595541	HQ708803	KJ595416
E	<i>G. middletonii</i>	CBS 528.74	HQ643694	KJ595457	HQ708738	AB362318
E	<i>G. multisporum</i>	CBS 470.50	HQ643700	KJ595455	HQ708744	AB362319
E	<i>G. terrestris</i>	CBS 112352	HQ643857	–	HQ708898	–
F	<i>G. mamillatum</i>	CBS 251.28	AY598703	AB512844	HQ708731	AB512918
F	<i>G. macrosporum</i>	CBS 575.80	AY598646	AY944860	HQ708728	AB512917
F	<i>G. intermedium</i>	CBS 224.68	AY598647	DQ071314	HQ708616	AB512898
F	<i>G. irregulare</i>	CBS 749.96	AY598702	DQ071319	HQ708646	MW006635
F	<i>G. paroecandrum</i>	CBS 157.64	AY598644	DQ071332	HQ708772	DQ071391
F	<i>G. attrantheridium</i>	DAOM230388	HQ643476	AB512824	HQ708524	AB512891
F	<i>G. oryzicola</i>	HT45-2	LC169738	–	LC169742	LC169751
F	<i>G. cylindrosporum</i>	CBS 218.94	AY598643	GU071877	HQ708562	GU071762
F	<i>G. cryptoirregulare</i>	CBS 118731	HQ643515	GU071888	HQ708561	GU071763
F	<i>G. spinosum</i>	CBS 275.67	AY598701	KJ595491	HQ708834	KJ595366
F	<i>G. sylvaticum</i>	CBS 453.67	AY598645	KJ595507	HQ708886	EU257622
F	<i>G. kunmingense</i>	CBS 550.88	AY598700	KJ595513	HQ708716	KJ595389
F	<i>G. debaryanum</i>	CBS 752.96	AY598704	KJ595523	HQ708565	KJ595399

Table S3. (Continued).

Clade	Species	Isolate Identification	GenBank Accession Number			
			ITS	<i>βtub</i>	<i>cox1</i>	<i>cox2</i>
F	<i>G. abappressorium</i>	CBS 110198	HQ643408	KJ595533	HQ708455	MN103371
F	<i>G. lucens</i>	CBS 113342	HQ643681	KJ595540	HQ708725	KJ595415
F	<i>G. viniferum</i>	CBS 119168	HQ643956	KJ595544	HQ708997	KJ595419.
F	<i>G. spiculum</i>	CBS 122645	HQ643790	KJ595549	HQ708831	KJ595425
F	<i>G. emineosum</i>	CBS 124057	GQ244427	KJ595557	GQ244423	KJ595432
F	<i>G. monoclinum</i>	IRAN2421c	MH203014	–	MG182702	–
G	<i>G. coniferarum</i>	GbCu04-2 = CBS 148568 =	<b>ON554847</b>	<b>MZ020764</b>	<b>MZ020754</b>	<b>MZ020759</b>
G		ChQu06 = CBS 148564 =	<b>ON554845</b>	<b>MZ020767</b>	<b>MZ020757</b>	<b>MZ020762</b>
G		ErCu18 = CBS 148565 =	<b>ON554846</b>	<b>MZ020766</b>	<b>MZ020756</b>	<b>MZ020761</b>
G		MgPi02 = CBS 148566 =	<b>ON554844</b>	<b>MZ020763</b>	<b>MZ020753</b>	<b>MZ020758</b>
G		ErLa03 = CBS 148567	<b>ON554843</b>	<b>MZ020765</b>	<b>MZ020755</b>	<b>MZ020760</b>
G	<i>G. okanoganense</i>	CBS 315.81	AY598649	KJ595498	HQ708755	KJ595373
G	<i>G. iwayamae</i>	CBS 156.64	AY598648	JX397965	JX397972	JX397979
G	<i>G. paddicum</i>	CBS 698.83	AY598707	JX397968	HQ708769	JX397982
G	<i>G. nagaii</i>	CBS 779.96	AY598705	KJ595526	HQ708749	KJ595402
G	<i>G. polare</i>	CBS 118203	AB299390	KJ595542	–	KJ595417
G	<i>G. canariense</i>	CBS 112353	HQ643482	JX397965	HQ708528	JX397983
G	<i>G. violae</i>	CBS 159.64	AY598706	JX397966	JX397973	JX397980
G	<i>G. sp. rooibos2</i>	STE-U7550	JQ412770	JQ412789	JQ412801	JQ412813
G	<i>G. cederbergense</i>	STE-U7555	JQ412768	JQ412785	JQ412797	JQ412809
I	<i>G. ultimum</i> var. <i>ultimum</i>	Py8.14	AY598657	MN663111	KX371319	MN715388
I	<i>G. splendens</i>	CBS 462.48	AY598655	KR706180	HQ708836	AB512921
J	<i>G. perplexum</i>	CBS 674.85	AY598657	KJ595519	HQ708785	KJ595395
J	<i>G. nunn</i>	CBS 808.96	AY598709	JAASFZ010001763*	EU350522	AF196609
J	<i>G. cystogenes</i>	CBS 675.85	HQ643518	KJ595520	HQ708564	KJ595396
J	<i>G. orthogonon</i>	CBS 376.72	AY598710	KJ595503	HQ708764	KJ595379
J	<i>G. acanthophoron</i>	CBS 337.29	AY598711	KJ595500	HQ708460	KJ595376
H	<i>Elangisporangium anandrum</i>	CBS 285.31	AY598650	KJ595450	HQ708482	AB362328

\*Derived from CBS 808.96 type species whole genome shut gun sequence (contig: 1764).

**Table S4**

**Table S4.** Base pair (bp) differences across *βtub*, ITS, *cox1*, and *cox2* sequences showing the inter- and intraspecific variation of *Globisporangium confiferarum* (CON), and other related species, including *G. nagaii* (NAG), *G. violae* (VIO), *G. paddicum* (PAD), *G. okanoganense* (OKA), *G. canariense* (CAN), *G. monoclimum* (MON), and *G. iwayamae* (IWA).

Region	Alignment length (bp)	Differences CON/NAG (bp)	Differences CON/VIO (bp)	Differences CON/PAD (bp)	Differences CON/OKA (bp)	Differences CON/CON/IWA (bp)	Differences CON/CAN (bp)	Differences CON/MON (bp)	Differences within CON (bp)
<i>βtub</i>	457	37	53	53	46	55	49	DN	0–3
ITS	1400	250	363	343	361	291	355	360	18
<i>cox1</i>	610	30	44	42	36	45	41	20	0
<i>cox2</i>	508	13	28	24	16	19	30	DN*	0
Total	3051	330	488	462	459	410	475	380	0–18

\*Data not available.