



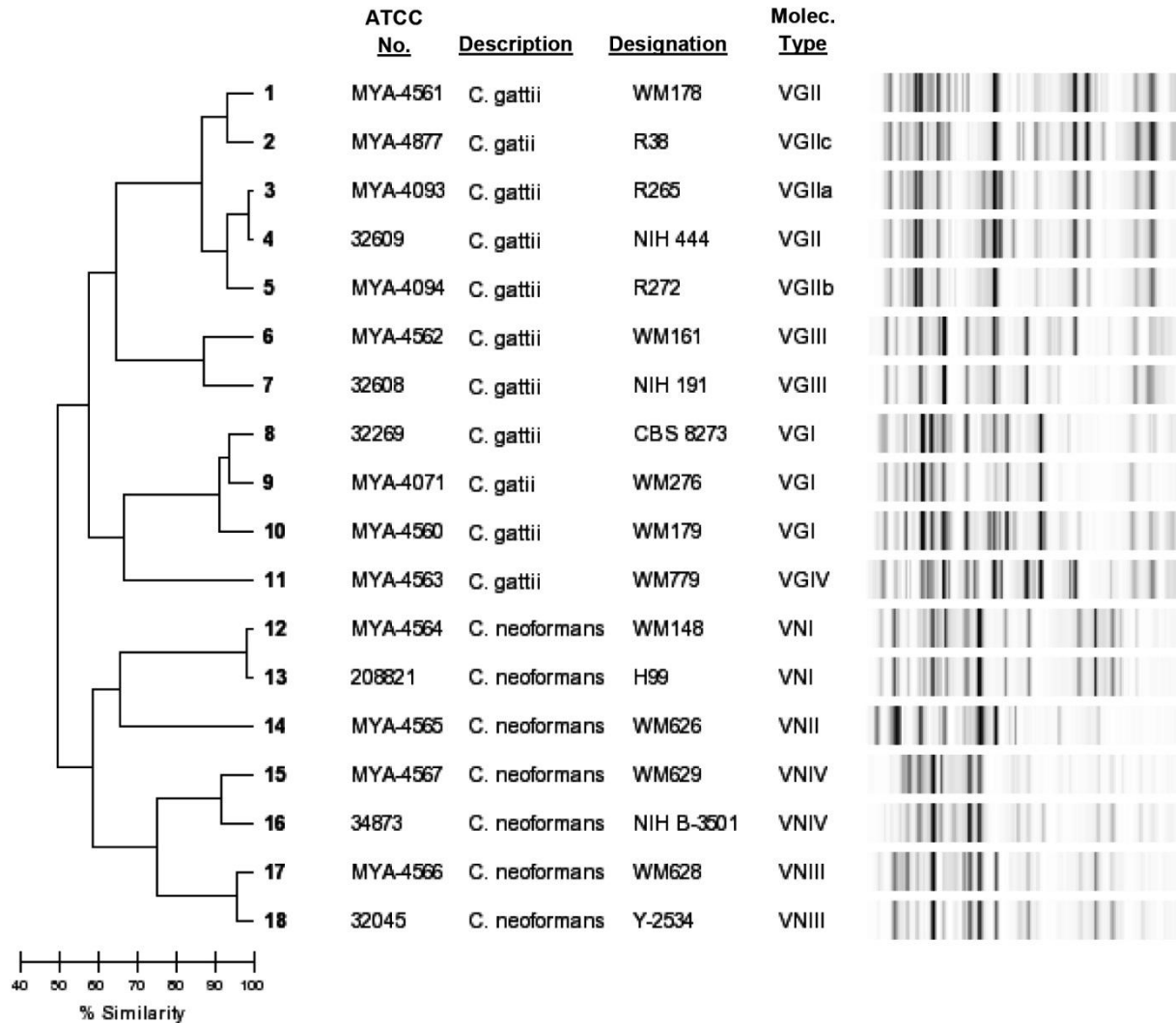
Pathogenic Cryptococcus Reference Strains

Cryptococcus isolates can be selected based on in-house antifungal susceptibility testing (AST) and genotyping (microsatellite PCR fingerprinting and MLST) data. An expanded panel can be assembled along with ATCC MP-11 by selecting five additional taxonomic Type strains representing *C. neoformans* var. *grubii* (ATCC 208821™), *C. neoformans* var. *neoformans* (ATCC 32045™), *Filobasidiella neoformans* (ATCC 34873™), *C. gattii* (ATCC 32269™), *F. bacillispora* (teleomorphic name of *C. gattii*, ATCC 32608™).

ATCC No.	Description	Designation	Molecular Type	MAT & Serotype	Isolation source*	Isolation location	Minimal growth inhibitory concentration (µg/mL) to Antifungal Drug**								
							AMB	ANF	MCF	CSF	5FC	POS	VOR	ITZ	FZ
MYA-4560™	<i>C. gattii</i>	WM179	VGI, AFLP4	Alpha, B	Human CSF	Sydney, Australia	0.25	>8	>8	>8	0.5	0.06	0.015	0.06	2
MYA-4561™	<i>C. gattii</i>	WM178	VGII, AFLP6	Alpha, B	Human CSF	Sydney, Australia	0.5	>8	>8	>8	2	0.06	0.06	0.06	8
MYA-4093™	<i>C. gattii</i>	R265	VGIIa, AFLP6A	Alpha, B	Human BAL	VI, B.C. Canada	0.5	>8	>8	>8	1	0.03	0.03	0.03	4
MYA-4094™	<i>C. gattii</i>	R272	VGIIb, AFLP6B	Alpha, B	Human BAL	VI, B.C. Canada	0.25	>8	>8	>8	1	0.12	0.06	0.12	8
MYA-4877™	<i>C. gattii</i>	R38	VGIIc, AFLP6C	Alpha, unknown	Human CSF	Oregon, USA	0.5	>8	>8	>8	1	0.06	0.06	0.06	4
MYA-4562™	<i>C. gattii</i>	WM161	VGIII, AFLP5	Alpha, B	Eucalyptus in a park	San Diego, USA	0.25	>8	>8	>8	0.5	0.03	0.03	0.015	2
MYA-4563™	<i>C. gattii</i>	WM779	VGIV, AFLP7	Alpha, C	Cheetah, veterinary	Johannesburg, SA	0.5	>8	>8	>8	1	0.06	0.03	0.06	8
MYA-4564™	<i>C. neoformans</i>	WM148	VNI, AFLP1	Alpha, A	Human CSF	Sydney, Australia	0.25	>8	>8	>8	2	0.12	0.06	0.12	8
MYA-4565™	<i>C. neoformans</i>	WM626	VNII, AFLP1A	Alpha, A	Human CSF	Sydney, Australia	0.5	>8	>8	>8	4	0.25	0.008	0.03	1
MYA-4566™	<i>C. neoformans</i>	WM628	VNIII, AFLP3	Alpha/a, AD	Human HIV, CSF	Melbourne, Australia	0.5	>8	>8	>8	4	0.03	0.03	0.015	4
MYA-4567™	<i>C. neoformans</i>	WM629	VNIV, AFLP2	Alpha, D	Human HIV, blood	Melbourne, Australia	0.25	>8	>8	>8	8	0.06	0.03	0.06	2
208821™	<i>C. neoformans</i> var. <i>grubii</i>	H99	VNI	Alpha, A	Human CSF	Durham, USA	0.12	>8	>8	>8	2	0.015	0.015	0.015	4
32045™	<i>C. neoformans</i> var. <i>neoformans</i>	NRRL Y-2534	VNIII	Alpha/a, AD	Fruit juice	Italy	0.25	>8	>8	>8	0.5	0.008	0.008	0.008	1
34873™	<i>C. neoformans</i>	NIH B-3501	VNIV	Alpha, D	Cross of ATCC 28957 & 28958	Bethesda USA	0.25	>8	>8	>8	8	0.03	0.015	0.015	2
32269™	<i>C. gattii</i> Type <i>C. gattii</i> (type of <i>Filobasidiella bacillispora</i>)	CBS 8273	VGI	a, B	Human CSF	Congo	0.5	>8	>8	>8	0.5	0.06	0.06	0.06	8
32608™		NIH 191	VGIII	a, C	Human CSF	San Fernando, USA	0.25	>8	>8	>8	1	0.06	0.06	0.03	8

*BAL - Bronchial alveolar lavage; CSF - Cerebrospinal fluid. ** Minimal growth inhibitory concentration (µg/mL) is obtained according to CLSI document M27-A2, using TREK Diagnostic System's YeastOne product. AMB, ANF, MCF, CSF, 5FC, POS, VOR, ITZ, and FZ stand for amphotericin B, anidulafungin, micafungin, caspofungin, 5-flucytosine, posaconazole, voriconazole, itraconazole, and fluconazole, respectively. The value is average of two independent testings, recorded at the 72 hour incubation, except for MYA-4565, which were recorded at 96 hour incubation.

Primer M13 PCR fingerprinting of *Cryptococcus gattii*/*neoformans* via Diversilab platform



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Cryptococcus gattii Multiple Locus Sequence Typing (MLST) Data Table

ATCC No.	Mol. type	CAP59	GPD1	IGS1	LAC1	PLB1	SOD1	URA5	Seq. Type
MYA-4560™	VGI	16	5	3	5	5	32	12	51
32269™	VGI	53	11	13	13	13	68	15	232
MYA-4071™	VGI	16	5	3	5	5	45	12	154
MYA-4561™	VGII	1	17	16	16	14	19	7	21
32609™	VGII	1	1	4	4	1	14	7	20
MYA-4093™	VGIIa	1	1	4	4	1	14	7	20
MYA-4094™	VGIIb	2	6	10	4	2	15	2	7
MYA-4877™	VGIIc	4	6	15	4	1	15	2	6
MYA-4562™	VGIII	18	18	14	3	6	28	19	60
32608™	VGIII	29	12	11	10	4	28	22	68
MYA-4563™	VGIV	17	10	8	18	3	37	11	70

Notes: Assignment of allele type (AT) and sequence type (ST) is performed according to the database at the website <http://mlst.mycologylab.org/defaultinfo.aspx?Page=CryptoHome>. For information on the rationale of gene selection for MLST, please refer to the paper by Meyer W. et al. Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii*. Med. Mycol. 47(6):561-570, 2009.