

# Blastomyces gilchristii as Cause of Fatal Acute Respiratory Distress Syndrome

## Technical Appendix

Strains		1	19	50
<i>B. gilchristii</i>	TB00029   JN562140	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	TB00037   JN562142	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	Strain 241   JN562106	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC 66136   JN562118	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC 62583   JN562117	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC 62541   JN562116	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC 60637   JN562115	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC 60636   JN562114	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	ATCC-MYA-2585   JN562119	GAAATGCGATAAGTAATG	<b>C</b>	GAATTGCAGAATTC
	<u>13BL347</u>	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
<i>B. dermatitidis</i>	ATCC-MYA-2586   JN562161	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
	ATCC 26197   JN562158	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
	ATCC 26199   JN562159	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
	ATCC 28306   JN562159	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
	UAMH 5635   JN562183	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
	TB00014   JN562146	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC
TB00042   JN562148	GAAATGCGATAAGTAATG	<b>T</b>	GAATTGCAGAATTC	
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**Technical Appendix Figure.** Clustal alignment of sequenced region of internal transcribed spacer 2 (ITS2) of *Blastomyces dermatitidis* and *B. gilchristii*. The ITS2 sequence of isolate 13BL347 was aligned to the ITS2 sequences of several well-characterized representatives of *B. dermatitidis* and *B. gilchristii* sequences (1,2), using the multiple sequence alignment tool, Clustal Omega (<http://www.ebi.ac.uk/tools/msa/clustalo>) using default settings (3). The single nucleotide polymorphism in ITS2 at position 19 is used for differentiation of *B. dermatitidis* from *B. gilchristii* (2). The sequence of 13BL347 ITS2 (underlined) possessed a cytosine at position 19 (bolded white text), which is diagnostic for *B. gilchristii*, while thymine (bolded black text) at that position is conserved in *B. dermatitidis*. Strains included in the alignment were *B. dermatitidis* strains ATCC MYA-2586 (JN562161), ATCC 26197 (JN562158), ATCC 26199 (JN562159), ATCC 28306 (JN562159), UAMH 5635 (JN562183), TB00014 (JN562146), TB00042 (JN562148) (2) and alpacaN13BD13\_0325 (KF543873) (1) and *B. gilchristii* strains ATCC MYA-2585 (JN562119), ATCC 60636 (JN562114), ATCC 60637 (JN562115), ATCC 62541 (JN562116), ATCC 62583 (JN562117), ATCC 66136 (JN562118), strain 241 (JN562106), TB0029 (JN562140), TB0037 (JN562142) (2). With the exception of KF543873, these strains were previously identified to species level by Brown et al. (2) through multilocus sequence typing scheme using *chs2*, *drk1*, *fads*, *pyrF*, *tub1*, *arf6*, and ITS2. \*Denotes a conserved nucleotide among strains in alignment.

## References

1. Meece JK, Anderson JL, Gruszka S, Sloss BL, Sullivan B, Reed KD. Variation in clinical phenotype of human infection among genetic groups of *Blastomyces dermatitidis*. J Infect Dis. 2013;207:814–22. [PubMed http://dx.doi.org/10.1093/infdis/jis756](http://dx.doi.org/10.1093/infdis/jis756)
2. Brown EM, McTaggart LR, Zhang SX, Low DE, Stevens DA, Richardson SE. Phylogenetic analysis reveals a cryptic species *Blastomyces gilchristii*, sp. nov. within the human pathogenic fungus *Blastomyces dermatitidis*. PLoS One. 2013;8:e59237. [PubMed http://dx.doi.org/10.1371/journal.pone.0059237](http://dx.doi.org/10.1371/journal.pone.0059237)
3. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, et al. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol. 2011;7:539. [PubMed http://dx.doi.org/10.1038/msb.2011.75](http://dx.doi.org/10.1038/msb.2011.75)