Blastomyces gilchristii as Cause of Fatal Acute Respiratory Distress Syndrome

Technical Appendix

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/maa/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), TB00029 (JN562140), TB00037 (JN562142), 9strain 241 (JN562106), ATCC 61136 (JN562118), ATCC 62583 (JN562117), ATCC 62541 (JN562116), ATCC 60637 (JN562115), ATCC 60636 (JN562114), ATCC-MYA-2585 (JN562119) 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), TB00029 (JN562140), TB00037 (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

