Supplementary Table 1: Results of amplification of fungal DNA by PCR combined with DNA sequencing

ITS1: 5’-TCC GTA GGT GAA CCT GCG G-3’

ITS2: 5’-GCT GCG TTC TTC ATC GAT GC-3’

ITS3: 5’-GCA TCG ATG AAG AAC GCA GC-3’

ITS4: 5’-TCC TCC GCT TAT TGA TAT GC-3’

NL1: 5’-GCA TAT CAA TAA GCG GAG GAA AA-3’

NL4: 5’-GGT CCG TGT TTC AAG ACG G-3’

ZM1: 5’-ATT ACC ATG AGC AAA TCA GA-3'

ZM2: 5’-TCC GTC AAT TCC TTT AAG TTT C-3'

ZM3: 5’-CAA TCC AAG AAT TTC ACC TCT AG-3’

ZM1 to ZM3 are Mucorales-specific primers. DNA sequencing was performed by PCR using the above primers, but only the ZM1-ZM3 region could be sequenced. The sequence was as follows (116 bp):

TATCATTACTATAGTACCTAAACCAACGAAAATAGGACTAAAGTCATATATTTCATTA
TTCCATGCTAACACACATTCAAGCTTAAAGCCTGCTTTAAACACTCTGATTTGCTC
ATGGT

The above sequence was checked against GenBank and found to be a 100% match with the genus *Rhizopus*, but since several species were lined up in the same row with a 100% match, we could only identify the genus (Rhizopus) and not the species.

DNA, deoxyribonucleic acid; PCR, polymerase chain reaction