# *Emergomyces orientalis* Emergomycosis Diagnosed by Metagenomic Next-Generation Sequencing Appendix
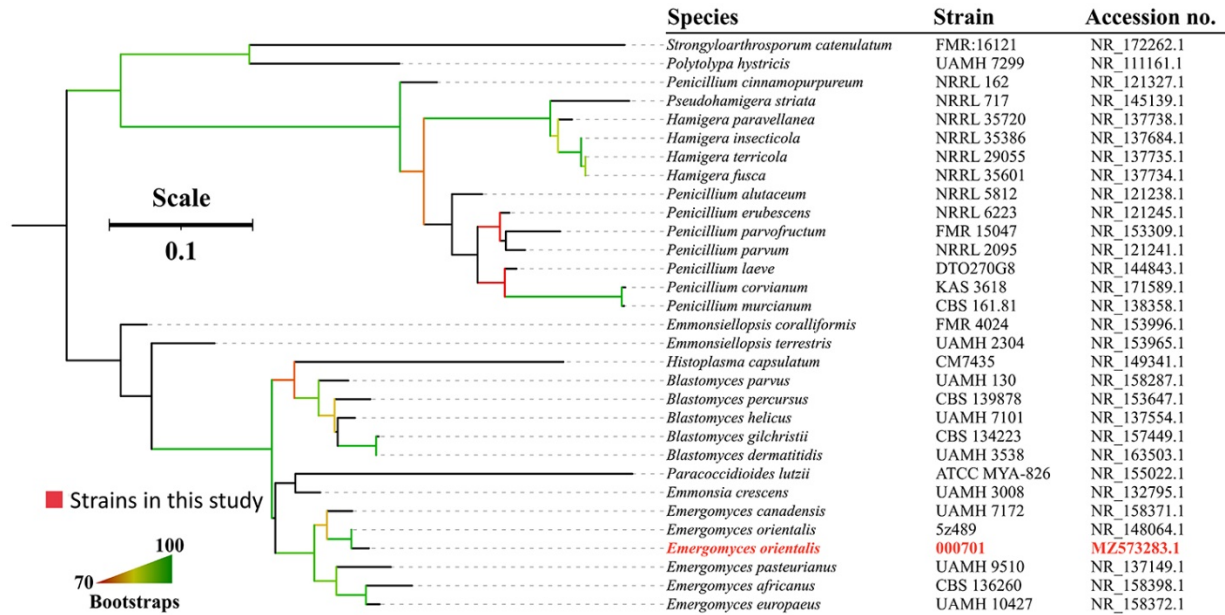
Appendix Table. Antimicrobial susceptibility test results*

Antimicrobials	MIC, µg/mL
amphotericin B	0.2
5-fluorocytosine	0.06
fluconazole	1
itraconazole	0.015
voriconazole	0.015
posaconazole	0.008
anidulafungin	8
caspofungin	1
micafungin	8

*Performed in the yeast phase using the fungal broth microdilution method.
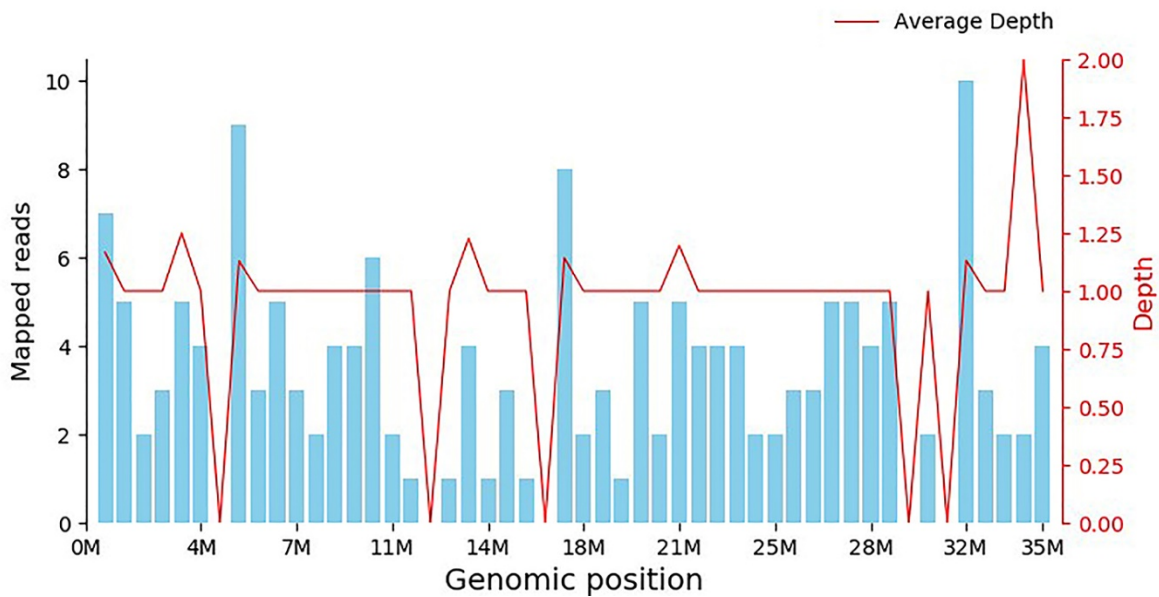
Appendix Figure 1. *Emergomyces orientalis* coverage map. The identified reads were mapped to the *Es. orientalis* reference genome (GenBank accession no. GCA_002110485.1). The abscissa is the genome position of *Es. orientalis* reference genome. The left-side scale shows the number of matched mNGS sequences in the alignment. The right-side scale shows the sequencing depth (i.e., the number of times the base pair site has been sequenced). The blue bars show the number of matched mNGS sequences corresponding to various positions in the genome of the fungus. The red line represents the average sequence depth distribution at different positions in the bacterial genome. M, position in the genome in millions of base pairs (x-axis scale)

Species	Strain	Accession no.
Strongyloarthrosporum catenulatum	FMR:16121	NR_172262.1
Polytolypa hystricis	UAMH 7299	NR_111161.1
Penicillium cinnamopurpureum	NRRL 162	NR_121327.1
Pseudohamigera striata	NRRL 717	NR_145139.1
Hamigera paravellanea	NRRL 35720	NR_137738.1
Hamigera insecticola	NRRL 35386	NR_137684.1
Hamigera terricola	NRRL 29055	NR_137735.1
Hamigera fusca	NRRL 35601	NR_137734.1
Penicillium alutaceum	NRRL 5812	NR_121238.1
Penicillium erubescens	NRRL 6223	NR_121245.1
Penicillium parvofructum	FMR 15047	NR_153309.1
Penicillium parvum	NRRL 2095	NR_121241.1
Penicillium laeve	DTO270G8	NR_144843.1
Penicillium corvianum	KAS 3618	NR_171589.1
Penicillium murcianum	CBS 161.81	NR_138358.1
Emmonsiellopsis coralliformis	FMR 4024	NR_153996.1
Emmonsiellopsis terrestris	UAMH 2304	NR_153965.1
Histoplasma capsulatum	CM7435	NR_149341.1
Blastomyces parvus	UAMH 130	NR_158287.1
Blastomyces percursus	CBS 139878	NR_153647.1
Blastomyces helicus	UAMH 7101	NR_137554.1
Blastomyces gilchristii	CBS 134223	NR_157449.1
Blastomyces dermatitidis	UAMH 3538	NR_163503.1
Paracoccidioides lutzii	ATCC MYA-826	NR_155022.1
Emmonsia crescens	UAMH 3008	NR_132795.1
Emergomyces canadensis	UAMH 7172	NR_158371.1
Emergomyces orientalis	5z489	NR_148064.1
Emergomyces orientalis	000701	MZ573283.1
Emergomyces pasteurianus	UAMH 9510	NR_137149.1
Emergomyces africanus	CBS 136260	NR_158398.1
Emergomyces europaeus	UAMH 10427	NR_158372.1

Appendix Figure 2. Phylogenetic tree of the ITS sequences amplified from the isolate in this study and sequences from reference strains in GenBank. A maximum likelihood tree was inferred using IQ-TREE under the TIM2+F+I+G4 model, chosen by the program according to the Bayesian information criterion and subjected to a 10,000-iteration bootstrap test to check the robustness. The supporting values were colored in gradients and the branch lengths were measured in terms of the number of substitutions per site. The scale bar represents number of substitutions per site.