

Table SI. The result of the genetic analysis using molecular biological techniques on the target genes of partial nucleotide sequence of β -tubulin (Bt) and internal transcribed spacer ribosomal deoxyribonucleic acid (ITSrDNA), from the white colony. Based on genetic identification of Bt1 and ITS rDNA, *Aspergillus hiratsukae* was identified.

Database	Target	Identified species	Homology	Accession No.
GeneBank	Bt1	<i>Aspergillus sp.</i>	98% 417/427	KX357795.1
	Bt2	<i>Neosartorya hiratsukae</i>	100% 442/442	FR775343.1
	ITSrDNA	<i>Aspergillus hiratsukae</i>	100% 186/186	MN347034.1

Table SII. The result of the genetic analysis using molecular biological techniques on the target genes of internal transcribed spacer ribosomal deoxyribonucleic acid (ITSrDNA) and 28S ribosomal deoxyribonucleic acid (28SrDNA), from the yellowish colony. Based on genetic identification of ITSrDNA and 28SrDNA, *Trichosporon faecale* was identified.

Database	Target	Identified spece	Homology	Accession No.
GeneBank	ITS1/4rDNA	<i>Trichosporon faecale</i>	100% 451/451	KY105736.1
	ITS1rDNA	<i>Trichosporon faecale</i>	100% 127/127	MT609903.1
	28SrDNA	<i>Trichosporon faecale</i>	100% 541/541	MN872895.1

Table SIII. The result of the genetic analysis using molecular biological techniques on the target genes of internal transcribed spacer ribosomal deoxyribonucleic acid (ITSrDNA) and 28S ribosomal deoxyribonucleic acid (28SrDNA), from the black colony. Based on genetic identification of ITSrDNA and 28SrDNA, *Exophiala xenobiotica* was identified.

Database	Target	Identified spece	Homology	Accession No.
NCBI	ITSrDNA	<i>Exophiala xenobiotica</i>	250/250(100%)	LC317597
	28SrDNA	<i>Exophiala xenobiotica</i>	375/375(100%)	MF630949
		<i>Exophiala spinifera</i>	375/375(100%)	LC228730
Mycobank	ITSrDNA	<i>Exophiala xenobiotica</i>	250/250(100%)	KU725776
	28SrDNA	<i>Exophiala xenobiotica</i>	375/375(100%)	491509