

## Supplementary Materials

**Identification of microorganisms dwelling on the 19th Century Lanna mural paintings from Northern Thailand using culture-dependent and -independent approaches.**

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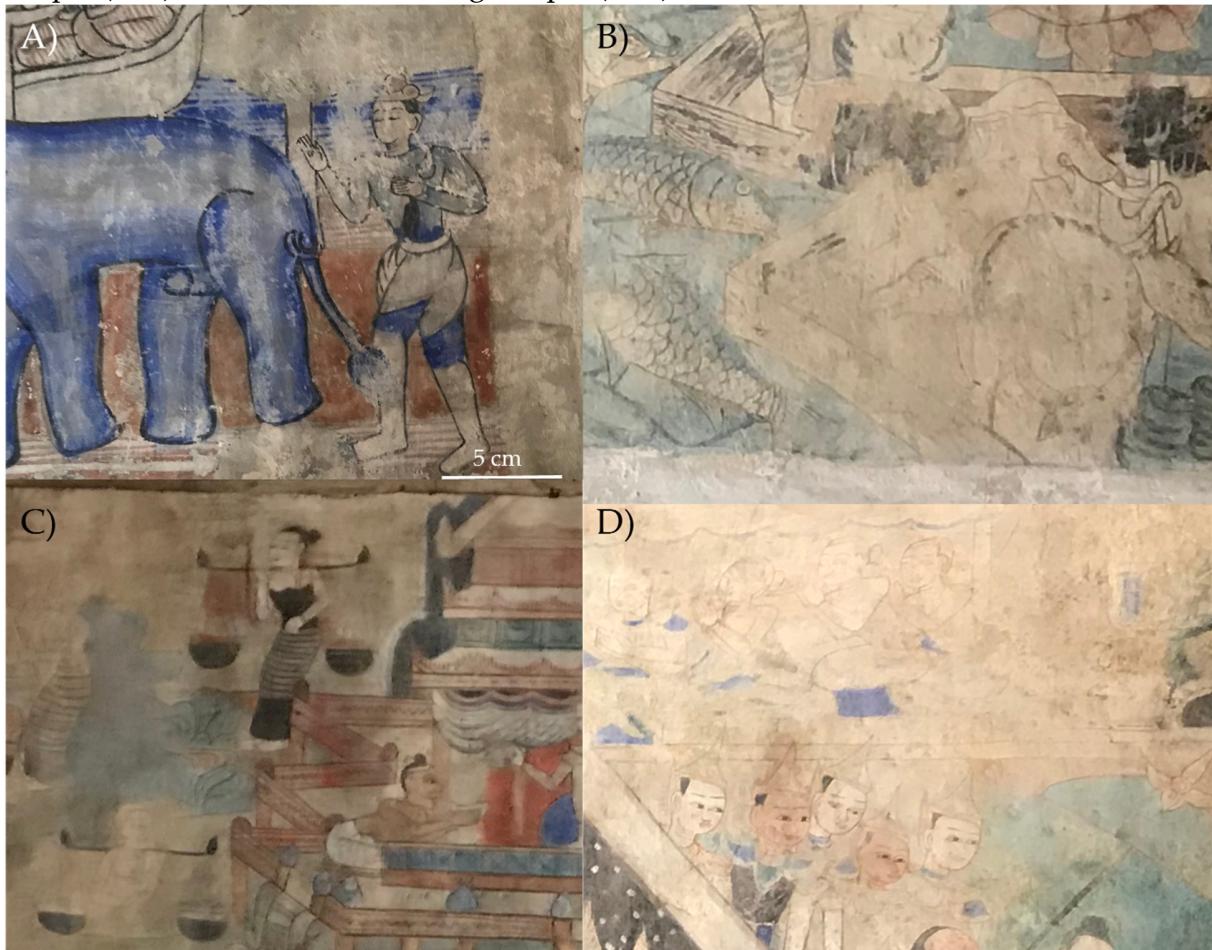
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8 The 7th Regional Office of Fine arts, Department of Fine art, Ministry of Culture, Chiang Mai 50300 , Thailand; klangjindasu@gmail.com; thanw3@yahoo.com

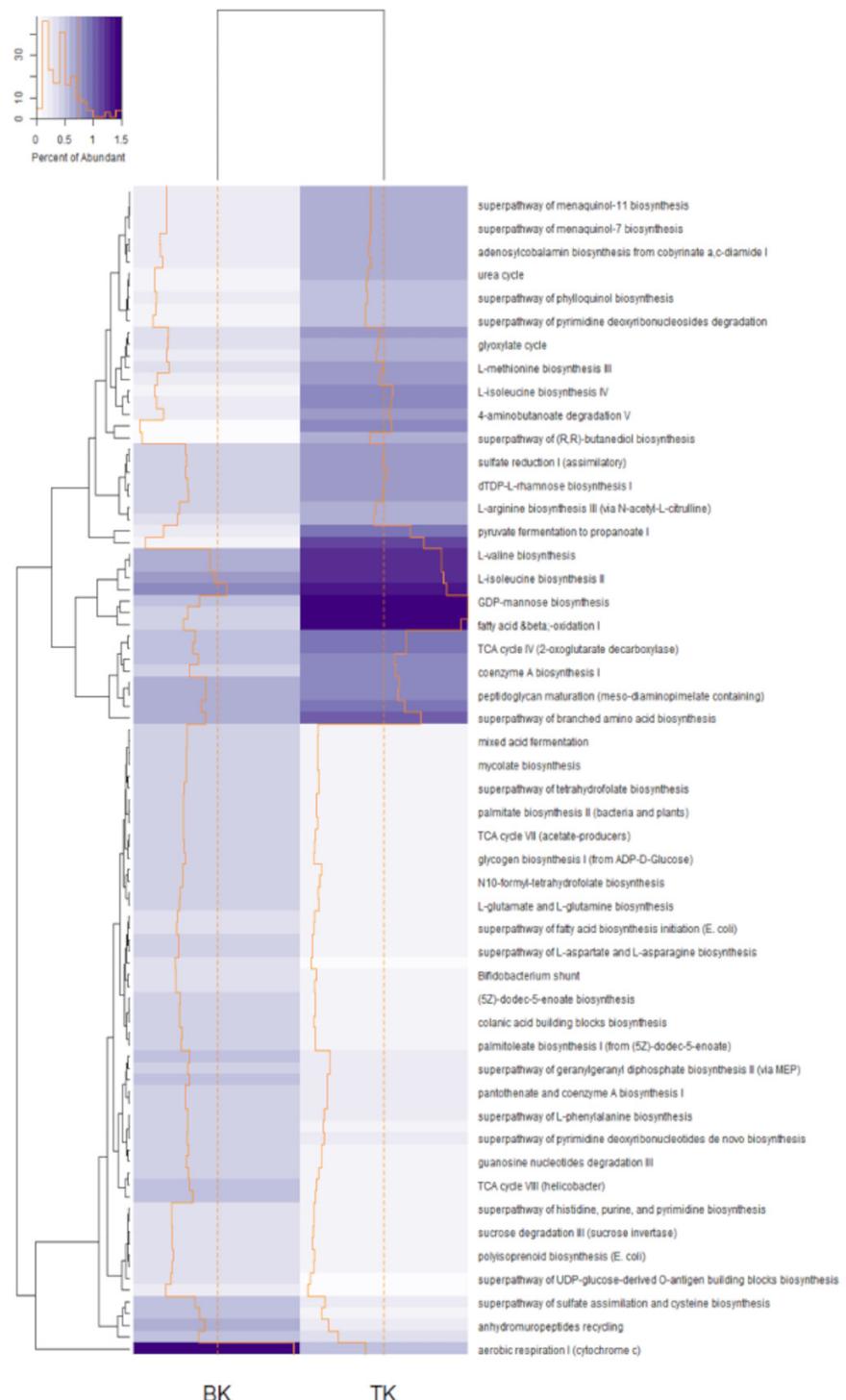
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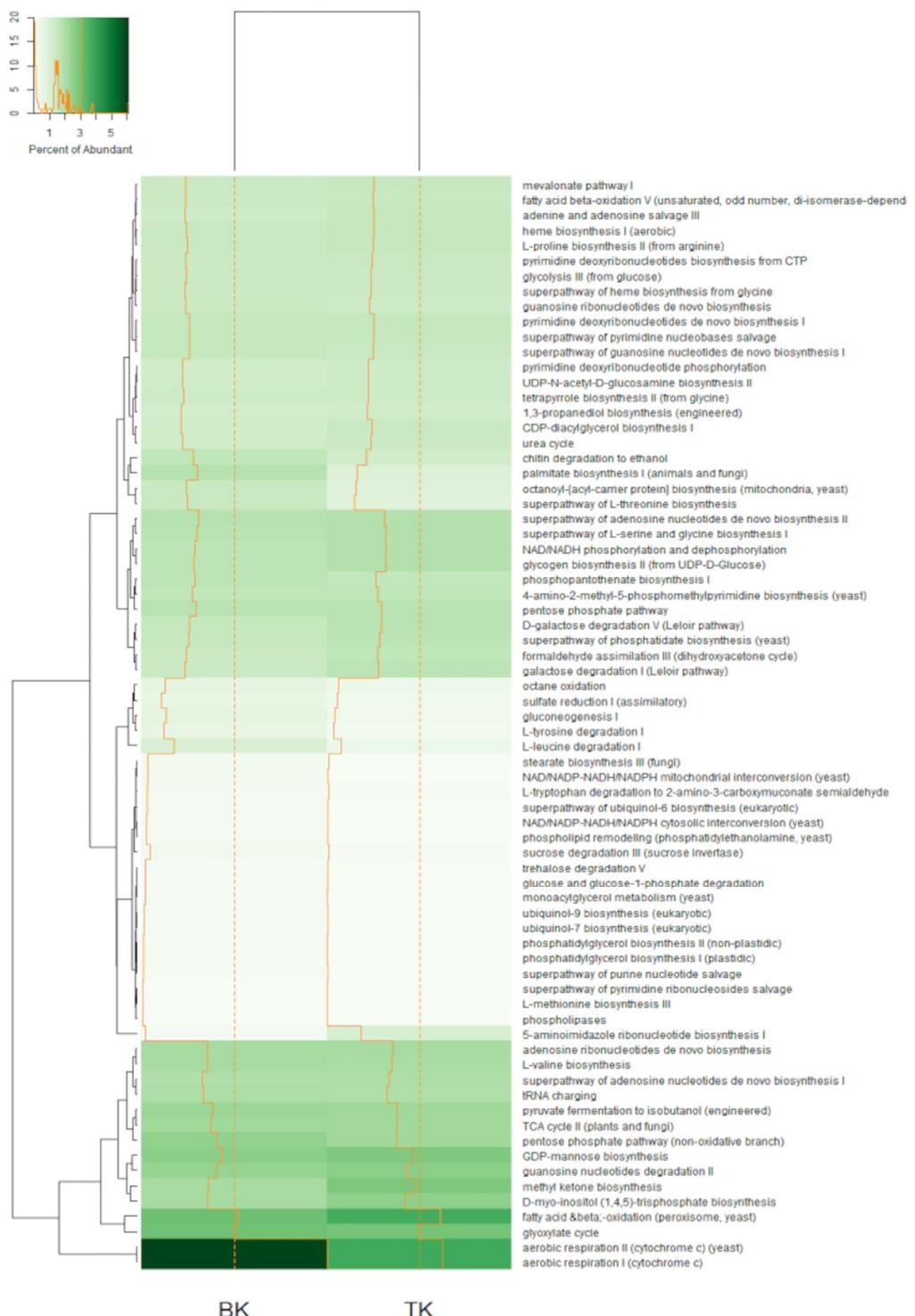
**Figure S1.** Background level of the deterioration on mural paintings from Tha Kham temple (A,B) and Buak Krok Luang temple (C,D).



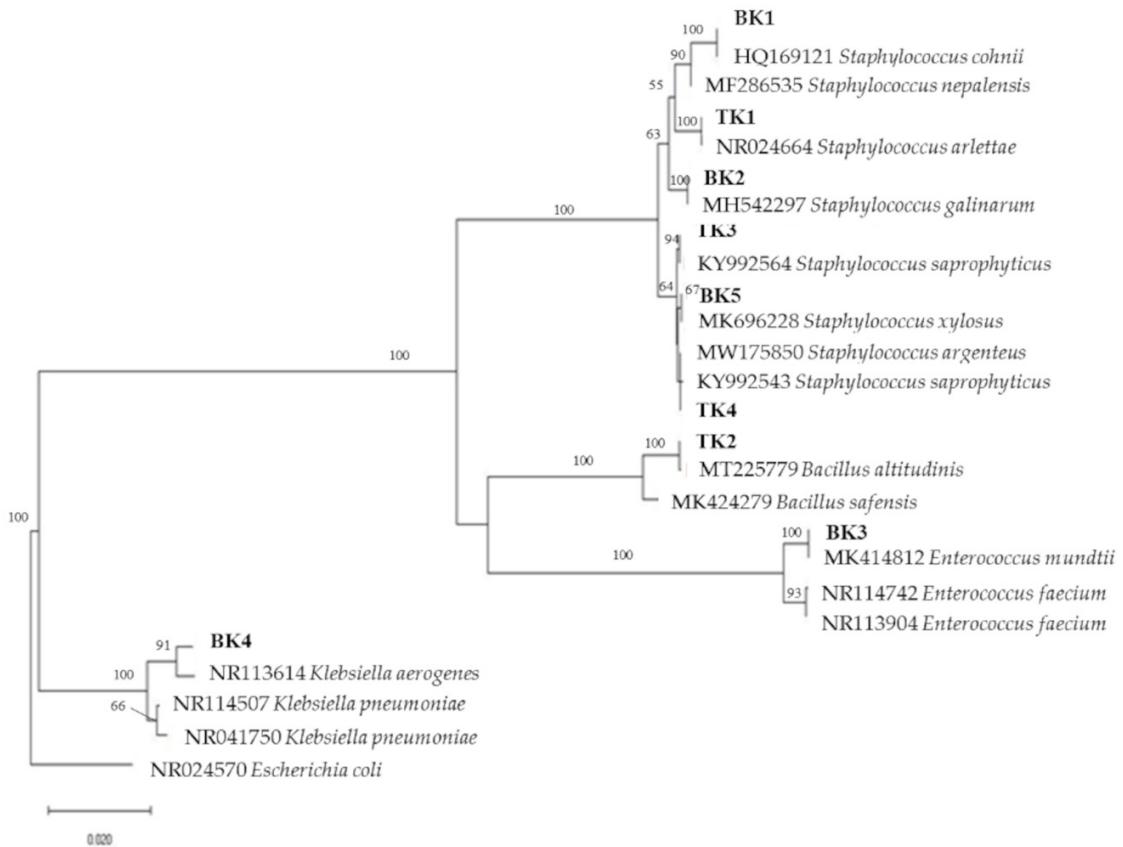
**Figure S2.** Bacterial function analysis heat map of samples from Buak Krok Luang and Tha Kham temples. The functional pathways are list on the right side of the heatmap.



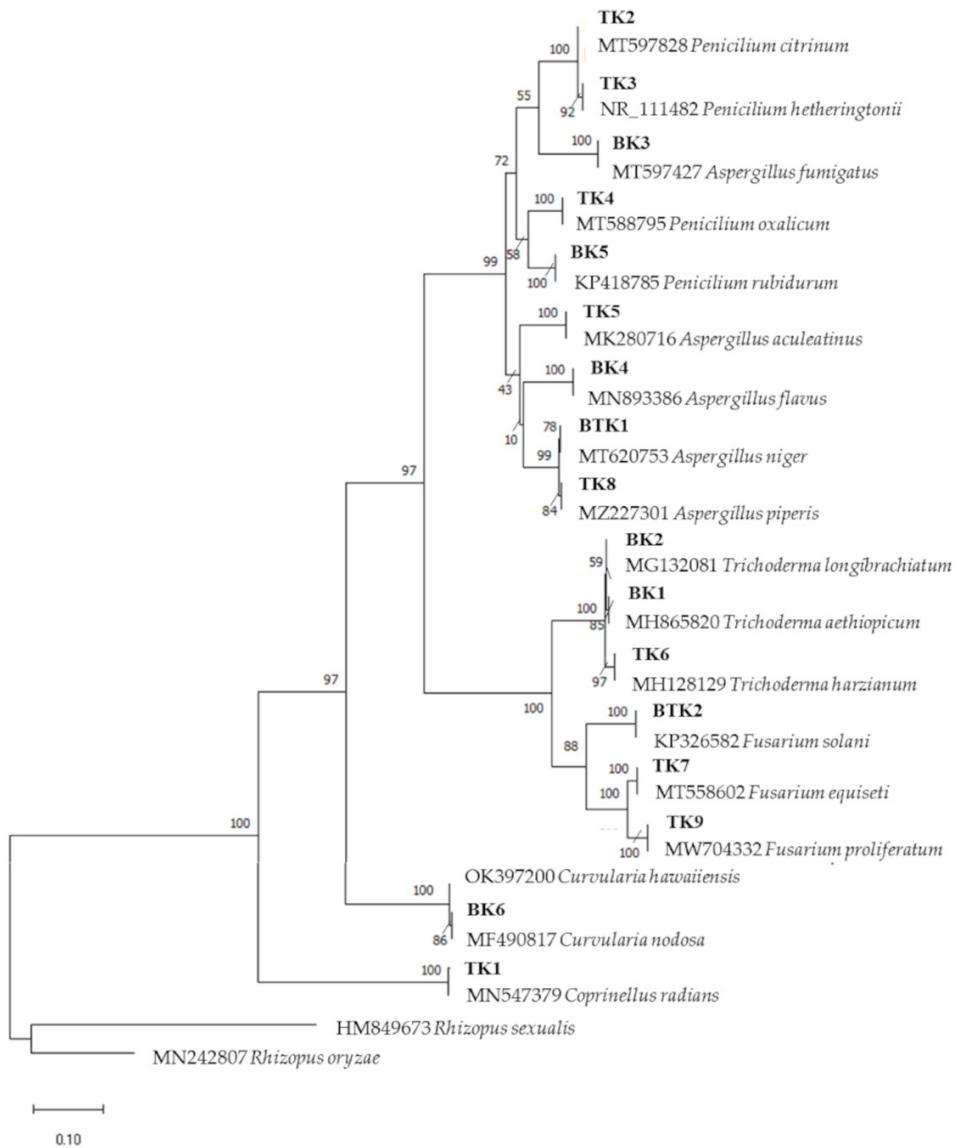
**Figure S3.** Fungal function analysis heat map from Buak Krok Luang and Tha Kham temples. The functional pathways are listed on the right side of the heat map.



**Figure S4.** Bacterial phylogenetic tree was constructed from sequences from the culturable bacteria using MEGA-X with kimura 2 model, the bootstrap values were shown on each branch.



**Figure S5.** Fungal phylogenetic tree was constructed from sequences from the culturable fungi using MEGA-X with kimura 2 model, the bootstrap values were shown on each branch.



**Table S1.** Bacterial biodeterioration activity on TSA mixed with crimson red (CR) and malachite green (MG) and fungal biodeterioration activity on PDA mixed with the same color.

Isolate	Code	MG	CR
Bacteria			
<i>S. cohnii</i>	BK1		
<i>S. galinarum</i>	BK2		
<i>S. xylosus</i>	BK5		
<i>S. arlettae</i>	TK1		
<i>S. argenteus</i>	TK4		
<i>S. saprophyticus</i>	TK3		
<i>K. aerogenes</i>	BK4		
<i>B. altitudinis</i>	TK2		
<i>E. mundtii</i>	BK3		
Fungi			
<i>T. aethiopicum</i>	BK1		
<i>T. longibrachiatum</i>	BK2		
<i>A. niger</i>	BTK1		
<i>F. solani</i>	BTK2		
<i>A. fumigatus</i>	BK3		
<i>P. citrinum</i>	TK2		
<i>P. hetheringtonii</i>	TK3		
<i>P. oxalicum</i>	TK4		
<i>A. aculeatinus</i>	TK5		
<i>T. harzianum</i>	TK6		
<i>A. piperis</i>	TK8		

**Table S2.** pH measurement of microorganism isolates, BK; Isolates from Buak Krok Luang temple, TK; Isolates from Tha Kham temple and BTK; Isolates from both temples.

Isolates	Initial pH	Final pH
Bacteria		
BK3	7.14	7.12 ± 0.04
BK4	7.14	7.15 ± 0.03
TK4	7.14	7.19 ± 0.03
Fungi		
BK1	5.36	4.41 ± 0.06
BK2	5.36	2.70 ± 0.05
BK3	5.36	3.98 ± 0.06
BTK1	5.36	3.88 ± 0.14
BTK2	5.36	2.81 ± 0.18
TK2	5.36	4.04 ± 0.06
TK3	5.36	4.14 ± 0.07
TK4	5.36	3.33 ± 0.07
TK5	5.36	3.72 ± 0.08
TK6	5.36	4.54 ± 0.11
TK8	5.36	4.16 ± 0.08

**Table S3.** Comparing between biodeterioration activities from the previously studies and microorganisms from culture-independent method in this study.

Organisms	Biodeterioration process	Researchers
Bacterial		
<i>Cyanobacteria</i> <i>Synechococcus</i> sp., <i>Chlorogloea</i> sp. <i>Chlorella</i> sp. <i>Chlorococcum</i> sp. <i>Chroococcus</i> sp. <i>Gloeocapsa aeruginosa</i> , <i>Nostoc muscorum</i> <i>Anabaena oscillarioides</i> <i>Brasilonema octagenarium</i>	-Biofilm formation -Creating patinas -Acid production -Rosy discoloration	Hueck, 1965, Sáiz-Jiménez, 1984, Viles, 1987, El-Gorj <i>et al.</i> , 2019, Imperi <i>et al.</i> , 2007 and Nugari <i>et al.</i> , 2009
<i>Arthrobacter parietis</i> <i>Arthrobacter castelli</i> <i>Arthrobacter monumenti</i> <i>Arthrobacter pigmenti</i> , <i>Arthrobacter tecti</i> <i>Arthrobacter tumbae</i> <i>Arthrobacter agilis</i> <i>Arthrobacter aureescens</i> <i>Micrococcus roseuss</i>	-Rosy discoloration -Biofilm formation	Tescari <i>et al.</i> , 2018, Heyrman <i>et al.</i> , 2008 and Altenburgera <i>et al.</i> , 1996
Fungi		
<i>Cladosporium cladosporioides</i> <i>Cladosporium oxysporum</i> <i>Cladosporium uredinicola</i> <i>Cladosporium sphaerospermum</i> <i>Cladosporium xylophilum</i> <i>Cladosporium macrocarpum</i> <i>Cladosporium herbarum</i> <i>Cladosporium tenuisimum</i>	-Staining -Creating patinas	Sterflinger and Piñar, 2013, Gorbushina <i>et al.</i> , 2004, Unković <i>et al.</i> , 2018, Jurado <i>et al.</i> , 2021, Vukojevi <i>et al.</i> , 2010

Table S4. Basic data relates to Figure 8. The table represents the microorganisms which are found in each country (dark gray indicates that this study did not focus on the organism).

Researchers	Organisms	
	Bacteria	Fungi
Gorbushina et al., 2004 (Germany)	Gammaproteobacteria Cyanobacteria Firmicutes Actinobacteria	<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp. <i>Fusarium</i> sp.
Tonolo and Giacobini, 1961 (Italy)		<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp.
Voronina, 1966 (Georgia)		<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp. <i>Alternaria</i> sp.
Kuritzyna, 1968 (Russia)		<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp.
Unković et al., 2016 (Serbia)		<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp.
Shirakawa et al., 2002 (Brazil)		<i>Aspergillus</i> sp. <i>Cladosporium</i> sp. <i>Fusarium</i> sp. <i>Curvularia</i> sp. <i>Alternaria</i> sp.
López-Miras et al., 2013 (Spain)	Gammaproteobacteria Firmicutes Actinobacteria	
Senbua and Wichitwechkam, 2019 (Thailand), Supaphimol et al., 2021 (Thailand)	Gammaproteobacteria Cyanobacteria Firmicutes Actinobacteria	<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Fusarium</i> sp. <i>Curvularia</i> sp. <i>Neodevriesia</i> sp.
Duan et al., 2018 (China), Duan et al., 2019 (China), Ma et al., 2020 (China)	Gammaproteobacteria Cyanobacteria Firmicutes Actinobacteria	<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp. <i>Fusarium</i> sp. <i>Alternaria</i> sp. <i>Mucor</i> sp. <i>Malassezia</i> sp. <i>Curvularia</i> sp.

Nikola <i>et al.</i> , 2018 (Serbia)		<i>Aspergillus</i> sp. <i>Penicillium</i> sp. <i>Cladosporium</i> sp.
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