

Supplementary materials

Microbiota associated with different developmental stages of the dry rot fungus

Serpula lacrymans

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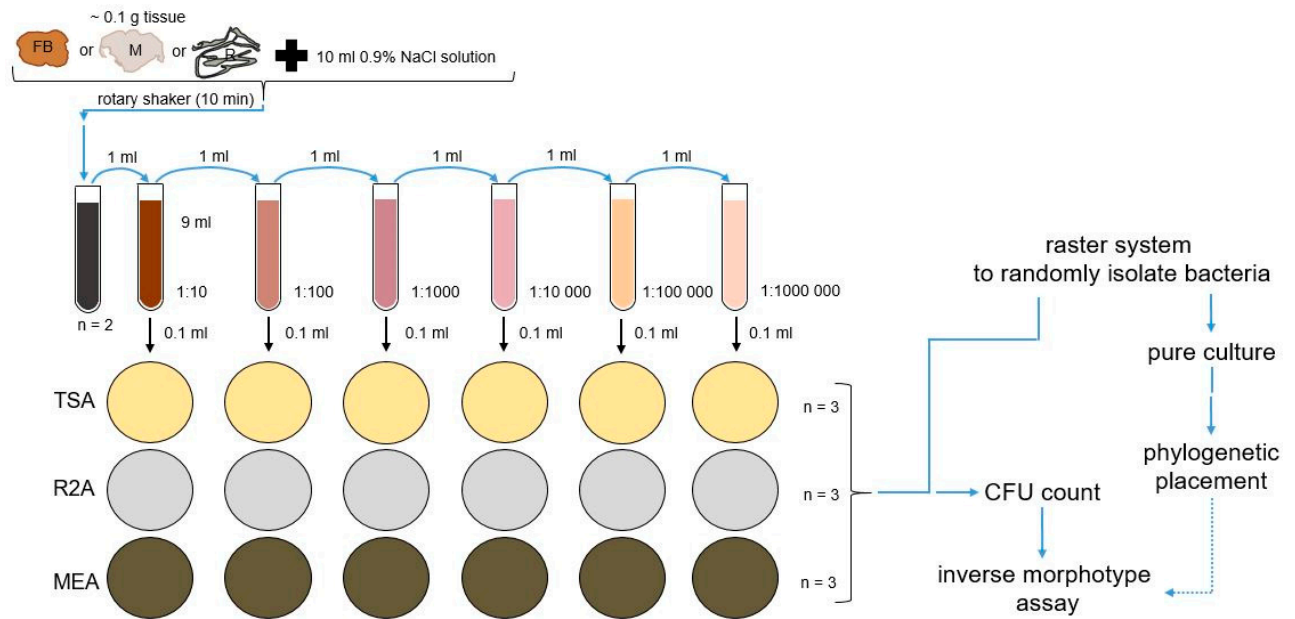


Figure S1 | Isolation and characterization of bacteria from tissues of *Serpula lacrymans*
– including 16S rRNA gene fingerprint and inverse morphotype assay: 0.1 - 1 g fungal tissue (FB: fruiting body, M: mycelia, R: rhizomorphs) were homogenized in 10 ml 0.9% NaCl solution. 100 µL of this suspension (or of a serial dilution therefrom) were plated on tryptone soy agar (TSA), R2A agar, and malt extract agar (MEA) in triplicates and incubated for 7 days at 25 °C. Petri dishes were checked daily. Petri dishes with 30 to 100 CFU were used for counting. Bacterial colonies were divided into morphotypes and the CFU of each morphotype were counted. From each plate 6 CFU were selected randomly (raster system) and bacterial pure cultures were created and identified upon their 16S rRNA gene. Each morphotype could therefore be assigned to 16S rRNA gene sequences.

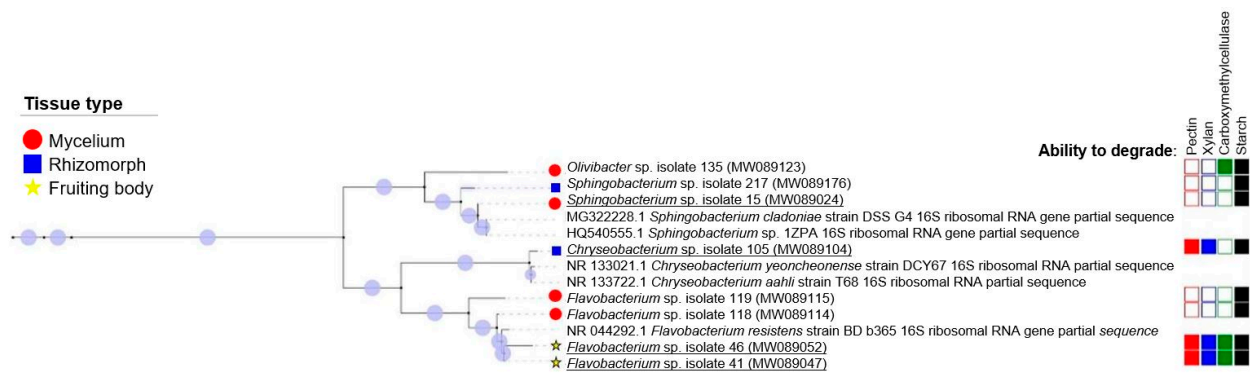


Figure S2 | Cladogram of bacteria belonging to the phylum Bacteroidetes (PHYML). 16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result. 13 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than 0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. Underlined isolates were tested in co-culture assays.

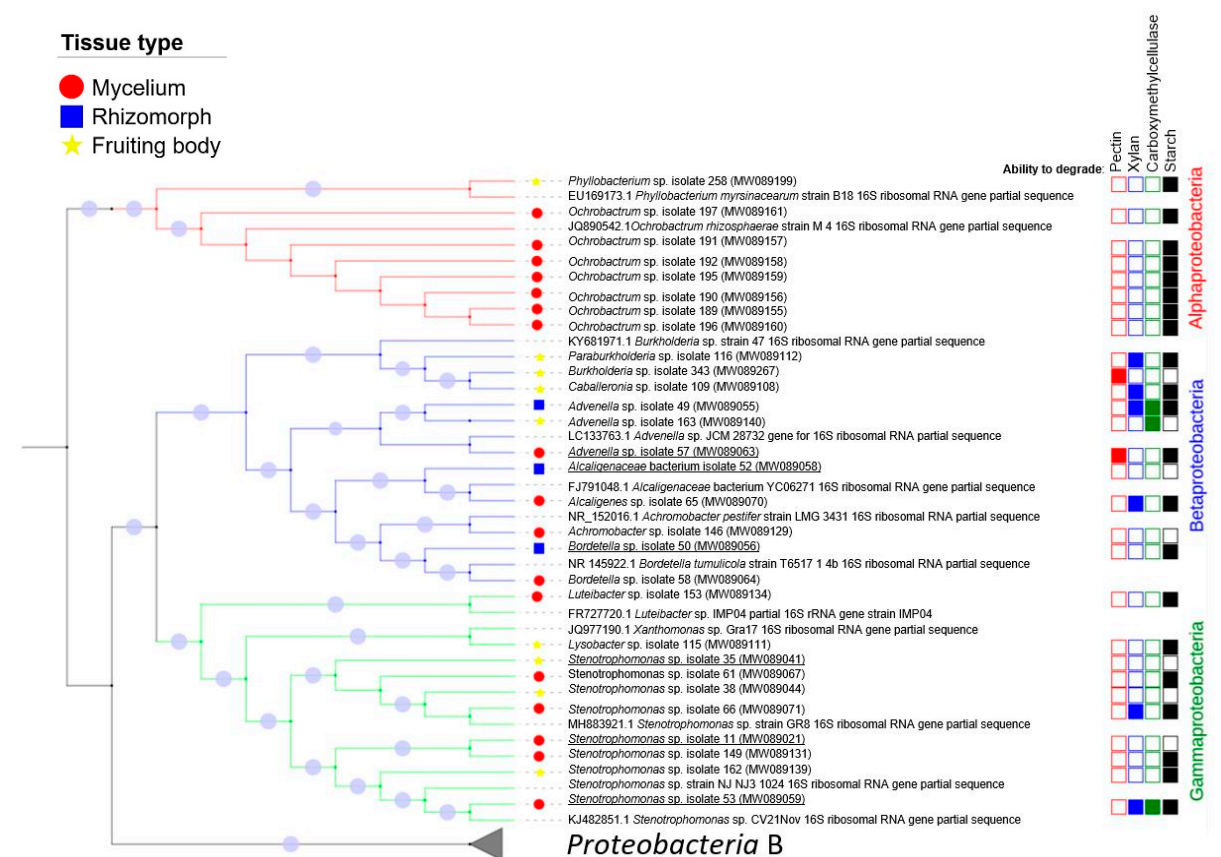


Figure S3 | Cladogram of bacteria belonging to the phylum Proteobacteria (part A) (PHYML). 16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result. 41 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than 0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. Red branches are Alphaproteobacteria, blue branches are Betaproteobacteria and green branches are Gammaproteobacteria. For *Proteobacteria* part B see figure S4. Underlined isolates were tested in co-culture assays

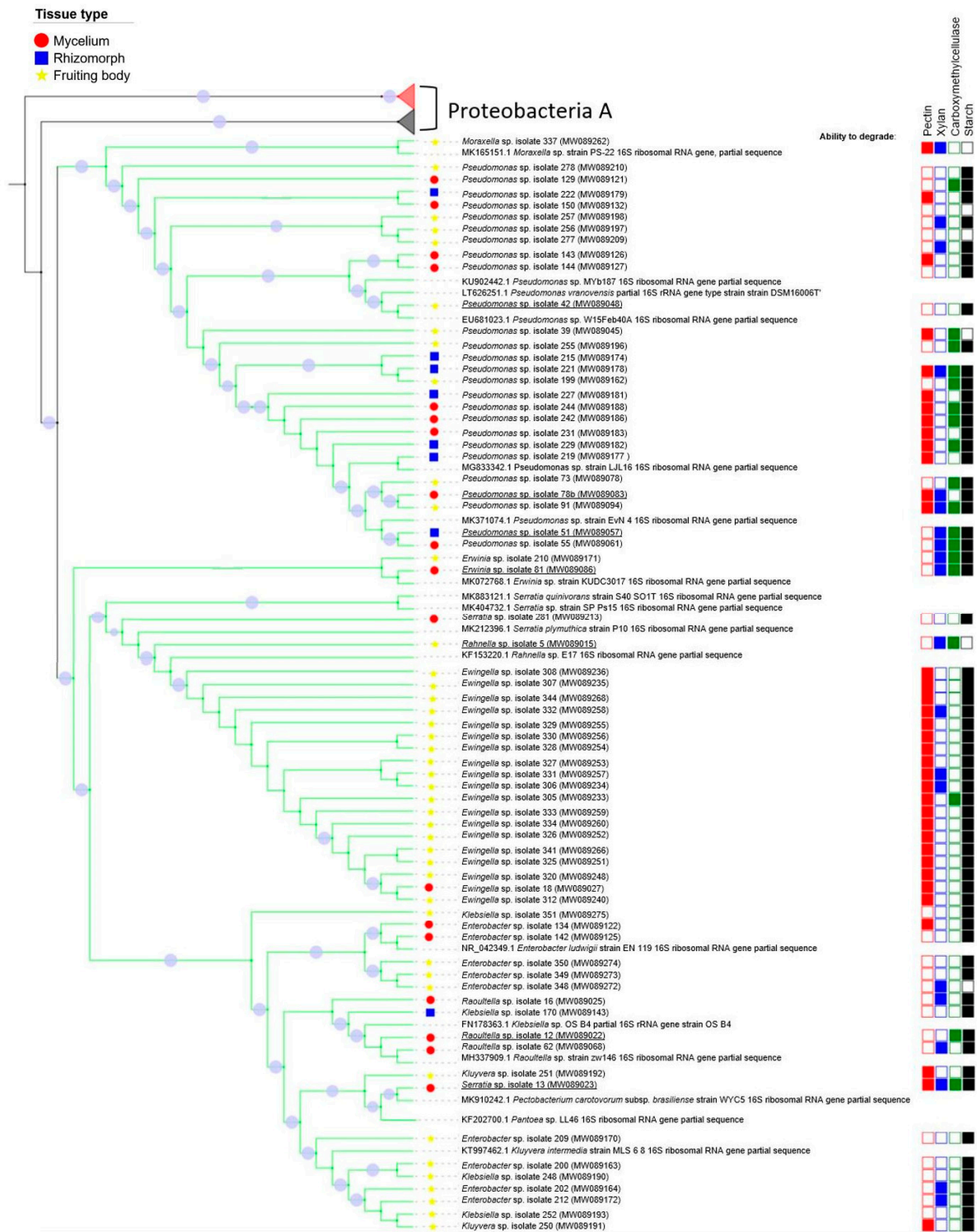


Figure S4 | Cladogram of bacteria belonging to the phylum Proteobacteria (part B) (PHYML). 16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result. 138 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than 0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. Green branches show Gammaproteobacteria. For Proteobacteria part A see figure S3. Underlined isolates were tested in co-culture assays.

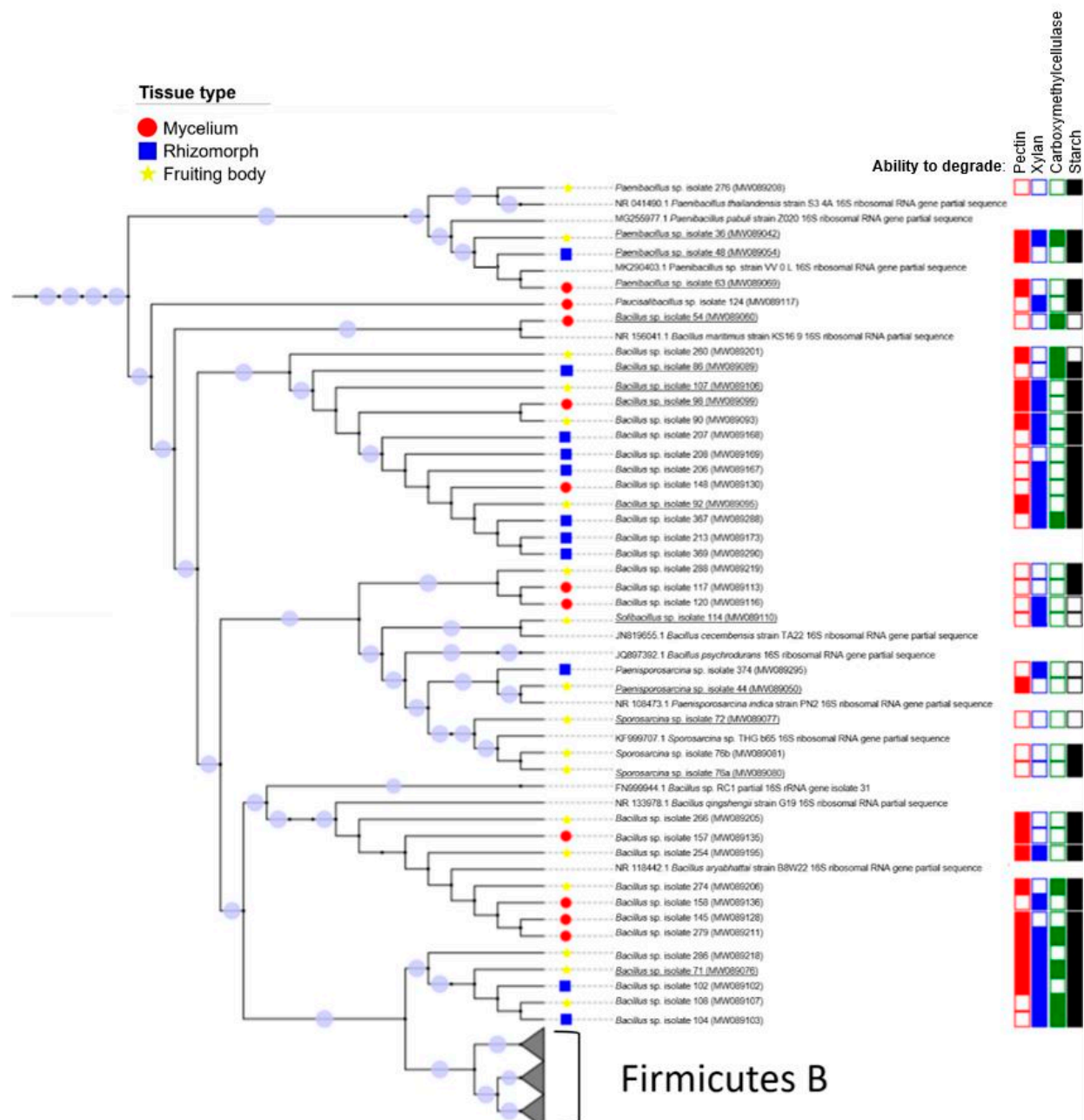


Figure S5 | Cladogram of bacteria belonging to the phylum Firmicutes (part A) (PHYML).

16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result. 102 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than 0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red

rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. For Firmicutes part B see figure S6. Underlined isolates were tested in co-culture assays.

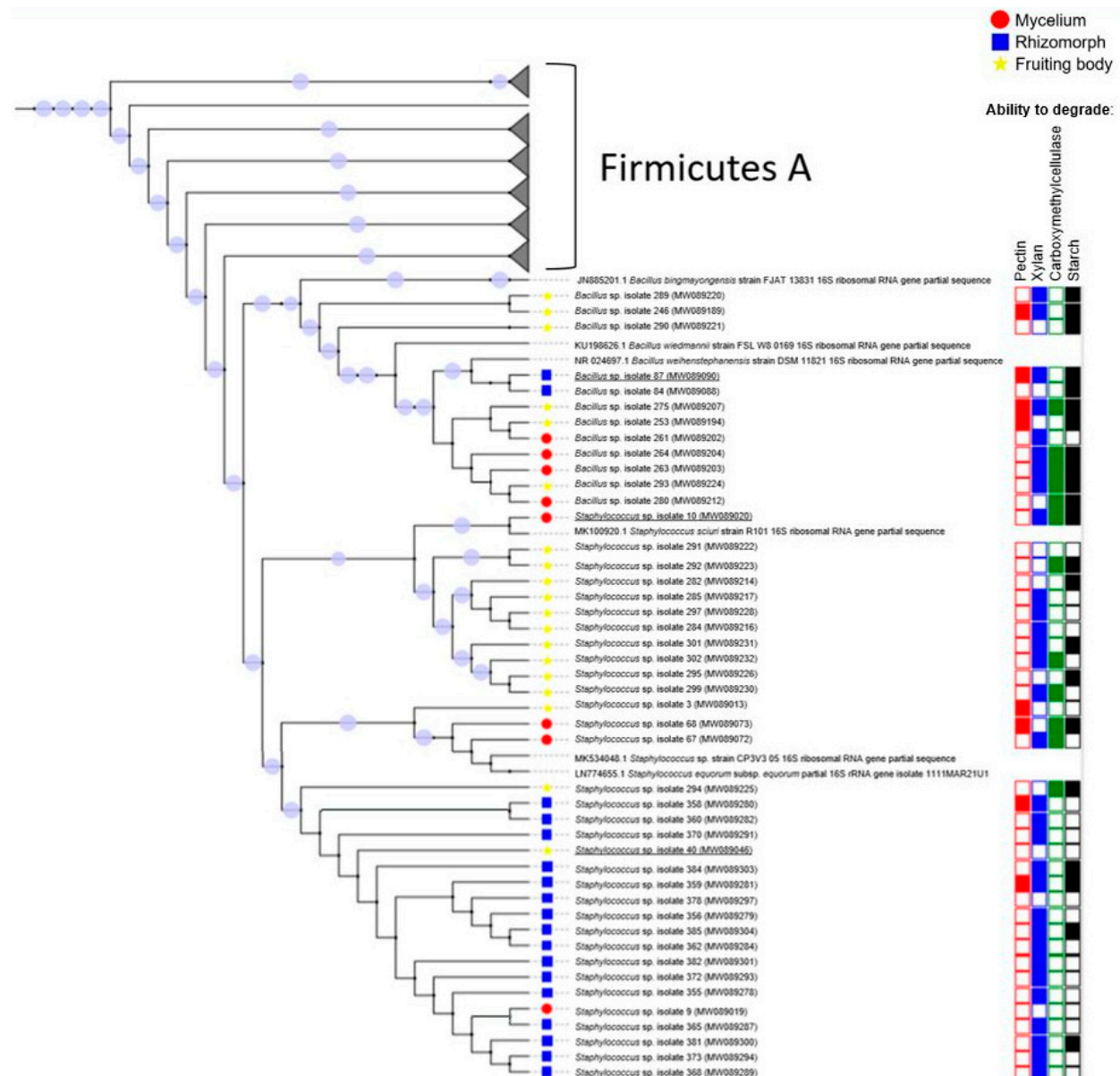


Figure S6 | Cladogram of bacteria belonging to the phylum Firmicutes (part B) (PHYML).

16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result. 102 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than

0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. For Firmicutes part A see figure S5. Underlined isolates were tested in co-culture assays.

Tissue type

- Mycelium
- Rhizomorph
- ★ Fruiting body

Ability to degrade:

- Pectin
- Xylan
- Carboxymethylcellulase
- Starch

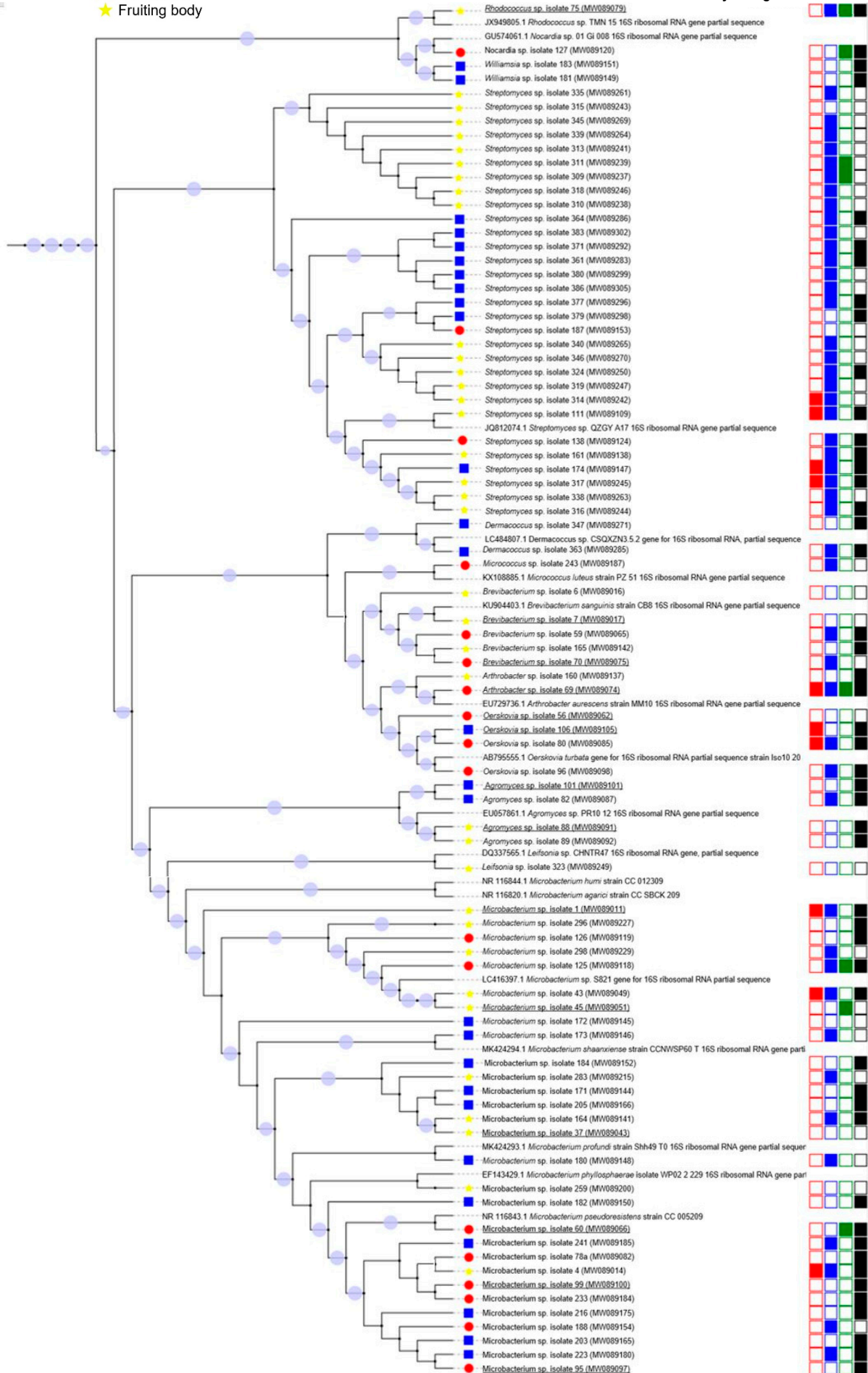


Figure S7 | Cladogram of bacteria belonging to the phylum Actinobacteria (PHYML).

16S rRNA gene sequences show the relationships between bacteria isolated from *S. lacrymans* tissue types. Most 16S rRNA gene sequences had high similarity with type species (>98%-100%); final assignment at genera level was based on the best blast result and the phylogenetic tree. 99 sequences were used for tree creation. Light blue circles indicate a χ^2 statistics greater than 0.75. Reference sequences were retrieved from NCBI. Symbols that indicate tissue of isolation: red circle = bacteria isolated from mycelium; star = bacteria isolated from fruiting body and blue rectangle = bacteria isolated from rhizomorphs. Symbols on the right: red rectangle indicates ability to degrade pectin, blue rectangle indicates ability to degrade xylan, green rectangle indicates ability to degrade carboxymethylcellulose and black rectangle indicates ability to degrade starch. Underlined isolates were tested in co-culture assays.

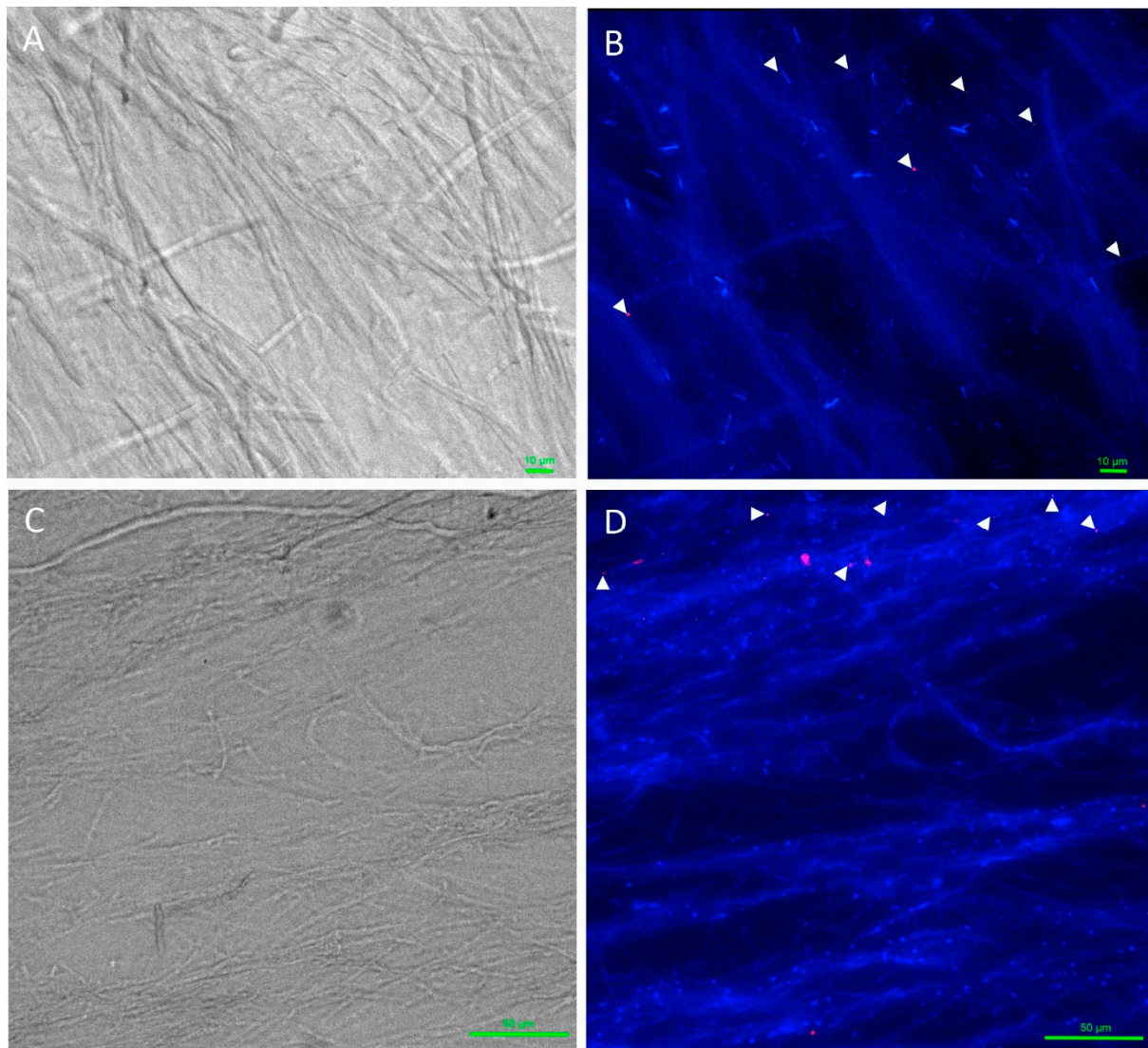


Figure S8 | Localization of bacteria on *S. lacrymans* rhizomorphs and mycelium. A Overlay of signals derived from EUB338 Mix-Cy5 and DAPI. Investigated tissue type = rhizomorph. **B** Transmitted light picture of rhizomorph. **C** Overlay of signals derived from EUB338 Mix-Cy5 and DAPI. Investigated tissue type = mycelium. **D** Transmitted light picture of fungal mycelium. The general bacterial EUB338 Mix probe gave red signals. Signals are highlighted with white arrows. Scale bars are 10 and 50 μm .

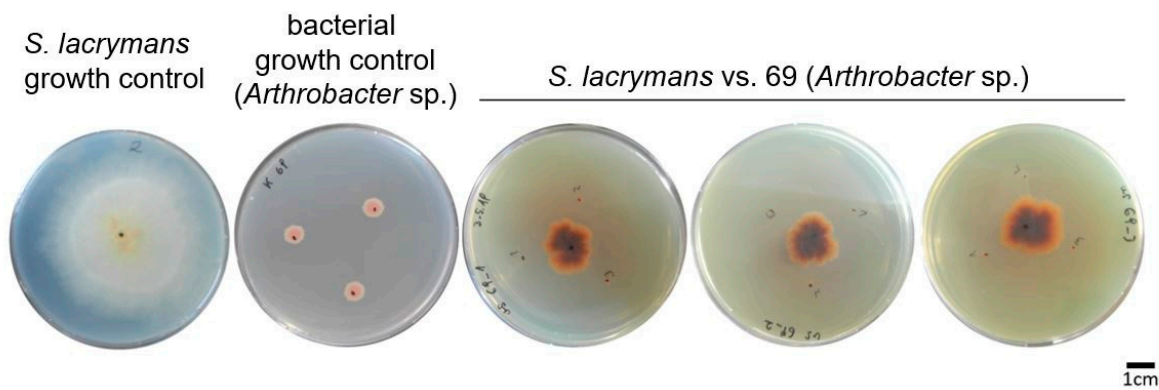


Figure S9 | Inhibition of bacterial growth by *S. lacrymans*. Growth impairment of bacterial isolate 69 (*Arthrobacter* sp.) during co-cultivation with *S. lacrymans*. Pictures were taken after cultivation for 31 days on minimal media at 25 °C.

Table S1: Accession numbers for sequences of bacterial isolates retrieved from NCBI:

Bacteria isolated from *Serpula lacrymans* or *Coniophora puteana* (CP) tissue (FB = Fruiting body, M = Mycelia, R = Rhizomorph) on either Tryptone Soy agar (TSA), R2A or Malt extract agar (MEA); + means sequences are included in the cladograms or – no consideration in the phylogenetic analysis.

Accession No.	Isolate No.	Species	isolation		included in Cladogram
			tissue	media	
MW089011	1	<i>Microbacterium</i> sp.	FB	TSA	+
MW089012	2	<i>Microbacterium</i> sp.	FB	TSA	-
MW089013	3	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089014	4	<i>Microbacterium</i> sp.	FB	TSA	+
MW089015	5	<i>Rahnella</i> sp.	FB	TSA	+
MW089016	6	<i>Brevibacterium</i> sp.	FB	TSA	+
MW089017	7	<i>Brevibacterium</i> sp.	FB	TSA	+
MW089018	8	<i>Microbacterium</i> sp.	M	TSA	-
MW089019	9	<i>Staphylococcus</i> sp.	M	TSA	+
MW089020	10	<i>Staphylococcus</i> sp.	M	TSA	+
MW089021	11	<i>Stenotrophomonas</i> sp.	M	TSA	+
MW089022	12	<i>Raoultella</i> sp.	M	TSA	+
MW089023	13	<i>Serratia</i> sp.	M	TSA	+
MW089024	15	<i>Sphingobacterium</i> sp.	M	TSA	+
MW089025	16	<i>Raoultella</i> sp.	M	TSA	+
MW089026	17	<i>Okibacterium</i> sp.	M	TSA	-
MW089027	18	<i>Ewingella</i> sp.	M	TSA	+
MW089028	20	<i>Microbacterium</i> sp.	FB CP	TSA	-
MW089029	21	<i>Pseudomonas</i> sp.	FB CP	TSA	-
MW089030	22	<i>Microbacterium</i> sp.	FB CP	TSA	-
MW089031	23	<i>Microbacterium</i> sp.	FB CP	TSA	-
MW089032	24	<i>Microbacterium</i> sp.	FB CP	TSA	-
MW089033	26	<i>Paenibacillus</i> sp.	M CP	TSA	-
MW089034	27	<i>Bacillus</i> sp.	M CP	TSA	-
MW089035	28	<i>Advenella</i> sp.	M CP	TSA	-
MW089036	29	<i>Pseudomonas</i> sp.	M CP	TSA	-
MW089037	30	<i>Bacillus</i> sp.	M CP	TSA	-
MW089038	31	<i>Staphylococcus</i> sp.	M CP	TSA	-
MW089039	33	<i>Sporosarcina</i> sp.	M CP	TSA	-
MW089040	34	<i>Bacillus</i> sp.	M CP	TSA	-
MW089041	35	<i>Stenotrophomonas</i> sp.	FB	TSA	+
MW089042	36	<i>Paenibacillus</i> sp.	FB	TSA	+
MW089043	37	<i>Microbacterium</i> sp.	FB	TSA	+
MW089044	38	<i>Stenotrophomonas</i> sp.	FB	TSA	+

MW089045	39	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089046	40	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089047	41	<i>Flavobacterium</i> sp.	FB	TSA	+
MW089048	42	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089049	43	<i>Microbacterium</i> sp.	FB	TSA	+
MW089050	44	<i>Paenispodosarcina</i> sp.	FB	TSA	+
MW089051	45	<i>Microbacterium</i> sp.	FB	TSA	+
MW089052	46	<i>Flavobacterium</i> sp.	FB	TSA	+
MW089053	47	<i>Bacillus</i> sp.	R	TSA	-
MW089054	48	<i>Paenibacillus</i> sp.	R	TSA	+
MW089055	49	<i>Advenella</i> sp.	R	TSA	+
MW089056	50	<i>Bordetella</i> sp.	R	TSA	+
MW089057	51	<i>Pseudomonas</i> sp.	R	TSA	+
MW089058	52	<i>Alcaligenaceae</i> <i>bacterium</i>	R	TSA	+
MW089059	53	<i>Stenotrophomonas</i> sp.	M	TSA	+
MW089060	54	<i>Bacillus</i> sp.	M	TSA	+
MW089061	55	<i>Pseudomonas</i> sp.	M	TSA	+
MW089062	56	<i>Oerskovia</i> sp.	M	TSA	+
MW089063	57	<i>Advenella</i> sp.	M	TSA	+
MW089064	58	<i>Bordetella</i> sp.	M	TSA	+
MW089065	59	<i>Brevibacterium</i> sp.	M	TSA	+
MW089066	60	<i>Microbacterium</i> sp.	M	TSA	+
MW089067	61	<i>Stenotrophomonas</i> sp.	M	TSA	+
MW089068	62	<i>Raoultella</i> sp.	M	TSA	+
MW089069	63	<i>Paenibacillus</i> sp.	M	TSA	+
MW089070	65	<i>Alcaligenes</i> sp.	M	TSA	+
MW089071	66	<i>Stenotrophomonas</i> sp.	M	TSA	+
MW089072	67	<i>Staphylococcus</i> sp.	M	TSA	+
MW089073	68	<i>Staphylococcus</i> sp.	M	TSA	+
MW089074	69	<i>Arthrobacter</i> sp.	M	TSA	+
MW089075	70	<i>Brevibacterium</i> sp.	M	TSA	+
MW089076	71	<i>Bacillus</i> sp.	FB	TSA	+
MW089077	72	<i>Sporosarcina</i> sp.	FB	TSA	+
MW089078	73	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089079	75	<i>Rhodococcus</i> sp.	FB	TSA	+
MW089080	76a	<i>Sporosarcina</i> sp.	FB	TSA	+
MW089081	76b	<i>Sporosarcina</i> sp.	FB	TSA	+
MW089082	78a	<i>Microbacterium</i> sp.	M	TSA	+
MW089083	78b	<i>Pseudomonas</i> sp.	M	TSA	+
MW089084	79	<i>Paenibacillus</i> sp.	M	TSA	-
MW089085	80	<i>Oerskovia</i> sp.	M	TSA	+
MW089086	81	<i>Erwinia</i> sp.	M	TSA	+
MW089087	82	<i>Agromyces</i> sp.	R	TSA	+
MW089088	84	<i>Bacillus</i> sp.	R	TSA	+

MW089089	86	<i>Bacillus</i> sp.	R	TSA	+
MW089090	87	<i>Bacillus</i> sp.	R	TSA	+
MW089091	88	<i>Agromyces</i> sp.	FB	TSA	+
MW089092	89	<i>Agromyces</i> sp.	FB	TSA	+
MW089093	90	<i>Bacillus</i> sp.	FB	TSA	+
MW089094	91	<i>Pseudomonas</i> sp.	FB	R2A	+
MW089095	92	<i>Bacillus</i> sp.	FB	R2A	+
MW089096	93	<i>Streptomyces</i> sp.	FB	R2A	-
MW089097	95	<i>Microbacterium</i> sp.	M	R2A	+
MW089098	96	<i>Oerskovia</i> sp.	M	R2A	+
MW089099	98	<i>Bacillus</i> sp.	M	R2A	+
MW089100	99	<i>Microbacterium</i> sp.	M	R2A	+
MW089101	101	<i>Agromyces</i> sp.	R	R2A	+
MW089102	102	<i>Bacillus</i> sp.	R	R2A	+
MW089103	104	<i>Bacillus</i> sp.	R	R2A	+
MW089104	105	<i>Chryseobacterium</i> sp.	R	R2A	+
MW089105	106	<i>Oerskovia</i> sp.	R	R2A	+
MW089106	107	<i>Bacillus</i> sp.	FB	R2A	+
MW089107	108	<i>Bacillus</i> sp.	FB	R2A	+
MW089108	109	<i>Caballeronia</i> sp.	FB	R2A	+
MW089109	111	<i>Streptomyces</i> sp.	FB	R2A	+
MW089110	114	<i>Solibacillus</i> sp.	FB	TSA	+
MW089111	115	<i>Lysobacter</i> sp.	FB	TSA	+
MW089112	116	<i>Paraburkholderia</i> sp.	FB	R2A	+
MW089113	117	<i>Bacillus</i> sp.	M	TSA	+
MW089114	118	<i>Flavobacterium</i> sp.	M	TSA	+
MW089115	119	<i>Flavobacterium</i> sp.	M	TSA	+
MW089116	120	<i>Bacillus</i> sp.	M	TSA	+
MW089117	124	<i>Paucisalibacillus</i> sp.	M	TSA	+
MW089118	125	<i>Microbacterium</i> sp.	M	TSA	+
MW089119	126	<i>Microbacterium</i> sp.	M	TSA	+
MW089120	127	<i>Nocardia</i> sp.	M	TSA	+
MW089121	129	<i>Pseudomonas</i> sp.	M	MEA	+
MW089122	134	<i>Enterobacter</i> sp.	M	TSA	+
MW089123	135	<i>Olivibacter</i> sp.	M	TSA	+
MW089124	138	<i>Streptomyces</i> sp.	M	TSA	+
MW089125	142	<i>Enterobacter</i> sp.	M	MEA	+
MW089126	143	<i>Pseudomonas</i> sp.	M	TSA	+
MW089127	144	<i>Pseudomonas</i> sp.	M	TSA	+
MW089128	145	<i>Bacillus</i> sp.	M	TSA	+
MW089129	146	<i>Achromobacter</i> sp.	M	TSA	+
MW089130	148	<i>Bacillus</i> sp.	M	TSA	+
MW089131	149	<i>Stenotrophomonas</i> sp.	M	TSA	+
MW089132	150	<i>Pseudomonas</i> sp.	M	TSA	+
MW089133	152	<i>Pseudomonas</i> sp.	M	R2A	-

MW089134	153	<i>Luteibacter</i> sp.	M	R2A	+
MW089135	157	<i>Bacillus</i> sp.	M	MEA	+
MW089136	158	<i>Bacillus</i> sp.	M	MEA	+
MW089137	160	<i>Arthrobacter</i> sp.	FB	TSA	+
MW089138	161	<i>Streptomyces</i> sp.	FB	TSA	+
MW089139	162	<i>Stenotrophomonas</i> sp.	FB	TSA	+
MW089140	163	<i>Advenella</i> sp.	FB	TSA	+
MW089141	164	<i>Microbacterium</i> sp.	FB	TSA	+
MW089142	165	<i>Brevibacterium</i> sp.	FB	TSA	+
MW089143	170	<i>Klebsiella</i> sp.	R	TSA	+
MW089144	171	<i>Microbacterium</i> sp.	R	TSA	+
MW089145	172	<i>Microbacterium</i> sp.	R	TSA	+
MW089146	173	<i>Microbacterium</i> sp.	R	TSA	+
MW089147	174	<i>Streptomyces</i> sp.	R	TSA	+
MW089148	180	<i>Microbacterium</i> sp.	R	R2A	+
MW089149	181	<i>Williamsia</i> sp.	R	R2A	+
MW089150	182	<i>Microbacterium</i> sp.	R	R2A	+
MW089151	183	<i>Williamsia</i> sp.	R	R2A	+
MW089152	184	<i>Microbacterium</i> sp.	M	R2A	+
MW089153	187	<i>Streptomyces</i> sp.	M	R2A	+
MW089154	188	<i>Microbacterium</i> sp.	M	TSA	+
MW089155	189	<i>Ochrobactrum</i> sp.	M	TSA	+
MW089156	190	<i>Ochrobactrum</i> sp.	M	TSA	+
MW089157	191	<i>Ochrobactrum</i> sp.	M	TSA	+
MW089158	192	<i>Ochrobactrum</i> sp.	M	TSA	+
MW089159	195	<i>Ochrobactrum</i> sp.	M	R2A	+
MW089160	196	<i>Ochrobactrum</i> sp.	M	R2A	+
MW089161	197	<i>Ochrobactrum</i> sp.	M	R2A	+
MW089162	199	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089163	200	<i>Enterobacter</i> sp.	FB	TSA	+
MW089164	202	<i>Enterobacter</i> sp.	FB	TSA	+
MW089165	203	<i>Microbacterium</i> sp.	R	TSA	+
MW089166	205	<i>Microbacterium</i> sp.	R	TSA	+
MW089167	206	<i>Bacillus</i> sp.	R	TSA	+
MW089168	207	<i>Bacillus</i> sp.	R	TSA	+
MW089169	208	<i>Bacillus</i> sp.	R	TSA	+
MW089170	209	<i>Enterobacter</i> sp.	FB	MEA	+
MW089171	210	<i>Erwinia</i> sp.	FB	MEA	+
MW089172	212	<i>Enterobacter</i> sp.	FB	MEA	+
MW089173	213	<i>Bacillus</i> sp.	R	MEA	+
MW089174	215	<i>Pseudomonas</i> sp.	R	MEA	+
MW089175	216	<i>Microbacterium</i> sp.	R	MEA	+
MW089176	217	<i>Sphingobacterium</i> sp.	R	MEA	+
MW089177	219	<i>Pseudomonas</i> sp.	R	MEA	+
MW089178	221	<i>Pseudomonas</i> sp.	R	R2A	+

MW089179	222	<i>Pseudomonas</i> sp.	R	R2A	+
MW089180	223	<i>Microbacterium</i> sp.	R	R2A	+
MW089181	227	<i>Pseudomonas</i> sp.	R	TSA	+
MW089182	229	<i>Pseudomonas</i> sp.	R	TSA	+
MW089183	231	<i>Pseudomonas</i> sp.	M	TSA	+
MW089184	233	<i>Microbacterium</i> sp.	M	TSA	+
MW089185	241	<i>Microbacterium</i> sp.	R	R2A	+
MW089186	242	<i>Pseudomonas</i> sp.	M	R2A	+
MW089187	243	<i>Micrococcus</i> sp.	M	R2A	+
MW089188	244	<i>Pseudomonas</i> sp.	M	R2A	+
MW089189	246	<i>Bacillus</i> sp.	FB	R2A	+
MW089190	248	<i>Klebsiella</i> sp.	FB	R2A	+
MW089191	250	<i>Kluyvera</i> sp.	FB	R2A	+
MW089192	251	<i>Kluyvera</i> sp.	FB	R2A	+
MW089193	252	<i>Klebsiella</i> sp.	FB	R2A	+
MW089194	253	<i>Bacillus</i> sp.	FB	TSA	+
MW089195	254	<i>Bacillus</i> sp.	FB	TSA	+
MW089196	255	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089197	256	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089198	257	<i>Pseudomonas</i> sp.	FB	TSA	+
MW089199	258	<i>Phyllobacterium</i> sp.	FB	TSA	+
MW089200	259	<i>Microbacterium</i> sp.	FB	TSA	+
MW089201	260	<i>Bacillus</i> sp.	FB	TSA	+
MW089202	261	<i>Bacillus</i> sp.	M	TSA	+
MW089203	263	<i>Bacillus</i> sp.	M	TSA	+
MW089204	264	<i>Bacillus</i> sp.	M	TSA	+
MW089205	266	<i>Bacillus</i> sp.	M	MEA	+
MW089206	274	<i>Bacillus</i> sp.	FB	R2A	+
MW089207	275	<i>Bacillus</i> sp.	FB	R2A	+
MW089208	276	<i>Paenibacillus</i> sp.	FB	R2A	+
MW089209	277	<i>Pseudomonas</i> sp.	FB	R2A	+
MW089210	278	<i>Pseudomonas</i> sp.	FB	R2A	+
MW089211	279	<i>Bacillus</i> sp.	M	R2A	+
MW089212	280	<i>Bacillus</i> sp.	M	R2A	+
MW089213	281	<i>Serratia</i> sp.	M	R2A	+
MW089214	282	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089215	283	<i>Microbacterium</i> sp.	FB	TSA	+
MW089216	284	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089217	285	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089218	286	<i>Bacillus</i> sp.	FB	TSA	+
MW089219	288	<i>Bacillus</i> sp.	FB	TSA	+
MW089220	289	<i>Bacillus</i> sp.	FB	TSA	+
MW089221	290	<i>Bacillus</i> sp.	FB	TSA	+
MW089222	291	<i>Staphylococcus</i> sp.	FB	TSA	+
MW089223	292	<i>Staphylococcus</i> sp.	FB	TSA	+

MW089224	293	<i>Bacillus</i> sp.	FB	R2A	+
MW089225	294	<i>Staphylococcus</i> sp.	FB	R2A	+
MW089226	295	<i>Staphylococcus</i> sp.	FB	R2A	+
MW089227	296	<i>Microbacterium</i> sp.	FB	R2A	+
MW089228	297	<i>Staphylococcus</i> sp.	FB	R2A	+
MW089229	298	<i>Microbacterium</i> sp.	FB	R2A	+
MW089230	299	<i>Staphylococcus</i> sp.	FB	MEA	+
MW089231	301	<i>Staphylococcus</i> sp.	FB	MEA	+
MW089232	302	<i>Staphylococcus</i> sp.	FB	MEA	+
MW089233	305	<i>Ewingella</i> sp.	FB	TSA	+
MW089234	306	<i>Ewingella</i> sp.	FB	TSA	+
MW089235	307	<i>Ewingella</i> sp.	FB	TSA	+
MW089236	308	<i>Ewingella</i> sp.	FB	TSA	+
MW089237	309	<i>Streptomyces</i> sp.	FB	TSA	+
MW089238	310	<i>Streptomyces</i> sp.	FB	TSA	+
MW089239	311	<i>Streptomyces</i> sp.	FB	TSA	+
MW089240	312	<i>Ewingella</i> sp.	FB	TSA	+
MW089241	313	<i>Streptomyces</i> sp.	FB	TSA	+
MW089242	314	<i>Streptomyces</i> sp.	FB	TSA	+
MW089243	315	<i>Streptomyces</i> sp.	FB	TSA	+
MW089244	316	<i>Streptomyces</i> sp.	FB	TSA	+
MW089245	317	<i>Streptomyces</i> sp.	FB	TSA	+
MW089246	318	<i>Streptomyces</i> sp.	FB	TSA	-
MW089247	319	<i>Streptomyces</i> sp.	FB	TSA	+
MW089248	320	<i>Ewingella</i> sp.	FB	TSA	+
MW089249	323	<i>Leifsonia</i> sp.	FB	TSA	+
MW089250	324	<i>Streptomyces</i> sp.	FB	TSA	+
MW089251	325	<i>Ewingella</i> sp.	FB	R2A	+
MW089252	326	<i>Ewingella</i> sp.	FB	R2A	+
MW089253	327	<i>Ewingella</i> sp.	FB	R2A	+
MW089254	328	<i>Ewingella</i> sp.	FB	R2A	+
MW089255	329	<i>Ewingella</i> sp.	FB	R2A	+
MW089256	330	<i>Ewingella</i> sp.	FB	R2A	+
MW089257	331	<i>Ewingella</i> sp.	FB	R2A	+
MW089258	332	<i>Ewingella</i> sp.	FB	R2A	+
MW089259	333	<i>Ewingella</i> sp.	FB	R2A	+
MW089260	334	<i>Ewingella</i> sp.	FB	R2A	+
MW089261	335	<i>Streptomyces</i> sp.	FB	R2A	+
MW089262	337	<i>Moraxella</i> sp.	FB	R2A	+
MW089263	338	<i>Streptomyces</i> sp.	FB	R2A	+
MW089264	339	<i>Streptomyces</i> sp.	FB	R2A	+
MW089265	340	<i>Streptomyces</i> sp.	FB	R2A	+
MW089266	341	<i>Ewingella</i> sp.	FB	R2A	+
MW089267	343	<i>Burkholderia</i> sp.	FB	R2A	+
MW089268	344	<i>Ewingella</i> sp.	FB	R2A	+

MW089269	345	<i>Streptomyces</i> sp.	FB	R2A	+
MW089270	346	<i>Streptomyces</i> sp.	FB	R2A	+
MW089271	347	<i>Dermacoccus</i> sp.	R	MEA	+
MW089272	348	<i>Enterobacter</i> sp.	FB	MEA	+
MW089273	349	<i>Enterobacter</i> sp.	FB	MEA	+
MW089274	350	<i>Enterobacter</i> sp.	FB	MEA	+
MW089275	351	<i>Klebsiella</i> sp.	FB	MEA	+
MW089276	352	<i>Klebsiella</i> sp.	FB	MEA	-
MW089277	353	<i>Staphylococcus</i> sp.	R	TSA	-
MW089278	355	<i>Staphylococcus</i> sp.	R	TSA	+
MW089279	356	<i>Staphylococcus</i> sp.	R	TSA	+
MW089280	358	<i>Staphylococcus</i> sp.	R	TSA	+
MW089281	359	<i>Staphylococcus</i> sp.	R	TSA	+
MW089282	360	<i>Staphylococcus</i> sp.	R	TSA	+
MW089283	361	<i>Streptomyces</i> sp.	R	TSA	+
MW089284	362	<i>Staphylococcus</i> sp.	R	TSA	+
MW089285	363	<i>Dermacoccus</i> sp.	R	TSA	+
MW089286	364	<i>Streptomyces</i> sp.	R	TSA	+
MW089287	365	<i>Staphylococcus</i> sp.	R	TSA	+
MW089288	367	<i>Bacillus</i> sp.	R	TSA	+
MW089289	368	<i>Staphylococcus</i> sp.	R	TSA	+
MW089290	369	<i>Bacillus</i> sp.	R	TSA	+
MW089291	370	<i>Staphylococcus</i> sp.	R	TSA	+
MW089292	371	<i>Streptomyces</i> sp.	R	TSA	+
MW089293	372	<i>Staphylococcus</i> sp.	R	TSA	+
MW089294	373	<i>Staphylococcus</i> sp.	R	TSA	+
MW089295	374	<i>Paenispodosarcina</i> sp.	R	TSA	+
MW089296	377	<i>Streptomyces</i> sp.	R	R2A	+
MW089297	378	<i>Staphylococcus</i> sp.	R	R2A	+
MW089298	379	<i>Streptomyces</i> sp.	R	R2A	+
MW089299	380	<i>Streptomyces</i> sp.	R	R2A	+
MW089300	381	<i>Staphylococcus</i> sp.	R	R2A	+
MW089301	382	<i>Staphylococcus</i> sp.	R	R2A	+
MW089302	383	<i>Streptomyces</i> sp.	R	R2A	+
MW089303	384	<i>Staphylococcus</i> sp.	R	R2A	+
MW089304	385	<i>Staphylococcus</i> sp.	R	R2A	+
MW089305	386	<i>Streptomyces</i> sp.	R	R2A	+

Table S2: Estimated abundances of bacterial species derived from different tissues of *S. lacrymans* (see Fig. 2). Abundances of bacterial species (in CFU g⁻¹) were estimated by an inverse morphotype approach. Because of the reciprocal approach, only relative abundances are indicated. Bacterial abundances of all used isolation media were summarized.

Genera	Tissue type			Sum [CFU g ⁻¹ ; %]
	Fruiting body	Mycelium	Rhizomorph	
<i>Paenibacillus</i> sp.	80720	1008.2	4448.4	11064384295; 52%
<i>Sporosarcina</i> sp.	4023216	-	-	
<i>Paenisporosarcina</i> sp.	1757400000	-	6081.9	
<i>Solibacillus</i> sp.	361800	-	-	
<i>Bacillus</i> sp.	1914474399	5871251379	71259161.5	
<i>Pausicalibacillus</i> sp.	-	385920000	-	
<i>Staphylococcus</i> sp.	1034950852	2414403.6	506825	
Firmicutes spp.	4711290988	6281316791	71776516.8	
<i>Microbacterium</i> spp.	130853242.9	123524399	6320480	1200427620; 6%
<i>Agromyces</i> spp.	217482	-	41653200	
<i>Oerskovia</i> spp.	-	195548222	-	
<i>Cellulomonas</i> spp.	-	161.36	-	
<i>Arhtrobacter</i> spp.	-	242.16	-	
<i>Brevibacterium</i> spp.	36340637.4	-	-	
<i>Streptomyces</i> spp.	331878384	16040000	111294715.4	
<i>Rhodococcus</i> spp.	4422	-	-	
<i>Nocardia</i> spp.	-	4020000	-	
<i>Micrococcus</i> spp.	n/a	n/a	n/a	
<i>Leifsonia</i> spp.	2032	-	-	
<i>Dermacoccus</i> spp.	202730000	-	-	
Actinobacteria spp.	702026200.3	339133024.56	159268395.4	
<i>Flavobacterium</i> spp.	769216000	40228140	-	809444547.6; 4%
<i>Sphingobacterium</i> spp.	-	407.6	-	
<i>Chryseobacterium</i> spp.	n/a	n/a	n/a	
<i>Pseudosphingobacterium</i> spp.	n/a	n/a	n/a	
Bacteroidetes spp.	769216000	40228547.6	0	
<i>Stenotrophomonas</i> spp.	166283.2	185483.64	2830800	
<i>Bordetella</i> spp.	-	80440	1124232000	
<i>Alcaligenes</i> spp.	-	161.36	6066	
<i>Advenella</i> spp.	-	804400	29925600	

<i>Pseudomonas</i> spp.	54622374	2183356548	1161025013	
<i>Erwinia</i> spp.	16800000	40360000	-	
<i>Rahnella</i> spp.	484,488	-	-	
<i>Ewingella</i> spp.	1538224	89672000	-	
<i>Pantoea</i> spp.	24120	-	-	
<i>Raoultella</i> spp.	-	1176,08	-	
<i>Serratia</i> spp.	-	247418581.52	24696	
<i>Achromobacter</i> spp.	-	103300000	-	
<i>Burkholderia</i> spp.	3341984	-	-	
<i>Enterobacter</i> spp.	18043920	-	-	
<i>Klebsiella</i> spp.	7190172	40450000	303400	
<i>Luteibacter</i> spp.	-	82.64	-	
<i>Ochrobactrum</i> spp.	-	99851500.8	-	
<i>Xanthomonas</i> spp.	n/a	n/a	n/a	
<i>Pectobacterium</i> spp.	137182.4	-	-	
<i>Kluyvera</i> spp.	2688000000	-	-	
<i>Phyllobacterium</i> spp.	4080000	-	-	
<i>Moraxella</i> spp.	125984	-	-	
<i>Proteobacteria</i> spp.	2794070728	2805480374	2318347575	7917898677; 38%
Total [CFU g⁻¹ tissue]	8976477932	9466158737	2549392487	20992029156
[%]	42.76	45.1	12.144	100

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Table S3: Results of Pectinase, Xylanase, Cellulase and Amylase Production Assays:

Bacteria isolated from *Serpula lacrymans* tissue (FB = Fruiting body, M = Mycelia, R = Rhizomorph); - means no production of according enzyme (i.e. no halo), ~ minimal production of enzyme (halo zone not more than 1 mm of the edges of the colonies), + enzymatic activity (halo zone smaller than 8 mm from the edges of the colonies), and ++ high enzymatic activity (halo zone larger than 8 mm). Plates were evaluated after 2 to 4 days (25 °C). * Bacterial isolate could not be identified based on the phylogenetic analysis.

Isolate No.	Species	tissue of Isolation	Enzyme produced			
			Pectinase	Xylanase	Cellulase	Amylase
01	<i>Microbacterium</i> sp.	FB	~	+	-	+
02	<i>Microbacterium</i> sp.	FB	~	-	-	-
03	<i>Staphylococcus</i> sp.	FB	~	-	-	-
04	<i>Microbacterium</i> sp.	FB	~	-	-	+
05	<i>Rahnella</i> sp.	FB	-	~	+	-
06	<i>Brevibacterium</i> sp.	FB	-	-	-	-
07	<i>Brevibacterium</i> sp.	FB	-	-	-	-
08	<i>Microbacterium</i> sp.	M	-	-	-	+
09	<i>Staphylococcus</i> sp.	M	-	-	-	-
10	<i>Staphylococcus</i> sp.	M	-	+	+	+
11	<i>Stenotrophomonas</i> sp.	M	-	-	-	-
12	<i>Raoultella</i> sp.	M	-	-	~	~
13	<i>Serratia</i> sp.	M	+	+	+	+
14	<i>Pseudomonas</i> sp.	M	+	-	++	+
15	<i>Sphingobacterium</i> sp.	M	-	-	-	+
16	<i>Raoultella</i> sp.	M	-	+	-	+
17	<i>Okibacterium</i> sp.	M	-	-	-	+
18	<i>Ewingella</i> sp.	M	+	-	-	+
19	<i>Paenibacillus</i> sp.	FB	-	-	-	+
20	<i>Microbacterium</i> sp.	FB	-	+	-	+
21	<i>Pseudomonas</i> sp.	FB	-	-	-	+
22	<i>Microbacterium</i> sp.	FB	+	-	-	+
23	<i>Microbacterium</i> sp.	FB	-	+	-	-
24	<i>Microbacterium</i> sp.	FB	-	-	~	-
25	<i>Psychrobacillus</i> sp.	M	-	+	-	+
26	<i>Paenibacillus</i> sp.	M	+	-	-	+
27	<i>Bacillus</i> sp.	M	+	-	-	+
28	<i>Advenella</i> sp.	M	-	-	-	-
29	<i>Pseudomonas</i> sp.	M	-	-	-	+
30	<i>Bacillus</i> sp.	M	+	-	-	+

31	<i>Staphylococcus</i> sp.	M	-	-	-	-
32	<i>Serratia</i> sp.	M	-	+	-	-
33	<i>Sporosarcina</i> sp.	M	-	-	-	-
34	<i>Bacillus</i> sp.	M	-	+	+	+
35	<i>Stenotrophomonas</i> sp.	FB	-	-	-	-
36	<i>Paenibacillus</i> sp.	FB	+	+	+	+
37	<i>Microbacterium</i> sp.	FB	-	-	-	-
38	<i>Stenotrophomonas</i> sp.	FB	-	-	-	-
39	<i>Pseudomonas</i> sp.	FB	~	-	+	-
40	<i>Staphylococcus</i> sp.	FB	-	-	-	-
41	<i>Flavobacterium</i> sp.	FB	+	+	+	+
42	<i>Pseudomonas</i> sp.	FB	-	-	-	+
43	<i>Microbacterium</i> sp.	FB	+	+	-	+
44	<i>Paenisporosarcina</i> sp.	FB	~	-	-	-
45	<i>Microbacterium</i> sp.	FB	-	-	+	-
46	<i>Flavobacterium</i> sp.	FB	+	+	+	+
47	<i>Bacillus</i> sp.	R	~	-	+	-
48	<i>Paenibacillus</i> sp.	R	+	-	-	+
49	<i>Advenella</i> sp.	R	-	~	+	+
50	<i>Bordetella</i> sp.	R	-	-	-	+
51	<i>Pseudomonas</i> sp.	R	-	+	~	+
52	<i>Alcaligenaceae</i> bacterium	R	-	-	-	-
53	<i>Stenotrophomonas</i> sp.	M	-	+	+	+
54	<i>Bacillus</i> sp.	M	-	-	~	-
55	<i>Pseudomonas</i> sp.	M	-	+	+	+
56	<i>Oerskovia</i> sp.	M	-	-	-	-
57	<i>Advenella</i> sp.	M	+	-	-	+
58	<i>Bordetella</i> sp.	M	-	-	+	-
59	<i>Brevibacterium</i> sp.	M	-	+	-	+
60	<i>Microbacterium</i> sp.	M	-	-	+	+
61	<i>Stenotrophomonas</i> sp.	M	-	-	-	~
62	<i>Raoultella</i> sp.	M	-	+	-	+
63	<i>Paenibacillus</i> sp.	M	+	-	-	+
64	<i>Cellulomonas</i> sp.	M	-	+	-	+
65	<i>Alcaligenaceae</i> sp.	M	-	+	-	+
66	<i>Stenotrophomonas</i> sp.	M	-	+	-	+
67	<i>Staphylococcus</i> sp.	M	-	+	+	-
68	<i>Staphylococcus</i> sp.	M	~	-	~	+
69	<i>Arthrobacter</i> sp.	M	+	+	+	+
70	<i>Brevibacterium</i> sp.	M	-	+	-	
71	<i>Bacillus</i> sp.	FB	+	~	+	+
72	<i>Sporosarcina</i> sp.	FB	-	-	-	-
73	<i>Pseudomonas</i> sp.	FB	-	-	~	+
74	<i>Pantoea</i> sp.	FB	+	-	+	-
75	<i>Rhodococcus</i> sp.	FB	-	~	~	~

76a	<i>Sporosarcina</i> sp.	FB	-	-	-	~
77	<i>Serratia</i> sp.	M	+	+	-	+
78a	<i>Microbacterium</i> sp.	M	-	-	-	+
78b	<i>Pseudomonas</i> sp.	M	+	+	-	+
79	<i>Paenibacillus</i> sp.	M	+	+	+	+
80	<i>Oerskovia</i> sp.	M	+	+	-	+
81	<i>Erwinia</i> sp.	M	-	+	+	+
82	<i>Agromyces</i> sp.	R	-	+	-	+
83	<i>Bacillus</i> sp.	R	-	+	-	+
84	<i>Bacillus</i> sp.	R	-	-	-	++
85	<i>Bacillus</i> sp.	R	-	+	-	+
86	<i>Bacillus</i> sp.	R	-	-	+	+
87	<i>Bacillus</i> sp.	R	~	+	-	+
88	<i>Agromyces</i> sp.	FB	-	-	-	+
89	<i>Agromyces</i> sp.	FB	-	-	-	+
90	<i>Bacillus</i> sp.	FB	+	+	-	+
91	<i>Pseudomonas</i> sp.	FB	+	+	+	+
92	<i>Bacillus</i> sp.	FB	+	+	-	+
93	<i>Streptomyces</i> sp.	FB	-	+	-	+
94	*	FB	-	+	-	+
95	<i>Microbacterium</i> sp.	M	-	-	-	+
96	<i>Oerskovia</i> sp.	M	-	+	-	+
98	<i>Bacillus</i> sp.	M	+	+	-	+
99	<i>Microbacterium</i> sp.	M	-	-	-	+
101	<i>Agromyces</i> sp.	R	-	-	-	+
102	<i>Bacillus</i> sp.	R	+	+	-	++
104	<i>Bacillus</i> sp.	R	-	+	+	++
105	<i>Chryseobacterium</i> sp.	R	+	+	-	+
106	<i>Oerskovia</i> sp.	R	+	-	-	+
107	<i>Bacillus</i> sp.	FB	+	+	-	+
108	<i>Bacillus</i> sp.	FB	-	+	+	++
109	<i>Caballeronia</i> sp.	FB	-	+	-	+
111	<i>Streptomyces</i> sp.	FB	~	+	-	+
113	<i>Pichia/Saccharomyces</i>	FB	-	+	-	+
114	<i>Solibacillus</i> sp.	FB	-	+	-	-
115	<i>Lysobacter</i> sp.	FB	-	-	-	+
116	<i>Paraburkholderia</i> sp.	FB	-	+	-	+
117	<i>Bacillus</i> sp.	M	-	-	-	+
118	<i>Flavobacterium</i> sp.	M	-	-	-	++
119	<i>Flavobacterium</i> sp.	M	-	-	-	+
120	<i>Bacillus</i> sp.	M	-	+	-	-
121	*	M	-	-	-	-
124	<i>Paucisalibacillus</i> sp.	M	-	+	-	~
125	<i>Microbacterium</i> sp.	M	-	+	+	+
126	<i>Microbacterium</i> sp.	M	-	-	-	~

127	<i>Nocardia</i> sp.	M	-	-	~	++
129	<i>Pseudomonas</i> sp.	M	-	-	+	+
134	<i>Enterobacter</i> sp.	M	+	-	-	+
135	<i>Pseudosphingobacterium</i> sp.	M	-	-	++	++
136	*	M	-	-	-	+
138	<i>Streptomyces</i> sp.	M	-	+	-	++
142	<i>Enterobacter</i> sp.	M	-	-	-	~
143	<i>Pseudomonas</i> sp.	M	+	-	-	+
144	<i>Pseudomonas</i> sp.	M	-	-	-	+
145	<i>Bacillus</i> sp.	M	++	-	-	+
146	<i>Achromobacter</i> sp.	M	-	-	-	-
147	*	M	-	-	-	+
148	<i>Bacillus</i> sp.	M	-	+	-	+
149	<i>Stenotrophomonas</i> sp.	M	-	-	-	+
150	<i>Pseudomonas</i> sp.	M	-	-	-	-
151	<i>Bacillus</i> sp.	M	-	-	-	+
152	<i>Pseudomonas</i> sp.	M	+	-	-	+
153	<i>Luteibacter</i> sp.	M	-	-	-	+
154	<i>Candida</i> sp.	M	+	+	+	+
155	<i>Pseudomonas</i> sp.	M	++	-	-	+
157	<i>Bacillus</i> sp.	M	++	-	-	+
158	<i>Bacillus</i> sp.	M	-	+	-	+
160	<i>Arthrobacter</i> sp.	FB	-	-	-	+
161	<i>Streptomyces</i> sp.	FB	-	+	-	++
162	<i>Stenotrophomonas</i> sp.	FB	-	-	-	~
163	<i>Advenella</i> sp.	FB	-	-	+	-
164	<i>Microbacterium</i> sp.	FB	-	+	-	+
165	<i>Brevibacterium</i> sp.	FB	-	-	-	+
170	<i>Klebsiella</i> sp.	R	-	-	-	~
171	<i>Microbacterium</i> sp.	R	-	-	-	+
172	<i>Microbacterium</i> sp.	R	-	-	-	-
173	<i>Microbacterium</i> sp.	R	-	+	-	-
174	<i>Streptomyces</i> sp.	R	+	+	-	+
180	<i>Microbacterium</i> sp.	R	-	+	-	-
181	<i>Williamsia</i> sp.	R	-	-	-	+
182	<i>Microbacterium</i> sp.	R	-	-	-	+
183	<i>Williamsia</i> sp.	R	-	-	-	~
184	<i>Microbacterium</i> sp.	R	-	-	-	+
186	*	M	-	-	-	-
187	<i>Streptomyces</i> sp.	M	-	-	-	-
188	<i>Microbacterium</i> sp.	M	-	+	-	-
189	<i>Ochrobactrum</i> sp.	M	-	-	-	+
190	<i>Ochrobactrum</i> sp.	M	-	-	-	+
191	<i>Ochrobactrum</i> sp.	M	-	-	-	+

192	<i>Ochrobactrum</i> sp.	M	-	-	-	+
195	<i>Ochrobactrum</i> sp.	M	-	-	-	+
196	<i>Ochrobactrum</i> sp.	M	-	-	-	+
197	<i>Ochrobactrum</i> sp.	M	-	-	-	++
198	*	FB	-	+	+	-
199	<i>Pseudomonas</i> sp.	FB	-	-	+	+
200	<i>Enterobacter</i> sp.	FB	-	-	-	+
201	<i>Bacillus</i> sp.	FB	-	+	+	+
202	<i>Enterobacter</i> sp.	FB	-	+	-	+
203	<i>Microbacterium</i> sp.	R	-	-	-	+
204	*	R	+	*	-	+
205	<i>Microbacterium</i> sp.	R	-	-	-	++
206	<i>Bacillus</i> sp.	R	-	+	-	+
207	<i>Bacillus</i> sp.	R	-	+	-	+
208	<i>Bacillus</i> sp.	R	-	-	-	+
209	<i>Enterobacter</i> sp.	FB	-	-	-	+
210	<i>Erwinia</i> sp.	FB	-	+	~	+
211	*	FB	+	-	-	+
212	<i>Enterobacter</i> sp.	FB	-	+	-	+
213	<i>Bacillus</i> sp.	R	-	+	~	+
215	<i>Pseudomonas</i> sp.	R	-	-	+	+
216	<i>Microbacterium</i> sp.	R	-	-	-	+
217	<i>Sphingobacterium</i> sp.	R	-	-	-	+
218	<i>Stenotrophomonas</i> sp.	R	~	-	-	~
219	<i>Pseudomonas</i> sp.	R	+	-	-	+
220	*	R	-	+	-	~
221	<i>Pseudomonas</i> sp.	R	+	+	+	+
222	<i>Pseudomonas</i> sp.	R	+	-	-	+
223	<i>Microbacterium</i> sp.	R	-	+	-	+
224	*	FB	-	+	-	+
225	*	FB	-	-	+	+
226	*	FB	-	+	-	+
227	<i>Pseudomonas</i> sp.	R	+	-	-	+
228	*	R	+	+	-	+
229	<i>Pseudomonas</i> sp.	R	+	-	+	+
230	*	M	-	+	-	+
231	<i>Pseudomonas</i> sp.	M	+	-	-	+
232	*	M	-	+	-	+
233	<i>Microbacterium</i> sp.	M	-	-	-	+
234	*	FB	-	+	-	+
235	<i>Pectobacterium</i> sp.	FB	-	+	-	+
236	*	R	-	+	-	+
238	*	R	+	+	-	+
239	*	M	+	-	-	+
240	<i>Serratia</i> sp.	R	+	-	-	+

241	<i>Microbacterium</i> sp.	R	-	~	-	+
242	<i>Pseudomonas</i> sp.	M	+	-	+	+
243	<i>Micrococcus</i> sp.	M	-	+	-	-
244	<i>Pseudomonas</i> sp.	M	+	-	+	+
245	*	FB	+	-	-	+
246	<i>Bacillus</i> sp.	FB	+	+	-	+
247	*	FB	-	+	+	-
248	<i>Klebsiella</i> sp.	FB	-	-	-	+
249	*	FB	+	-	-	+
250	<i>Kluyvera</i> sp.	FB	+	-	-	+
251	<i>Kluyvera</i> sp.	FB	+	*	-	+
252	<i>Klebsiella</i> sp.	FB	-	-	-	+
253	<i>Bacillus</i> sp.	FB	+	-	-	++
254	<i>Bacillus</i> sp.	FB	++	+	-	+
255	<i>Pseudomonas</i> sp.	FB	-	-	+	+
256	<i>Pseudomonas</i> sp.	FB	-	-	-	-
257	<i>Pseudomonas</i> sp.	FB	-	+	-	+
258	<i>Phyllobacterium</i> sp.	FB	-	-	-	+
259	<i>Microbacterium</i> sp.	FB	-	-	-	-
260	<i>Bacillus</i> sp.	FB	+	-	+	-
261	<i>Bacillus</i> sp.	M	-	++	-	-
262	<i>Klebsiella</i> sp.	M	-	-	-	+
263	<i>Bacillus</i> sp.	M	-	+	+	+
264	<i>Bacillus</i> sp.	M	-	+	+	+
265	<i>Serratia</i> sp.	M	+	+	-	-
266	<i>Bacillus</i> sp.	FB	+	-	-	+
268	*	M	~	-	-	-
269	*	M	-	-	-	-
274	<i>Bacillus</i> sp.	FB	++	-	+	+
275	<i>Bacillus</i> sp.	FB	~	+	+	++
276	<i>Paenibacillus</i> sp.	FB	-	-	-	+
277	<i>Pseudomonas</i> sp.	FB	-	+	-	+
278	<i>Pseudomonas</i> sp.	FB	-	-	-	+
279	<i>Bacillus</i> sp.	M	++	+	+	+
280	<i>Bacillus</i> sp.	M	-	-	++	++
281	<i>Serratia</i> sp.	M	-	-	-	+
282	<i>Staphylococcus</i> sp.	FB	-	-	-	+
283	<i>Microbacterium</i> sp.	FB	-	+	-	-
284	<i>Staphylococcus</i> sp.	FB	-	+	-	-
285	<i>Staphylococcus</i> sp.	FB	-	+	-	-
286	<i>Bacillus</i> sp.	FB	+	+	-	++
287	<i>Bacillus</i> sp.	FB	-	+	~	+
288	<i>Bacillus</i> sp.	FB	-	-	-	-
289	<i>Bacillus</i> sp.	FB	-	+	-	+
290	<i>Bacillus</i> sp.	FB	-	-	-	+

291	<i>Staphylococcus</i> sp.	FB	-	-	-	-
292	<i>Staphylococcus</i> sp.	FB	-	-	+	+
293	<i>Bacillus</i> sp.	FB	-	++	+	+
294	<i>Staphylococcus</i> sp.	FB	-	-	+	+
295	<i>Staphylococcus</i> sp.	FB	-	-	-	+
296	<i>Microbacterium</i> sp.	FB	-	-	-	++
297	<i>Staphylococcus</i> sp.	FB	-	+	-	-
298	<i>Microbacterium</i> sp.	FB	-	++	-	-
299	<i>Staphylococcus</i> sp.	FB	-	++	+	-
301	<i>Staphylococcus</i> sp.	FB	-	+	-	+
302	<i>Staphylococcus</i> sp.	FB	-	++	+	-
305	<i>Ewingella</i> sp.	FB	~	-	+	+
306	<i>Ewingella</i> sp.	FB	+	~	-	+
307	<i>Ewingella</i> sp.	FB	+	-	-	+
308	<i>Ewingella</i> sp.	FB	+	-	-	+
309	<i>Streptomyces</i> sp.	FB	-	+	~	-
310	<i>Streptomyces</i> sp.	FB	-	+	-	-
311	<i>Streptomyces</i> sp.	FB	-	+	+	-
312	<i>Ewingella</i> sp.	FB	+	-	-	+
313	<i>Streptomyces</i> sp.	FB	-	+	-	-
314	<i>Streptomyces</i> sp.	FB	~	+	-	-
315	<i>Streptomyces</i> sp.	FB	-	-	-	-
316	<i>Streptomyces</i> sp.	FB	-	+	-	+
317	<i>Streptomyces</i> sp.	FB	+	+	-	+
318	<i>Streptomyces</i> sp.	FB	-	+	-	-
319	<i>Streptomyces</i> sp.	FB	-	+	-	-
320	<i>Ewingella</i> sp.	FB	+	-	-	++
321	*	FB	-	+	-	++
322	*	FB	-	-	-	-
323	<i>Leifsonia</i> sp.	FB	-	-	-	-
324	<i>Streptomyces</i> sp.	FB	-	+	-	++
325	<i>Ewingella</i> sp.	FB	+	-	-	~
326	<i>Ewingella</i> sp.	FB	+	-	-	~
327	<i>Ewingella</i> sp.	FB	+	-	-	+
328	<i>Ewingella</i> sp.	FB	+	-	-	+
329	<i>Ewingella</i> sp.	FB	+	-	-	+
330	<i>Ewingella</i> sp.	FB	+	-	-	+
331	<i>Ewingella</i> sp.	FB	+	+	-	+
332	<i>Ewingella</i> sp.	FB	~	+	-	+
333	<i>Ewingella</i> sp.	FB	+	-	-	+
334	<i>Ewingella</i> sp.	FB	+	-	-	+
335	<i>Streptomyces</i> sp.	FB	-	+	-	-
337	<i>Moraxella</i> sp.	FB	~	+	-	-
338	<i>Streptomyces</i> sp.	FB	-	+	-	-
339	<i>Streptomyces</i> sp.	FB	-	+	-	-

340	<i>Streptomyces</i> sp.	FB	-	+	-	-
341	<i>Ewingella</i> sp.	FB	+	-	-	~
343	<i>Burkholderia</i> sp.	FB	+	-	-	-
344	<i>Ewingella</i> sp.	FB	+	-	-	+
345	<i>Streptomyces</i> sp.	FB	-	+	-	-
346	<i>Streptomyces</i> sp.	FB	-	+	-	-
347	<i>Dermaococcus</i> sp.	R	-	-	-	+
348	<i>Enterobacter</i> sp.	FB	-	++	-	-
349	<i>Enterobacter</i> sp.	FB	-	-	-	+
350	<i>Enterobacter</i> sp.	FB	-	-	-	+
351	<i>Klebsiella</i> sp.	FB	-	-	-	+
352	<i>Klebsiella</i> sp.	FB	-	-	-	+
353	<i>Staphylococcus</i> sp.	R	-	+	-	-
355	<i>Staphylococcus</i> sp.	R	-	~	-	-
356	<i>Staphylococcus</i> sp.	R	-	+	-	-
357	*	R	-	+	-	+
358	<i>Staphylococcus</i> sp.	R	+	+	-	-
359	<i>Staphylococcus</i> sp.	R	+	+	-	~
360	<i>Staphylococcus</i> sp.	R	-	~	-	-
361	<i>Streptomyces</i> sp.	R	-	++	-	+
362	<i>Staphylococcus</i> sp.	R	-	~	-	-
363	<i>Dermaococcus</i> sp.	R	-	+	-	+
364	<i>Streptomyces</i> sp.	R	-	+	-	+
365	<i>Staphylococcus</i> sp.	R	-	~	-	-
366 a)	*	R	-	-	-	+
366 b)	*	R	+	+	+	+
367	<i>Bacillus</i> sp.	R	-	+	+	+
368	<i>Staphylococcus</i> sp.	R	-	~	-	-
369	<i>Bacillus</i> sp.	R	-	-	-	+
370	<i>Staphylococcus</i> sp.	R	-	~	-	-
371	<i>Streptomyces</i> sp.	R	-	+	-	+
372	<i>Staphylococcus</i> sp.	R	-	+	-	-
373	<i>Staphylococcus</i> sp.	R	-	+	-	-
374	<i>Paenisporosarcina</i> sp.	R	-	+	-	-
375	<i>Dermaococcus</i> sp.	R	-	+	-	++
376	*	R	-	+	-	-
377	<i>Streptomyces</i> sp.	R	-	+	-	+
378	<i>Staphylococcus</i> sp.	R	-	-	-	-
379	<i>Streptomyces</i> sp.	R	-	-	-	+
380	<i>Streptomyces</i> sp.	R	-	+	-	-
381	<i>Staphylococcus</i> sp.	R	-	~	-	+
382	<i>Staphylococcus</i> sp.	R	-	+	-	-
383	<i>Streptomyces</i> sp.	R	-	+	-	-
384	<i>Staphylococcus</i> sp.	R	-	~	-	~
385	<i>Staphylococcus</i> sp.	R	-	~	-	~

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386	<i>Streptomyces</i> sp.	R	-	+	-	-
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