

Biodiversity of *Vitis vinifera* endophytes in conventional and biodynamic vineyard

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Electronic supplementary material

Supplementary Figures S1–S2
Supplementary Tables S1–S2

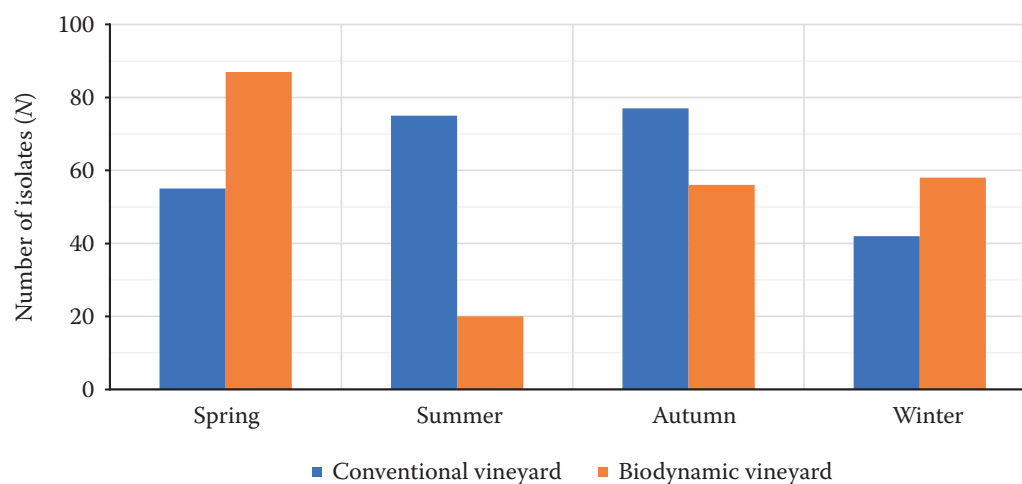


Figure S1. The number of isolated endophytes in the vineyards depending on the season

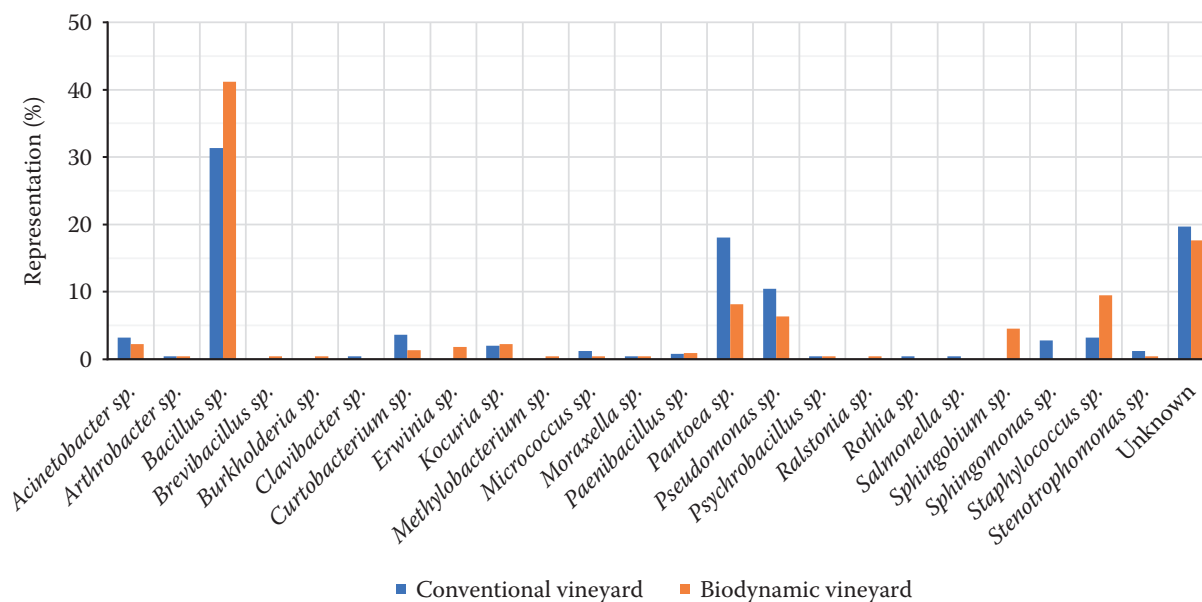


Figure S2. Percentage of endophytes in vineyards by species

Table S1. Identification of endophytes by matrix-assisted laser desorption-time-of-flight mass spectrometry (MALDI-TOF MS) method in spring, summer, autumn and winter from leaves and shoots from a conventional vineyard in Prague from Riesling varieties, Pinot Gris, Pinot Noir, Müller Thurgau

Isolate	Identification	Score	Isolate	Identification	Score
SP RR 1 S	<i>Bacillus subtilis</i>	2.179	SU MT 18 L	<i>Staphylococcus aureus</i>	2.105
SP RR 2 S	<i>Bacillus</i> sp.	1.743	SU MT 19 L	<i>Bacillus</i> sp.	1.989
SP RR 3 S	<i>Bacillus</i> sp.	1.977	SU MT 20 L	<i>Staphylococcus aureus</i>	2.238
SP RR 4 L	<i>Bacillus subtilis</i>	2.028	SU MT 21 L	<i>Bacillus cereus</i>	2.167
SP RR 5 L	<i>Bacillus</i> sp.	1.873	SU MT 22 L	<i>Staphylococcus aureus</i>	2.171
SP RR 6 L	<i>Bacillus subtilis</i>	2.166	SU MT 23 L	–	
SP RR 7 L	–		SU MT 24 L	–	
SP RR 8 L	<i>Bacillus subtilis</i>	2.176	SU MT 25 L	<i>Bacillus</i> sp.	1.897
SP RR 9 L	<i>Bacillus</i> sp.	1.894	SU MT 26 L	<i>Staphylococcus</i> sp.	1.765
SP RR 10 L	<i>Bacillus</i> sp.	1.752	A RR 1 S	<i>Bacillus pumilus</i>	2.03
SP RR 11 L	<i>Bacillus cereus</i>	2.337	A RR 2 S	<i>Pseudomonas koreensis</i>	2.294
SP RR 12 L	<i>Bacillus</i> sp.	1.839	A RR 3 S	<i>Bacillus pumilus</i>	2.049
SP RR 13 L	<i>Bacillus</i> sp.	1.878	A RR 4 S	–	
SP RR 14 L	<i>Bacillus subtilis</i>	2.109	A RR 5 S	<i>Pantoea agglomerans</i>	2.473
SP RR 15 L	<i>Bacillus</i> sp.	1.762	A RR 6 S	<i>Pantoea agglomerans</i>	2.311
SP PN 1 S	<i>Bacillus cereus</i>	2.324	A RR 7 S	<i>Curtobacterium flaccumfaciens</i>	2.29
SP PN 2 S	<i>Bacillus subtilis</i>	2.042	A RR 8 S	<i>Stenotrophomonas</i> sp.	1.705
SP PN 3 S	<i>Bacillus subtilis</i>	2.229	A RR 9 S	<i>Pseudomonas koreensis</i>	2.236
SP PN 4 S	<i>Bacillus subtilis</i>	2.276	A RR 10 S	<i>Pantoea agglomerans</i>	2.302
SP PN 5 S	<i>Bacillus</i> sp.	1.953	A RR 11 S	<i>Pantoea agglomerans</i>	2.356
SP PN 6 S	<i>Bacillus subtilis</i>	2.185	A RR 12 S	<i>Bacillus</i> sp.	1.901
SP PN 7 S	<i>Bacillus subtilis</i>	2	A RR 13 S	<i>Bacillus cereus</i>	2.367
SP PN 8 S	<i>Bacillus pumilus</i>	2.192	A RR 14 S	–	
SP PN 9 S	<i>Bacillus subtilis</i>	2.193	A RR 15 S	<i>Curtobacterium flaccumfaciens</i>	2.224
SP PN 10 L	<i>Kocuria rhizophila</i>	2.046	A RR 16 S	<i>Pantoea agglomerans</i>	2.408
SP PN 11 L	<i>Bacillus subtilis</i>	2.211	A RR 17 L	<i>Pantoea agglomerans</i>	2.335
SP PN 12 L	<i>Bacillus</i> sp.	1.89	A RR 18 L	<i>Pantoea agglomerans</i>	2.316
SP PN 13 L	<i>Bacillus subtilis</i>	2.022	A PN 1 S	<i>Pantoea agglomerans</i>	2.259
SP PN 14 L	<i>Bacillus cereus</i>	2.364	A PN 2 S	–	
SP PG 1 S	<i>Bacillus subtilis</i>	2.141	A PN 3 S	–	
SP PG 2 S	–		A PN 4 S	<i>Pantoea agglomerans</i>	2.234
SP PG 3 S	<i>Bacillus subtilis</i>	2.291	A PN 5 S	–	
SP PG 4 S	<i>Bacillus subtilis</i>	2.037	A PN 6 S	<i>Pantoea agglomerans</i>	2.134
SP PG 5 S	–		A PN 7 S	<i>Pantoea agglomerans</i>	2.326
SP PG 6 S	–		A PN 8 S	–	
SP PG 7 L	<i>Bacillus subtilis</i>	2.115	A PN 9 S	<i>Pantoea agglomerans</i>	2.346
SP PG 8 L	<i>Bacillus cereus</i>	2.138	A PN 10 S	–	
SP PG 9 L	–		A PN 11 S	–	
SP PG 10 L	<i>Bacillus</i> sp.	1.974	A PN 12 L	<i>Bacillus subtilis</i>	2.134
SP PG 11 L	<i>Bacillus subtilis</i>	2.026	A PN 13 L	<i>Bacillus</i> sp.	1.772
SP MT 1 S	<i>Kocuria</i> sp.	1.853	A PN 14 L	<i>Pantoea agglomerans</i>	2.51
SP MT 2 S	<i>Kocuria</i> sp.	1.896	A PN 15 L	<i>Bacillus subtilis</i>	2.226
SP MT 3 S	–		A PN 16 L	<i>Bacillus subtilis</i>	2.167
SP MT 4 S	<i>Bacillus</i> sp.	1.882	A PG 1 S	–	

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Table S1. To be continued

Isolate			Identification	Score	Isolate			Identification	Score
SP	MT 5	S	<i>Bacillus subtilis</i>	2.199	A	PG 2	S	<i>Bacillus</i> sp.	1.858
SP	MT 6	S	<i>Bacillus</i> sp.	1.812	A	PG 3	S	–	
SP	MT 7	S	<i>Kocuria</i> sp.	1.968	A	PG 4A	S	<i>Bacillus cereus</i>	2.433
SP	MT 8	S	<i>Kocuria</i> sp.	1.75	A	PG 4B	S	<i>Pantoea agglomerans</i>	2.495
SP	MT 9	L	<i>Bacillus subtilis</i>	2.054	A	PG 5	S	<i>Curtobacterium flaccumfaciens</i>	2.135
SP	MT 10	L	<i>Bacillus</i> sp.	1.842	A	PG 6	S	<i>Pantoea agglomerans</i>	2.394
SP	MT 11	L	<i>Bacillus subtilis</i>	2.116	A	PG 7	S	<i>Pantoea agglomerans</i>	2.456
SP	MT 12	L	<i>Bacillus</i> sp.	1.864	A	PG 8	S	<i>Pantoea agglomerans</i>	2.434
SP	MT 13	L	<i>Bacillus subtilis</i>	2.241	A	PG 9	L	<i>Bacillus</i> sp.	1.972
SP	MT 14	L	<i>Bacillus</i> sp.	1.782	A	PG 10	L	<i>Acinetobacter</i> sp.	1.875
SP	MT 15	L	<i>Bacillus cereus</i>	2.134	A	PG 11	L	<i>Curtobacterium</i> sp.	1.946
SP	MT 16	L	<i>Bacillus cereus</i>	2.181	A	PG 12	L	<i>Bacillus</i> sp.	1.867
SP	MT 17	L	<i>Bacillus</i> sp.	1.963	A	PG 13	L	<i>Bacillus</i> sp.	1.959
SU	RR 1	S	<i>Pantoea agglomerans</i>	2.397	A	PG 14	L	–	
SU	RR 2	S	<i>Pantoea agglomerans</i>	2.248	A	PG 15	L	<i>Pseudomonas</i> sp.	1.788
SU	RR 3	S	–		A	PG 16	L	–	
SU	RR 4	S	<i>Paenibacillus amylolyticus</i>	2.309	A	PG 17	L	<i>Bacillus cereus</i>	2.055
SU	RR 5	S	<i>Pantoea agglomerans</i>	2.376	A	MT 1	S	<i>Pantoea agglomerans</i>	2.464
SU	RR 6	S	<i>Micrococcus luteus</i>	2.101	A	MT 2	S	<i>Bacillus simplex</i>	2.048
SU	RR 7	S	<i>Bacillus</i> sp.	1.813	A	MT 3	S	<i>Pantoea agglomerans</i>	2.366
SU	RR 8	S	<i>Micrococcus</i> sp.	1.87	A	MT 4	S	<i>Bacillus subtilis</i>	2.247
SU	RR 9	S	<i>Pseudomonas</i> sp.	1.975	A	MT 5	S	<i>Pantoea agglomerans</i>	2.41
SU	RR 10	S	<i>Pantoea agglomerans</i>	2.381	A	MT 6	S	<i>Curtobacterium flaccumfaciens</i>	2.116
SU	RR 11	S	<i>Paenibacillus amylolyticus</i>	2.249	A	MT 7	S	<i>Pantoea agglomerans</i>	2.503
SU	RR 12	L	–		A	MT 8	S	<i>Arthrobacter polychromogenes</i>	2.335
SU	PN 1	S	<i>Stenotrophomonas</i> sp.	1.999	A	MT 9	S	–	
SU	PN 2	S	<i>Pseudomonas koreensis</i>	2.382	A	MT 10	S	<i>Pantoea agglomerans</i>	2.368
SU	PN 3	S	<i>Pseudomonas koreensis</i>	2.255	A	MT 11	S	<i>Pantoea agglomerans</i>	2.463
SU	PN 4	S	<i>Pseudomonas koreensis</i>	2.359	A	MT 12	S	<i>Pantoea agglomerans</i>	2.366
SU	PN 5	S	<i>Stenotrophomonas rhizophila</i>	2.392	A	MT 13	S	–	
SU	PN 6	S	<i>Pseudomonas koreensis</i>	2.262	A	MT 14	S	<i>Pantoea agglomerans</i>	2.299
SU	PN 7	S	<i>Stenotrophomonas rhizophila</i>	2.485	A	MT 15	S	<i>Curtobacterium flaccumfaciens</i>	2.198
SU	PN 8	S	–		A	MT 16	S	<i>Moraxella osloensis</i>	2.05
SU	PN 9	S	<i>Pseudomonas koreensis</i>	2.262	A	MT 17	S	<i>Pantoea agglomerans</i>	2.458
SU	PN 10	S	–		A	MT 18	S	<i>Bacillus subtilis</i>	2.177
SU	PN 11	S	–		A	MT 19	S	<i>Pantoea agglomerans</i>	2.494
SU	PN 12	S	–		A	MT 20	L	<i>Pseudomonas graminis</i>	2.351
SU	PN 13	S	<i>Pseudomonas rhodesiae</i>	2.012	A	MT 21	L	<i>Bacillus subtilis</i>	2.316
SU	PN 14	S	<i>Pseudomonas koreensis</i>	2.314	A	MT 22	L	<i>Bacillus cereus</i>	2.276
SU	PN 15	S	<i>Pseudomonas koreensis</i>	2.375	A	MT 23	L	<i>Bacillus cereus</i>	2.349
SU	PN 16	S	<i>Pseudomonas</i> sp.	1.937	A	MT 24	L	<i>Acinetobacter lwoffii</i>	2.172
SU	PN 17	S	<i>Pseudomonas koreensis</i>	2.289	A	MT 25	L	<i>Bacillus</i> sp.	1.863
SU	PN 18	S	–		W	RR 1	S	<i>Sphingomonas aerolata</i>	2.185
SU	PN 19	S	<i>Pseudomonas vancoverensis</i>	2.002	W	RR 2	S	<i>Pantoea agglomerans</i>	2.269
SU	PN 20	S	<i>Pseudomonas jessenii</i>	2.037	W	RR 4	S	–	

Table S1. To be continued

Isolate	Identification	Score	Isolate	Identification	Score
SU PN 21 S	–		W RR 5 S	<i>Curtobacterium flaccumfaciens</i>	2.169
SU PN 22 S	–		W RR 6 S	<i>Bacillus</i> sp.	1.897
SU PN 23 S	<i>Pseudomonas koreensis</i>	2.043	W RR 7 S	<i>Pantoea agglomerans</i>	2.161
SU PN 24 S	<i>Pseudomonas chloraphis</i>	2.017	W RR 8 S	–	
SU PN 25 S	–		W RR 9 S	<i>Sphingomonas</i> sp.	1.97
SU PN 26 L	–		W RR 10 S	<i>Bacillus</i> sp.	1.777
SU PN 27 L	<i>Bacillus</i> sp.	1.717	W RR 11 S	–	
SU PN 28 L	–		W RR 12 S	<i>Salmonella</i> sp.	1.733
SU PN 29 L	<i>Bacillus cereus</i>	2.072	W RR 13 S	<i>Sphingomonas aerolata</i>	2.153
SU PN 30 L	<i>Bacillus</i> sp.	1.828	W RR 15 S	<i>Sphingomonas</i> sp.	1.831
SU PG 1 S	–		W RR 16 S	<i>Curtobacterium flaccumfaciens</i>	2.089
SU PG 2 S	<i>Pantoea agglomerans</i>	2.43	W RR 17 S	<i>Bacillus cereus</i>	2.126
SU PG 3 S	<i>Pantoea agglomerans</i>	2.352	W RR 18 S	–	
SU PG 4 S	–		W PN 1 S	<i>Pantoea agglomerans</i>	2.321
SU PG 5 S	–		W PN 2 S	<i>Curtobacterium flaccumfaciens</i>	2.128
SU PG 6 S	<i>Pantoea agglomerans</i>	2.345	W PN 3 S	<i>Acinetobacter</i> sp.	1.81
SU PG 7 S	<i>Pantoea agglomerans</i>	2.34	W PN 4 S	–	
SU PG 8 S	–		W PN 6 S	<i>Clavibacter michiganensis</i>	2.136
SU PG 9 S	<i>Pantoea agglomerans</i>	2.273	W PN 7 S	<i>Acinetobacter</i> sp.	1.807
SU PG 10 S	–		W PN 8 S	–	
SU PG 11 S	<i>Pantoea agglomerans</i>	2.126	W PN 9 S	<i>Sphingomonas aerolata</i>	2.21
SU PG 12 S	<i>Pantoea agglomerans</i>	2.257	W PG 1 S	<i>Acinetobacter radioresistens</i>	2.244
SU PG 13 S	–		W PG 2 S	<i>Bacillus cereus</i>	2.187
SU PG 14 L	–		W PG 3 S	<i>Pantoea agglomerans</i>	2.268
SU PG 15 L	<i>Rothia</i> sp.	1.962	W PG 4 S	<i>Acinetobacter</i> sp.	1.900
SU PG 16 L	<i>Pantoea agglomerans</i>	2.276	W PG 5 S	<i>Sphingomonas aerolata</i>	2.197
SU MT 1 S	–		W PG 8 S	<i>Acinetobacter</i> sp.	1.861
SU MT 2 S	<i>Pseudomonas viridiflava</i>	2.034	W PG 9 S	–	
SU MT 3 S	<i>Pantoea agglomerans</i>	2.362	W PG 10 S	<i>Acinetobacter</i> sp.	1.752
SU MT 4 S	<i>Pseudomonas viridiflava</i>	2.01	W MT 1 S	–	
SU MT 5 S	<i>Pseudomonas viridiflava</i>	2.038	W MT 2 S	<i>Pseudomonas</i> sp.	1.854
SU MT 6 S	<i>Pseudomonas extremorientalis</i>	2.043	W MT 4 S	–	
SU MT 7 S	<i>Pantoea agglomerans</i>	2.253	W MT 6 S	–	
SU MT 8 S	–		W MT 7 S	–	
SU MT 9 S	<i>Pseudomonas viridiflava</i>	2.028	W MT 8 S	<i>Sphingomonas</i> sp.	1.746
SU MT 10 S	<i>Psychrobacillus</i> sp.	1.757	W MT 10 S	–	
SU MT 11 S	–		W MT 12 S	–	
SU MT 12 S	<i>Staphylococcus hominis</i>	2.33	W MT 13 S	<i>Pseudomonas</i> sp.	1.911
SU MT 13 S	–		W MT 14 S	<i>Pseudomonas</i> sp.	1.757
SU MT 14 S	<i>Micrococcus luteus</i>	2.066	W MT 15 S	–	
SU MT 15 L	<i>Bacillus</i> sp.	1.82	W MT 16 S	–	
SU MT 16 L	<i>Staphylococcus aureus</i>	2.341	W MT 20 S	<i>Staphylococcus hominis</i>	2.298
SU MT 17 L	<i>Staphylococcus aureus</i>	2.342			

– unidentified bacteria: 1.700–1.999 – probable identification at the genus level; 2.000–2.299 – secure identification at the genus level, probable identification at the species level; 2.300–3.000 – high probability of identification at the species level; SP – spring, SU – summer, A – autumn; W – winter; L – leaves; S – shoots; RR – Riesling; PG – Pinot Gris; PN – Pinot Noir; MT – Müller Thurgau

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Table S2. Identification of endophytes by MALDI-TOF MS method in spring, summer, autumn and winter from leaves and shoots from a biodynamic vineyard in Kutná Hora from Riesling varieties, Pinot Gris, Pinot Noir, Müller Thurgau

Isolate	Identification	Score	Isolate	Identification	Score
SP RR 1 S	<i>Bacillus cereus</i>	2.348	A PN 8A S	<i>Erwinia persicina</i>	2.078
SP RR 2 S	<i>Bacillus</i> sp.	1.891	A PN 8B S	<i>Pantoea agglomerans</i>	2.025
SP RR 3 S	<i>Bacillus subtilis</i>	2.323	A PN 9 S	<i>Pseudomonas</i> sp.	1.713
SP RR 4 S	<i>Bacillus subtilis</i>	2.051	A PN 11 S	<i>Pantoea agglomerans</i>	2.338
SP RR 5 S	<i>Bacillus cereus</i>	2.396	A PN 12 S	–	
SP RR 6 S	<i>Bacillus</i> sp.	1.879	A PN 16 S	<i>Erwinia</i> sp.	1.94
SP RR 7 S	<i>Bacillus</i> sp.	1.949	A PN 17 S	–	
SP RR 8 S	<i>Bacillus</i> sp.	1.711	A PN 18 S	<i>Bacillus simplex</i>	2.061
SP RR 9 S	–		A PN 19 S	–	
SP RR 10 S	<i>Bacillus cereus</i>	2.016	A PN 20 S	<i>Pantoea agglomerans</i>	2.265
SP RR 11 S	<i>Bacillus subtilis</i>	2.139	A PN 21 S	<i>Pantoea agglomerans</i>	2.302
SP RR 12 S	–		A PN 23 S	–	
SP RR 13 S	<i>Bacillus</i> sp.	1.99	A PN 24 L	<i>Pantoea agglomerans</i>	2.208
SP RR 14 S	<i>Bacillus</i> sp.	1.85	A PN 26 L	<i>Arthrobacter aureus</i>	2.169
SP RR 15 S	<i>Bacillus cereus</i>	2.195	A PG 1 S	–	
SP RR 16 S	<i>Bacillus subtilis</i>	2.112	A PG 2 S	–	
SP RR 17 L	<i>Bacillus subtilis</i>	2.02	A PG 3 S	–	
SP RR 18 L	<i>Bacillus subtilis</i>	2.156	A PG 4 S	<i>Bacillus subtilis</i>	2.291
SP RR 19 L	<i>Bacillus</i> sp.	1.89	A PG 5 S	<i>Pseudomonas monteilii</i>	2.028
SP RR 20 L	<i>Bacillus circulans</i>	2.023	A PG 6 S	<i>Pantoea agglomerans</i>	2.006
SP RR 21 L	<i>Acinetobacter lwoffii</i>	2.117	A PG 7 S	<i>Pseudomonas</i> sp.	1.984
SP RR 22 L	<i>Staphylococcus epidermidis</i>	2.296	A PG 9 S	–	
SP RR 23 L	–		A PG 11 S	<i>Pantoea agglomerans</i>	2.278
SP RR 24 L	<i>Bacillus subtilis</i>	2.022	A PG 12 S	–	
SP RR 25 L	–		A PG 13 S	<i>Pantoea agglomerans</i>	2.11
SP RR 26 L	<i>Acinetobacter lwoffii</i>	2.257	A PG 14 S	<i>Pantoea agglomerans</i>	2.426
SP RR 27 L	<i>Acinetobacter lwoffii</i>	2.125	A PG 15 L	<i>Staphylococcus saprophyticus</i>	2.198
SP RR 28 L	<i>Bacillus</i> sp.	1.873	A PG 16 L	<i>Bacillus subtilis</i>	2.306
SP RR 29 L	<i>Kocuria</i> sp.	1.936	A PG 17 L	–	
SP PN 1 S	<i>Bacillus</i> sp.	1.979	A PG 18 L	–	
SP PN 2 S	<i>Bacillus</i> sp.	1.925	A PG 19 L	<i>Bacillus</i> sp.	1.943
SP PN 3 S	–		A RŠ 20 L	<i>Bacillus cereus</i>	2.244
SP PN 4 S	<i>Bacillus</i> sp.	1.825	A RŠ 21 L	<i>Kocuria rosea</i>	2.359
SP PN 5 S	<i>Bacillus subtilis</i>	2.139	A RŠ 22 L	<i>Bacillus</i> sp.	1.773
SP PN 6 S	<i>Bacillus cereus</i>	2.245	A RŠ 23 L	<i>Bacillus cereus</i>	2.221
SP PN 7 S	<i>Bacillus</i> sp.	1.925	A MT 1 S	<i>Burkholderia fungorum</i>	2.341
SP PN 8 S	<i>Bacillus flexus</i>	2.382	A MT 2 S	<i>Paenibacillus pasadenensis</i>	2.157
SP PN 9 S	<i>Bacillus subtilis</i>	2.145	A MT 3 S	<i>Bacillus</i> sp.	1.829
SP PN 10 S	<i>Bacillus</i> sp.	1.812	A MT 4 S	–	
SP PN 11 L	<i>Bacillus subtilis</i>	2.043	A MT 5 S	–	
SP PN 12 L	<i>Bacillus subtilis</i>	2.038	A MT 6 S	<i>Pantoea agglomerans</i>	2.51
SP PG 1 S	<i>Bacillus cereus</i>	2.206	A MT 7 L	<i>Stenotrophomonas</i> sp.	1.974
SP PG 2 S	<i>Bacillus subtilis</i>	2.323	A MT 8 L	<i>Acinetobacter lwoffii</i>	2.166
SP PG 3 S	<i>Bacillus cereus</i>	2.385	A MT 9 L	<i>Acinetobacter lwoffii</i>	2.167
SP PG 4 S	<i>Bacillus cereus</i>	2.168	A MT 10 L	<i>Pantoea agglomerans</i>	2.335

Table S2. To be continued

Isolate				Identification	Score	Isolate				Identification	Score
SP	PG 5	S		<i>Kocuria rhizophila</i>	2.262	A	MT 11	L		<i>Pantoea agglomerans</i>	2.163
SP	PG 6	S		<i>Bacillus subtilis</i>	2.141	A	MT 12	L		<i>Ralstonia insidiosa</i>	2.057
SP	PG 7	S		<i>Bacillus subtilis</i>	2.146	A	MT 13	L		<i>Pseudomonas</i> sp.	1.834
SP	PG 8	S		<i>Bacillus subtilis</i>	2.995	W	RR 2	S		<i>Sphingomonas</i> sp.	1.969
SP	PG 9	S		<i>Bacillus subtilis</i>	2.105	W	RR 3	S		<i>Kocuria</i> sp.	1.843
SP	PG 10	L		<i>Brevibacillus agri</i>	2.385	W	RR 5	S		<i>Sphingobium</i> sp.	1.82
SP	MT 1	S		<i>Bacillus cereus</i>	2.322	W	RR 7	S		<i>Staphylococcus epidermidis</i>	2.165
SP	MT 2	S		<i>Bacillus cereus</i>	2.197	W	RR 8	S		<i>Staphylococcus epidermidis</i>	2.186
SP	MT 3	S		<i>Bacillus cereus</i>	2.064	W	RR 12	S		<i>Sphingomonas</i> sp.	1.939
SP	MT 4	S		<i>Bacillus cereus</i>	2.285	W	RR 14	S		<i>Staphylococcus epidermidis</i>	2.248
SP	MT 5	S		<i>Bacillus cereus</i>	2.259	W	RR 15	S		<i>Staphylococcus</i> sp.	1.86
SP	MT 6	S		<i>Staphylococcus epidermidis</i>	2.163	W	RR 16	S		–	
SP	MT 7	S		<i>Bacillus</i> sp.	1.758	W	RR 17	S		<i>Staphylococcus epidermidis</i>	2.202
SP	MT 8	S		<i>Bacillus cereus</i>	2.37	W	RR 20	S		<i>Staphylococcus</i> sp.	1.836
SP	MT 9	S		<i>Bacillus subtilis</i>	2.232	W	RR 21	S		<i>Sphingomonas aerolata</i>	2.315
SP	MT 10	S		<i>Kocuria palustris</i>	2.135	W	RR 22	S		<i>Staphylococcus</i> sp.	1.928
SP	MT 11	L		<i>Psychrobacillus psychrotolerans</i>	2.11	W	PN 1	S		<i>Pseudomonas graminis</i>	2.257
SP	MT 12	L		<i>Bacillus cereus</i>	2.268	W	PN 2	S		<i>Sphingomonas aurantiaca</i>	2.039
SP	MT 13	L		<i>Bacillus cereus</i>	2.278	W	PN 3	S		<i>Pseudomonas</i> sp.	1.771
SP	MT 14	L		<i>Bacillus cereus</i>	2.26	W	PN 4	S		<i>Pseudomonas</i> sp.	1.747
SP	MT 15	L		<i>Bacillus subtilis</i>	2.278	W	PN 5	S		<i>Staphylococcus epidermidis</i>	2.076
SP	MT 16	L		<i>Bacillus</i> sp.	1.997	W	PN 6	S		<i>Staphylococcus epidermidis</i>	2.092
SP	MT 17	L		<i>Bacillus weihenstephanensis</i>	2.069	W	PN 7	S		<i>Micrococcus luteus</i>	2.178
SP	MT 18	L		<i>Bacillus cereus</i>	2.41	W	PN 8	S		–	
SP	MT 19	L		<i>Bacillus cereus</i>	2.096	W	PN 9	S		<i>Staphylococcus epidermidis</i>	2.19
SP	MT 20	L		<i>Bacillus</i> sp.	1.961	W	PN 10	S		<i>Staphylococcus epidermidis</i>	2.007
SP	MT 21	L		<i>Bacillus cereus</i>	2.225	W	PN 12	S		<i>Sphingomonas</i> sp.	1.791
SP	MT 22	L		<i>Bacillus cereus</i>	2.364	W	PN 13	S		<i>Pseudomonas</i> sp.	1.953
SP	MT 23	L		<i>Bacillus cereus</i>	2.053	W	PN 15	S		<i>Pseudomonas</i> sp.	1.746
SP	MT 24	L		<i>Curtobacterium flaccumfaciens</i>	2.107	W	PN 16	S		<i>Bacillus cereus</i>	2.155
SP	MT 25	L		<i>Bacillus cereus</i>	2.311	W	PN 17	S		<i>Pseudomonas</i> sp.	1.88
SP	MT 26	L		<i>Bacillus cereus</i>	2.11	W	PN 18	S		<i>Pseudomonas</i> sp.	1.889
SP	MT 27	L		<i>Staphylococcus epidermidis</i>	2.185	W	PN 19	S		–	
SP	MT 28	L		<i>Bacillus cereus</i>	2.074	W	PN 20	S		<i>Moraxella</i> sp.	1.844
SP	MT 29	L		<i>Bacillus subtilis</i>	2.101	W	PN 21	S		<i>Bacillus</i> sp.	1.96
SP	MT 30	L		<i>Bacillus</i> sp.	1.85	W	PG 1	S		–	
SP	MT 31	L		<i>Bacillus</i> sp.	1.703	W	PG 2	S		<i>Bacillus</i> sp.	1.726
SP	MT 32	L		<i>Curtobacterium</i> sp.	1.977	W	PG 4	S		<i>Sphingomonas faeni</i>	2.179
SP	MT 33	L		<i>Bacillus</i> sp.	1.959	W	PG 5	S		<i>Curtobacterium flaccumfaciens</i>	2.256
SP	MT 34	L		–		W	PG 7	S		<i>Staphylococcus</i> sp.	1.998
SP	MT 35	L		<i>Bacillus subtilis</i>	2.169	W	PG 8	S		<i>Streptomyces</i> sp.	1.78
SP	MT 36	L		<i>Bacillus cereus</i>	2.31	W	PG 9	S		<i>Pseudomonas</i> sp.	1.734
SP	MT 37	L		–		W	PG 11	S		<i>Methylobacterium mesophilicum</i>	2.087
SP	MT 38	L		<i>Bacillus</i> sp.	1.714	W	PG 12	S		<i>Staphylococcus hominis</i>	2.262
SU	RR 1	S		<i>Paenibacillus</i> sp.	1.998	W	PG 13	S		<i>Pseudomonas</i> sp.	1.814

Table S2. To be continued

Isolate			Identification	Score	Isolate			Identification	Score
SU	RR 2	S	–		W	PG 14	S	<i>Bacillus simplex</i>	2.014
SU	RR 3	S	<i>Pantoea agglomerans</i>	2.42	W	PG 16	S	<i>Staphylococcus epidermidis</i>	2.144
SU	RR 4	S	–		W	PG 17	S	<i>Sphingomonas</i> sp.	1.932
SU	RR 5	S	–		W	PG 18	S	<i>Pseudomonas graminis</i>	2.167
SU	RR 6	S	<i>Bacillus cereus</i>	2.435	W	PG 19	S	<i>Sphingomonas</i> sp.	1.811
SU	RR 7	L	<i>Bacillus</i> sp.	1.942	W	PG 20	S	–	
SU	PN 1	S	–		W	PG 21	S	<i>Sphingomonas</i> sp.	1.784
SU	PN 2	S	<i>Bacillus megaterium</i>	2.286	W	MT 3	S	<i>Clavibacter michiganensis</i>	2.009
SU	PN 3	S	–		W	MT 4	S	<i>Pseudomonas savastanoi</i>	2.165
SU	PN 4	S	<i>Bacillus cereus</i>	2.439	W	MT 5	S	–	
SU	PN 5	L	<i>Bacillus cereus</i>	2.276	W	MT 8	S	<i>Pseudomonas caricapapayae</i>	2.167
SU	PG1	S	<i>Bacillus</i> sp.	1.73	W	MT 9	S	–	
SU	PG 2	L	<i>Bacillus</i> sp.	1.761	W	MT 10	S	–	
SU	PG 3	L	<i>Bacillus pumilus</i>	2.038	W	MT 11	S	<i>Pseudomonas</i> sp.	1.807
SU	PG 4	L	<i>Bacillus</i> sp.	1.803	W	MT 13	S	<i>Pseudomonas syringae</i>	2.09
SU	MT 1	S	<i>Bacillus</i> sp.	1.732	W	MT 14	S	–	
SU	MT 2	S	<i>Pantoea</i> sp.	1.937	W	MT 15	S	<i>Pseudomonas</i> sp.	1.745
SU	MT 3	S	–		W	MT 16	S	<i>Staphylococcus hominis</i>	2.259
SU	MT 4	L	<i>Bacillus licheniformis</i>	2.219	W	MT 17	S	–	
SU	MT 5	L	<i>Pantoea agglomerans</i>	2.441	W	MT 18	S	<i>Sphingomonas aerolata</i>	2.113
SU	MT 6	L	<i>Staphylococcus hominis</i>	2.291	W	MT 19	S	–	
A	RR 2A	L	<i>Pseudomonas monteilii</i>	2.038	W	MT 20	S	–	
A	RR 3	L	<i>Pantoea agglomerans</i>	2.258	W	MT 21	S	<i>Pseudomonas savastanoi</i>	2.129
A	RR 4	L	–		W	MT 22	S	–	
A	PN 3	S	<i>Pantoea agglomerans</i>	2.312	W	MT 23	S	<i>Staphylococcus epidermidis</i>	2.064
A	PN 4	S	<i>Curtobacterium flaccumfaciens</i>	2.309	W	MT 24	S	<i>Staphylococcus</i> sp.	1.823
A	PN 5	S	<i>Erwinia persicina</i>	2.096	W	MT 25	S	<i>Pseudomonas graminis</i>	2.345
A	PN 6	S	<i>Pantoea agglomerans</i>	2.223	W	MT 26	S	<i>Sphingomonas</i> sp.	1.78
A	PN 7	S	<i>Erwinia</i> sp.	1.972	W	MT 28	S	<i>Sphingomonas</i> sp.	1.721

– unidentified bacteria; 1.700–1.999 – probable identification at the genus level; 2.000–2.299 – secure identification at the genus level, probable identification at the species level; 2.300–3.000 – high probability of identification at the species level; SP – spring, SU – summer, A – autumn; W – winter; L – leaves; S – shoots; RR – Riesling; PG – Pinot Gris; PN – Pinot Noir; MT – Müller Thurgau