Supplementary material

Marine fungi from the sponge *Grantia compressa*: biodiversity, chemodiversity and biotechnological potential

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Bayesian phylogram of the genus *Emericellopsis* based on a combined dataset of ITS and betatubulin partial sequences. MUT 2273 and MUT 2274 were identified as *Emericellopsis pallida*.Branch numbers indicate BPP values.

Effect of different growth conditions on the HPLC-UV 280 nm chemical fingerprint of fungi,

Table S4.expressed as classes 1, 2, 3 and 4 at the increasing of the metabolic diversity. Exclusive peaks
of each condition indicated in parenthesis. The changing in colours from dark to light blue
and white indicated the increasing of the metabolic diversity.

Effect of different growth conditions on the development of the fungus (-, +, ++, +++); production of exudates (e), soluble pigments (s) and high sporulation (h); fungal-bacteria

Table S5. interaction as antagonistic response (*a*), predominance of the fungus (*p*) or complete inhibition of the bacterial growth (*n*). The changing in colours from dark to light blue and white, underlined the increasing of growth classes.

Table S1. Gene loci sequenced, primers for molecular analysis and PCR programs.

Fungi	Gene loci and DNA regions sequenced ^a	Primers (Forward and Reverse)	PCR amplification Conditions	References for primers	
Penicillium, Emericellopsis	ТИВ	BT–2a and BT–2b	94 °C: 4 min, (94 °C: 35 sec, 58 °C: 35 sec, 72 °C: 50 sec) × 35 cycles; 72 °C: 5 min	[92]	
Cladosporium	ACT	ACT-512F and ACT-783R	94 °C: 8 min, (94 °C: 15 sec, 61 °C: 20 sec, 72 °C: 40 sec) × 35 cycles; 72 °C: 10 min	[93]	
Sterile mycelia and taxa for which no specific primers are required	ITS	ITS1 and ITS4	95 °C: 5 min, (95 °C:40 s, 55 °C: 50 s, 72 °C: 50 sec) × 35 cycles; 72 °C: 8 min	[94]	
Sterile mycelia	LSU	LROR and LR7	95 °C: 5 min, (95 °C: 1 min, 50 °C: 1 min, 72 °C: 2 min) × 35 cycles; 72 °C: 10 min	[95]	

^a TUB: partial beta-tubulin gene; ACT: partial actin gene; ITS: internal transcribed spacer regions and intervening 5.8S nrRNA gene; LSU: partial nuclear ribosomal DNA large subunit.

Table S2. List of taxa used for the phylogenetic analysis of *Emericellopsis* spp. and their GenBank accession number.

		GenBank ac	cession number
Species	Strain	ITS	TUB
Acremonium exuviarum	UAMH 9995	AY882946	AY882947
Acremonium fuci	CBS 112868	AY632653	AY632690
Acremonium potronii	CBS 379.70F	AY632655	AY632691
Acremonium sclerotigenum	A130	KC987166	KC987128
Emericellopsis alkalina	CBS 127350	KC987171	KC987133
Emericellopsis alkalina	CBS 120044	KC987169	KC987131
Emericellopsis alkalina	CBS 120049	KC987170	KC987132
Emericellopsis donezkii	CBS 489.71	AY632658	AY632674
Emericellopsis glabra	A.R. 3614	HM484860	HM484879
Emericellopsis humicola	CBS 180.56	AY632659	AY632675
Emericellopsis maritima	CBS 491.71	KC987175	KC987137
Emericellopsis microspora	CBS 380.62	AY632663	AY632679
Emericellopsis minima	CBS 190.55	KC987173	KC987135
Emericellopsis minima	CBS 871.68	KC987174	KC987136
Emericellopsis pallida	CBS 490.71	KC987176	KC987138
Emericellopsis pallida	CBS 624.73	AY632667	AY632683
Emericellopsis robusta	CBS 489.73	AY632664	AY632680
Emericellopsis salmosynnemata	CBS 382.62	AY632666	AY632682
Emericellopsis stolkiae	CBS 159.71	AY632668	AY632684
Emericellopsis synnematicola	CBS 176.60	AY632665	AY632681
Emericellopsis terricola	CBS 229.59	AY632662	AY632678

Table S3. List of fungal strains isolated from G. compressa with Mycotheca Universitatis Taurinensis (MUT) and GenBank

MUT CODE	Tava	GenBank accession number							
MUTCODE	1 dXd	ITS	LSU	ACT	TUB				
2282	Convinallus on	MF140467	MF140459						
2332	Coprineitus sp.	MF140469	MF140461						
2288	Ceriporia lacerata	MF125292	MF125289						
2307	Cladosnonium allisiuum			-					
2313				MH383514					
2314	Cladosporium cladosporioides			MH383515					
2315	Cladosporium pseudocladosporioides			MH383516					
2273	Emericellopsis pallida	MH399734	MG845233		MH480660				
2274	Emericellopsis pallida	MH399735	MG845234		MH480663				
2316	Eurotium chevalieri	MH399736			MH383517				
2334	Euthypella scoparia	MH399739	MG845235						
2317	Fusarium solani	MH399737							
2321	Penicillium chrysogenum				MH383518				
2328	Penicillium oxalicum	MH399738							
2322	Davisillium nausum				MH383519				
2326	Fenicilium puneum				MH383520				
2331	Psathyrella candolleana	MF125293	MF125290						
2415	Rhodotorula mucilaginosa	MF423718							
-	Tetracladium sp.								
2410	Talumaladium adinduaran	MH399740							
2413	топуросшанит сунпаговрогит	MH399741							

accession number.

Echinulin (1):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 8.05 (1H, s, 1-NH), 7.13 (1H, s, H-4), 6.80 (1H, s, H-6), 6.10 (1H, dd, *J* = 17.3, 10.6, H-2'), 5.42 (1H, t, *J* = 6.8, H-2'''), 5.35 (1H, m, H-2''), 5.14 (2H, m, H-3'), 4.41 (1H, m, H-9), 4.10 (1H, q, *J* = 6.8, H-12), 3.66 (1H, dd, *J* = 14.6, 3.2, H-8), 3.53 (2H, d, *J* = 7.1, H-1'''), 3.39 (2H, d, *J* = 7.1, H-1''), 3.18 (1H, dd, *J* = 14.6, 11.8, H-8), 1.87 (3H, s, CH₃-3'''), 1.81 (3H, s, CH₃-3'''), 1.74 (3H, overlapped, CH₃-3''), 1.51 (3H, overlapped, CH₃-1').

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 168.6 (C-10), 167.9 (C-13), 145.9 (C-2'), 141.5 (C-2), 134.0 (C-5), 133.1 (C-3'''), 132.4 (C-7a), 131.7 (C-3''), 129.1 (C-3a), 124.6 (C-2''), 123.5 (C-7), 123.0 (C-2'''), 123.0 (C-6), 115.2 (C-4), 112.5 (C-3'), 104.2 (C-3), 54.7 (C-9), 51.0 (C-12), 39.1 (C-1'), 34.7 (C-1''), 31.5 (C-1'''), 29.6 (C-8), 28.1 (CH₃-1'), 27.9 (CH₃-1'), 25.9 (CH₃-3''), 25.9 (CH₃-3''), 20.0 (C-15), 18.1 (CH₃-3'''), 18.1 (CH₃-3'').

LR-ESI-MS: *m*/*z* 462.2 [M + H]⁺.

Neoechinulin A (2):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 8.33 (1H, s, 1-NH), 7.36 (1H, d, *J* = 8.0, H-4), 7.27 (1H, d, *J* = 7.5, H-7), 7.18 (1H, m, H-6), 7.07 (1H, m, H-5), 6.08 (1H, dd, *J* = 17.4, 10.6, H-2'), 5.21 (2H, m, H-3'), 4.22 (1H, q, *J* = 6.0, H-12), 1.60 (6H, overlapped, CH₃-1'), 1.53 (3H, d, *J* = 6.0, CH₃-12).

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 165.8 (C-13), 160.0 (C-10), 144.4 (C-2'), 143.9 (C-2), 134.4 (C-7a), 126.2 (C-3a), 124.5 (C-9), 122.5 (C-6), 121.2 (C-5), 119.0 (C-4), 113.5 (C-8), 112.1 (C-7), 111.4 (C-3'), 103.1 (C-3), 51.8 (C-12), 39.4 (C-1'), 27.5 (CH₃-1'), 21.0 (CH₃-12).

LR-ESI-MS: *m*/*z* 324.1 [M + H]⁺.

Physcion (3):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 12.31 (1H, s, 5-OH), 12.11 (1H, s, 4-OH), 7.63 (1H, s, H-1), 7.37 (1H, d, *J* = 2.0, H-8), 7.08 (1H, s, H-3), 6.69 (1H, d, *J* = 2.0, H-6), 3.94 (3H, s, 7-OCH₃), 2.45 (3H, s, 2-CH₃).

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 190.9 (C-10), 182.2 (C-9), 166.7 (C-7), 165.3 (C-5), 162.6 (C-4), 148.6 (C-2), 135.4 (C-8a), 133.4 (C-1a), 124.7 (C-3), 121.4 (C-1), 113.8 (C-4a), 110.4 (C-5a), 108.4 (C-6), 106.9 (C-8), 56.2 (3-OCH₃), 22.3 (2-CH₃).

LR-ESI-MS: m/z 285.1 [M + H]⁺.

Dihydroauroglaucin (4):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 11.8 (1H, s, 5-OH), 10.01 (1H, s, 1-CHO), 6.90 (1H, s, H-4), 6.56 (1H, d, *J* = 15.9, H-1'), 6.44 (1H, ddd, *J* = 15.9, 10.2, 0.6, H-2'), 6.27 (1H, ddt, *J* = 15.1, 10.2, 1.4, H-3'), 5.89 (dt, *J* = 15.0, 7.0 Hz, H-4'), 5.30 (1H, m, H-2''), 4.93 (1H, 2-OH), 3.31 (2H, d, *J* = 7.5, H-1''), 2.15 (2H, m, H-5'), 1.76 (3H, s, H-4''), 1.70 (3H, s, H-5''), 1.47 (2H, m, H-6'), 0.94 (3H, t, *J* = 6.0, H-7').

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 196.4 (1-CHO), 155.4 (C-5), 145.2 (C-2), 140.1 (C-4'), 139.1 (C-2'), 134.2 (C-3''), 130.6 (C-3), 129.7 (C-6), 125.3 (C-4), 124.2 (C-2''), 121.1 (C-3'), 119.5 (C-1'), 117.2 (C-1), 35.0 (C-5'), 27.4 (C-1''), 26.0 (C-4''), 22.4 (C-6'), 17.9 (C-5''), 13.9 (C-7').

LR-ESI-MS: m/z 301.1 [M + H]⁺.

Flavoglaucin (5):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 11.91 (1H, s, 5-OH), 10.25 (1H, s, 1-CHO), 6.89 (1H, s, H-4), 5.28 (1H, m, H-2"), 4.43 (1H, 2-OH), 3.29 (2H, d, *J* = 7.5, H-1"), 2.88 (2H, t, *J* = 7.5, H-1'), 1.76 (3H, s, H-4"), 1.69 (3H, s, H-5"), 1.57 (2H, m, H-2'), 1.40 (2H, m, H-3'), 1.27 (6H, overlapped, H-4', 5', 6'), 0.88 (3H, t, *J* = 6.0, H-7').

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 195.7 (1-CHO), 155.9 (C-5), 145.1 (C-2), 134.0 (C-3"), 128.7 (C-3, C-6), 125.8 (C-4), 121.3 (C-2"), 117.5 (C-1), 32.2 (C-5'), 31.9 (C-4'), 29.7 (C-3'), 29.3 (C-2'), 27.1 (C-1"), 25.9 (C-4"), 24.1 (C-1"), 22.8 (C-6'), 17.9 (C-5'), 14.2 (C-7").

LR-ESI-MS: *m*/*z* 305.1 [M + H]⁺.

Isodihydroauroglaucin (6):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 11.93 (1H, s, 5-OH), 10.23 (1H, s, 1-CHO), 6.90 (1H, s, H-4), 6.01 (1H, overlapped, H-4'), 5.99 (1H, overlapped, H-5'), 5.59 (1H, overlapped, H-3'), 5.59 (1H, overlapped, H-6'), 5.30 (1H, m, H-2''), 4.43 (1H, 2-OH), 3.29 (2H, d, *J* = 7.5, H-1"), 2.98 (2H, t, *J* = 7.5, H-1'), 2.34 (2H, m, H-2'), 1.76 (3H, s, H-4"), 1.73 (3H, d, *J* = 6.0, H-7'), 1.69 (3H, s, H-5").

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 195.5 (1-CHO), 156.0 (C-5), 145.2 (C-2), 134.1 (C-3"), 132.2 (C-5'), 131.3 (C-6'), 129.5 (C-4'), 129.1 (C-6), 128.5 (C-3'), 127.5 (C-3), 126.0 (C-4), 117.4 (C-1), 34.4 (C-2'), 29.9 (C-2''), 27.2 (C-1''), 26.0 (C-4''), 24.3 (C-1'), 18.2 (C-5''), 17.9 (C-7').

LR-ESI-MS: m/z 301.1 [M + H]⁺.

Neoechinulin D (7):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 8.18 (1H, s, 1-NH), 7.16 (1H, m, H-4), 7.21 (1H, s, H-7), 7.00 (1H, dd, *J* = 8.0, 1.5, H-5), 6.05 (1H, dd, *J* = 17.4, 10.6, H-2'), 5.23 (1H, m, H-2"), 5.21 (2H, m, H-3'), 4.29 (1H, q, *J* = 6.0, H-12), 3.43 (2H, d, *J* = 7.5, H-1"), 1.76 (3H, s, H-4"), 1.74 (3H, s, H-5"), 1.60 (6H, overlapped, CH₃-1'), 1.51 (3H, d, *J* = 6.0, CH₃-12).

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 165.7 (C-13), 160.0 (C-10), 144.5 (C-2'), 143.4 (C-2), 124.3 (C-6), 123.8 (C-7a), 122.4 (C-3"), 124.3 (C-3a), 123.8 (C-9), 122.4 (C-5), 118.9 (C-4), 113.4 (C-8), 112.4 (C-7), 110.6 (C-3'), 103.2 (C-3), 51.8 (C-12), 39.4 (C-1'), 27.6 (CH₃-1'), 27.5 (CH₃-1'), 25.9 (CH₃-4''), 21.1 (CH₃-12), 18.0 (CH₃-5''). LR-ESI-MS: *m/z* 392.2 [M + H]⁺.

Asperflavin (8):

¹H NMR (500 MHz, CD₃OD, δ/ppm, *J*/Hz): 6.81 (1H, s, H-10), 6.54 (1H, d, *J* = 2.0, H-5), 6.45 (1H, d, *J* = 2.0, H-7), 3.92 (3H, s, CH₃O-8), 3.01 (2H, s, H-4), 2.79 (1H, d, *J* = 16.9, H-2a), 2.79 (1H, d, *J* = 16.9, H-2b), 1.37 (3H, s, CH₃-3).

¹³C NMR (125 MHz, CD₃OD, δ/ppm,): 204.5 (C-1), 166.9 (C-9), 163.3 (C-8), 162.4 (C-6), 144.1 (C-10a), 138.8 (C-4a), 118.1 (C-10), 110.7 (C-8a), 103.8 (C-9a), 99.3 (C-5), 97.8 (C-7), 71.7 (C-3), 56.7 (CH₃O-8), 52.9 (C-2), 44.6 (C-4), 29.3 (CH₃-3).

LR-ESI-MS: *m*/*z* 287.1 [M – H][–].

Cinnalutein (9):

¹H NMR (500 MHz, CD₃OD, *δ*/ppm, *J*/Hz): 7.51 (1H, s, H-4), 7.22 (1H, s, H-5), 6.94 (1H, s, H-7), 3.94 (3H, s, 6-OCH₃), 2.43 (3H, s, 3-COCH₃).

¹³C NMR (125 MHz, CD₃OD, δ/ppm): 188.3 (C-9), 184.1 (C-10), 174.3 (-COOH), 170.2 (C-1 or C-8), 165.4 (C-6), 159.2 (C-1 or C-8), 142.0 (C-2 or C3), 139.5 (C-10a), 138.8 (C-4a), 131.9 (C-2 or C-3), 121.1 (C-4), 116.2 (C-9a), 109.5 (C-8a), 105.9 (C-5), 102.9 (C-7), 56.7 (1C, 6-OCH₃), 20.2 (1C, 3-COCH₃). LR-ESI-MS: *m/z* 327.1 [M + H]⁻.

Cyclo-L-Trp- L-Ala (10):

¹H NMR (500 MHz, CDCl₃, δ/ppm, *J*/Hz): 8.52 (1H, s, 1-NH), 7.60 (1H, d, *J* = 8.0, H-4), 7.32 (1H, d, *J* = 8, H-7), 7.06 (2H, m, H-2, H-6), 6.99 (1H, t, *J* = 8, H-5), 4.27 (1H, t, *J* = 4.5, H-9), 3.59 (1H, q, *J* = 7.0, H-12), 3.45 (1H, dd, *J* = 14.9, 3.9, H-8), 3.14 (1H, dd, *J* = 14.9, 3.9, H-8), 0.36 (3H, d, *J* = 7.0, H-13).

¹³C NMR (125 MHz, CDCl₃, δ/ppm): 170.6 (C-10), 169.5 (C-13), 137.8 (C-7a), 129.2 (C-3a), 125.8 (C-2), 122.5 (C-5), 120.1 (C-4), 120.0 (C-6), 112.1 (C-7), 109.3 (C-3), 57.5 (C-9), 51.7 (C-12), 30.8 (C-8), 20.0 (C-15).

LR-ESI-MS: *m*/*z* 258.1 [M + H]⁺.



Figure S1. ¹H NMR spectrum of echinulin **(1)** in CDCl₃ at 500 MHz.



Figure S2. ¹³C NMR spectrum of echinulin (1) in CDCl₃ at 125 MHz.



Figure S3. ¹H NMR spectrum of neoechinulin A (2) in CDCl₃ at 500 MHz.



Figure S4. ¹³C NMR spectrum of neoechinulin A (2) in CDCl₃ at 125 MHz.



Figure S5. ¹H NMR spectrum of physcion (3) in CDCl₃ at 500 MHz.



Figure S6. ¹³C NMR spectrum of physcion (3) in CDCl₃ at 125 MHz.



Figure S7. ¹H NMR spectrum of dihydroauroglaucin (4) in CDCl₃ at 500 MHz.



Figure S8. ¹³C NMR spectrum of dihydroauroglaucin (4) in CDCl₃ at 125 MHz.



Figure S9. ¹H NMR spectrum of flavoglaucin (5) in CDCl₃ at 500 MHz.



Figure S10. ¹³C NMR spectrum of flavoglaucin (5) in CDCl₃ at 125 MHz.



Figure S11. ¹H NMR spectrum of isodihydroauroglaucin (6) in CDCl₃ at 500 MHz.



Figure S12. ¹³C NMR spectrum of isodihydroauroglaucin (6) in CDCl₃ at 125 MHz.



Figure S13. ¹H NMR spectrum of neoechinulin D (7) in CDCl₃ at 500 MHz.



Figure S14. ¹³C NMR spectrum of neoechinulin D (7) in CDCl₃ at 125 MHz.



Figure S15. ¹H NMR spectrum of asperflavin (8) in CD₃OD at 500 MHz.



Figure S16. ¹³C NMR spectrum of asperflavin (8) in CD₃OD at 125 MHz.



Figure S17. ¹H NMR spectrum of cinnalutein (9) in CD₃OD at 500 MHz.



Figure S18. ¹³C NMR spectrum of cinnalutein (9) in CD₃OD at 125 MHz.



Figure S19. ¹H NMR spectrum of cyclo-L-Trp- L-Ala (10) in CD₃OD at 500 MHz.



Figure S20. ¹³C NMR spectrum of cyclo-L-Trp- L-Ala (10) in CD₃OD at 125 MHz.



Figure S21. Bayesian phylogram of the genus *Emericellopsis* based on a combined dataset of ITS and beta tubulin partial sequences. MUT 2273 and MUT 2274 were identified as *Emericellopsis pallida*. Branch numbers indicate BPP values.

MUT code	Таха	Pure culture							Co-culture				
MOT code	T unu	WH	WHS	PDA	PDAS	GA	GAS	WH	WHS	PDA	PDAS	GA	GAS
2288	Ceriporia lacerata	2	1	1	1	1	1	1 (1)	1	1	1	1	1
2307	Cladosporium allicinum	2 (2)	2	2 (2)	2	2	1	1	1	2 (1)	2	2	1
2313	Cladosporium allicinum	2 (2)	2 (1)	2	2 (1)	2	2	2 (2)	2	1	1	2	2
2314	Cladosporium cladosporioides	3	2	2	2	1	1	2	1 (1)	2	2	1 (3)	1
2315	Cladosporium pseudocladosporioides	2 (1)	1	2 (1)	1 (2)	2	2	1	2	2 (1)	2	2 (2)	1
2282	Coprinellus sp.	2 (1)	1 (1)	1	1 (1)	1	1	1	1	1	1	1	1
2332	Coprinellus sp.	2	1 (1)	1	1	1	1	. 1	1 (1)	1 (1)	2	1	1
2273	Emericellopsis pallida	2	2	4 (1)	3	2	1	1 (2)	1 (1)	3 (3)	3	1	1
2274	Emericellopsis pallida	1 (1)	1 (1)	2	1	1	1	. 1	1 (1)	2	1	1 (2)	1
2316	Eurotium chevalieri	4	4 (1)	4 (1)	4 (4)	1	1	4	4 (2)	4 (3)	4	1 (1)	1(1)
2334	Euthypella scoparia	2 (2)	1 (1)	1	1	1	1 (1)	1 (3)	1	1	1 (1)	1	1
2317	Fusarium solani	1	1	4	2	2	1	1	1	3	2	2	1
2321	Penicillium chrysogenum	1	2	2	4	1 (1)	1	3	2	4	3	1	1
2328	Penicillium oxalicum	4	3 (1)	3	3	2	2	3 (1)	4 (2)	4	3 (1)	1	1
2322	Penicillium paneum	2 (1)	2	2	3	1	1	2	2	3	3	2	1
2326	Penicillium paneum	2	2	2 (2)	2	1	1	2	2	2	2	1	1
2331	Psathyrella candolleana	2 (2)	1	1	1	1	1	2	2	3	1	1 (1)	1
2415	Rhodotorula mucillaginosa	2	2	1 (1)	1 (1)	1	1	1	2	1	1	1	1
2413	Tolypocladium cylindrosporum	1 (1)	2 (1)	2	2	2	2	2	2 (1)	2	2 (1)	1	1
2410	Tolypocladium cylindrosporum	3 (1)	2 (2)	2 (2)	1 (1)	2	2	3	2	1	2	2 (1)	1

Table S4. Effect of different growth conditions on the HPLC-UV 280 nm chemical fingerprint of fungi, expressed as classes 1, 2, 3 and 4 at the increasing of the metabolic diversity. Exclusive peaks of each condition indicated in parenthesis. The changing in colours from dark to light blue and white indicated the increasing of the metabolic diversity.

MUT codo	Таха			Pure cul	ture		Co-culture						
WICT Code	1 828	WH	WHS	PDA	PDAS	GA	GAS	WH	WHS	PDA	PDAS	GA	GAS
2288	Ceriporia lacerata	+++ (e, s)	++	+++	+++	+++	+++	+++ (e, s, <mark>p</mark>)	+++	+++ (p)	+++ (n)	+++	++
2307	Cladosporium allicinum	+++ (h)	+++ (h)	+++ (h)	+++ (h)	++ (h)	++	++ (h, <mark>a</mark>)	++ (h, <mark>a</mark>)	++ (h, <mark>a</mark>)	+++ (h, <mark>p</mark>)	+ (h)	+
2313	Cladosporium allicinum	+++ (h)	+++ (h)	+++ (h)	+++ (h)	++ (h)	+	+++ (h, <mark>a</mark>)	+++ (h, <mark>a</mark>)	+++ (h, <mark>a</mark>)	+++ (h, <mark>a</mark>)	++ (h)	+
2314	Cladosporium cladosporioides	+++ (h)	+++ (h)	+++ (h)	+++ (h)	+++ (h)	++	+++ (h, <mark>a</mark>)	+++ (h, <mark>a</mark>)	+++ (h, <mark>a</mark>)	+++ (h, <mark>p</mark>)	++ (h)	++
2315	Cladosporium pseudocladosporioides	+++ (h)	+++ (h)	+++ (h)	+++ (h)	++ (h)	+	+++ (h, <mark>a</mark>)	+++ (h, a)	+++ (h)	+++ (h, <u>n</u>)	+ (h)	+
2282	Coprinellus sp.	+++	+++	+++	+++	+++	+	+++ <mark>(p)</mark>	++	+++ <mark>(p)</mark>	++	++	+
2332	Coprinellus sp.	+++	++	+++	+++	+++	-	++ (p)	+	+++ <mark>(p)</mark>	++	+	+
2273	Emericellopsis pallida	+++	+++	+++	+++	++	+++	+++ (a)	+++	+++ (a)	+++	++	++
2274	Emericellopsis pallida	+++	+++	+++	+++	+++	+++	+++ (a)	+++ (p)	+++ (a)	+++ (p)	++	++
2316	Eurotium chevalieri	+++ (e, h, s)	+++ (h, s)	+++ (h, s)	+++ (h, s)	+	++	++ (e, h, s)	+++ (h, s, a)	++ (h, s)	+++ (h, s, n)	+	++
2334	Eutypella scoparia	+++	+++	+++	+++	++	++	+++	+++	+++	++	++	-
2317	Fusarium solani	+++ (s)	+++	+++ (s)	+++	+++	+++	+++(s)	+++ (p)	+++(s, p)	+++ (p)	+++	+++
2321	Penicillium chrysogenum	+++ (h, s)	+++ (h, s)	+++ (h)	+++ (h)	+++ (h, s)	+++ (h)	+++ (h, s, a)	+++ (h, s, a)	+++ (h)	+++ (h, <u>n</u>)	++ (h, s)	++ (h)
2328	Penicillium oxalicum	+++ (h)	+++ (h)	+++ (h)	+++ (h)	++	++	+++ (h, p)	+++ (h, p)	+++ (h, p)	+++ (h, p)	+++	+++
2322	Penicillium paneum	+++	+++	+++ (h)	+++ (h)	++	+	+++ (a)	+++ (a)	+++ (h, p)	+++ (h, p)	+++	+
2326	Penicillium paneum	+++	+++	+++ (h)	+++ (h)	+++	++	+++ (a)	+++ (a)	+++ (h)	+++ (h, <u>n</u>)	+++	+
2331	Psathyrella candolleana	+++	+	+++	-	+++	-	++ (a)	+	+++ (a)	-	++	-
2415	Rhodotorula mucillaginosa	+++	+++	+++	+++	+	+	+++	+++	+++	+++		+
2413	Tolypocladium cylindrosporum	+++	+++	+++	+++	+++	+++	+++ (a)	+++ (a)	+++	+++	++	++
2410	Tolypocladium cylindrosporum	+++	+++	++	++	++	+	++	++	++	++	+	+

Table S5. Effect of different growth conditions on the development of the fungus (-, +, ++, +++); production of exudates (*e*), soluble pigments (*s*) and high sporulation (*h*); fungalbacteria interaction as antagonistic response (*a*), predominance of the fungus (*p*) or complete inhibition of the bacterial growth (*n*). The changing in colours from dark to light blue and white, underlined the increasing of growth classes.