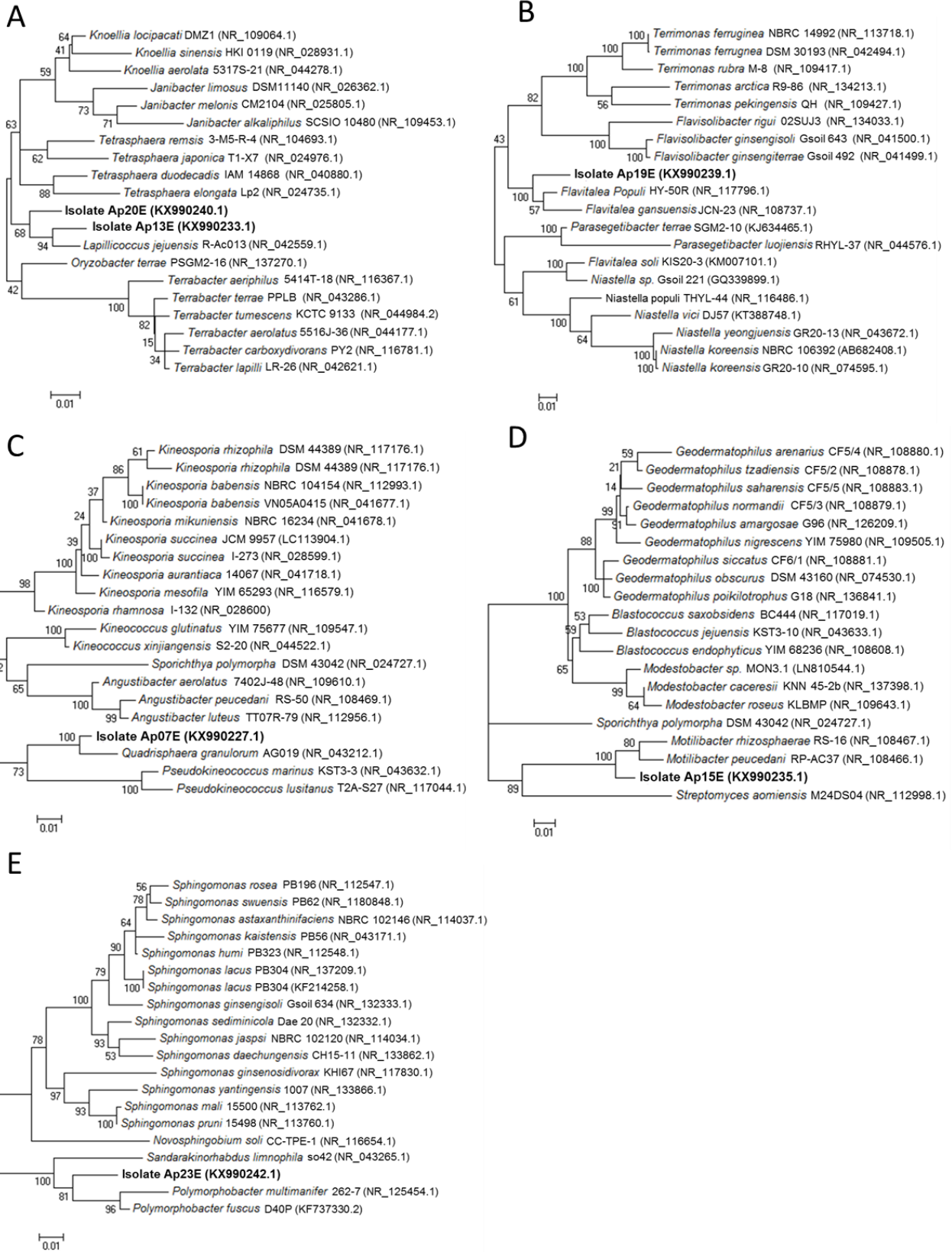
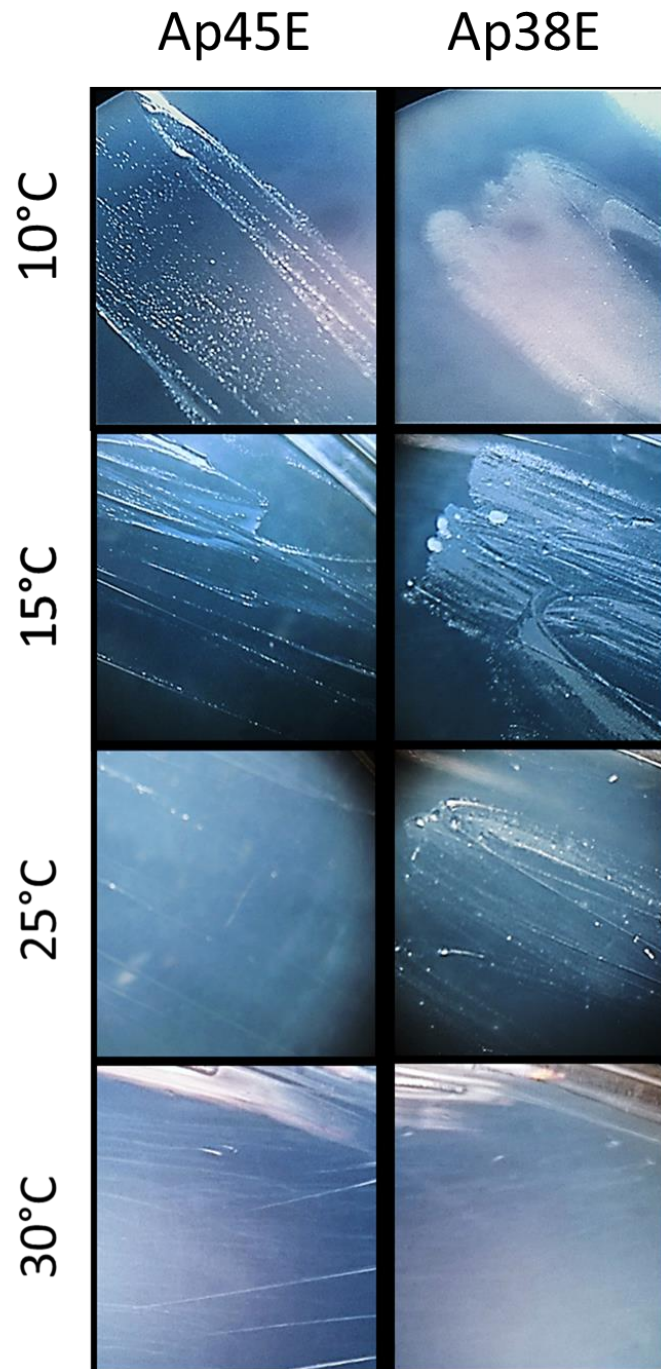


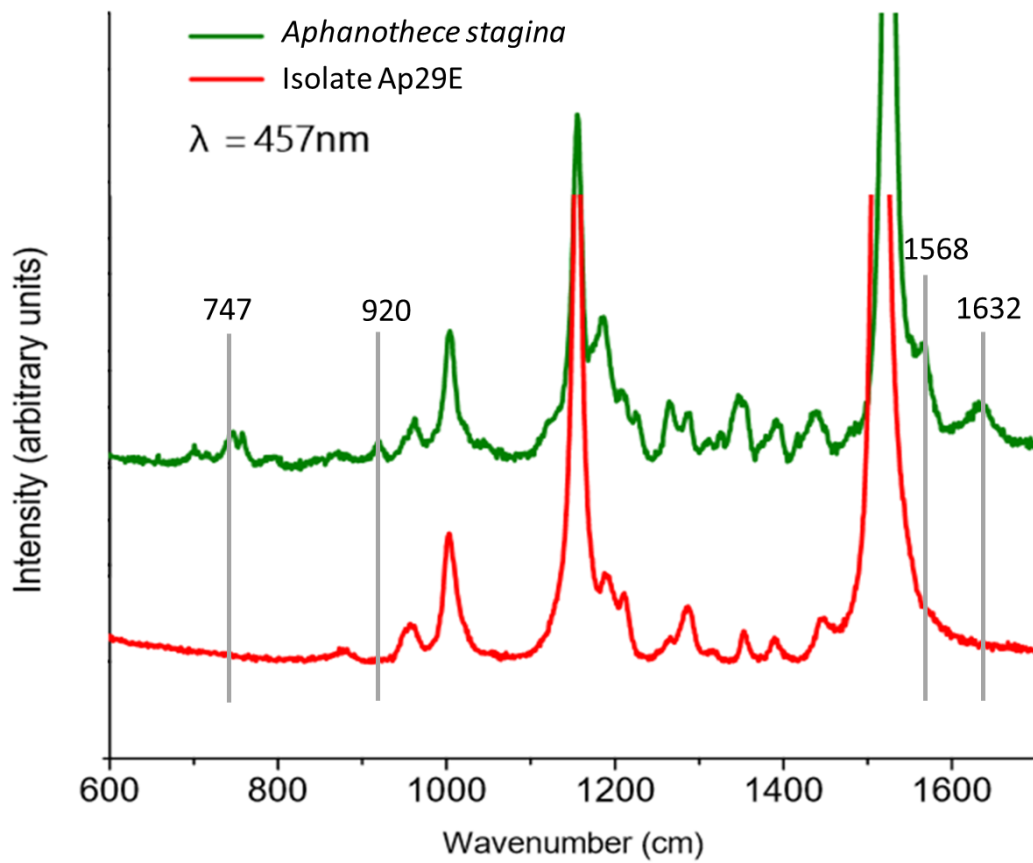
Supplementary Material



Supplementary Figure 1. Phylogenetic affiliation of the isolates Ap20E, Ap13E, Ap19E, Ap07E, Ap23E and Ap15E and most similar type material 16S sequences. (A) Ap20E and Ap13E; (B) Ap19E; (C) Ap07E; (D) Ap23E; (E) Ap15E



Supplementary Figure 3. Growth at different temperatures for the isolates Ap45E and Ap38E, on DNB 10% media after 80 days of incubation. As can be observed, growth occurs at 10°C and 15°C, whereas little or no growth is observed at higher temperatures. At 25°C weak growth is observed for Ap38E, whereas no growth was observed for Ap45E. At 30°C, no growth was detected for both isolates.



Supplementary Figure 4. Raman spectra acquired with the blue laser (457nm) of the isolate Ap29E and *Aphanothece stagina*.

Supplementary Table 1. Slow-growing isolates obtained using 1/100 NB Gellan gum plates

Isolate code	Weeks until isolation	Accession code	Highest 16S sequence similarity (Cultured - Ezbiotaxon)	Highest 16S sequence similarity (Genbank)
Ap02E	4	KX990222.1	<i>Sphingomonas molluscorum</i> (99.78%) – [AB248285]	<i>Sphingomonas</i> sp. PA223 (99%) – [AM900786.1]
Ap03E	4	KX990223.1	<i>Sphingomonas mali</i> IFO 15500 (97.7%) – [Y09638.1]	<i>Sphingomonas</i> sp. R-36505 (98%) – [FR682707.1]
Ap04E	4	KX990224.1	<i>Phycococcus ochangensis</i> I1b-b9 (98.04%) – [NR_132688.1]	Uncultured bacterium clone AK1DE1_08H (99%) – [GQ396990.1]
Ap05E	4	KX990225.1	<i>Sphingomonas daechungensis</i> CH15-11 (97.17%) – [JQ772481]	Uncultured bacterium mus-a20 (99%) – [JN023506.1]
Ap06E	4	KX990226.1	<i>Sphingomonas daechungensis</i> CH15-11 (97.28%) – [JQ772481]	Uncultured bacterium mus-a20 (99%) – [JN023506.1]
Ap07E	5	KX990227.1	<i>Quadrisphaera granulorum</i> AG019 (98.2%) – [AY831385]	<i>Quadrisphaera granulorum</i> strain CS4 (99%) – [AM887695.2]
Ap08E	5	KX990228.1	<i>Friedmanniella okinawensis</i> FB1 (99.34%) – [NR_112796.1]	<i>Friedmanniella okinawensis</i> FB1 (99%) – [NR_112796.1]
Ap09E	4	KX990229.1	<i>Phycococcus ochangensis</i> I1b-b9 (97.9%) – [NR_132688.1]	<i>Phycococcus aerophilus</i> S32341 (98%) – [AB649009.1]
Ap10E	4	KX990230.1	<i>Methylobacterium goesingense</i> iEII3 (99.63%) – [AY364020]	<i>Methylobacterium adhaesivum</i> z88a (100%) – [AB698722.1]
Ap11E	4	KX990231.1	<i>Methylobacterium goesingense</i> iEII3 (99.63%) – [AY364020]	<i>Methylobacterium adhaesivum</i> z88a (100%) – [AB698722.1]
Ap12E	7	KX990232.1	<i>Sphingomonas sediminicola</i> Dae 20 (97.28%) – [AB258386]	Uncultured bacterium clone ANTLV1_H10 (99%) – [DQ521501.1]
Ap13E	5	KX990233.1	<i>Lapillicoccus jejuensis</i> R-Ac013 (98.4%) – [AM398397]	<i>Lapillicoccus jejuensis</i> R-Ac013 (98%) – [AM398397]
Ap14E	5	KX990234.1	<i>Polaromonas vacuolata</i> 34-P (98.2%) – [U14585]	<i>Polaromonas</i> sp. R-36500 (99%) – [FR682711.1]
Ap15E	4	KX990235.1	<i>Motilibacter peucedani</i> RP-AC37 (97.46%) – [FM998003]	<i>Actinomycetales bacterium</i> OS1-23 (98%) – [FN649461.1]
Ap16E	4	KX990236.1	<i>Albidiferax ferrireducens</i> T118 (98.72%) – [CP000267]	<i>Albidiferax</i> sp. R-37567 (99%) – [FR691423.1]
Ap17E	8	KX990237.1	<i>Kineosporia rhamnosa</i> JCM 9954 (99.05%) – [AB003935]	<i>Kineosporia rhamnosa</i> strain I-132 (99%) – [NR_028600.1]
Ap18E	6	KX990238.1	<i>Nocardioides deserti</i> SC8A-24 (96.89%) – [KM816582]	<i>Nocardioides</i> sp. R-36473 (99%) – [FR682687.1]
Ap19E	7	KX990239.1	<i>Flavitalea populi</i> HY-50R (96.72%) – [HM130561]	Uncultured <i>Flavitalea</i> clone SNNP_2012-54 (99%) – [JX114387.1]
Ap20E	8	KX990240.1	<i>Lapillicoccus jejuensis</i> R-Ac013 (98.12%) – [AM398397]	Uncultured <i>Lochheadia</i> sp. clone Plot4-B02 (98%) – [EU449557.1]
Ap21E	6	KX990241.1	<i>Sphingomonas sediminicola</i> Dae 20 (97.2%) – [AB258386]	Uncultured bacterium clone ANTLV1_H10 (99%) – [DQ521501.1]
Ap23E	8	KX990242.1	<i>Polymorphobacter multimanifer</i> 272-7 (95.66%) – [AB649056]	Uncultured alpha proteobacterium clone IC4022 (99%) – [HQ622730.1]
Ap24E	6	KX990243.1	<i>Hymenobacter antarcticus</i> VUG-A42aa (98.12%) – [EU155012]	<i>Hymenobacter</i> sp. TMT1-67 (99%) – [JX949782.1]
Ap25E	9	KX990244.1	<i>Frankia alni</i> ACN14A (93.35%) – [CT573213]	Uncultured bacterium clone MA03C08 (98%) – [FM873556.1]
Ap26E	9	KX990245.1	<i>Nocardioides islandensis</i> MSL 26 (96.36%) – [EF466123]	Uncultured bacterium clone D3-119 (97%) – [KC554926.1]
Ap27E	9	KX990246.1	<i>Sphingomonas oligophenolica</i> JCM 12082 (99.06%) – [AB018439]	Uncultured bacterium BF0002C010 (99%) – [AM697313.1]
Ap28E	8	KX990247.1	<i>Rhizobacter fulvus</i> Gsoil 322 (98.92%) – [AB245356]	Uncultured bacterium clone JFJ-ICE-Bact-28 (99%) – [AJ867658.1]
Ap29E	9	KX990248.1	<i>Rhodospila globiformis</i> DSM 161 (93.49%) – [D86513]	Uncultured alpha proteobacterium clone IC4004 (96%) – [HQ622721.1]
Ap31E	7	KX990249.1	<i>Sphingomonas sediminicola</i> Dae 20 (97.18%) – [AB258386]	Uncultured bacterium clone ANTLV1_H10 (99%) – [DQ521501.1]
Ap32E	8	KX990250.1	<i>Paracraurococcus ruber</i> NS89 (95.62%) – [D85827]	Uncultured endolithic bacterium clone SM_01_BAC (99%) – [AB473915.1]

Ap33E	6	KX990251.1	<i>Nakamurella panacisegetis</i> P4-7 (98.92%) – [HE599560]	<i>Nakamurella panacisegetis</i> P4-7 (99%) – [HE599560]
Ap35E	8	KX990252.1	<i>Angustibacter luteus</i> TT07R-79 (98.26%) – [AB512285]	<i>Angustibacter luteus</i> strain AL8 (98%) – [KU258205.1]
Ap36E	13	KX990253.1	<i>Beijerinckia derxii</i> subsp. <i>Venezuelae</i> DSM 2329 (94.28%) – [AJ563934]	Uncultured bacterium clone 1174-901-15 (98%) – [AB128887.1]
Ap37E	9	KX990254.1	<i>Sphingomonas mali</i> IFO 15500 (98.07%) – [Y09638]	Uncultured <i>Sphingomonas</i> sp. clone DOL43 (99%) – [HM224424.1]
Ap38E	13	KX990255.1	<i>Conexibacter woesei</i> DSM 14684 (93.7%) – [CP001854]	Rubrobacteridae bacterium Gsoil 1167 (99%) – [AB245333.1]
Ap41E	13	KX990256.1	<i>Bradyrhizobium erythrophlei</i> CCBAU 53325 (98.43%) – [KF114645]	Uncultured bacterium clone B8-55 (99%) – [KF494604.1]
Ap42E	10	KX990257.1	<i>Acidothermus cellulolyticus</i> ATCC 43068 (92.08%) – [CP000481]	Uncultured bacterium clone ncd260b10c1 (97%) – [HM270084.1]
Ap43E	12	KX990258.1	<i>Rhodopila globiformis</i> DSM 161 (92.55%) – [D86513]	Uncultured bacterium clone Bas-7-52 (97%) – [GQ495410.1]
Ap44E	12	KX990259.1	<i>Modestobacter versicolor</i> CP153-2 (94.5%) – [AJ871304]	Uncultured bacterium clone 3-952 (98%) – [KC554168]
Ap45E	14	KX990260.1	<i>Conexibacter arvalis</i> KV-962 (94.46%) – [AB597950]	Uncultured actinobacterium clone UMAB-cl- 13 (98%) – [FN811197.1]
Ap46E	11	KX990261.1	<i>Frankia alni</i> ACN14A (93.39%) – [CT573213]	Uncultured bacterium clone MA03C08 (98%) – [FM873556.1]
Ap47E	10	KX990262.1	<i>Marmoricola solisilvae</i> KIS18-7 (98.84%) – [KM199638]	Uncultured bacterium clone 11-312 (99%) – [KC554620.1]

Supp. Table 2. Growth profile of isolates Ap25E, Ap42E, Ap38E and Ap45E on different media plates

	Isolate Ap25E	Isolate Ap42E	Isolate Ap38E	Isolate Ap45E
NB 5% pH 7	++	+++	+++	++
NB 100% pH 7	0	++	0	0
TSA 5% pH 7	0	+++	0	0
TSA 100% pH 7	0	++	0	0
R2 10% pH 7	0	+++	+++	+
R2 100% pH 7	0	+++	+	0
R2(Agar) 100% pH 7	0	0	0	0
NB 5% pH 5	0	+	0	0
NB 100% pH 5	0	0	0	0
TSA 5% pH 5	0	+	0	0
TSA 100% pH 5	0	0	0	0
R2 10% pH 5	0	+	0	0
R2 100% pH 5	0	0	0	0
Growth temperature (NB 5%)				
30°C	0	0	0	0
20°C	++	++	++	+
10°C	++	+++	+++	++

+++ = good growth ++ = moderate growth + = weak growth 0 = no growth detected

* All plates were solidified with Gellan gum 0.7% (w/v), with exception of the R2(Agar) media, which was solidified with 1.5% (w/v) Bacto Agar