

Study on syntaxonomic diversity of algal cenoses in soils of the Russian Far East, using integrative taxonomic approach

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Table S1. Results of genotyping of the isolated algal strains from soils using the BLAST algorithm.

Taxa	Strain	GenBank accession number	Phylogenetic DNA region	Percentage of identity with the closest strain from NCBI
<i>Coelastrella aeroterrestrica</i> Tschaikner, Gärtner & Kofler	VCA-240 Ch	OQ873174	ITS rDNA	100.00% – <i>Coelastrella aeroterrestrica</i> SWK1_2 JX513879
	VCA-227 Ch	OQ873175	ITS rDNA	100.00% – <i>Coelastrella aeroterrestrica</i> IT2-2-2 MW013807
	VCA-231 Ch	OQ873176	ITS rDNA	100.00% – <i>Coelastrella aeroterrestrica</i> HP-29P MZ969857
	VCA-221 Ch	OQ873177	ITS rDNA	99.29% – <i>Coelastrella aeroterrestrica</i> Ru-1-8 MH703752
	VCA-34 Ch	OQ873178	ITS rDNA	100.00% – <i>Coelastrella aeroterrestrica</i> SWK1_2 JX513879
	VCA-32 Ch	OQ873179	ITS rDNA	99.88% – <i>Coelastrella aeroterrestrica</i> SWK1_2 JX513879
	VCA-225 Ch	OQ873180	ITS rDNA	100.00% – <i>Coelastrella aeroterrestrica</i> SWK1_2 JX513879
<i>Vischeria magna</i> (Petersen) Kryvenda, Rybalka, Wolf & Friedl	VCA-233 Eu	OQ873181	ITS rDNA	98.63% – <i>Eustigmatos magnus</i> SAG 2554 MG596348
	VCA-27 Eu	OQ873182	ITS rDNA	100.00% – <i>Vischeria magna</i> ACSSI 013 MK228872
	VCA-29 Eu	OQ873183	ITS rDNA	98,88% – <i>Eustigmatos magnus</i> SAG 2554 MG596348
	VCA-218 Eu	OQ873184	ITS rDNA	99.76% – <i>Eustigmatos magnus</i> SAG 2554 MG596348

	VCA-219 Eu	OQ873185	ITS rDNA	99.76% – <i>Eustigmatos magnus</i> SAG 2554 MG596348
	VCA-241 Eu	OQ873164	18S rDNA	100.00% – <i>Vischeria magna</i> ACSSI 081 MK228873
	VCA-242 Eu	OQ873186	ITS rDNA	99.09% – <i>Vischeria magna</i> SAG 2554 MG596348
<i>Heterochlamydomonas</i> cf. <i>callunae</i> (Ettl) Mikhailyuk & Demchenko	VCA-229 Ch	OQ915509	18S rDNA	99.75% – <i>Chlamydomonas callunae</i> Us-1-5 MH703756
	VCA-224 Ch	OQ915510	18S rDNA	99.75% – <i>Chlamydomonas callunae</i> Us-1-5 MH703756
<i>Bracteacoccus bullatus</i> Fuciková, Flechtner & L.A.Lewis	VCA-228 Ch	OQ873187	ITS rDNA	99.57% – <i>Bracteacoccus bullatus</i> SAG 2032 JQ281848
	VCA-223 Ch	OQ873188	ITS rDNA	99.57% – <i>Bracteacoccus bullatus</i> SAG 2032 JQ281848
	VCA-238 Ch	OQ873165	18S rDNA	100.00% – <i>Bracteacoccus bullatus</i> ACSSI MG582205
	VCA-216 Ch	OQ873189	ITS rDNA	99.64% – <i>Bracteacoccus bullatus</i> MZ-Ch11 KY066480
	VCA-244 Ch	OQ873190	ITS rDNA	99.34% – <i>Bracteacoccus bullatus</i> SAG 2032 MW075321
<i>Humidophila contenta</i> (Grunow) Lowe, Kociolek, J.R. Johansen, Van de Vijver, Lange-Bertalot & Kopalová	VCA-214 Ba	OQ835556*	<i>rbcL</i>	93.21% – <i>Pinnularia</i> cf. <i>gibba</i> 12 EF143304
<i>Chloromonas</i> cf. <i>chlorococcoides</i> (H.Ettl & K.Schwarz) Matsukaki, Y.Hara & Nozaki	VCA-243 Ch	OQ873191	ITS rDNA	98.83% – <i>Chloromonas chlorococcoides</i> SAG72.81 AB624573
<i>Coelastrella striolata</i> Chodat	VCA-217 Ch	OQ873192	ITS rDNA	100% – <i>Coelastrella striolata</i> ACSSI 355 MZ920145
<i>Coelastrella terrestris</i> (Reisigl) Hegewald & N.Hanagata	VCA-222 Ch	OQ873166	18S rDNA	99.27% – <i>Coelastrella terrestris</i> IRK-A 173 MK504637
	VCA-234 Ch	OQ873193	ITS rDNA	99.53% – <i>Coelastrella terrestris</i> IRK-A MK504637
<i>Chloromonas</i> cf. <i>reticulata</i> (Goroschankin) Gobi	VCA-226 Ch	OQ873167	18S rDNA	98.49% – <i>Chloromonas reticulata</i> ARK-S12-19 OM729982
<i>Edaphochlorella mirabilis</i> (V.M.Andreyeva) Darienko & Pröschold in Darienko & al.	VCA-215 Ch	OQ873171	18S rDNA	100% – <i>Edaphochlorella mirabilis</i> ACSSI 102 MG696560
<i>Mayamaea arida</i> (Bock) Lange-Bertalot	VCA-44 Ba	MZ400876*	<i>rbcL</i>	94.84% – <i>Mayamaea terrestris</i> NIES-4281 LC648449
<i>Vischeria calaminaris</i> (Trzcinska et Pawlik-Skowronska) Kryvenda, Rybalka, Wolf & Friedl	VCA-220 Eu	OQ873194	ITS rDNA	99.72% – <i>Vischeria calaminaris</i> E120 JX202554
<i>Vischeria vischeri</i> (Hibberd) Kryvenda, Rybalka, Wolf & Friedl	VCA-30 Eu	MW013808	ITS rDNA	99.88% – <i>Eustigmatos vischeri</i> CCAP 860/7 KJ713283
<i>Monodopsis subterranea</i> (J.B.Petersen) D.J.Hibberd	VCA-28 Eu	MW013813	ITS rDNA	99,69% – <i>Monodopsis subterranea</i> U41054
<i>Chlamydomonas asymmetrica</i> Korshikov	VCA-235 Ch	OQ873195	ITS rDNA	99.81% – <i>Chlamydomonas asymmetrica</i> A2WS ON077054
<i>Chloromonas</i> sp.	VCA-239 Ch	OQ873172	18S rDNA	99.75% – <i>Chloromonas</i> sp. ACSSI 397 OQ363207

<i>Spongiochloris spongiosa</i> (Vischer) R.C.Starr	VCA-236 Ch	OQ873168	18S rDNA	99.90% – <i>Spongiochloris spongiosa</i> CCAP 3/1 MK541715
<i>Protosiphon botryoides</i> (Kützinger) Klebs	VCA-230 Ch	OQ873169	18S rDNA	100.00% – <i>Protosiphon botryoides</i> GTD4b-3 KC149964
<i>Bracteacoccus minor</i> (Schmidle ex Chodat) Petrová	VCA-232 Ch	OQ915508	18S rDNA	99.07% – <i>Bracteacoccus minor</i> SAG 221-1 MW075319
<i>Coelastrella ellipsoidea</i> (P.M.Novis & G.Visnovksy) K.Gopalakrishnan, P.M.Novis & G.Visnovsky	VCA-237 Ch	OQ873170	18S rDNA	99.62% – <i>Coelastrella ellipsoidea</i> LCR-CG7 KC861672
<i>Parietochloris pseudoalveolaris</i> (T.R.Deason & Bold) Shin Watanabe & G.L.Floyd in Deason, Silva, Watanabe & Floyd	VCA-38 Ch	MW013814	ITS rDNA	99.84% – <i>Ettlia pseudoalveolaris</i> NV-5 MT735204
<i>Tetrastichococcus jenerensis</i> (Neustupa, Eliás & Sejnohová) Pröschold & Darienko	VCA-213 Ch	OQ873173	18S rDNA	100.00% – <i>Tetrastichococcus jenerensis</i> KP09HW3001 KX094816
<i>Deuterostichococcus epilithicus</i> Pröschold & Darienko	VCA-245 Ch	OQ873196	ITS rDNA	98.8% – <i>Deuterostichococcus epilithicus</i> SAG 2060 MT07816
<i>Coccomyxa subellipsoidea</i> E.Acton	VCA-246 Ch	OQ873197	ITS rDNA	99.56% – <i>Coccomyxa subellipsoidea</i> C-169 FAHX137-B20 AC277064

Notes: * – represent the sequences of new species for the NCBI.