Supplement to the article: MIKHAILYUK et al.

Terrestrial algae and cyanobacteria of the Holosiiv National Nature Park (Kyiv, Ukraine), with the description of *Leptochlorella arboricola* sp. nov. (*Trebouxiophyceae*, *Chlorophyta*).

Ukrainian Botanical Journal, 82(1)

Table S1. **Percent identity (%) of the 18S rRNA gene of the different strains of *Leptochlorella***

		1	2	3	4	5	6
1	PV102507 *Leptochlorella arboricola* Golos-2-1						
2	HE984579 *Leptochlorella corticola* CAUPH8401*	92					
3	FJ946881 *Trebouxiophyceae* sp. SC2-2	90	90				
4	KF693810 *Leptochlorella* sp. UTEX EE84	90	86	86			
5	FJ790649 Uncultured *Trebouxiophyceae* clone QE17	92	86	88	89		
6	FJ790655 Uncultured *Trebouxiophyceae* clone QE29	93	87	89	89	96	
7	EU878373 *Parietochloris alveolaris* UTEX 836 as outgroup	70	67	68	67	66	67

Table S2. **p-distance (units) of the 18S rRNA gene of the different strains of *Leptochlorella***

		1	2	3	4	5	6
1	PV102507 *Leptochlorella arboricola* Golos-2-1						
2	HE984579 *Leptochlorella corticola* CAUPH8401*	0.008					
3	FJ946881 *Trebouxiophyceae* sp. SC2-2	0.010	0.010				
4	KF693810 *Leptochlorella* sp. UTEX EE84	0.010	0.014	0.014			
5	FJ790649 Uncultured *Trebouxiophyceae* clone QE17	0.008	0.014	0.012	0.011		
6	FJ790655 Uncultured *Trebouxiophyceae* clone QE29	0.007	0.013	0.011	0.011	0.004	
7	EU878373 Parietochloris alveolaris UTEX 836 as outgroup	0.030	0.033	0.032	0.033	0.034	0.033

Table S3. **Percent identity (%) of the *rbc*L gene of the different *Leptochlorella* strains**

		1	2
1	PV102579 *Leptochlorella arboricola* Golos-1-2		
2	HE984583 *Leptochlorella corticola* I2e	59	
3	KF693821 *Leptochlorella* sp. UTEX EE84	28	34

Table S4. **p-distance (units) of the *rbc*L gene of the different *Leptochlorella* strains**

		1	2
1	PV102579 *Leptochlorella arboricola* Golos-1-2		
2	HE984583 *Leptochlorella corticola* I2e	0.041	
3	KF693821 *Leptochlorella* sp. UTEX EE84	0.072	0.066

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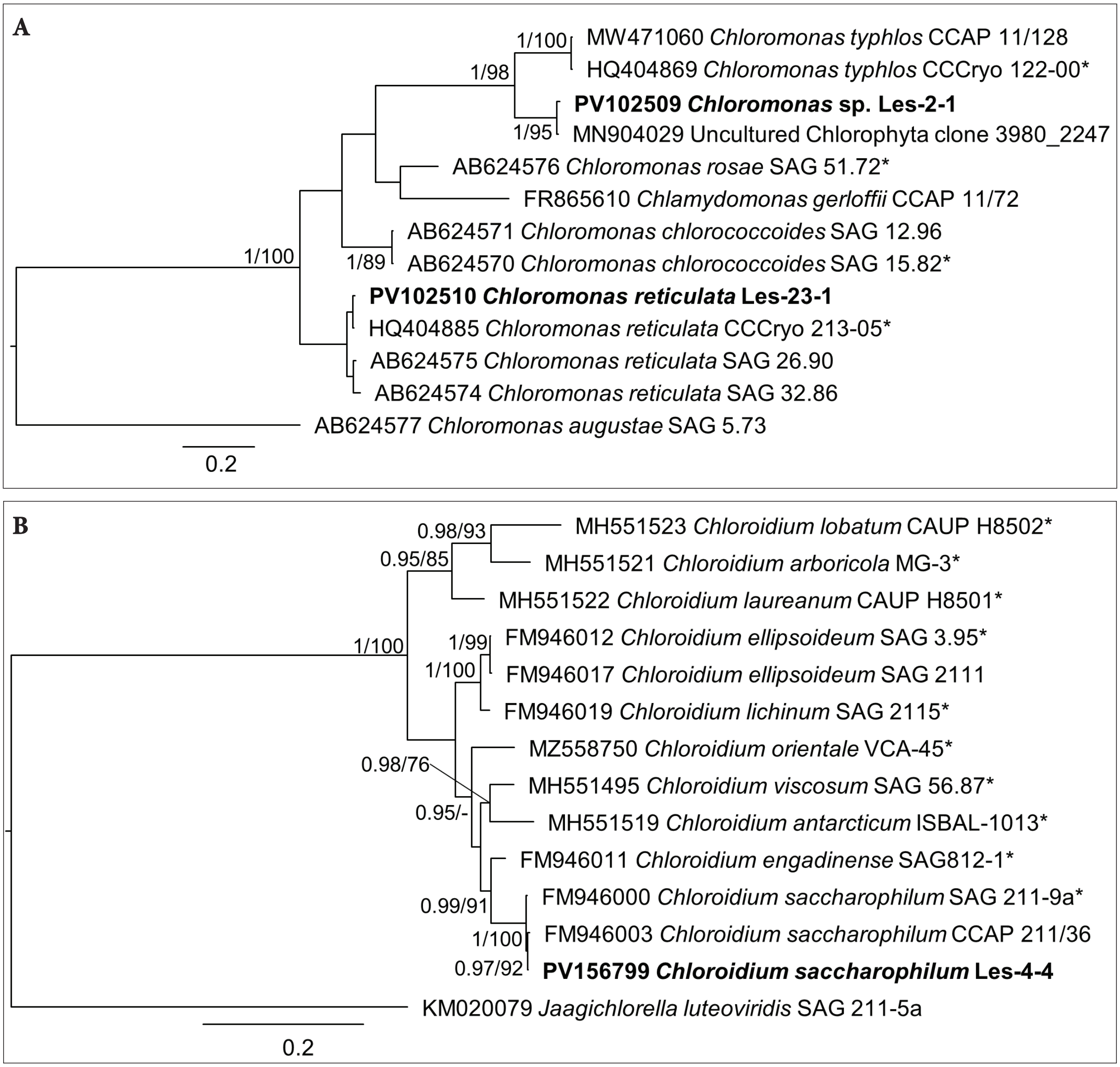

Fig. S1. Molecular phylogeny based on comparison of the nucleotide sequences of sites containing the ITS region. A: *Chloromonas*, ITS 2; B: *Chloroidium*, 18S rRNA and ITS 1,2. Phylogenetic trees in Figs S1–S2 were inferred by the Bayesian Posterior Probabilities (PP) values (left) and Maximum Likelihood bootstrap support (BP, right). Only values of PP above 0.8 and BP above 50% are specified. Sequences in bold represent newly sequenced strains. Authentic strains are marked with an asterisk

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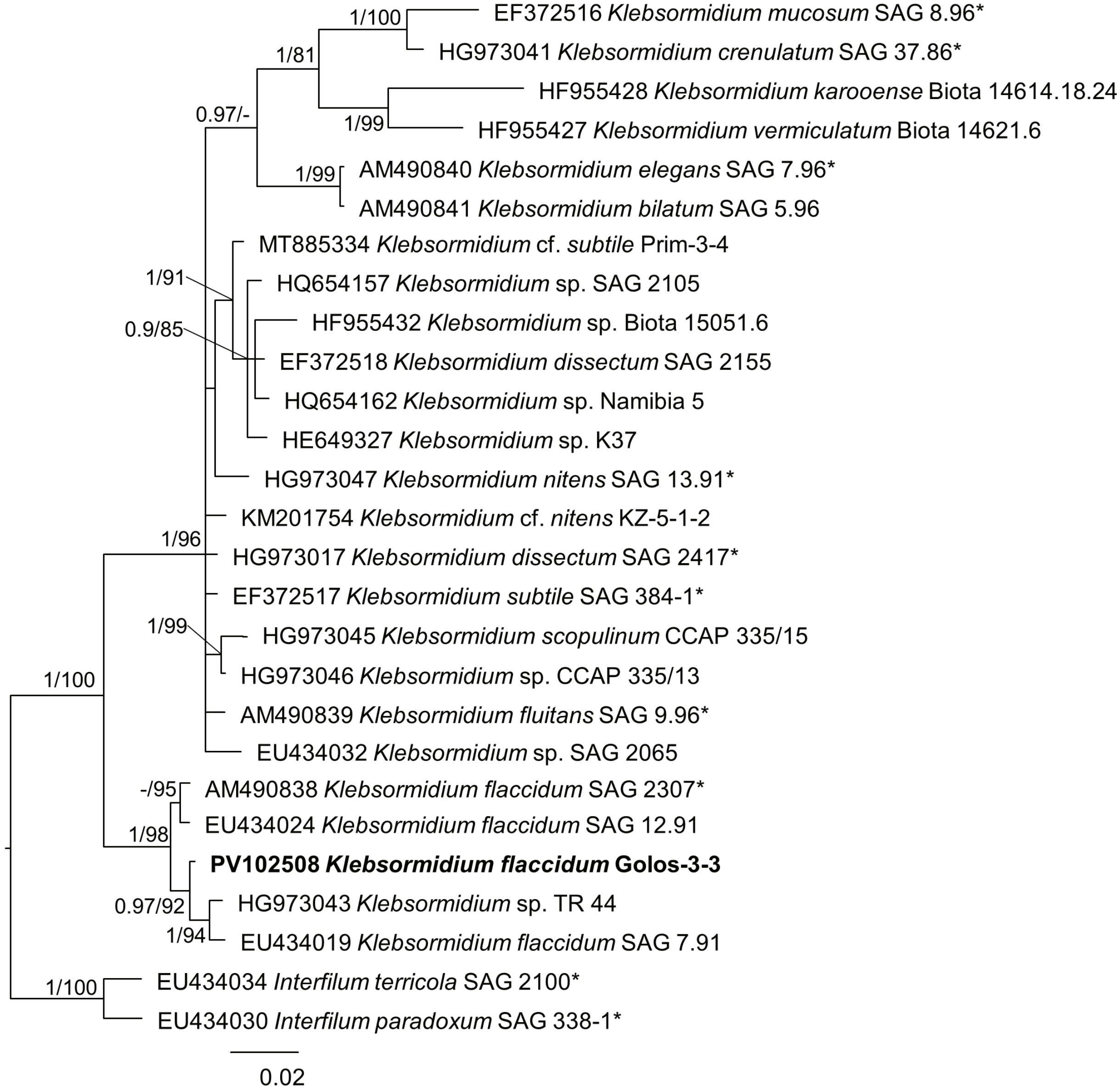

Fig. S2. Molecular phylogeny based on comparison of the nucleotide sequences of ITS 1,2 of *Klebsormidiales*

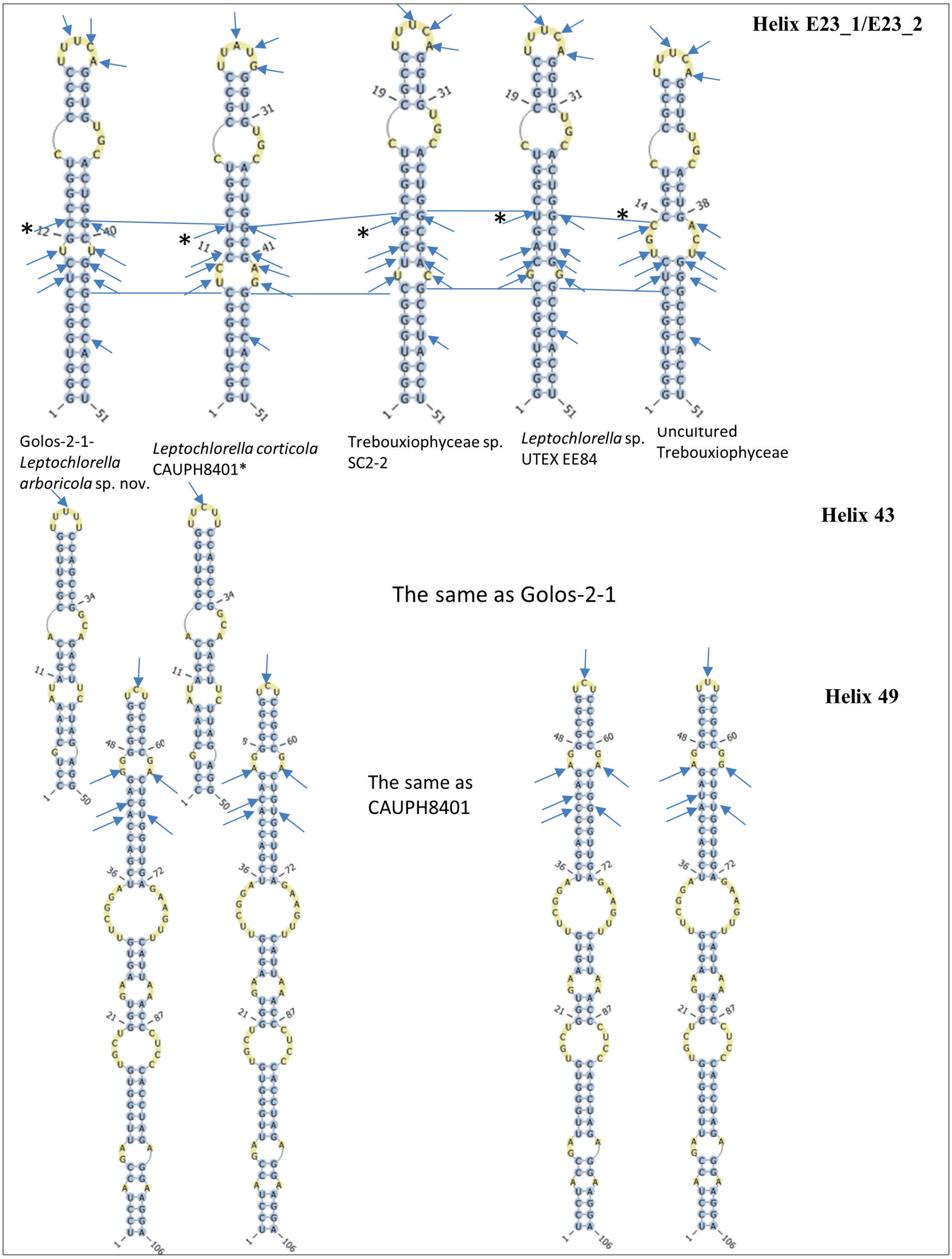

Fig. S3. Secondary structure of the most informative helices of 18S rRNA in different strains of *Leptochlorella*. Lines indicate homologous places, arrows indicate variable bases, asterisks indicate hCBC

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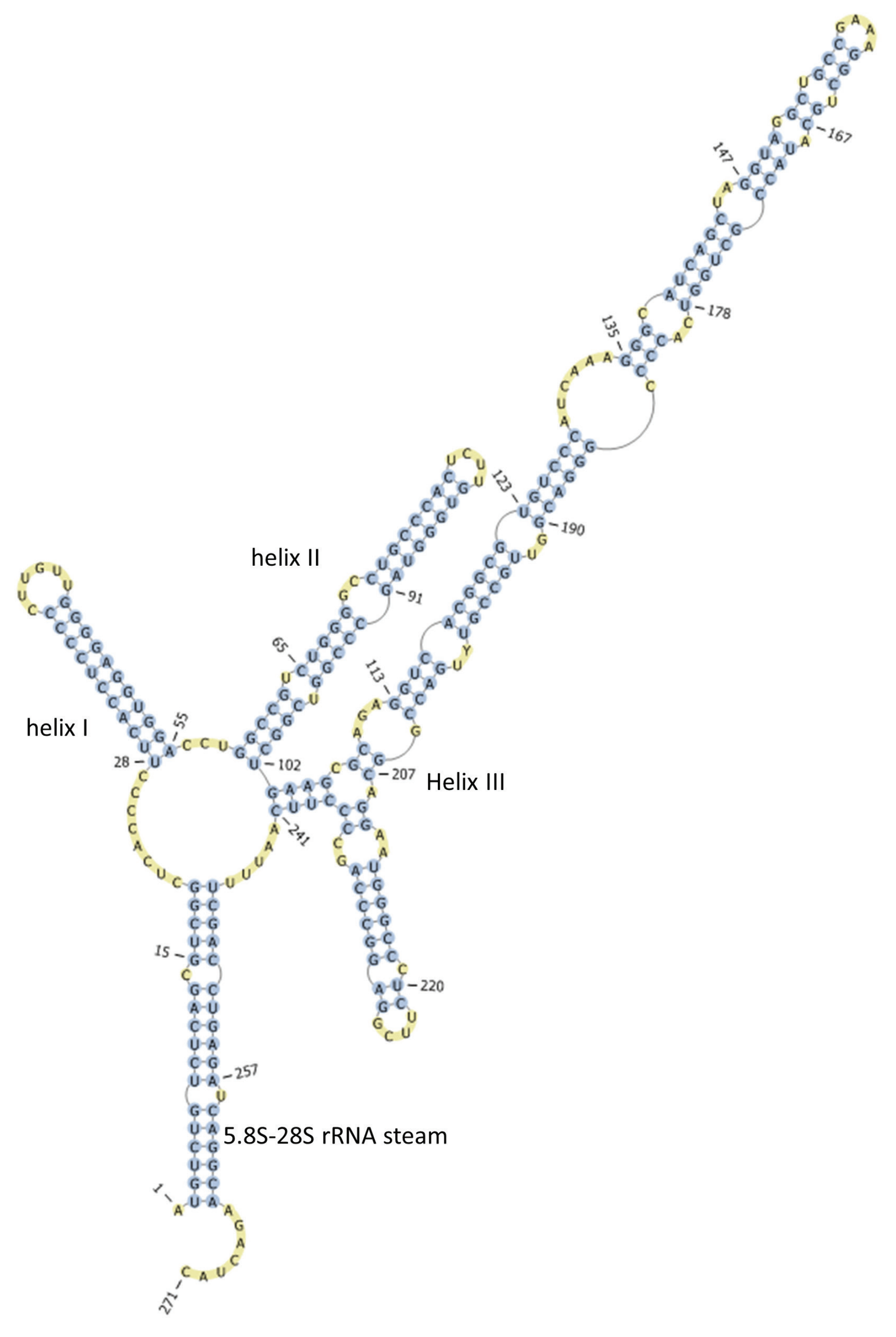

Fig. S4. ITS 2 secondary structure of *Leptochlorella arboricola* sp. nov.