

Table S2: Comparison of nucleotide length of the 16S-23S ITS regions of *C. solincola* KUT1-PS and *C. badium* 18C-PS with their phylogenetically related taxa based on 16S rRNA gene

Species/Strains	Leader	D1-D1' Helix	spacer+D2	spacer +D3+spacer	tRNA ^{isoleucine}	spacer+V2+spacer	tRNA ^{alanine}	Spacer+BoxB+spacer	BoxA	Spacer+D4+spacer	V3	End of ITS	Total ITS length
<i>C. solincola</i> KUT1-PS	7	64	35	16	75	85	73	160	11	29	34	25	614
<i>C. badium</i> 18C-PS	7	64	31	16	75	84	73	164	11	27	41	20	613
<i>C. stagnale</i> PCC 7417 (CP003642)	7	64	32	16	75	84	73	160	11	29	33	29	613
<i>C. alatosporum</i> CCALA 988 (KF052599)	7	64	31	16	75	86	73	158	11	29	35	30	615
<i>C. alatosporum</i> CCALA 994 (KF052609)	7	64	31	16	75	86	73	159	11	30	35	30	617
<i>C. catenatum</i> CCALA 990 (KF052601)	7	64	31	16	75	86	73	160	11	28	41	26	618
<i>C. catenatum</i> CCALA 991 (KF052603)	7	64	31	16	75	86	73	160	11	28	41	26	618
<i>C. catenatum</i> CCALA 996 (KF052611)	7	64	31	16	75	86	73	160	11	28	41	26	618
<i>C. catenatum</i> CCALA 999 (KF052615)	7	64	31	16	75	86	73	160	11	28	41	26	618
<i>C. muscicola</i> SAG 44.79 (KF111150)	7	64	31	16	75	86	73	160	11	28	41	25	617
<i>C. badium</i> CCALA 1000 (KF052616)	7	64	31	16	75	86	73	160	11	27	41	26	617
<i>C. moravicum</i> CCALA 993 (KF052607)	7	64	31	16	75	84	73	159	11	28	41	26	615