

**Table S3. Comparative percent dissimilarity matrix of 16S-23S ITS region of *C. solincola* KUT1-PS and *C. badium* 18C-PS with their phylogenetically related taxa based on 16S rRNA gene**

No.	Strains	1	2	3	4	5	6	7	8	9	10	11
1	<i>C. solincola</i> KUT1-PS (OQ055347)	-										
2	<i>C. badium</i> 18C-PS (OQ055346)	13.6	-									
3	<i>C. muscicola</i> SAG 44.79 (KF111150)	12.6	8.2	-								
4	<i>C. badium</i> CCALA 1000 operon 1 (KF052616)	14.5	4.1	7.9	-							
5	<i>C. catenatum</i> CCALA 999 operon 1 (KF052615)	15.3	7.3	8.4	5.9	-						
6	<i>C. catenatum</i> CCALA 996 operon 1 (KF052611)	15.3	7.3	8.4	5.9	0.0	-					
7	<i>C. alatosporum</i> CCALA 994 operon 1 (KF052609)	12.2	14.6	13.8	15.0	14.6	14.6	-				
8	<i>C. moravicum</i> CCALA 993 operon 1 (KF052607)	15.0	5.5	7.8	7.1	6.1	6.1	13.4	-			
9	<i>C. catenatum</i> CCALA 991 operon 1 (KF052603)	15.4	7.9	8.9	6.6	1.4	1.4	15.4	6.8	-		
10	<i>C. catenatum</i> CCALA 990 operon 1 (KF052601)	15.4	8.1	8.9	6.4	1.9	1.9	15.0	7.1	2.4	-	
11	<i>C. alatosporum</i> CCALA 988 operon 1 (KF052599)	13.3	13.6	13.2	14.6	13.7	13.7	8.4	13.0	14.7	13.9	-
12	<i>C. stagnale</i> PCC 7417 (CP003642)	15.5	16.6	15.9	16.8	16.0	16.0	13.8	15.2	16.6	16.6	12.2