Table S2. Pairwise nucleotide sequence comparisons between taxa for the aligned LSU rDNA sequences (1292 nt) (below the diagonal) and for *cox1* sequences (588 nt). In bold is represented the genetic intraspecific divergence.

LSU	1 *Lobucirruatus infloresco*	2 *Allobacciger* spp.	3 *Alloinfundiburictus haemuli*	4 *Monorchis monorchis*	5 *Sinistroporomonorchis* sp. (‘*Lasiotocus* sp.’)	6 *S. lizae*	7 *S. glebulentus*	8 *S. mexicanus* n. sp.	9 *S. minutus* n. sp.	10 *S. yucatanensis* n. sp.
1 *Lobucirruatus infloresco*	–	–	–	–	–	–	–	–	–	
2 *Allobacciger* spp.	8.3-8.8	**1.5-2.3**	–	–	–	–	–	–	–	
3 *Alloinfundiburictus haemuli*	11.3-13.6	11.7-15.4	**0-0.3**	–	–	–	–	–	–	
4 *Monorchis monorchis*	11.1	12.3-13.3	12.8-17	**–**	–	–	–	–	–	
5 *Sinistroporomonorchis* sp. (‘*Lasiotocus* sp.’)	8.6	10.6-11.4	11.1-14.2	10	**–**	–	–	–	–	
6 *S. lizae*	9.3-9.7	11.2-12.7	12.1-16.2	10.6-11.2	4.2-5	**–**	–	–	–	
7 *S. glebulentus*	9.3-9.7	11.2-12.7	12.1-16.2	10.6-11.2	4.2-5	2.1-2.2	**0**	–	–	
8 *S. mexicanus* n. sp.	9.3-9.7	11.2-12.7	12.1-16.2	10.6-11.2	4.2-5	2.7-2.8	0.9-1	**0**	–	
9 *S. minutus* n. sp.	9-9.5	10-11.6	10.4-14.5	10.9-11.9	5.2-5.7	6.3-7	5.7-6.4	6-6.9	**0-0.1**	
10 *S. yucatanensis* n. sp.	9-9.5	10-11.6	10.4-14.5	10.9-11.9	5.2-5.7	6.3-7	5.7-6.4	6-6.9	2.6-2.9	**0-0.08**

cox 1	1 *Lobucirruatus infloresco*	2 *Allobacciger* spp.	3 *Alloinfundiburictus haemuli*	7 *S. glebulentus*	8 *S. mexicanus* n. sp.	9 *S. minutus* n. sp.	10 *S. yucatanensis* n. sp.
1 *Lobucirruatus infloresco*		–	–	–	–	–	
2 *Allobacciger* spp.	18.3-20.4	**15.1**	–	–	–	–	
3 *Alloinfundiburictus haemuli*		17.8-20.4	**0.3**	–	–	–	
7 *S. glebulentus*	17.3-18.1	18-22.1	17.2-18.3	**0.2-0.8**	–	–	
8 *S. mexicanus* n. sp.	17.3-18.1	18-22.1	17.2-18.3	9-9.4	**0**	–	
9 *S. minutus* n. sp.	19.1-22.5	18-24.4	19.2-21.4	14.9-16.4	14.4-18.2	**9.2**	
10. *S. yucatanensis* n. sp.	19.1-22.5	18-24.4	19.2-21.4	14.9-16.4	14.4-18.2	14.4-15.6	**0.1-1.1**