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Genomic characterization of a new species of Pseudoparacreptotrema (Digenea: Allocreadiidae) from Puerto Rico, with comments on the biogeography of the genus

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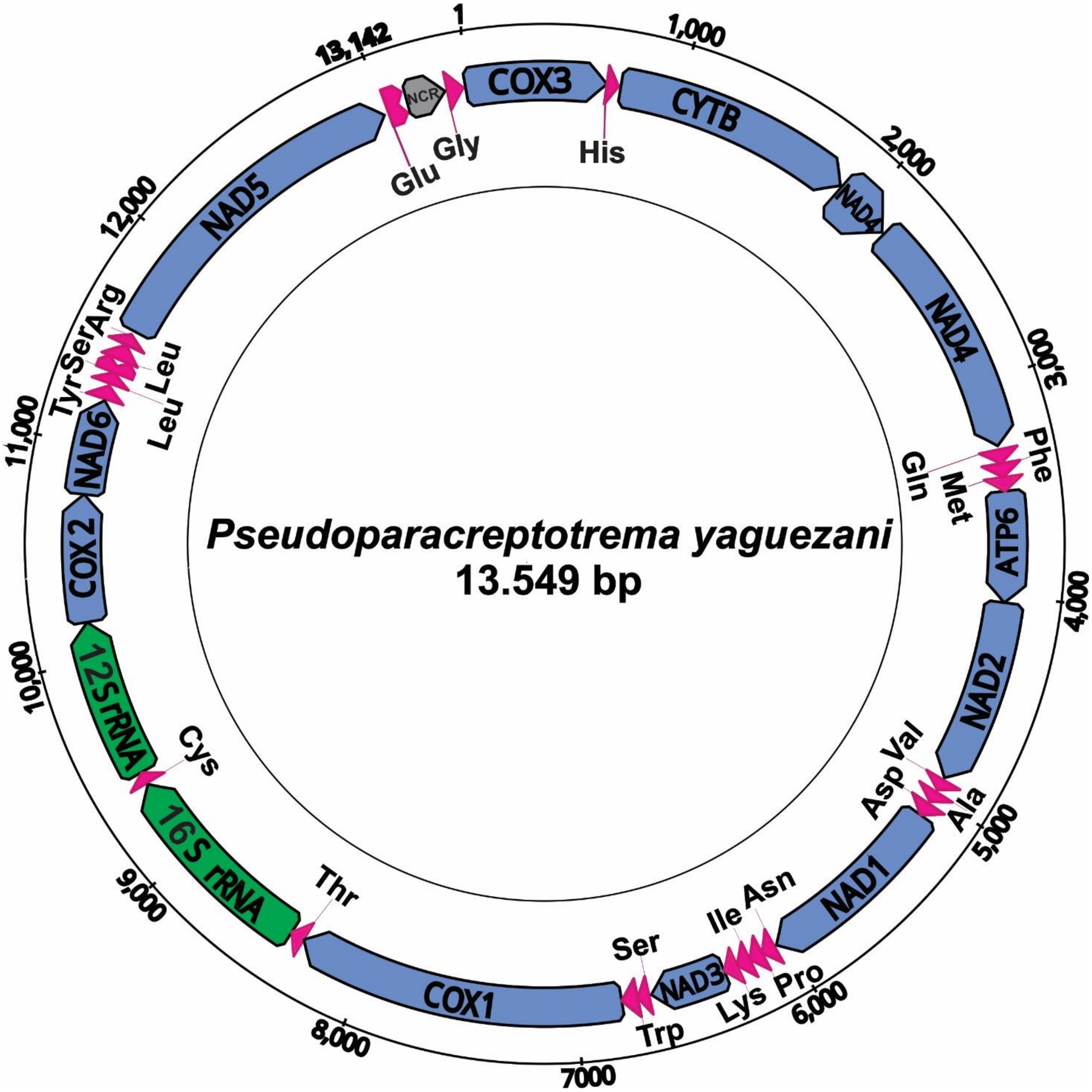
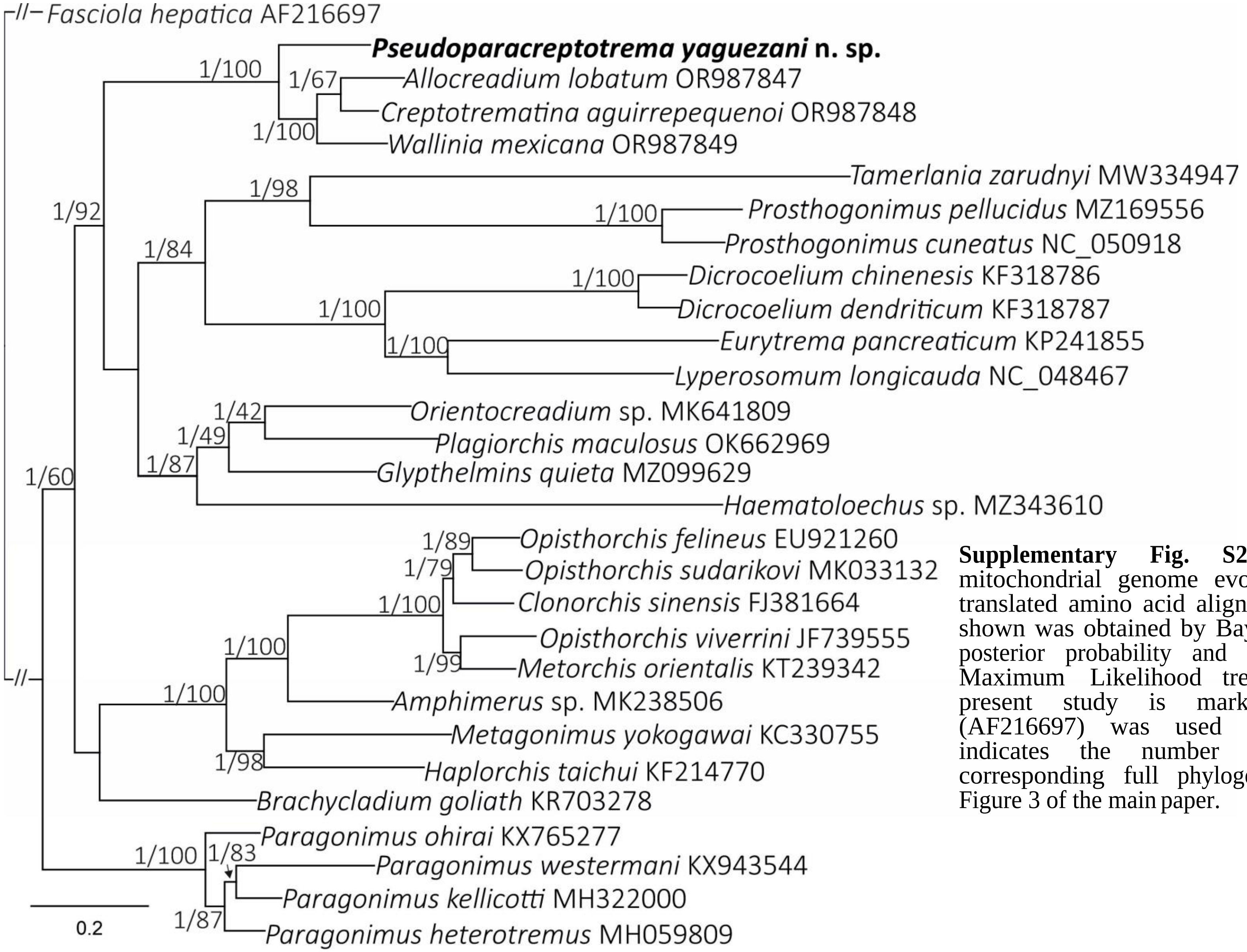
Supplementary Table S1**.** Organization of the mitochondrial genome of *Pseudaparacreptotrema yaguezani* n. sp.

Genes	Length	Start Position	End Position	Initiation Codon	Stop Codon
Cox3	645	1	645	ATG	TAA
tRNA-His	53	663	715		
Cytb	1110	724	1833	ATG	TAA
nad4L	187	1918	2104	TTG	TAA
nad4	125	2055	3321	ATG	TAA
tRNA-Gln	83	3324	3384		
tRNA-Phe	63	3386	3448		
tRNA-Met	68	3449	3516		
ATP6	516	3517	4032	ATG	TAA
Nad2	867	4039	4905	ATG	TAA
tRNA-Val	53	4918	4970		
tRNA-Ala	65	4973	5037		
tRNA-Asp	65	5047	5111		
Nad1	906	5112	6017	ATG	TAA
tRNA-Asn	67	6029	6095		
tRNA-Pro	63	6096	6158		
tRNA-Ile	64	6459	6222		
tRNA-Lys	66	6226	6291		
Nad3	360	6293	6652	ATG	TAG
tRNA-Ser	60	11357	6715		
tRNA-Trp	67	6717	6783		
Cox1	1539	6790	8328	ATG	TAG
tRNA-Thr	64	8329	8392		
16S	956	8393	9348		
tRNA-Cys	59	9365	9423		
12S	722	9429	10150		
Cox2	600	10171	10770	ATG	TAA
Nad6	450	10773	11222	ATG	TAG
tRNA-Tyr	64	11228	11291		
tRNA-Leu	63	11297	11359		
tRNA-Ser	64	11357	6715		
tRNA-Leu	68	11424	11491		

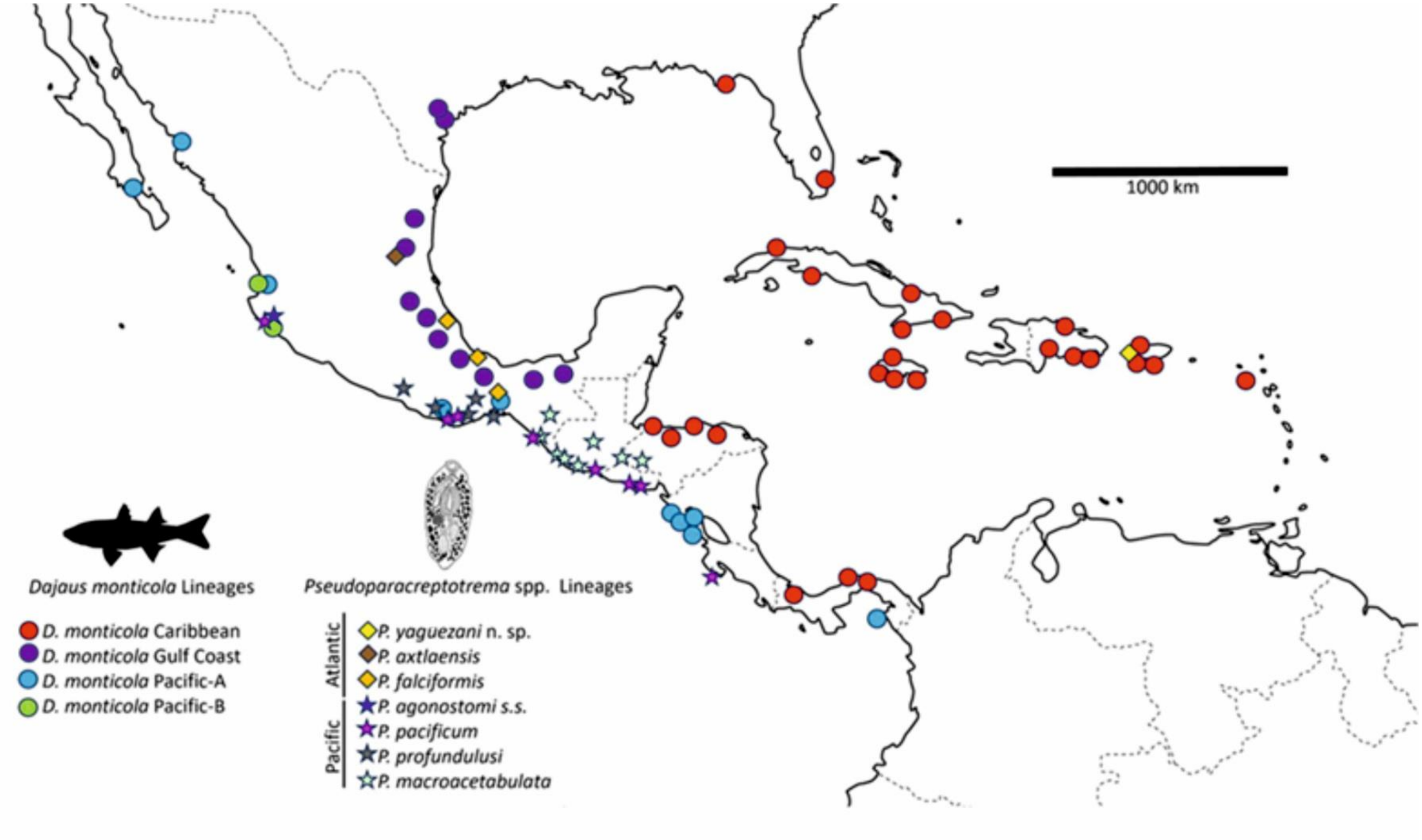
tRNA-Arg	60	11495	11554		
Nad5	1572	11557	13128	GTG	TAA
tRNA-Glu	87	13172	13258		
tRNA-Gly	83	13465	13547		



Supplementary Fig. S1. Mitochondrial genome of *Pseudoparacreptotrema yaguezani* n. sp. NCR, non-coding regions.



Supplementary Fig. S2. Phylogenetic reconstruction of mitochondrial genome evolution in the Allocreadiidae (3098 translated amino acid alignment) and other digeneans. The tree shown was obtained by Bayesian Inference (BI); nodal support is posterior probability and bootstrap values from a separate Maximum Likelihood tree (BI/ML). Sequence from the present study is marked in bold. *Fasciola hepatica* (AF216697) was used as an outgroup. The scale bar indicates the number of substitutions per site. The corresponding full phylogenetic analysis of nucleotides is in Figure 3 of the main paper.



Supplementary Fig. S3. Distribution of lineages of *Dajaus monticola* and *Pseduoparacreptotrema* spp. Colored circles indicate the locations where lineages of *D. monticola* were sampled by McMahan et al. (2013), Díaz-Murillo et al. (2017), Schmidt & McMullin, (2017), and Kubicek et al. (2019). Colored lozenges indicate the locations where Atlantic *Pseudoparacreptotrema* spp. lineages were sampled in *D. monticola* by Pérez-Ponce de León et al. (2016, 2020) and in the present study. Colored stars indicate localities in Pacific drainages where Pacific *Pseudoparacreptotrema* spp. were sampled in *Profundulus* spp. by Pérez-Ponce de León et al. (2016).

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