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The importance of integrative approaches in nematode taxonomy: the validity of *Parapharyngodon* and *Thelandros* as distinct genera

Amanda De Sousa, Fátima Jorge, Miguel Angel Carretero, David James Harris, Vicente Roca and Ana Perera

Table S1. Matrix with the average genetic distances (uncorrected p-distance) for the three genes analysed (18S, 28S and COI).

Table S2. Results of the correlations between the first three principal components (PC1, PC2 and PC3) and the linear measurements of Parapharyngodon and Thelandros individuals.

Fig. S1. Morphology of the three genetic lineages. a-c) *P. echinatus* lineage: a) general view of an adult male, b) anterior end of the lateral alae, c) posterior end of male, ventral view; d-g) *T. galloti* lineage: d) general view of an adult male, e) anterior end of the lateral alae, f-g) posterior end of male, ventral view; h-k) *Thelandros* clade: h) general view of an adult male, i) anterior end highlighting the nerve ring position, j-k) posterior end of male. LA, lateral alae; CA, caudal alae; CP, caudal papillae; ClP, cloacal papillae; Sp, spicula; NR, nerve ring.

Fig. S2. Phylogenetic trees of the estimated relationships based on the BI analysis of the a) 18S rRNA, b) 28S rRNA and c) COI single genes.

Table S1. Matrix with the average genetic distances (uncorrected *p*-distances) for the three genes analyzed (18S, 28S and COI). Values in the diagonal represent within-group distances. Below diagonal values refer to the distances between groups.

18S rRNA	*P. echinatus* lineage	*T. galloti* lineage	*P. scleratus*	*P. cubensis* lineage	*Thelandros* clade
P. echinatus lineage	**0,003**				
T. galloti lineage	0,005	**0,000**			
P. scleratus	0,012	0,012	**0,004**		
P. cubensis lineage	0,011	0,010	0,014	**0,010**	
Thelandros clade	0,017	0,017	0,021	0,021	**0,004**

28S rRNA	*P. echinatus* lineage	*T. galloti* lineage	*Thelandros* clade
P. echinatus lineage	**0,007**		
T. galloti lineage	0,016	**0,001**	
Thelandros clade	0,104	0,106	**0,023**

COI	*P. echinatus* lineage	*T. galloti* lineage	*P. scleratus*	*P. cubensis* lineage	*Parapharyngodon* sp.	*Thelandros* clade
P. echinatus lineage	**0,083**					
T. galloti lineage	0,117	**0,026**				
P. scleratus	0,207	0,207	**0,000**			
P. cubensis lineage	0,219	0,215	0,224	**0,185**		
Parapharyngodon sp.	0,195	0,195	0,192	0,206	**0,000**	
Thelandros clade	0,225	0,230	0,246	0,205	0,200	**0,113**

Table S2. Results of the correlations between the first three principal components (PC1, PC2 and PC3) and the linear measurements of *Parapharyngodon* and *Thelandros* individuals. Males and females were analysed separately. Values in bold represent the most contributing variables. For each axis, eigenvalues and percentage of contribution to the total variation are provided.

	MALES			FEMALES		
	PC1	PC2	PC3	PC1	PC2	PC3
BL	**-0.667**	-0.327	0.337	**-0.958**	-0.040	0.185
BW	**-0.733**	-0.410	-0.268	**-0.961**	-0.032	0.077
LAW	-0.488	0.104	-0.054	-	-	-
LAL	-0.091	**-0.829**	-0.309	-	-	-
TL	-0.490	**0.657**	-0.145	**-0.900**	**0.328**	-0.241
TW1	-0.577	0.490	-0.431	-	-	-
TW2	-0.566	0.478	-0.524	-	-	-
Spi	-0.606	0.070	-0.181	-	-	-
SW	-0.151	0.379	0.600	-	-	-
NR	-0.485	0.264	**0.674**	**-0.786**	-0.255	**-0.551**
OL	-0.487	-0.109	-0.145	**-0.972**	-0.206	0.026
OW	-0.654	-0.045	0.156	**-0.906**	**-0.368**	0.154
OBW	**-0.792**	-0.370	0.113	**-0.974**	-0.169	0.111
OBL	**-0.860**	-0.214	0.247	**-0.928**	**0.304**	0.121
TW	-	-	-	**-0.940**	0.211	-0.035
VL	-	-	-	**-0.932**	0.135	0.011
Vu	-	-	-	**-0.982**	0.099	0.077
Ewa	-	-	-	**-0.965**	0.062	-0.085
Ela	-	-	-	**-0.978**	-0.093	0.043
Eigenvalue	4.779	2.287	1.731	11.449	0.559	0.470
% variation	34.133	16.338	12.366	88.068	4.300	3.617
% total	34.133	50.472	62.837	88.068	92.368	95.986

Figure S1. Morphology of the three genetic lineages. a-c) *P. echinatus* lineage: a) general view of an adult male, b) anterior end of the lateral alae, c) posterior end of male, ventral view; d-g) *T. galloti* lineage: d) general view of an adult male, e) anterior end of the lateral alae, f-g) posterior end of male, ventral view; h-k) *Thelandros* clade: h) general view of an adult male, i) anterior end highlighting the nerve ring position, j-k) posterior end of male. LA, lateral alae; CA, caudal alae; CP, caudal papillae; ClP, cloacal papillae; Sp, spicula; NR, nerve ring.

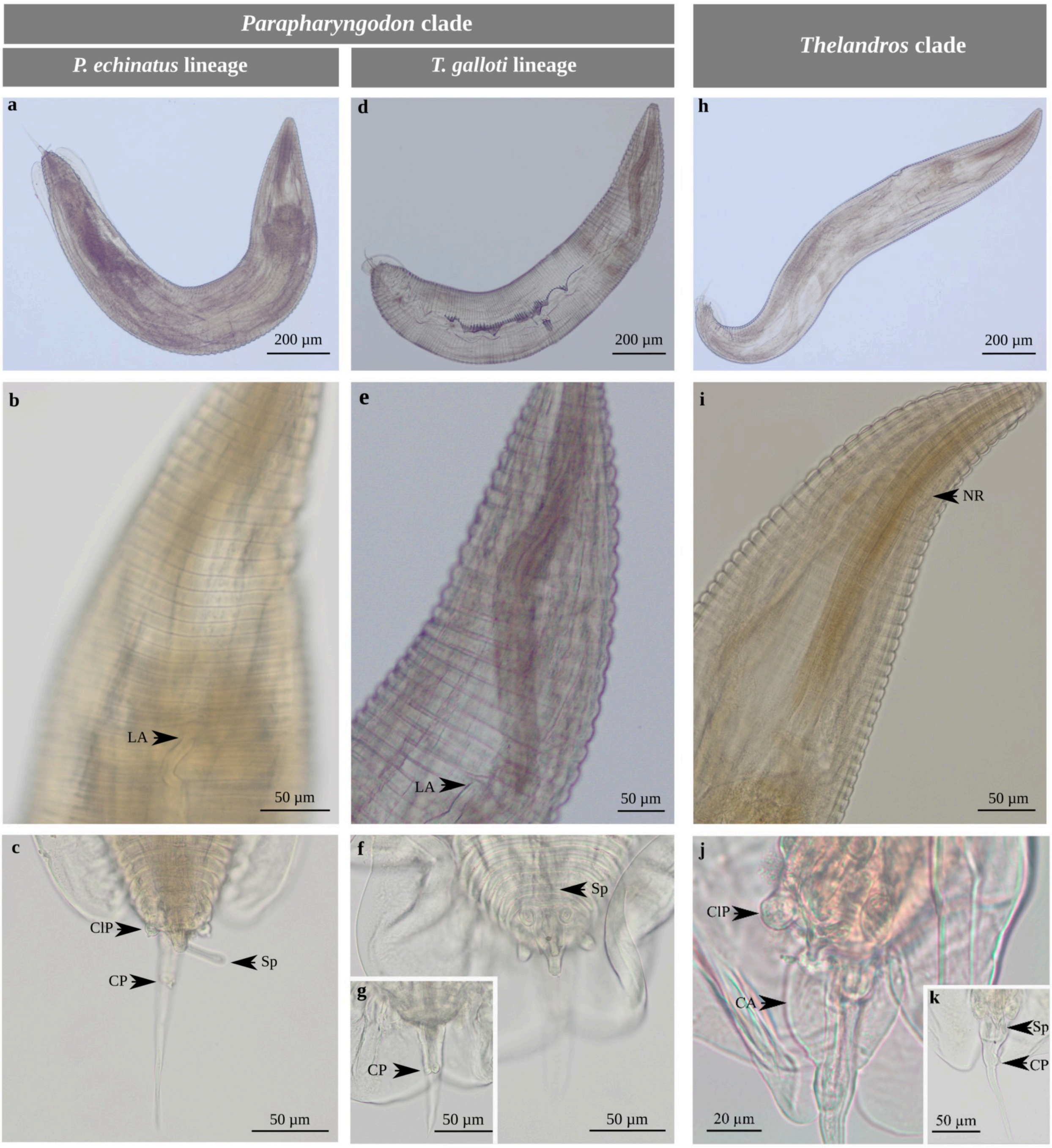

Figure S2a. Phylogenetic trees of the estimated relationships based on the BI analysis of the 18S rRNA gene. Bayesian posterior probabilities are given on the nodes. Additional information regarding sample codes is provided in Table 1.

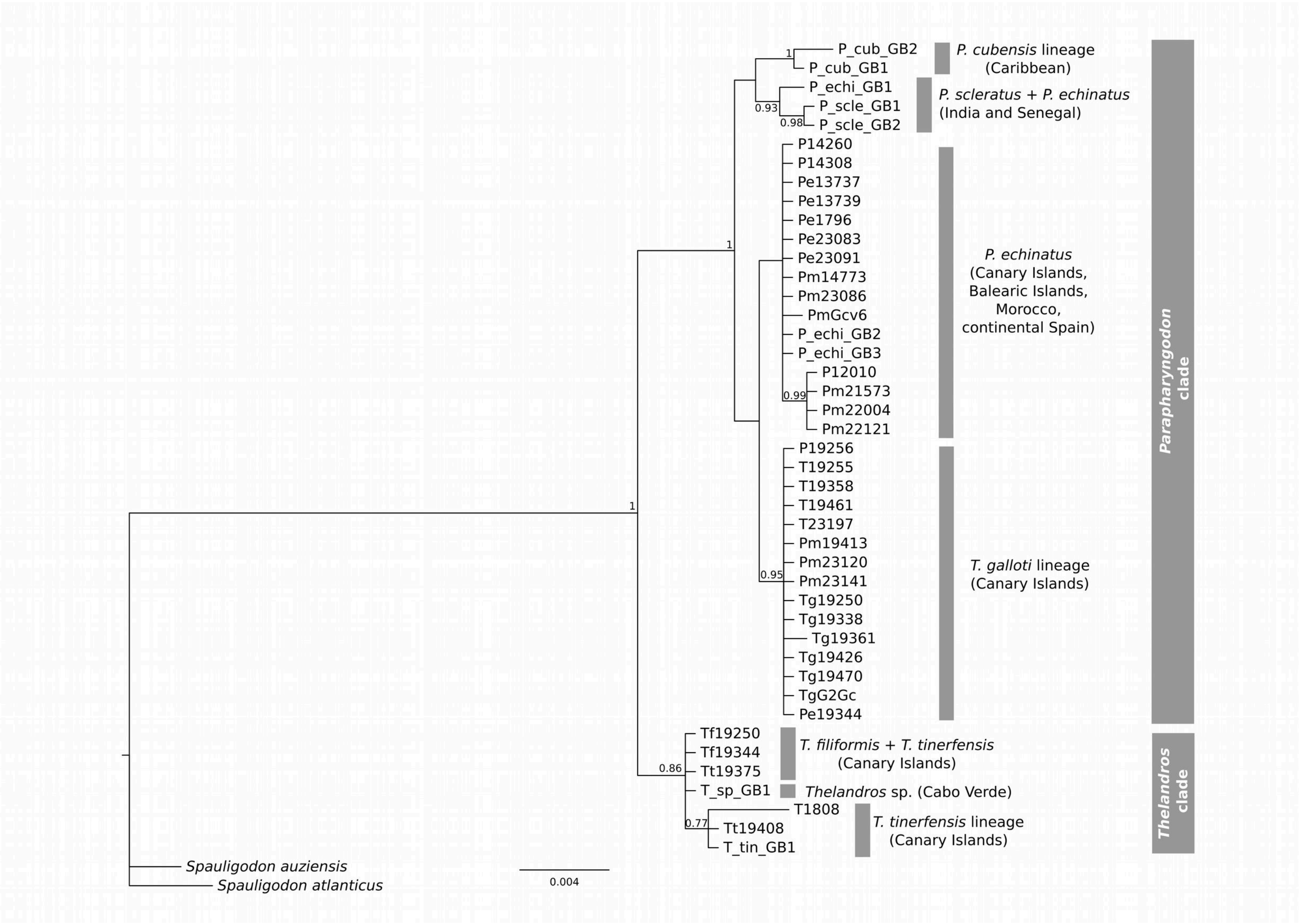

Figure S2b. Phylogenetic trees of the estimated relationships based on the BI analysis of the 28S rRNA gene. Bayesian posterior probabilities are given on the nodes. Additional information regarding sample codes is provided in Table 1.

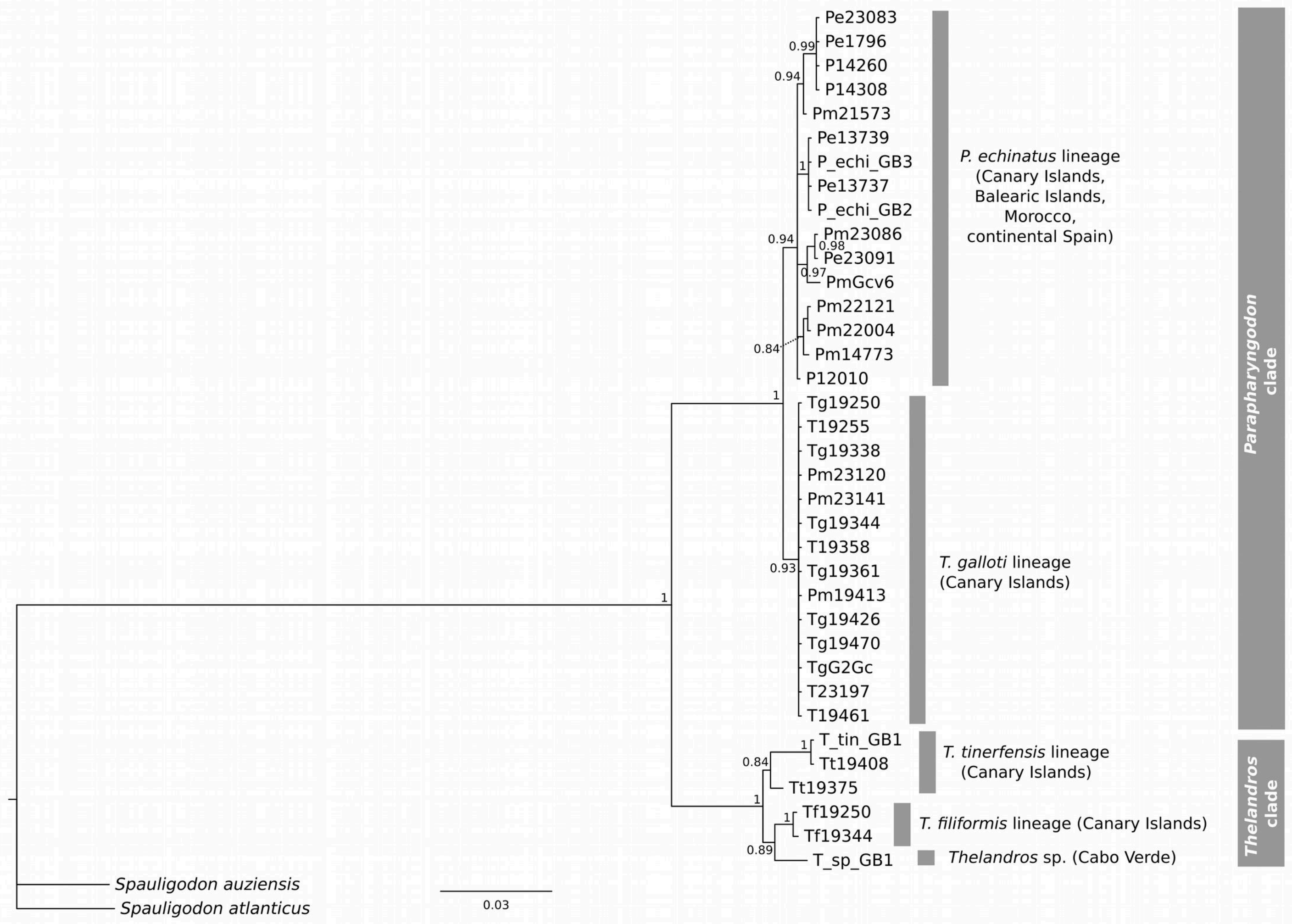

Figure S2c. Phylogenetic trees of the estimated relationships based on the BI analysis of the COI gene. Bayesian posterior probabilities are given on the nodes. Additional information regarding sample codes is provided in Table 1.