

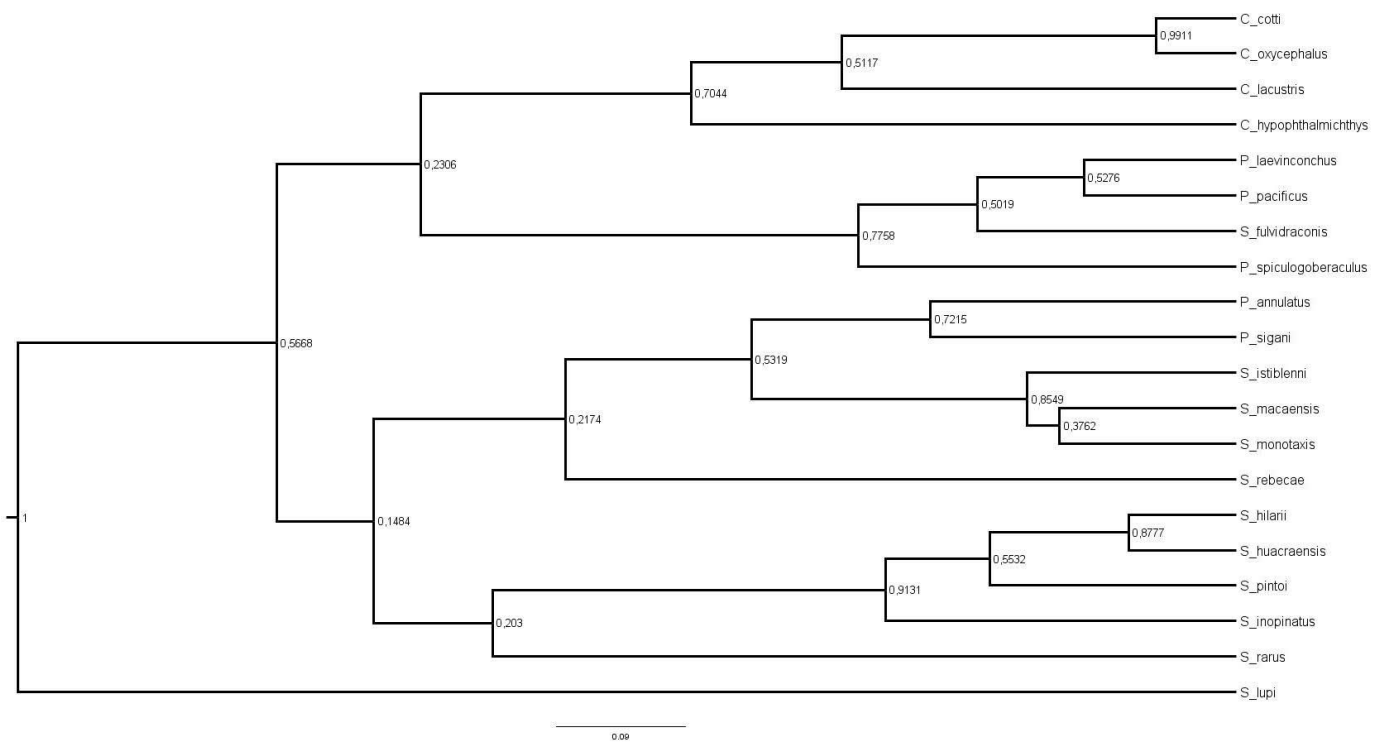
Deep in the systematics of Camallanidae (Nematoda): using integrative taxonomy to better understand the phylogeny and consistency of diagnostic traits

**Running title:** Integrative taxonomic assessment of Camallanidae

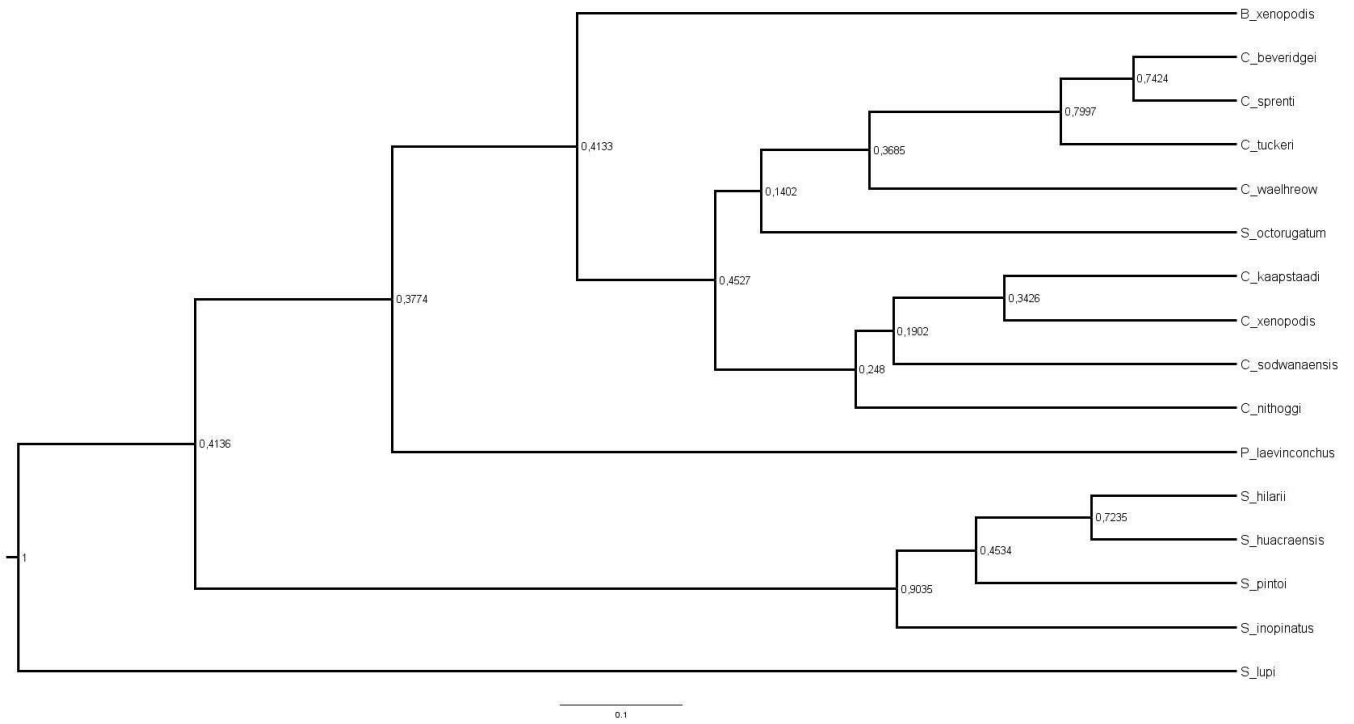
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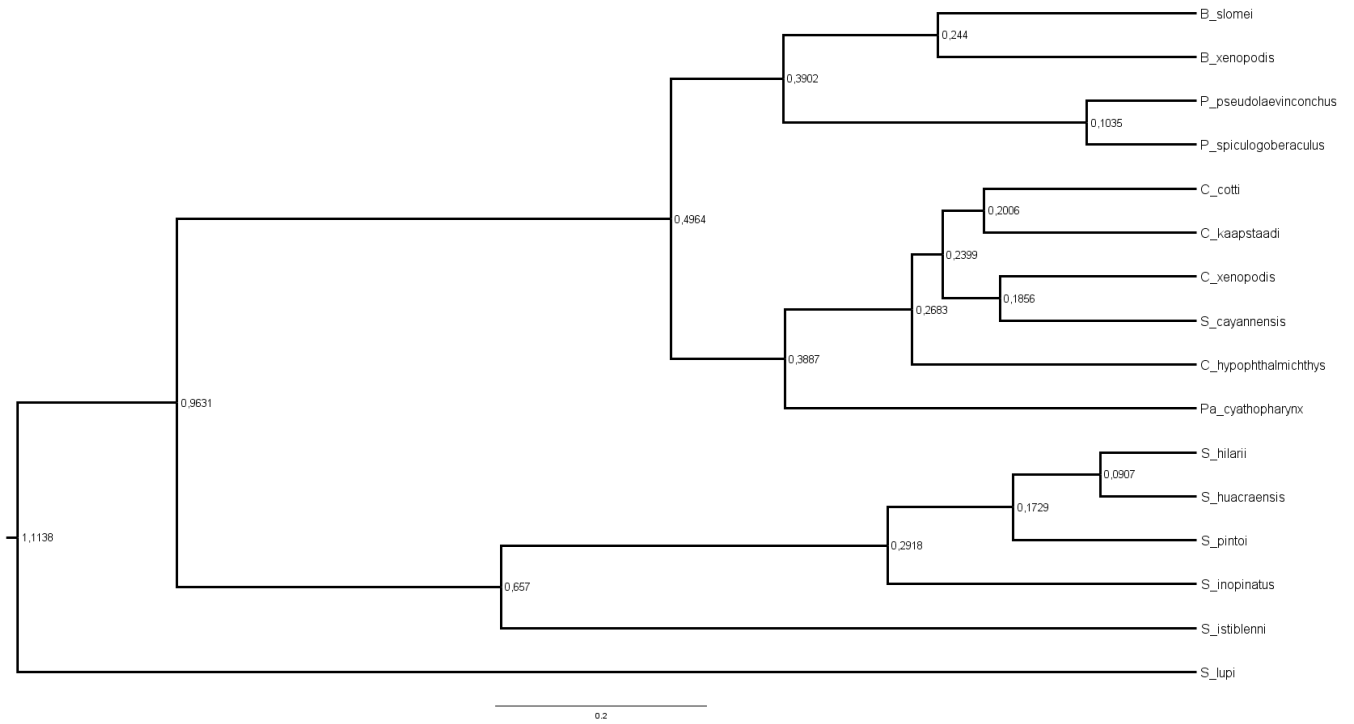
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**Fig. 1** Phylogenetic hypothesis based on morphological and life history traits of camallanids, used in the database of 18S rDNA, generated from Bayesian inference, under the Markovian Mk<sub>v</sub> model of character change, using BEAST 2.5. Nodal supports were estimated after running the Markov chain Monte Carlo for  $10 \times 10^6$  generations, sampling every  $5 \times 10^3$  generation and discarding the first 25% as burn-in.



**Fig. 2** Phylogenetic hypothesis based on morphological and life history traits of camallanids, used in the database of 28S rDNA, generated from Bayesian inference, under the Markovian Mkv model of character change, using BEAST 2.5. Nodal supports were estimated after running the Markov chain Monte Carlo for  $10 \times 10^6$  generations, sampling every  $5 \times 10^3$  generation and discarding the first 25% as burn-in.



**Fig. 3** Phylogenetic hypothesis based on morphological and life history traits of camallanids, used in the database of COI mtDNA, generated from Bayesian inference, under the Markovian MkV model of character change, using BEAST 2.5. Nodal supports were estimated after running the Markov chain Monte Carlo for  $10 \times 10^6$  generations, sampling every  $5 \times 10^3$  generation and discarding the first 25% as burn-in.