Supporting Information

The phylogenetic position of the Black-collared Bulbul *Neolestes torquatus*

Dario Zuccon & Per G. P. Ericson

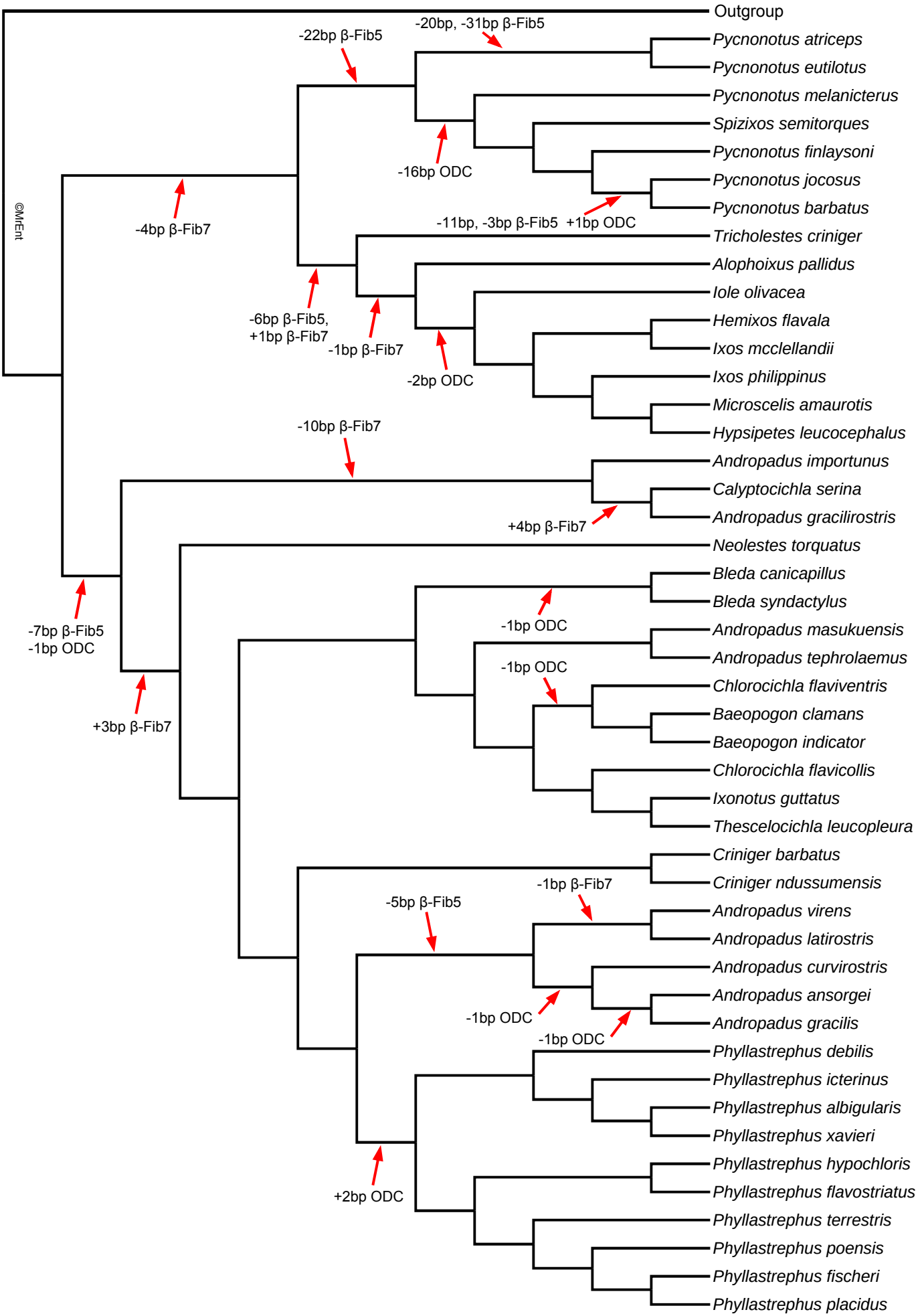
Figure S1. Mapping onto the Baysian topology (see Fig. 1) of inferred synapomorphic insertions and deletions in the four introns. A plus indicates an inferred insertion, a minus an inferred deletion.

Figures S2-S7. Trees recovered from the analysis of the individual genes. S2: β-Fibrinogen intron 5; S3: β-Fibrinogen intron 7; S4: Myoglobin intron 2; S5: Ornithine decarboxylase introns 6-7; S6: NADH dehydrogenase II; S7: NADH dehydrogenase III. A: Bayesian inference (posterior probability indicated at the node); B: maximum likelihood (bootstrap support indicated at the node).

Figure S8. Trees recovered from the analysis of the concatenated dataset without ND2. A: Bayesian inference (posterior probability indicated at the node); B: maximum likelihood (bootstrap support indicated at the node).

Table S1. Primer pairs used for the amplification and sequencing of the longer genes of *Neolestes torquatus* (β-fibrinogen intron 5, myoglobin intron 2, ornithine decarboxylase introns 6-7 and NADH dehydrogenase II). For all combinations, the amplification profile was: initial denaturation 5' at 95°C, 40 cycles of denaturation 40" at 95°C, annealing 40" at the temperature indicated for each primer pair, extension 60" at 72°C, with a final extension of 5' at 72°C. ND3 and β-Fib7 were short enough for direct amplification using standard primers (see main text). [1]: Fuchs *et al.* 2004; [2]: Irestedt *et al.* 2002; [3]: Allen & Omland 2003 (see the main text for the full references).

Table S2. Sequence characteristics of the six genes analyzed.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Pycnonotus barbatus
Tricholestes criniger
Alophoixus pallidus
Iole olivacea
Hemixos flavala
Ixos mcclellandii
Ixos philippinus
Microscelis amaurotis
Hypsipetes leucocephalus
Andropadus importunus
Calyptocichla serina
Andropadus gracilirostris
Neolestes torquatus
Bleda canicapillus
Bleda syndactylus
Andropadus masukuensis
Andropadus tephrolaemus
Chlorocichla flaviventris
Baeopogon clamans
Baeopogon indicator
Chlorocichla flavicollis
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Criniger ndussumensis
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Andropadus curvirostris
Andropadus ansorgei
Andropadus gracilis
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Phyllastrephus albigularis
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Phyllastrephus terrestris
Phyllastrephus poensis
Phyllastrephus fischeri
Phyllastrephus placidus
-20bp, -31bp β-Fib5
-22bp β-Fib5
-16bp ODC
-4bp β-Fib7
-11bp, -3bp β-Fib5
+1bp ODC
-6bp β-Fib5,
+1bp β-Fib7
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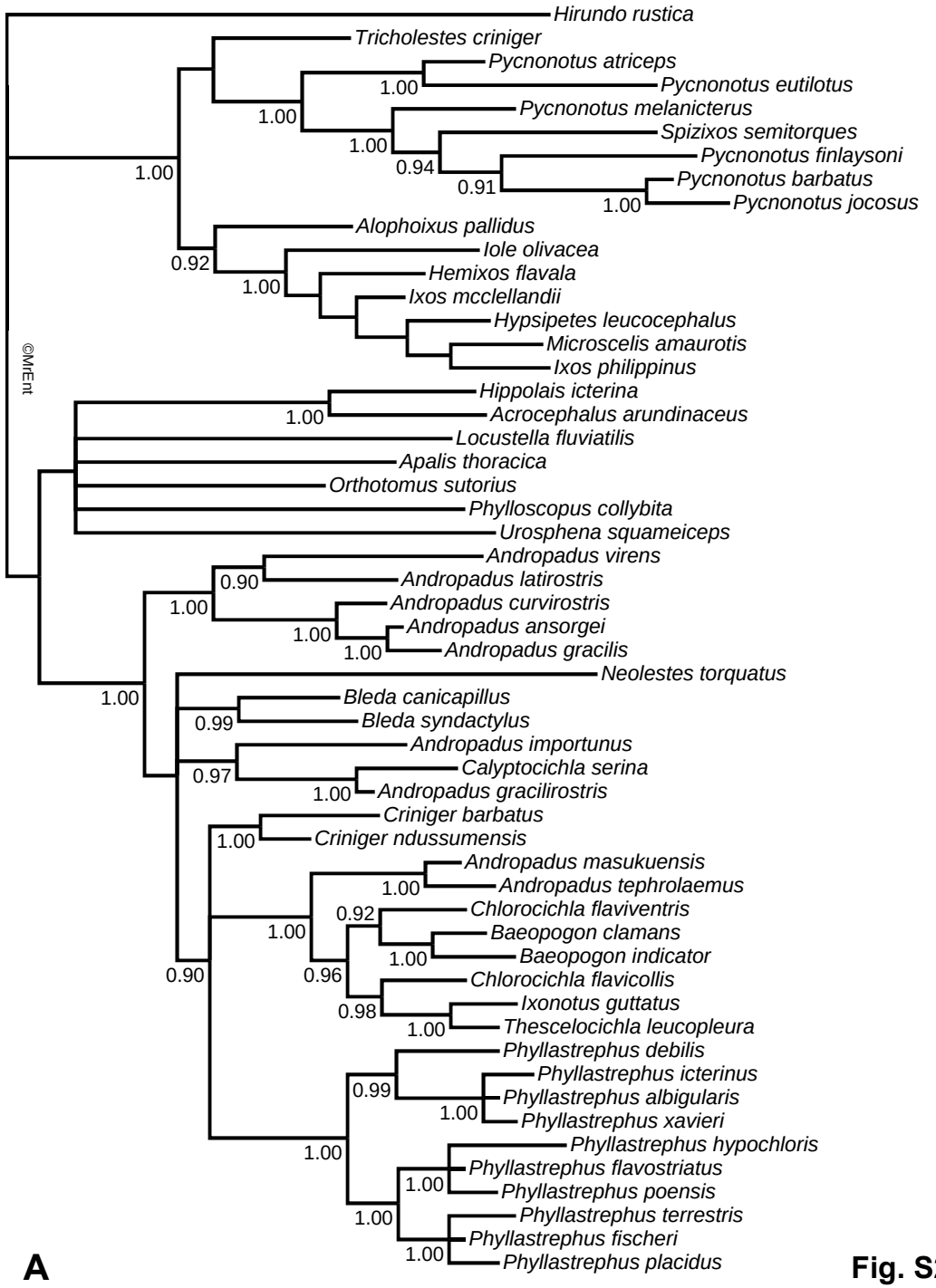
Fig. S1.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Phyllastrephus placidus
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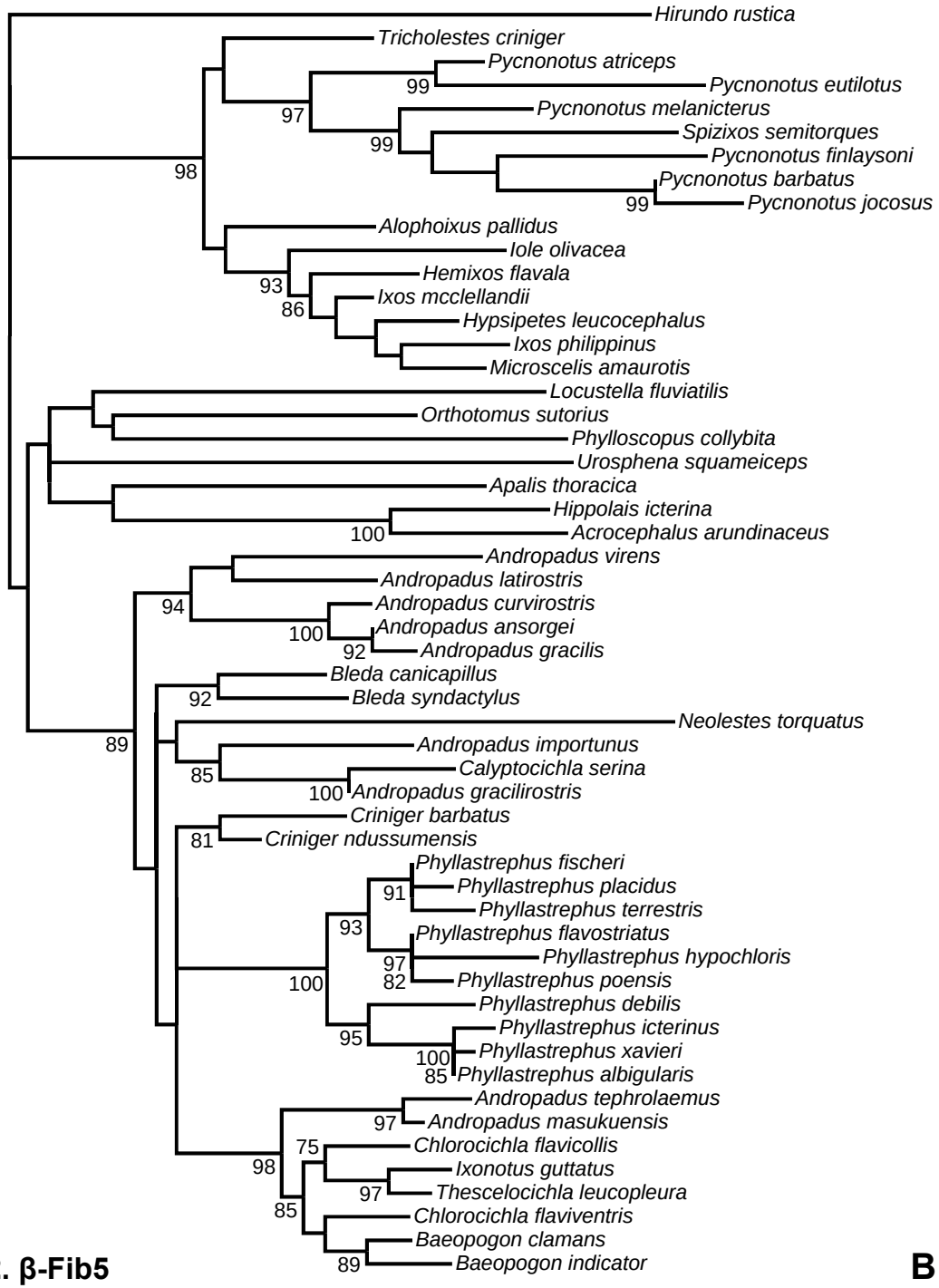
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Baeopogon indicator
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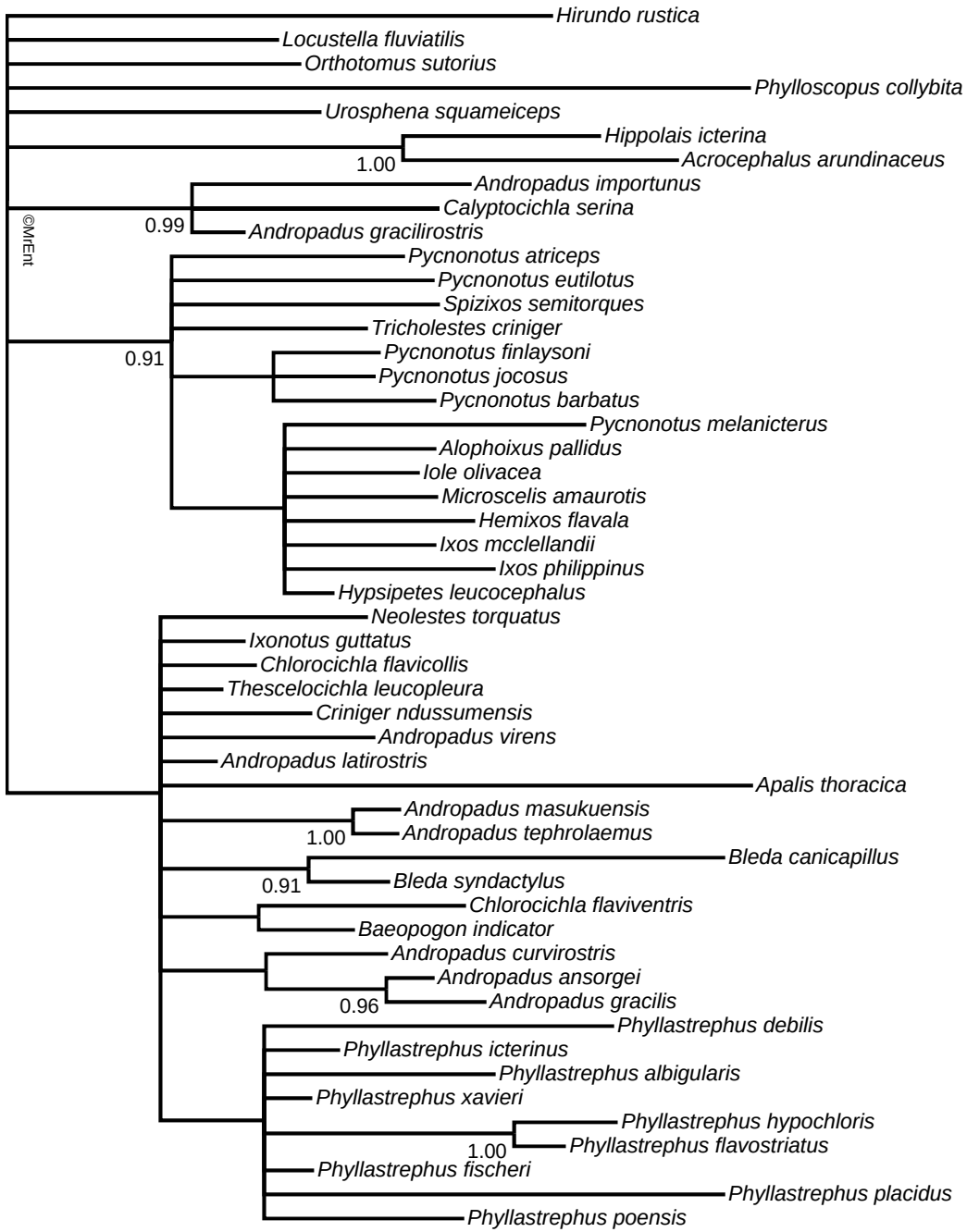
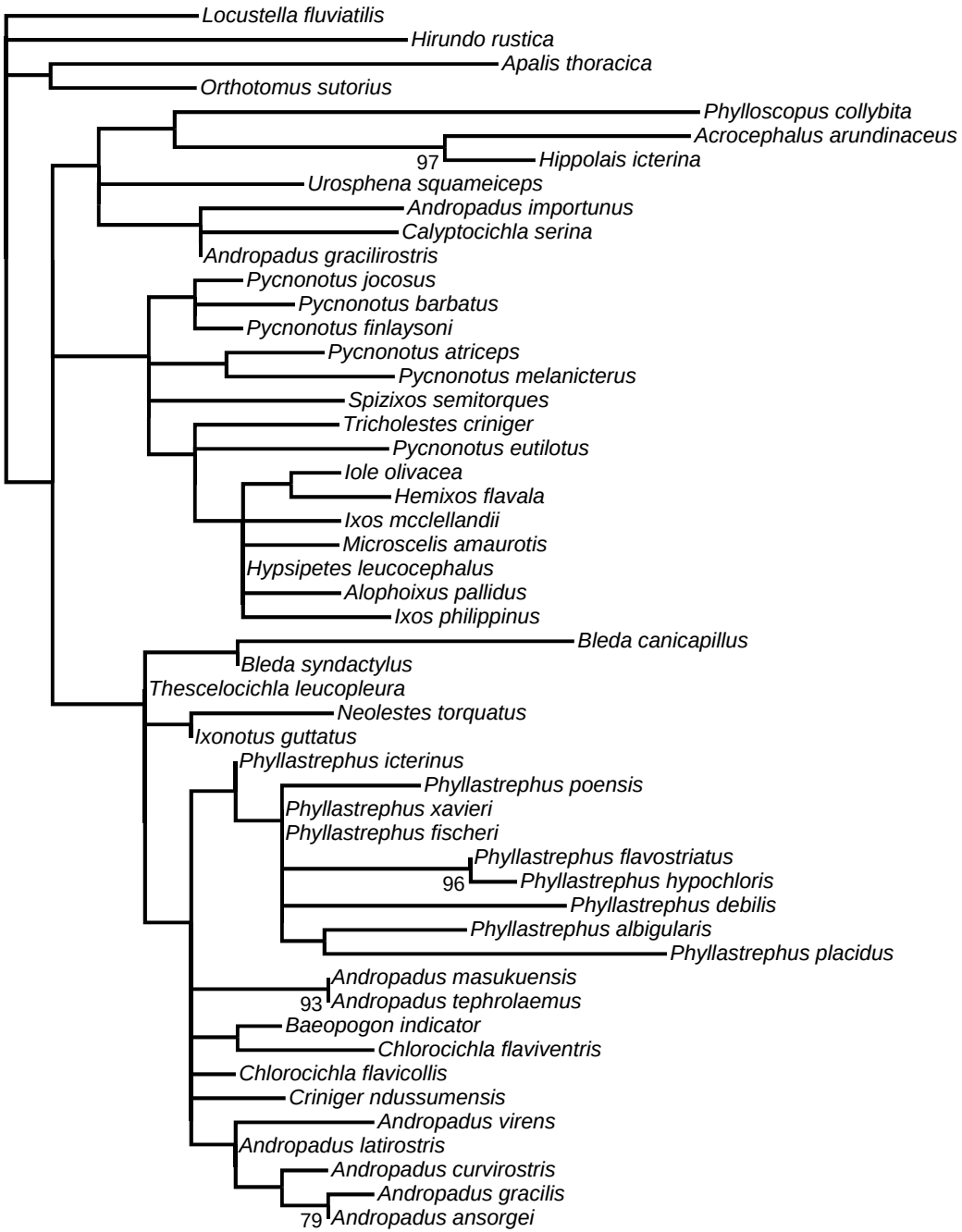
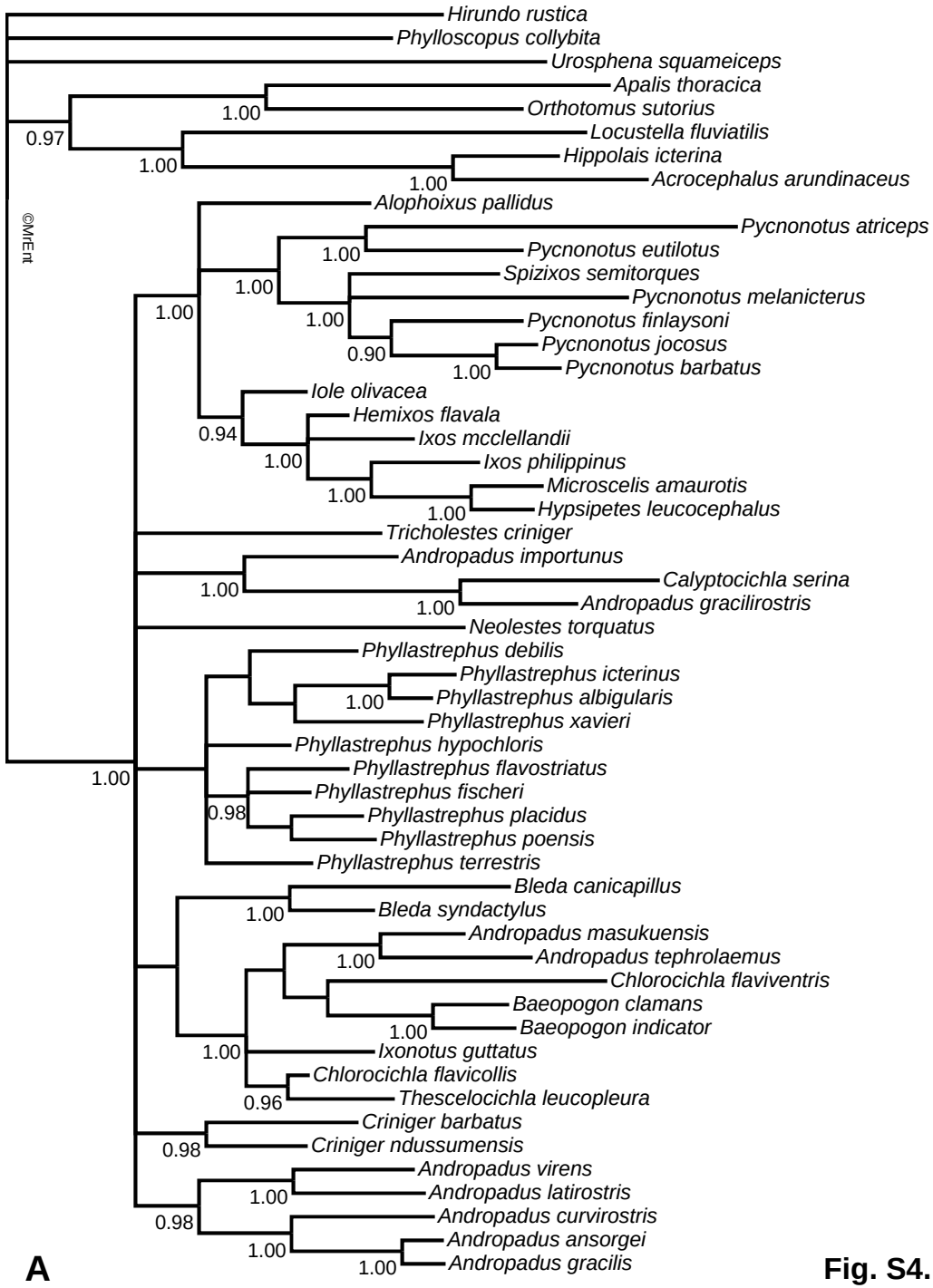
Fig. S2. β-Fib5





A **Fig. S3. β-Fib7** **B**



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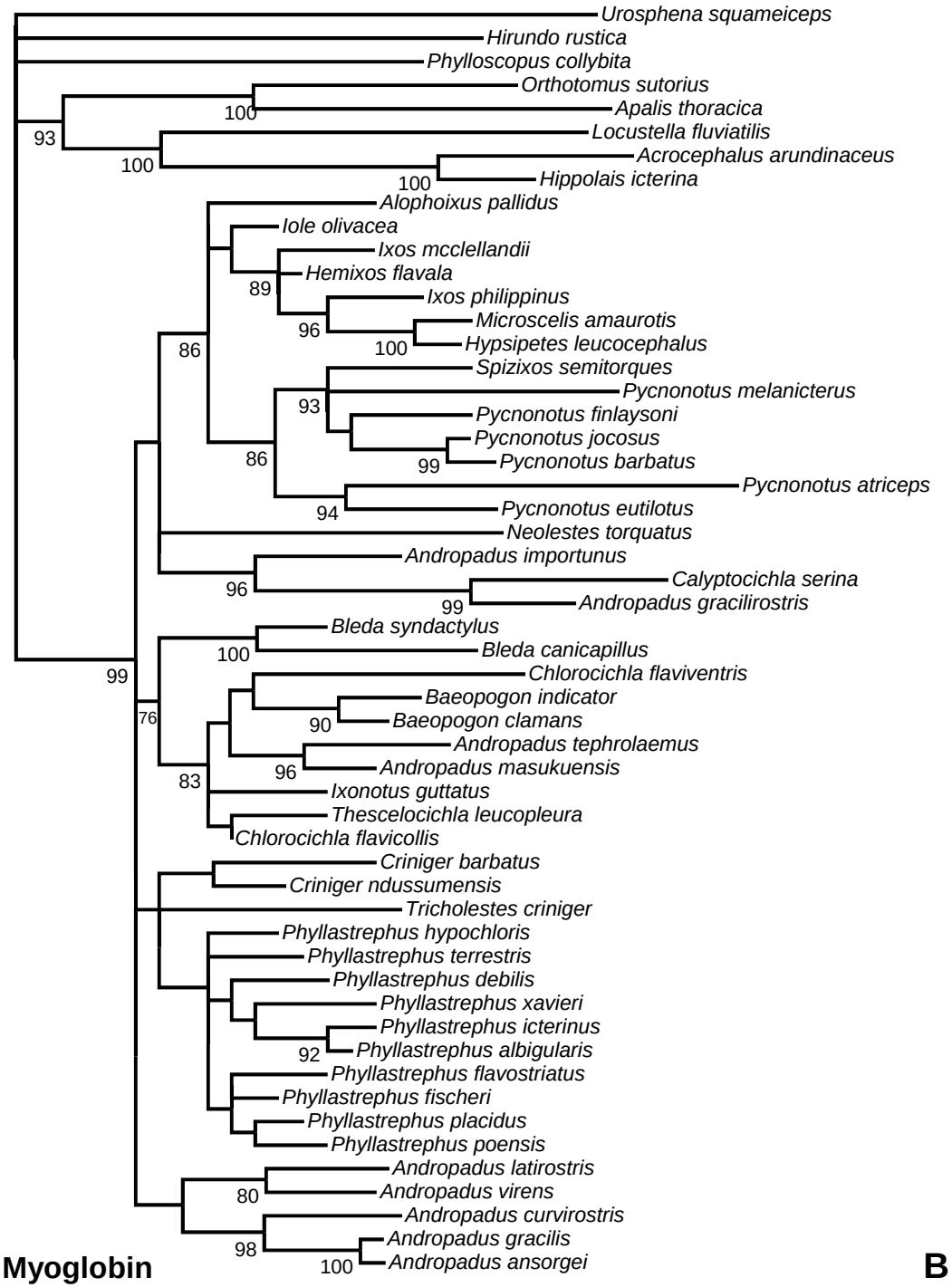

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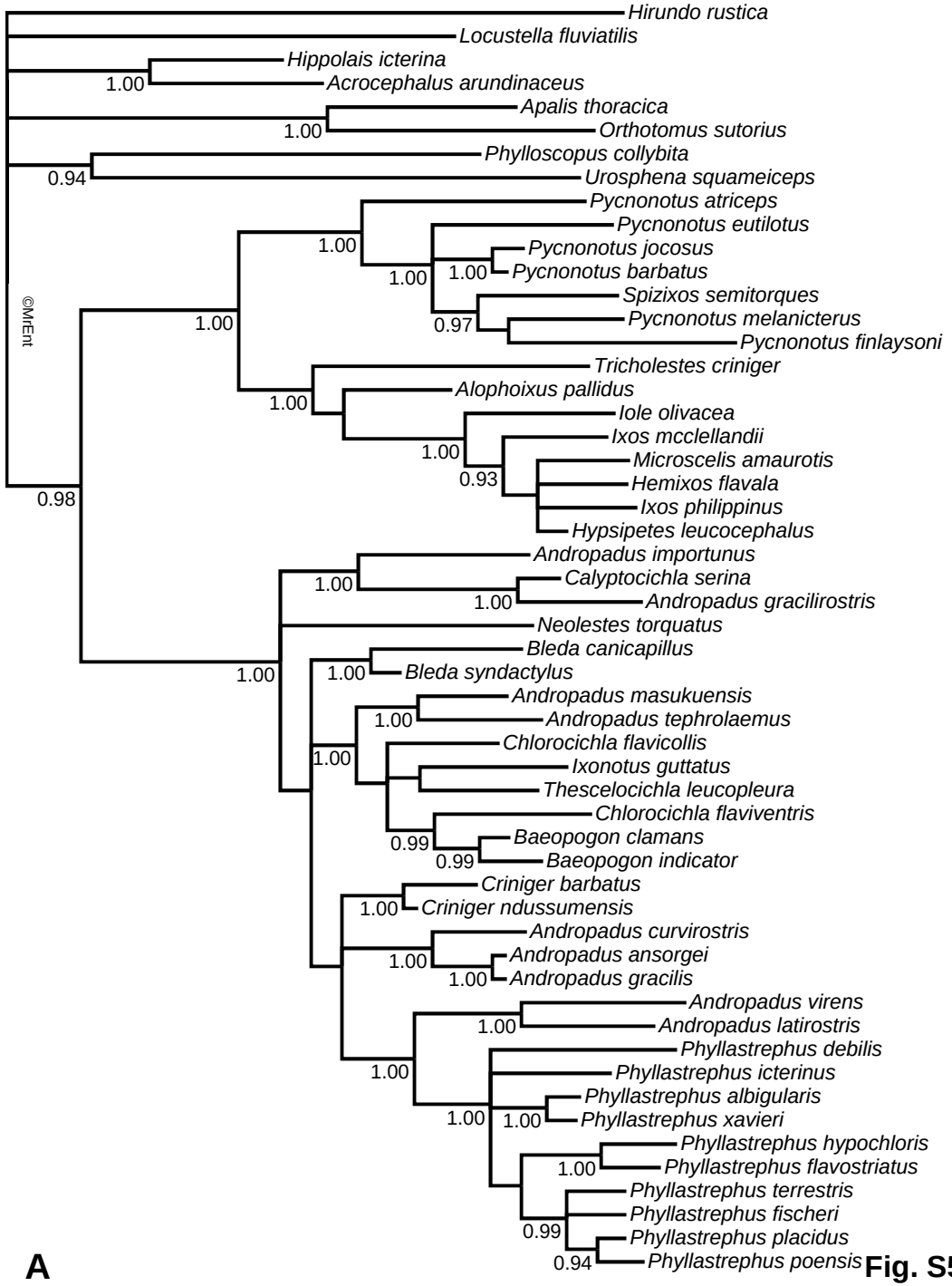
Fig. S4. Myoglobin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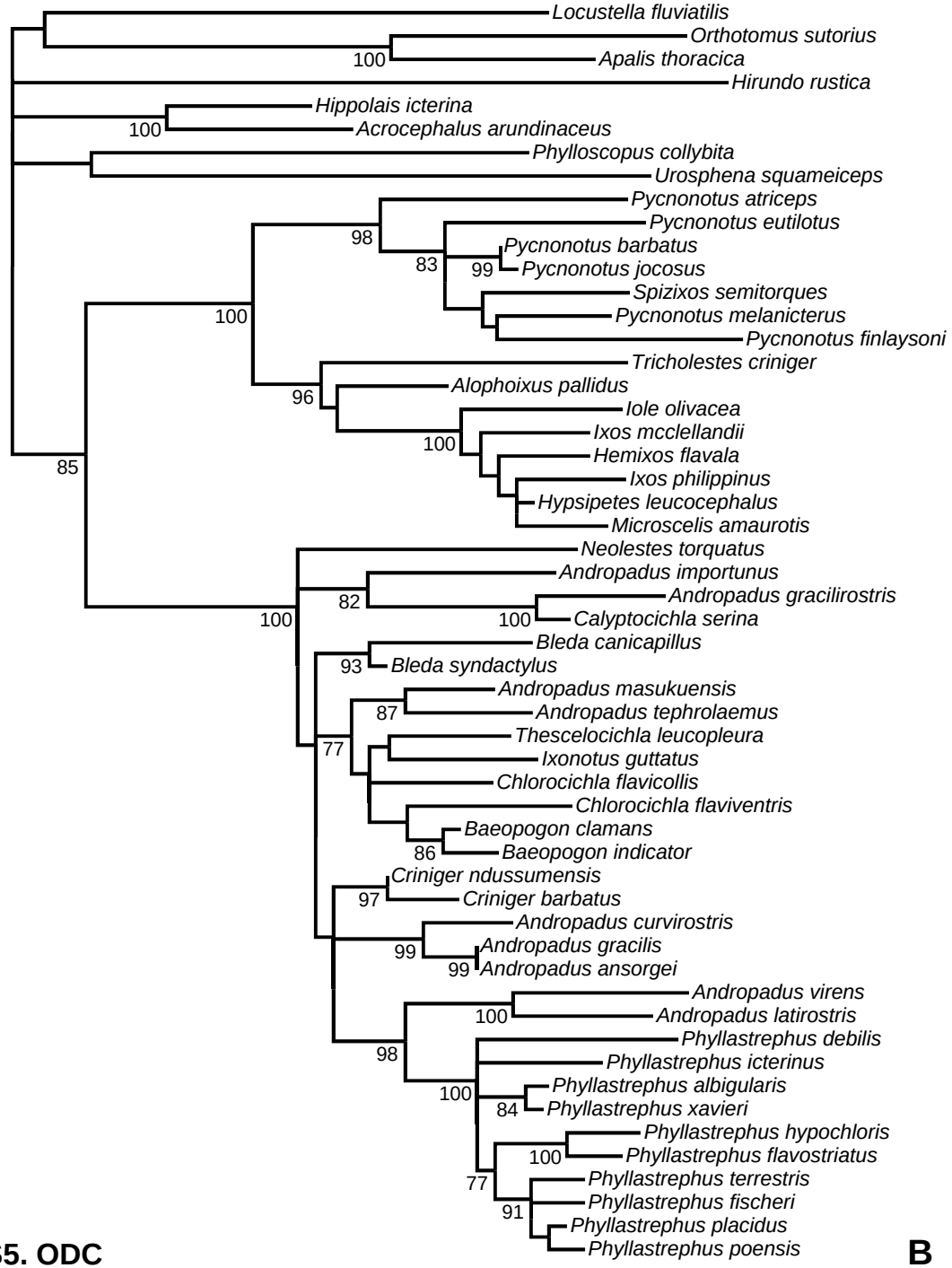
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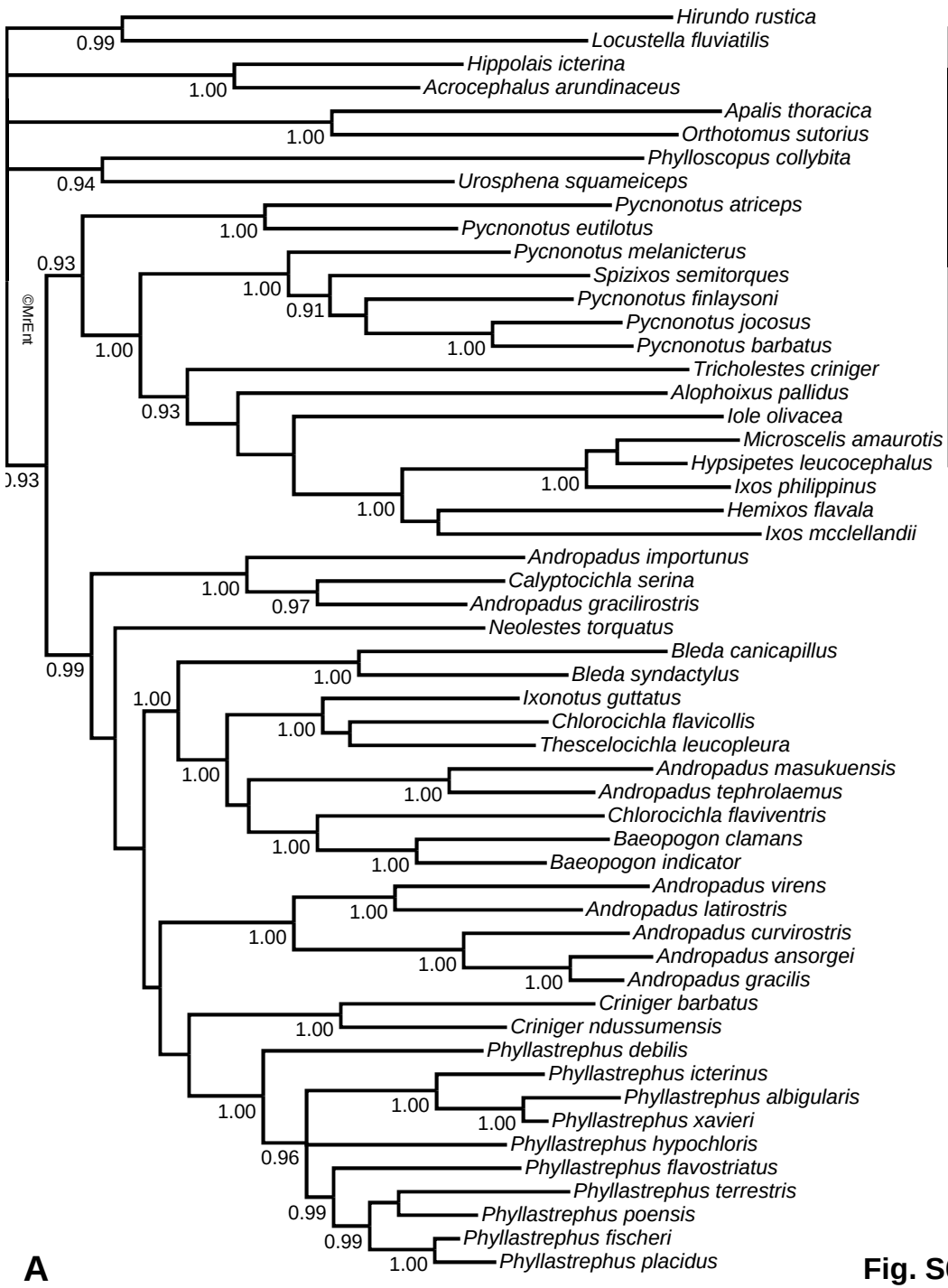
Fig. S5. ODC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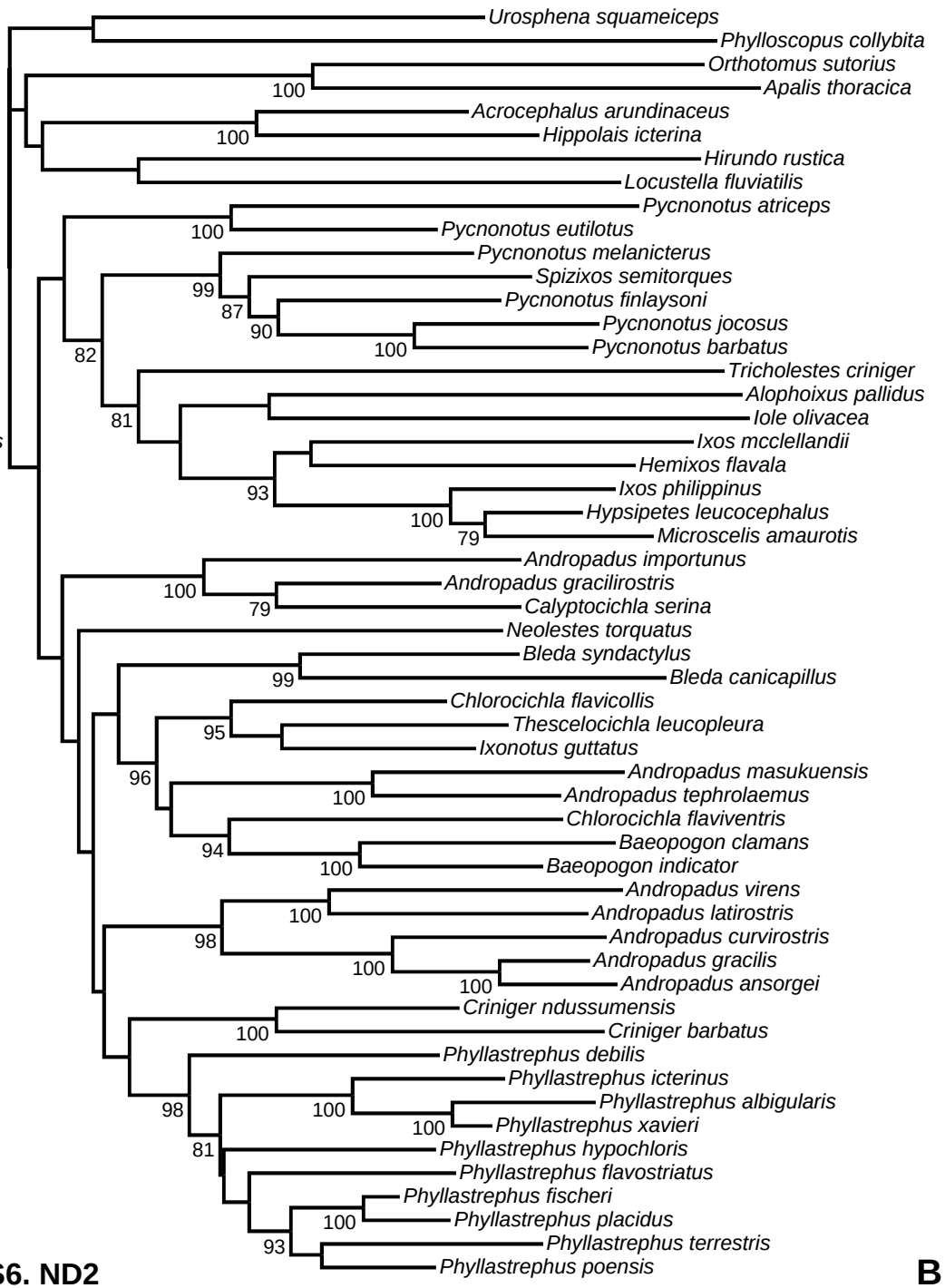
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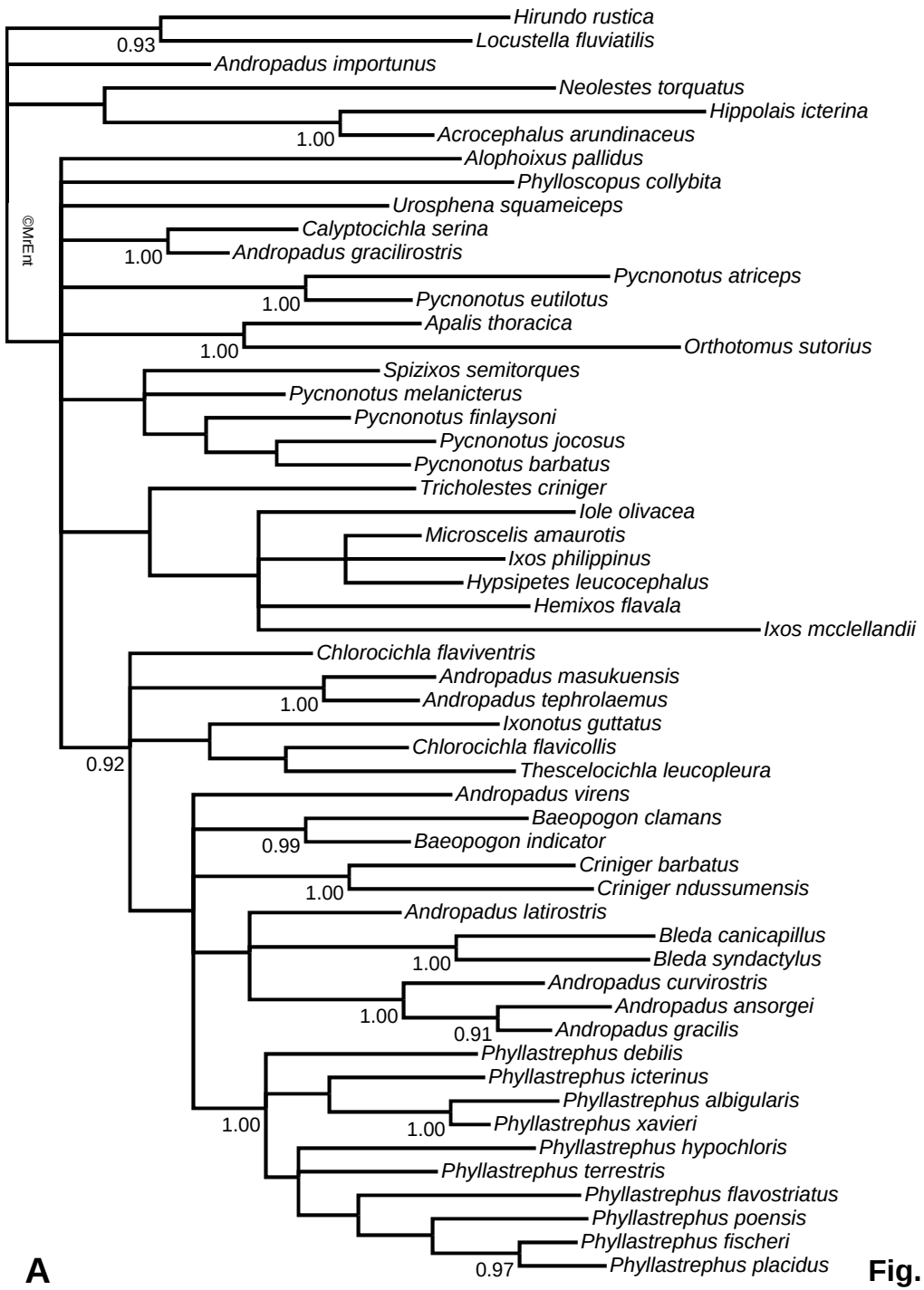
Fig. S6. ND2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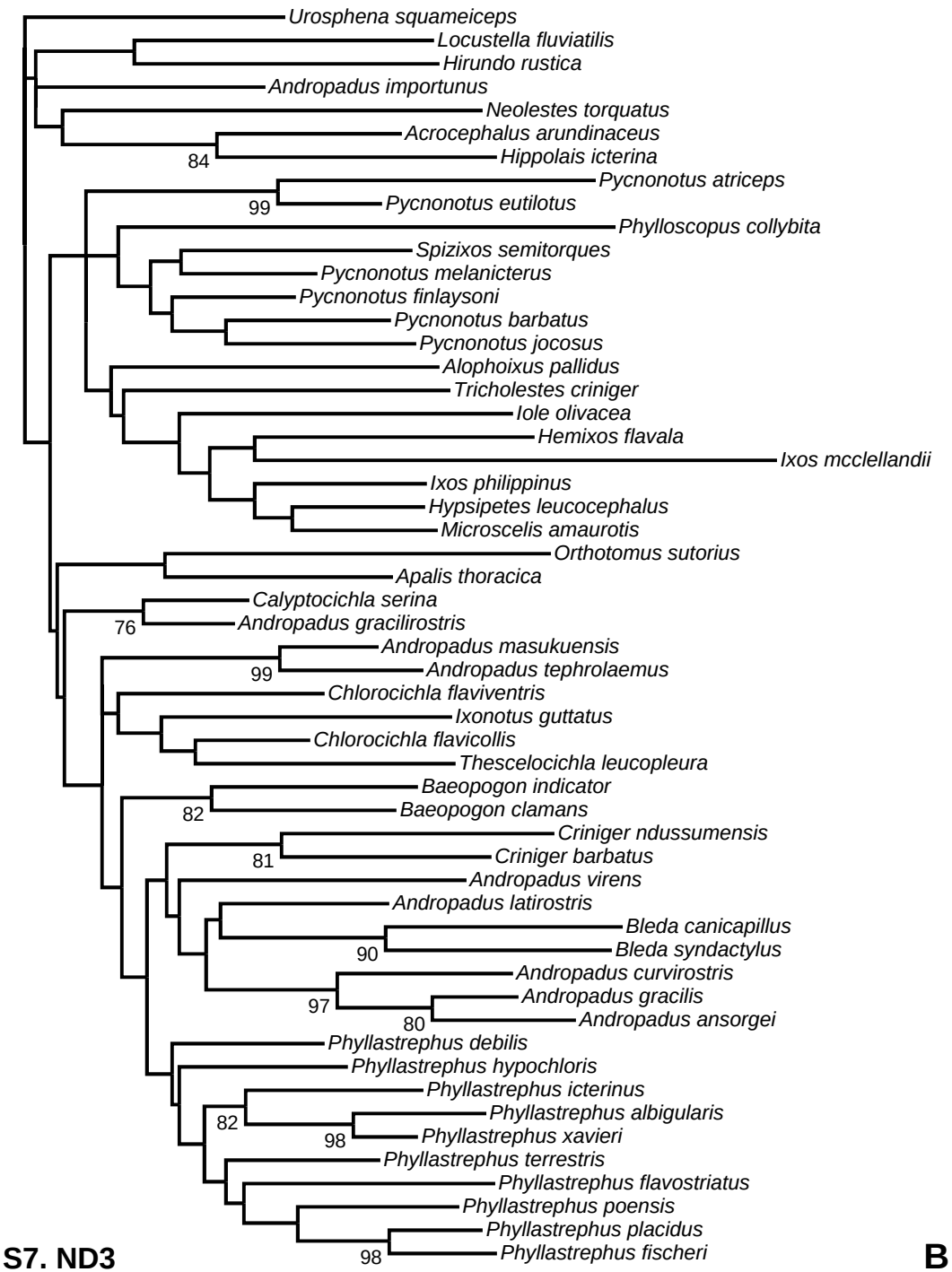
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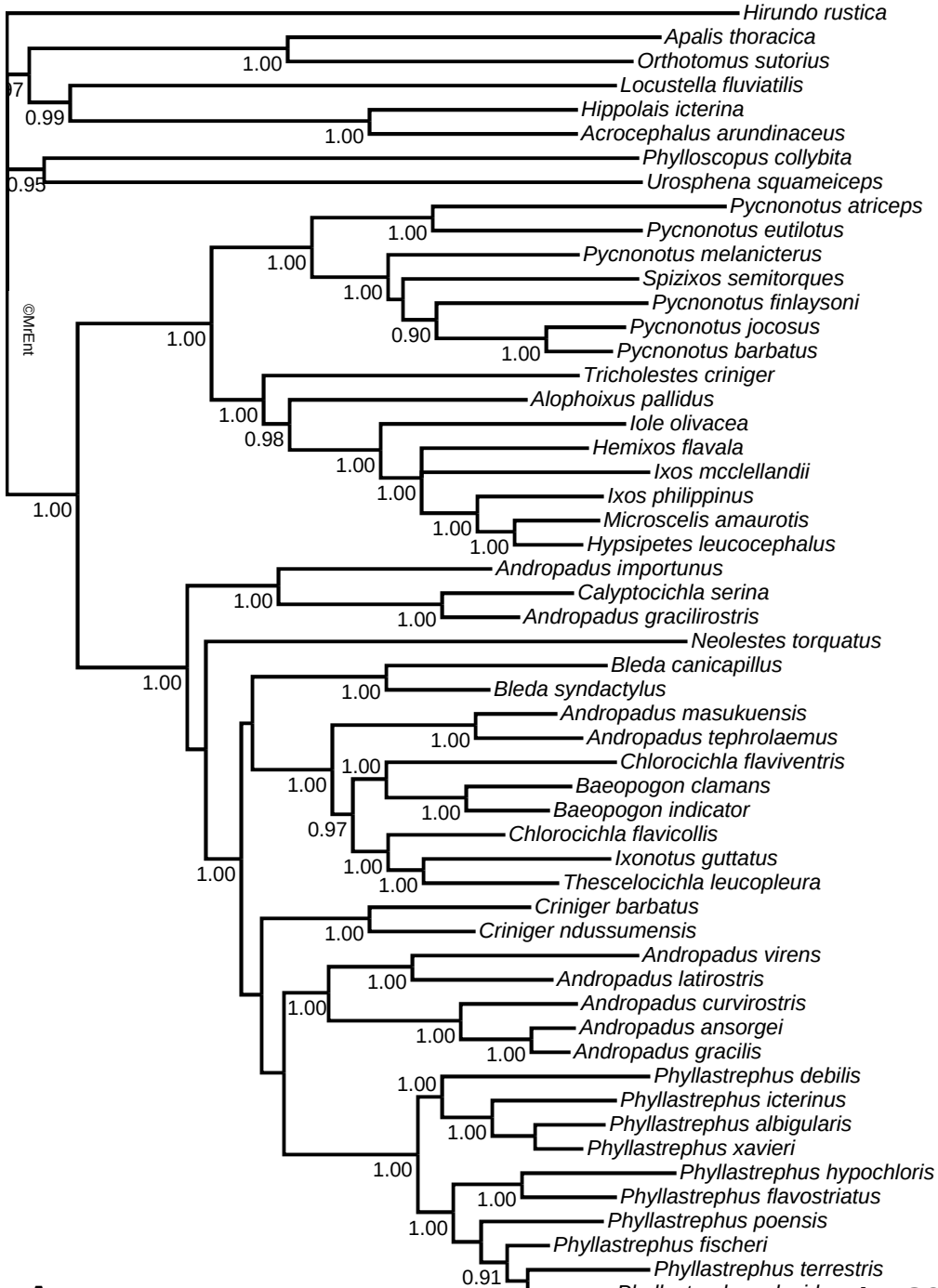

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Fig. S8. without ND2

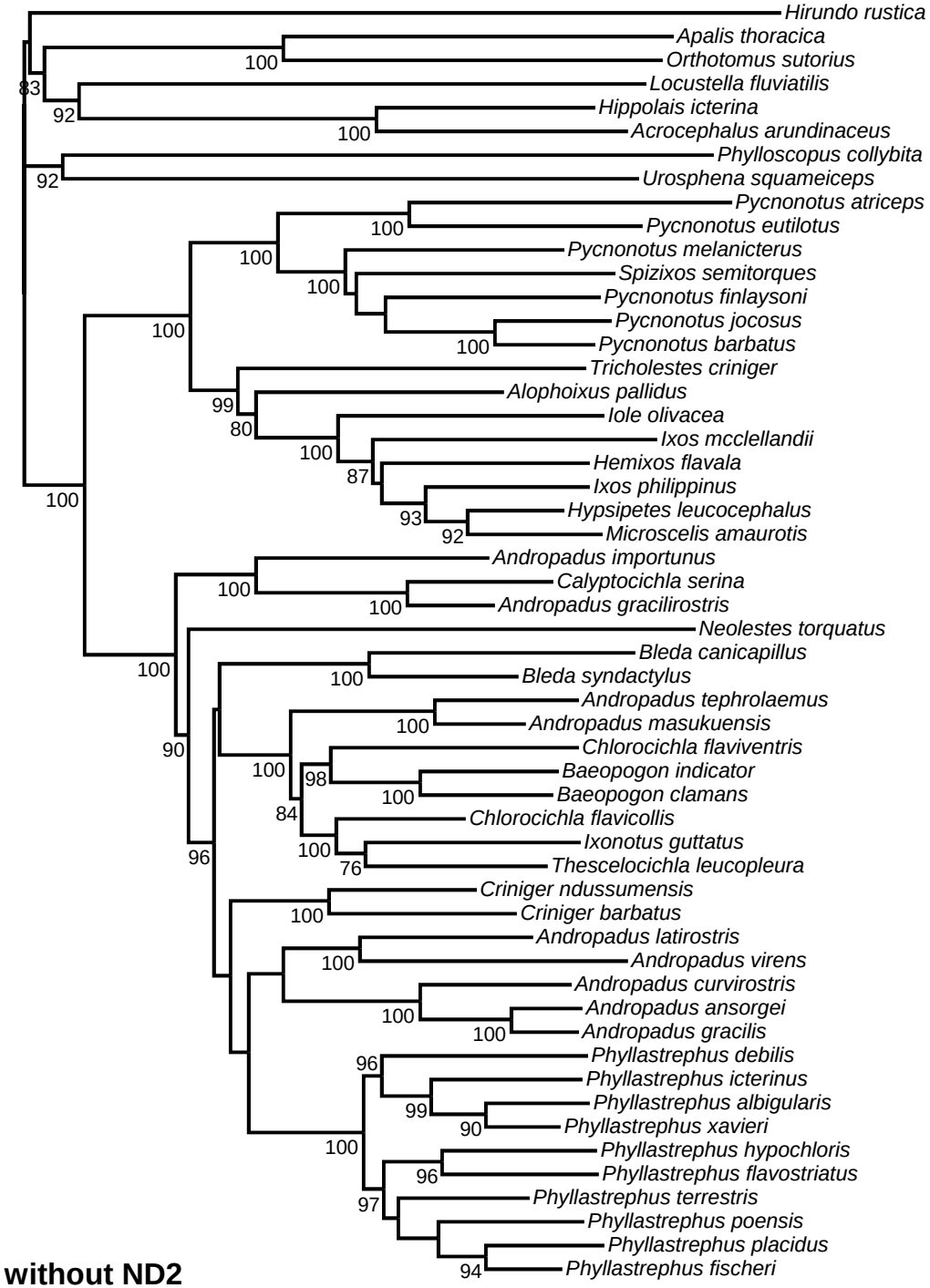

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Table S1. Primer pairs used for the amplification and sequencing of the longer genes of *Neolestes torquatus* (β-fibrinogen intron 5, myoglobin intron 2, ornithine decarboxylase introns 6-7 and NADH dehydrogenase II). For all combinations, the amplification profile was: initial denaturation 5' at 95°C, 40 cycles of denaturation 40" at 95°C, annealing 40" at the temperature indicated for each primer pair, extension 60" at 72°C, with a final extension of 5' at 72°C. ND3 and β-Fib7 were short enough for direct amplification using standard primers (see main text). [1]: Fuchs *et al.* 2004; [2]: Irestedt *et al.* 2002; [3]: Allen & Omland 2003 (see the main text for the full references).

Forward		**Reverse**		**Annealing Temp.**
Fib5 [1]	5'-CGCCATACAGAGTATACTGTGACAT-3'	bFib5-R325	5'-AAGGATGrCCCTGGTCTTTTsTC-3'	56
bFib5-F292	5'-TGGCTCATTTCTTACCCTGCTCCA-3'	Fib6 [1]	5'-GCCATCCTGGCGATTCTGAA-3'	56
Myo2 [2]	5'-GCCACCAAGCACAAGATCCC-3'	Myo-R180	5'-TGAGCCTTTTCTGTGCCTCCTGCT-3'	59
MyoF138	5'-CAGTGAGCTCTCCCTCAAGTCCA-3'	MyoR340	5'-TCCCTTGTGTCCGGTCACTGACA-3'	59
MyoF291	5'-AGCCTATGCATGCCTGGGAAACTG-3'	MyoR546	5'-GGAGCCTGGGCTAGGCAGAAGCA-3'	59
MyoF493	5'-GGTCTACTCAAGGTCATGAAGCA-3'	Myo3F [2]	5'-AAGTCATTATCAAGGTCCTTGCTGAA-3'	61
OD6 [3]	5'-GACTCCAAAGCAGTTTGTCGTCTCAGTGT-3'	ODC-R255	5'-TGTACATCCACTTCCAACGTGGAA-3'	57
ODC-F202	5'-ACTAATTTGCCAAATAGCAAGTGATA-3'	ODC-R506	5'-ATTGAGCTRCCARTTTTAGTGCAT-3'	56
ODC-F469	5'-AGCTTACTTTGACCAGCTTGGCAA-3'	OD8R [3]	5'-ATTGGTGGTGGCTTCCCTGGCTCTGAAGA-3'	58
ND2-ExtF	5'-AGCTATCGGGCCCATACCCCGAA-3'	ND2-R387	5'-TGGTGGGAATTTTATGGCTGTGGA-3'	58
ND2-F308	5'-AAAACTAGGACTAGCCCCCTTCCA-3'	ND2-R571	5'-TTTGGGGCTGTAGACTATGACGA-3'	58
ND2-F476	5'-CTCTGCAGCCCTAGGCGGAT-3'	ND2-R768	5'-AGTCATTTGGGGAGGAAGCCTGT-3'	58
ND2-F701	5'-GAGCAAAAACCCCAGCTTTAAGCGC-3'	ND2-R873	5'-TGCGCAGTATGCAAGTCGGAGGTA-3'	58
ND2-F828	5'-GTAGCAACAATCATCGCCCTCCT-3'	ND2-ExtR	5'-TTGAAGGCCTTCGGTTTAGGTGA-3'	56

Table S2. Sequence characteristics of the six genes analyzed.

Locus	**βFib5**	**βFib7**	**Myoglobin**	**ODC**	**ND2**	**ND3**
Alignment length	611	296	734	787	1041	351
Number of variable bases (%)	198 (32.4%)	98 (33.1%)	291 (39.6%)	337 (42.8%)	644 (61.9%)	199 (56.7%)
Number of parsimony informative bases (%)	150 (24.5%)	41 (39.6%)	133 (18.1%)	162 (20.6%)	577 (55.4%)	181 (51.6%)
% A nucleotides (range)	29.1 (27.6-30.1)	33.4 (25-37.2)	28.0 (27.3-29.9)	28.0 (27.0-30.0)	30.4 (27.7-33.4)	28.4 (24.9-32.2)
% C (range)	17.1 (16.1-18.0)	18.5 (12.9-25)	22.4 (21.2-23.2)	16.8 (15.4-17.9)	34.5 (31.7-37.0)	33.2 (30.5-36.2)
% G (range)	21.4 (20.0-22.6)	16.8 (9.57-25.0)	23.0 (22.0-23.7)	20.4 (19.5-21.4)	11.1 (8.83-12.8)	13.6 (11.7-16.2)
% T (range)	32.3 (31.5-34.2)	31.3 (25.0-38.0)	26.6 (25.7-27.9)	34.8 (33.5-36.5)	24.0 (21.8-26.0)	24.8 (22.8-27.4)
χ^2 (d.f. = 159)	12.25 (P = 1.00)	90.37 (P = 0.99)	10.60 (P = 1.00)	18.88 (P = 1.00)	131.84 (P = 0.94)	56.50 (P = 1.00)
Selected substitution model	GTR+Γ	GTR+Γ	HKY+Γ	GTR+Γ	GTR+Γ+I	GTR+Γ+I