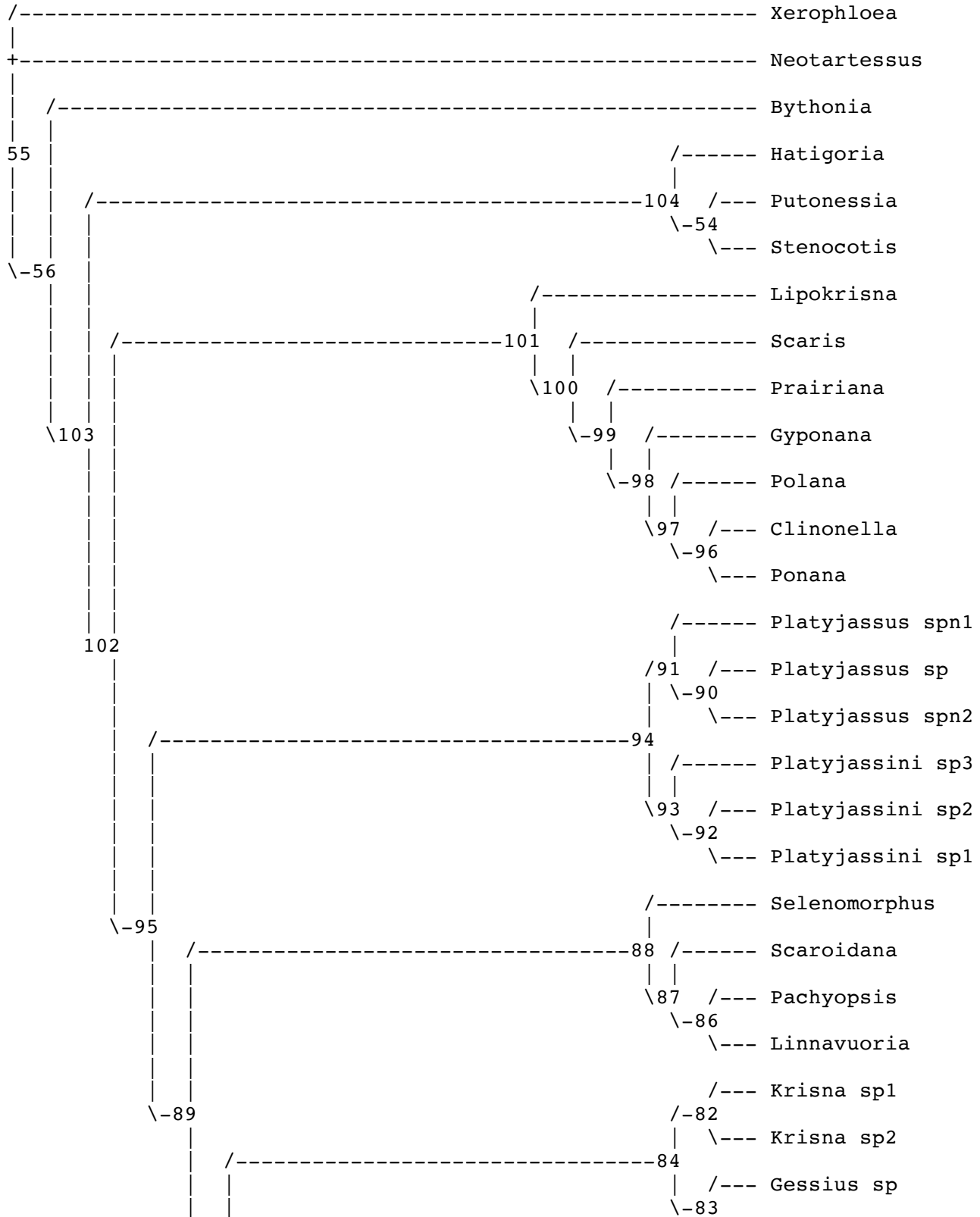
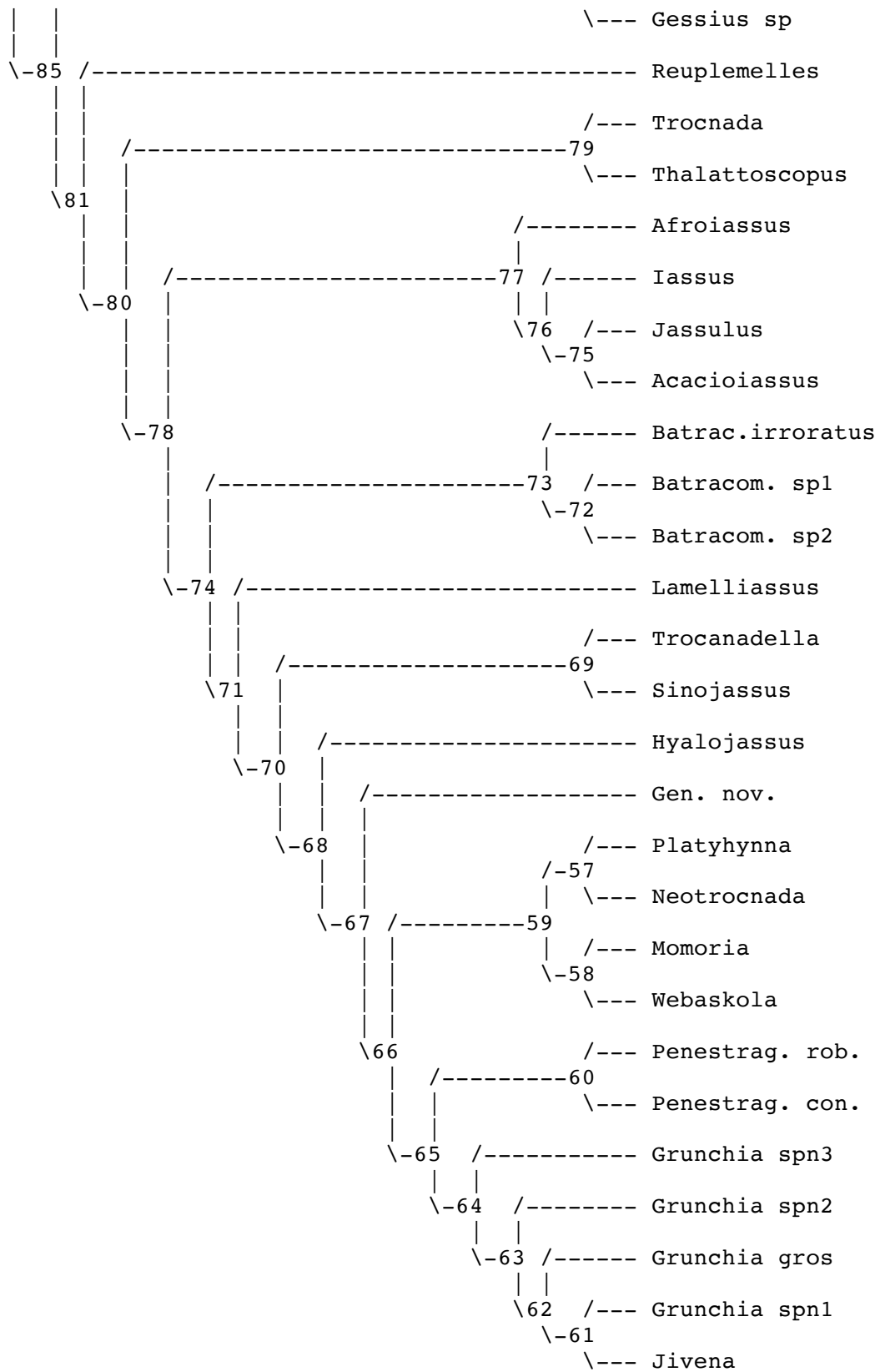


Appendix S1. Morphological apomorphies.

Numbered nodes on the following tree diagram correspond to those in the list of apomorphies given below. ACCTRAN character optimization was used.

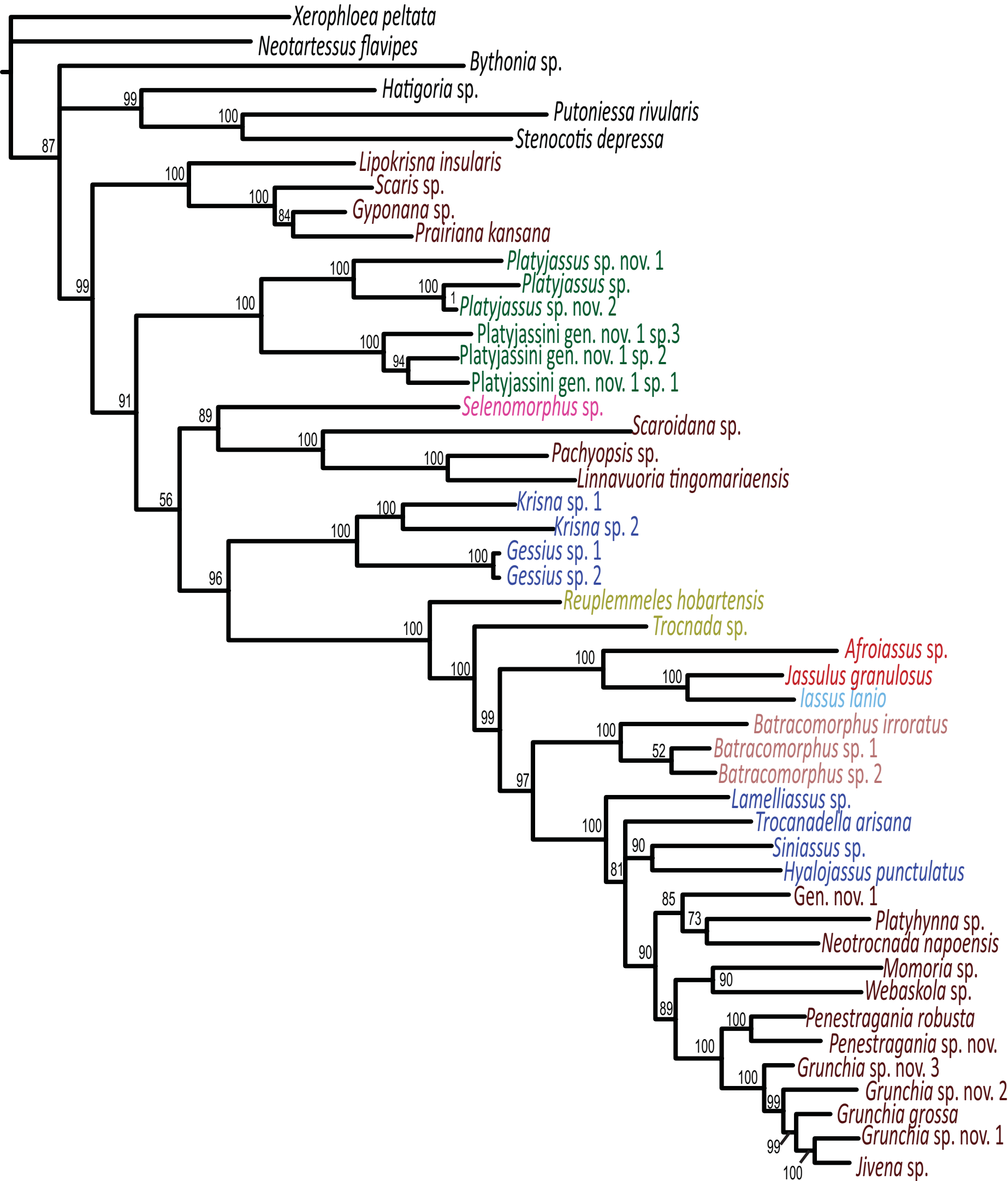




Apomorphy list (character number from S3 followed by state in parentheses; non-homoplasious changes indicated in **bold**). Nodes not listed were resolved on the trees resulting from analysis of combined DNA+morphological data but lack morphological synapomorphies.

node	apomorphies
104	47(1), 61(1), 67(1), 69(0)
103	17(1), 42(1), 43(1), 53(1)
102	16(0), 19(1), 34(1), 44(0), 46(1), 49(1), 57(1), 73(1), 91(1)
100	13(0), 16(1), 19(0), 21(1), 41(0), 49(0), 57(0), 67(2), 83(2)
99	69(0), 79(1), 81(0)
98	8(1), 76(1)
97	7(0), 16(0), 81(1)
95	37(2), 76(1), 77(0)
94	5(1), 6(1), 13(0), 21(1), 29(2), 35(1), 38(1), 41(0), 48(1)
93	57(0), 82(1)
92	50(2), 70(1), 76(0)
91	15(0), 22(1), 34(0), 84(1)
90	21(0), 77(1)
89	61(1), 81(0), 90(1)
88	3(1), 34(0), 37(0), 42(0), 69(0), 70(2), 73(0)
87	4(0), 7(0), 13(2), 18(1), 19(0)
86	27(1), 45(1), 47(1), 70(0), 76(0)
85	76(0)
84	39(1), 47(1), 50(2), 54(1)
83	4(0), 7(0), 77(1)
81	16(1), 17(2), 19(0), 36(1) , 37(1), 38(1), 51(1) , 81(2)
80	1(0), 2(0), 4(0), 7(0), 13(2), 29(1), 35(1), 46(0), 52(1), 57(0), 73(0), 76(1), 77(1), 82(1)
79	3(1), 42(0), 50(1), 81(1)
78	33(1), 45(1)
77	52(0), 53(0), 71(1), 73(1), 78(0), 81(0), 88(1)
76	17(1), 37(0), 42(0), 44(2), 45(0), 47(1), 69(0), 89(1)
75	16(0), 33(0), 34(0), 43(0)
74	59(1)
73	50(1)
71	23(1), 33(0), 61(0), 62(1.000 1), 67(1), 72(1), 74(0), 75(1), 76(0)
70	34(0), 42(0), 58(1), 69(0), 81(1), 82(0)
69	56(2), 59(0)
68	17(1), 27(1), 28(1), 67(0)
67	33(1), 73(1), 77(0)
66	23(0), 29(0)
65	67(1), 68(1.000 1), 85(1)
60	32(1), 59(0), 63(1), 77(1), 87(1)
64	50(1), 55(1), 70(1), 81(0)
63	81(2)
62	54(1), 77(1), 79(1)
61	53(0)
59	17(2), 28(0), 72(0), 75(0), 79(1)
58	32(1), 54(1), 80(1.000 1), 87(1)
57	15(0), 22(1), 29(1), 35(0), 37(0), 53(0), 82(1), 90(0)
56	20(0), 41(1), 48(0), 49(0), 52(0), 73(0), 81(1)
54	3(1), 20(1), 37(0), 42(0), 53(0), 67(2), 81(0)
<i>Acacioiassus</i>	44(4), 47(0), 69(1), 81(1)
<i>Afroiassus</i>	23(1)
<i>Batracomor</i> sp1	17(1), 28(1), 29(0), 42(0), 59(0), 76(0), 77(0), 82(0)
<i>Batracomor</i> sp2	45(0)

Bythonia 1(0), 2(0), 3(1), 9(1), 27(1), 50(2), 83(1)
Clinonella 19(1), 23(1), 34(0), 40(0), 50(2)
Grunchia gros 44(1), 81(0)
Grunchia sp.n.1 55(0), 77(0)
Grunchia sp.n.2 55(0), 56(1)
Grunchia sp.n.3 17(2), 56(2), 76(1), 82(1)
Gen.nov. 40(0), 44(1), 47(1), **60(1)**, 61(1), 64(1), 66(1)
Hatigoria 2(2), 5(1), 9(1), 13(1), 14(0), 15(0), 17(0), 24(2), 27(1), 78(0)
Hyalojassus 9(1), 18(1), 26(1), 37(0), 45(0), 72(0), 75(0), 79(1), 82(1), 83(1), 87(1)
Iassus 3(1), 28(1)
Jassulus 15(0), 23(1), 26(1), 70(1), 71(0), 82(0), 89(0)
Jivena 56(2), 59(0), 69(1), 70(0), 76(1), 81(1)
Krisna sp.1 12(1), 14(0), 29(2), 40(0), 48(1), 50(0), 85(1)
Krisna sp.2 2(0)
Lamelliassus 29(0), 54(1), 66(2), 77(0), 87(1)
Linnavuoria 4(1), 7(1), 15(0), 17(0), 20(1), 43(0), 44(1), 46(0), 77(1), 79(1), 81(2)
Lipokrisna 5(1), 12(1), 14(0), 29(2), 35(1), 40(0), 48(1), 84(1)
Momoria 10(1.000 1), 28(1), 61(1), 67(1), 75(1), 85(1)
Neotartessus 3(1), 7 (0), 19(1), 39(1), 40(0), 42(1), 44(4), 46(1), 50(1), **51(2)**, 53(1), 63(1), 76(1), **80(2)**
Neotrocnada 23(1), 27(0), 33(0), 47(1), 59(0), 61(1), 64(1), 66(1), 76(1), 77(1), 81(0)
Pachyopsis 48(1), 69(1)
Platyhyinna 1(1), 2(2), 4 (1), 5 (1), 13(0), 24(1), 26(1), 29(2), 34(1), 44(3), 50(2), 58(0), 72(1), 79(0)
Platyjassus sp. 19(0), 22(0), 24(3), 28(1), 41(1), 48(0), 52(1), 69(0), 74(0), 76(0), 81(0)
Platyjassus spn1 29(0), 40(0), 84(2), 91(2)
Platyjassus spn2 34(1), 47(1), 70(1), 85(1)
Platyjassini sp1 12(1), 16(1), 19(0), **65(1)**, 83(2)
Platyjassini sp2 21(0), 22(1), 29(0), 82(0)
Platyjassini sp3 5(0), 6 (0), 35(0), 48(0), 57(1), 83(1), 91(0)
Polana 4(0), 8 (0), 63(1), 83(0), 84(1)
Ponana 7(1), 59(1)
Prairiana 15(0), 84(1)
Putonessia 4(0), 7(0), 18(1), 41(0), 46(1), 47(0), 52(1), 58(1), 63(1), 71(1), 81(2)
Reuplemmeles 5(1), 12(1), 40(0), 48(1), 70(1), 83(2), 90(0)
Scaris 4(0), 7(0), 23(1), 50(2), 61(1), 63(1), 77(0)
Scaroidana 42(1), 54(1)
Selenomorphus 81(2), 88(1)
Siniassus 33(1), 66(2), 70(1), 85(1)
Stenocotis 8(1), **11(1)**, 21(1), 29(1), 40(0), 43(0), 48(1), 49(1), 50(2), 69(1)
Thalattoscopus 7(1), 53(0)
Trocnada 1(1), 16(0), 22(1), 23(1), 44(4), 84(1)
Trocanadella 16(0), 45(0), 54(1), 75(0), 79(2), 81(0)
Webaskola 56(1), 59(0), 70(1), 77(1), 81(0)
Xerophloea 2(2), 5(1), 13(0), 15(0), 17(1), 24(2), 37(0), 43(1), 67(2), 69(0), 79(1)



0.03

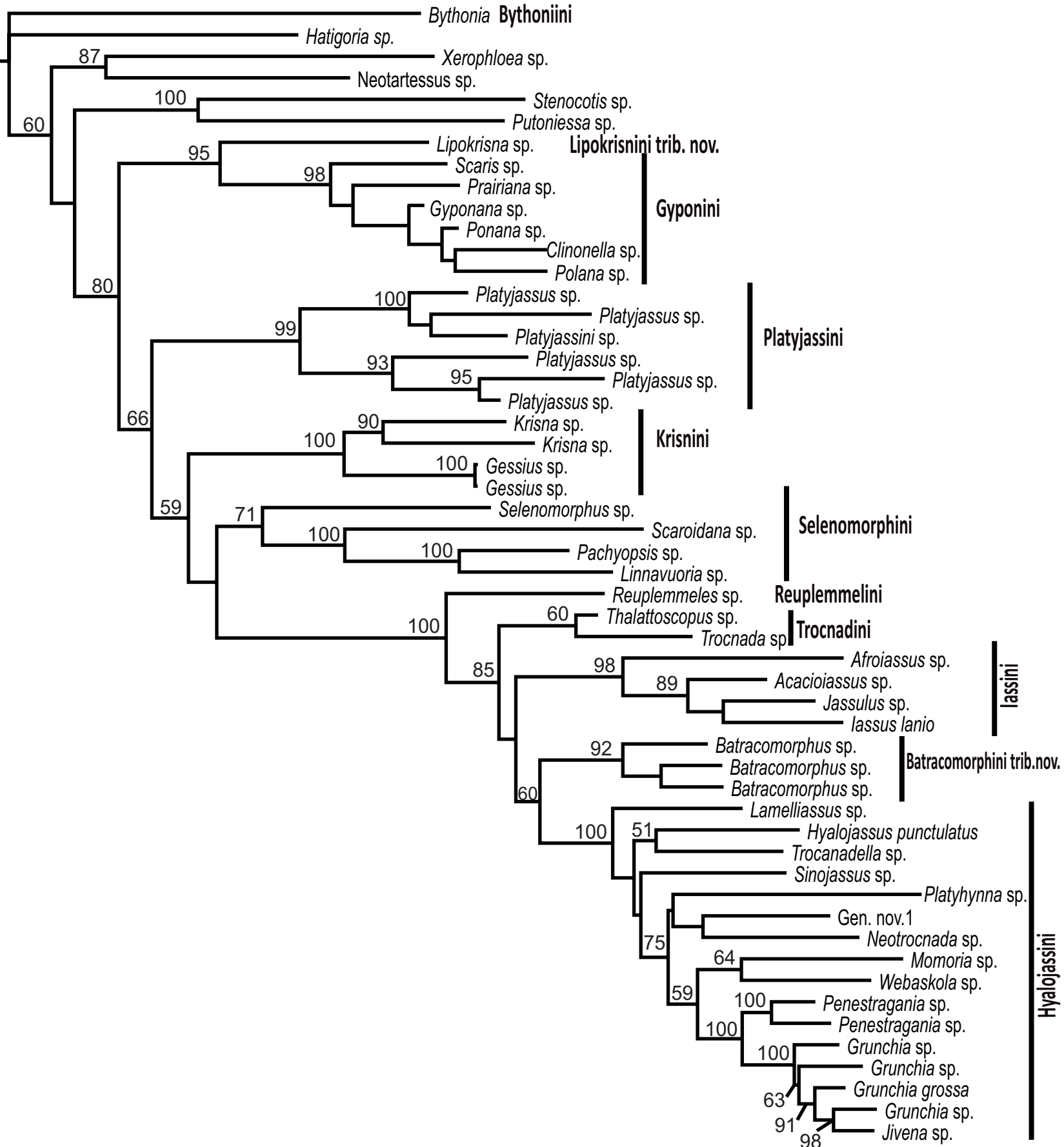


Table S1. List of taxa and DNA sequences included in the study

Taxa	Family	Voucher ID	Location	GenBank Accession numbers			
				28S D2	28S D8	Histone	12S
<i>Xerophloea peltata</i>	Ledrinae	LH21	North America: USA	AF304617*	AF304617*	KC753649	KC753617
<i>Neotartessus sp.</i>	Hylicinae	LH168	Asia: Taiwan	AF304663*	AF304664*	KC753646	KC753614
<i>Neotartessus flavipes</i>	Tartessinae	Ah7	Australia	AF304615*	AF304615*	KC753650	KC753618
<i>Putoniessa rivularis</i>	Tartessinae	Ah3	Australia	AF304612*	AF304612*	KC753647	KC753615
<i>Stenocotis depressa</i>	Tartessinae	Ah5	Australia	AF304613*	AF304613*	KC753648	KC753616
<i>Bythonia sp.</i>	Iassinae (Tribe Bythoniini)	PR49	South America: Ecuador	AF304673*	AF304673*	KC753651	KC753619
<i>Lipokrisna insularis</i>	Iassinae (Tribe Lipokrisnini)	IAS25	Peurto Rico	KC753577	KC753612	KC753686	–
<i>Scaris sp.</i>	Iassinae (Tribe Gyponini)	LH175	South America: Peru	KC753549	KC753579	–	–
<i>Prairiana kansana</i>	Iassinae (Tribe Gyponini)	LH20	North America: USA	KC753551	KC753581	KC753653	–
<i>Gyponana sp.</i>	Iassinae (Tribe Gyponini)	106	North America: USA	KC753550	KC753580	–	–
<i>Platyjassus sp.nov.1</i>	Iassinae (Tribe Platyjassini)	MIAS2	Madagascar	KC753558	KC753589	KC753662	KC753640
<i>Platyjassus sp.</i>	Iassinae (Tribe Platyjassini)	MIAS1	Madagascar	–	KC753588	KC753661	–
<i>Platyjassus sp.nov.2</i>	Iassinae (Tribe Platyjassini)	MIAS4	Madagascar	KC753559	KC753590	KC753663	KC753641
<i>Platyjassini gen. nov.1 sp3</i>	Iassinae (Tribe Platyjassini)	MIAS15	Madagascar	–	KC753611	KC753685	KC753645
<i>Platyjassini gen. nov.1 sp2</i>	Iassinae (Tribe Platyjassini)	MIAS13	Madagascar	–	KC753591	KC753664	KC753642
<i>Platyjassini gen. nov.1 sp1</i>	Iassinae (Tribe Platyjassini)	MIAS11	Madagascar	–	KC753610	KC753684	KC753644
<i>Selenomorphus sp.</i>	Iassinae (Tribe Selenomorphini)	LH183	New Caledonia	KC753552	KC753582	–	–
<i>Scaroidana sp.</i>	Iassinae (Tribe Selenomorphini)	PR50	South America: Ecuador	AF304677*	AF304677*	KC753654	KC753621
<i>Pachyopsis sp.</i>	Iassinae (Tribe Selenomorphini)	IAS1	South America: Peru	KC753553	KC753583	KC753655	KC753622
<i>Linnavuoria tingomariaensis</i>	Iassinae (Tribe Selenomorphini)	IAS3	South America: Peru	KC753554	KC753584	KC753656	KC753623
<i>Krisna sp.1</i>	Iassinae (Tribe Krisnini)	PR56	Asia: Thailand	AF304678*	AF304678*	KC753657	–
<i>Krisna sp. 2</i>	Iassinae (Tribe Krisnini)	IAS23	Asia: Taiwan	KC753557	KC753587	KC753660	KC753625
<i>Gessius curvatus</i>	Iassinae (Tribe Krisnini)	IAS11	Asia: Taiwan	KC753555	KC753585	KC753658	KC753624
<i>Gessius curvatus</i>	Iassinae (Tribe Krisnini)	IAS12	Asia: Taiwan	KC753556	KC753586	KC753659	–
<i>Reuplemmeles hobartensis</i>	Iassinae (Tribe Reuplemmellini)	MIAS14	Australia	KC753576	KC753609	KC753683	KC753643
<i>Trocnada sp.</i>	Iassinae (Tribe Trocnadini)	LH109	Australia	AF304636*	AF304636*	KC753665	KC753626
<i>Afroissus anteros</i>	Iassinae (Tribe Iassini)	IAS17	Africa: Zambia	KC753561	KC753593	KC753667	KC753628
<i>Jassulus granulatus</i>	Iassinae (Tribe Iassini)	IAS16	Africa: Zambia	KC753560	KC753592	KC753666	KC753627
<i>Iassus lanio</i>	Iassinae (Tribe Iassini)	MIAS9	Europe: France	KC753564	KC753596	–	KC753629
<i>Batracomorphus irroratus</i>	Iassinae (Tribe Batracomorphini)	Ah2	Asia: Taiwan	AF304583*	AF304583*	–	–
<i>Batracomorphus sp. 1</i>	Iassinae (Tribe Batracomorphini)	IAS10	Asia: Taiwan	KC753562	KC753594	KC753668	–
<i>Batracomorphus sp. 2</i>	Iassinae (Tribe Batracomorphini)	IAS14	Asia: Taiwan	KC753563	KC753595	KC753669	–
<i>Lamelliassus sp.</i>	Iassinae (Tribe Hyalojassini)	IAS21	Asia: Thailand	KC753568	KC753600	KC753673	KC753632
<i>Trocnadella arisana</i>	Iassinae (Tribe Hyalojassini)	IAS13	Asia: Taiwan	KC753565	KC753597	KC753670	–
<i>Siniassus compressus</i>	Iassinae (Tribe Hyalojassini)	IAS19	Asia: Thailand	KC753566	KC753598	KC753671	KC753630
<i>Hyalojassus punctulatus</i>	Iassinae (Tribe Hyalojassini)	IAS20	Asia: Thailand	KC753567	KC753599	KC753672	KC753631
Gen. nov. 1	Iassinae (Tribe Hyalojassini)	IAS24	South America: Peru	–	KC753601	KC753674	KC753633
<i>Platyhyyna sp.</i>	Iassinae (Tribe Hyalojassini)	LH179	South America: Peru	KC753548	–	KC753652	KC753620
<i>Neotrocnada napoensis</i>	Iassinae (Tribe Hyalojassini)	IAS26	South America: Ecuador	KC753578	KC753613	KC753687	–
<i>Momoria sp.</i>	Iassinae (Tribe Hyalojassini)	59m	South America: Peru	AF304601*	AF304601*	–	–
<i>Webaskola ecorusta</i>	Iassinae (Tribe Hyalojassini)	IAS9	South America: Peru	KC753575	KC753608	KC753682	KC753639
<i>Penestragania robusta</i>	Iassinae (Tribe Hyalojassini)	LH63	South America: Peru	AF304627*	AF304627*	KC753675	–
<i>Penestragania confusa</i>	Iassinae (Tribe Hyalojassini)	IAS2	South America: Peru	KC753569	KC753602	KC753676	KC753634
<i>Grunchia sp. nov. 3</i>	Iassinae (Tribe Hyalojassini)	IAS4	South America: Peru	KC753570	KC753603	KC753677	–
<i>Grunchia sp. nov. 2</i>	Iassinae (Tribe Hyalojassini)	IAS8	South America: Peru	KC753574	KC753607	KC753681	KC753638
<i>Grunchia grossa</i>	Iassinae (Tribe Hyalojassini)	IAS5	South America: Peru	KC753571	KC753604	KC753678	KC753635
<i>Grunchia sp. nov. 1</i>	Iassinae (Tribe Hyalojassini)	IAS6	South America: Peru	KC753572	KC753605	KC753679	KC753636
<i>Jivena sp.</i>	Iassinae (Tribe Hyalojassini)	IAS7	South America: Peru	KC753573	KC753606	KC753680	KC753637

* Numbers indicate GenBank Accession for samples not sequenced for 28S during this study

Table S2. Oligonucleotide primers used in this study

Primer	Primer sequence	Source
28SD2F	TGA CCA CGA GAC CGA TAG AA	Modified from Dietrich <i>et al.</i> (2001)
28SD2R	TTC GGG TCC CAA CGT GTA CG	Dietrich <i>et al.</i> (2001)
28SD8F	CCT CGG ACC TTG AAA ATC C	Dietrich <i>et al.</i> (2001)
28SD8R	TGT CTC CTT ACA GTG CCA GA	Dietrich <i>et al.</i> (2001)
28SD9F	GTA GCC AAA TGC CTC GTC A	Dietrich <i>et al.</i> (2001)
28SD9R	CAC AAT GAT AGG AAG AGC C	Dietrich <i>et al.</i> (2001)
HexAF	ATG GCT CGT ACC AAG CAG ACG GC	Ogden & Whiting (2003)
HexAR	ATA TCC TTG GGC ATG ATG GTG AC	Ogden & Whiting (2003)
12Sai	AAA CTA GGA TTA GAT ACC CTA TTA T	Simon <i>et al.</i> (1994)
12Sbi	AAG AGC GAC GGG CGA TGT GT	Simon <i>et al.</i> (1994)

Table S3. List of morphological characters used in phylogenetic analyses

Head

1. Body: 0, Robust, ovoid (Fig. 4E); 1, cylindrical, elongate (Fig. 4A).
2. Face: 0, much shorter than wide (Fig. 5C); 1, approximately as tall as wide (Fig. 5F); 2, taller than wide.
3. Head: 0, distinctly narrower than pronotum (Figs 5A-B); 1, subequal to or wider than pronotum.
4. Head: 0, rounded to face, transition poorly delimited (Fig. 4E); 1, with anterior margin strongly carinate, transition from crown to face well delimited (Fig. 4A-B).
5. Crown: 0, parallel margined or slightly produced (Fig. 5A); 1, strongly produced or elongate, much longer medially than next to eye (Fig. 4H).
6. Crown margin: 0, not extended across eye (Fig. 4A-E); 1, extended across eye (Fig. 4H).
7. Crown: 0, convex (Fig. 4E); 1, flat or concave (Fig. 4A).
8. Crown: 0, without oblique or longitudinal rugae; 1, with oblique and longitudinal rugae.
9. Crown and pronotum: 0, without fine setae; 1, with many fine setae.
10. Rostrum: 0, parallel sided; 1, expanded distally (Dai & Dietrich 2012: Fig. 2A).
11. Rostrum: 0, not extended to hind coxae; 1, extended to or beyond hind coxae.
12. Ocelli: 0, mesad of antennal bases (Fig. 5C); 1, laterad of antennal bases (Fig. 5D).
13. Ocelli: 0, on crown well separated from anterior margin and eyes (Fig. 5B); 1, on crown near anterolateral margin; 2, on face (Fig. 5G); 3, on crown margin (Figs 4A, 5E-F).
14. Distance from ocellus to eye: 0, equal to or shorter than own diameter from adjacent eye (Fig. 4A); 1, more than twice diameter of ocellus (Fig. 5C).
15. Head transverse striations: 0, absent; 1, present.
16. Striation development: 0, restricted to area dorsad of antennal ledges; 1, extended well ventrad of antennal ledges [scored as ? if no striations present].
17. Lateral frontal sutures: 0, well developed, extended nearly to ocelli (Figs 5D-E); 1, reduced, extended less than half distance from antennal ledges to ocelli (Fig. 5G); 2, obsolete (Fig. 5C).
18. Lower part of face: 0, not expanded in males; 1, expanded in males, anteclypeus broadened and inflated.
19. Anteclypeus apex: 0, no wider than at midlength (Figs 5D-E); 1, distinctly wider than at midlength (Figs 5C, F).
20. Anteclypeus: 0, not extended beyond gena (Figs 5C-D); 1, extended beyond gena.
21. Clypeal suture (separating anteclypeus from postclypeus): 0, well delimited (Figs 5C-G); 1, obsolete at least medially.
22. Face below antennal ledges: 0, not strongly depressed; 1, strongly depressed, horizontal (Fig. 4H).
23. Pronotum shape: 0, depressed, only slightly convex (Fig. 4A); 1, distinctly humped, becoming vertical anteriorly (Fig. 4D).
24. Pronotum texture: 0, finely transversely striate (Fig. 4H); 1, irregularly rugose; 2, coarsely punctate; 3, smooth or finely punctate (Fig. 4E).
25. Scutellum: 0, short, not extended beyond apex of clavus; 1, elongate; extended well beyond apex of clavus (Dietrich 1993: Figs 2-3).
26. Scutellum: 0, flat or only slightly convex; 1, distinctly humped.

Forewing

27. Membrane: 0, without conspicuous setae; 1, with conspicuous setae (Fig. 4C).
28. Venation: 0, well delimited (Fig. 4B); 1, obscure (Fig. 4C).

29. Venation: 0, not reticulate, without supranumerary crossveins (Fig. 4F); 1, with extra branches of vein R but otherwise not reticulate (Fig. 5H); 2, reticulate (Fig. 4B).
30. Crossvein r-m1: 0, absent (Fig. 4F); 1, present (Fig. 5H).
31. Crossvein m-cu2: 0, absent (Fig. 4F); 1, present (Fig. 5H).
32. Inner apical cell: 0, well delimited by complete submarginal vein (Fig. 5H); 1, partially delimited (Fig. 4C); 2, absent.
33. Inner apical cell: 0, same texture as other apical cells (Fig. 4F); 1, membranous, contrasting with texture of other cells (Fig. 4C).
34. Inner apical cell: 0, broad, no more than 3 times longer than wide (Fig. 4F); 1, narrow, more than 5 times longer than wide (Fig. 5J).
35. Forewing second apical cell: 0, parallel-sided or broadened distally (Fig. 5J); 1, distinctly narrowed distally (Fig. 5H).
36. Forewing CuP: 0, not recurved distally (Fig. 5J); 1, recurved distally (Fig. 5H).
37. Appendix: 0, narrow, wings not overlapping at rest (Fig. 4G); 1, broad, wings overlapping at rest (4A-D).

Hind wing

38. Veins RP and MA: 0, free, connected by crossvein (Figs 4G, 5K); 1, partially or completely confluent (Fig. 5I).
39. Submarginal vein: 0, not extended onto jugum (Fig. 5I); 1, extended onto jugum (Fig. 5K).

Legs

40. Front femur row AM: 0, with one or more preapical macrosetae; 1, without preapical macrosetae (Dai et al. 2010: Fig. 25).
41. Front femur intercalary row: 0, uniseriate; 1, multiseriate (Dai et al. 2010: Fig. 25).
42. Front femur row AV: 0, without macrosetae; 1, with several macrosetae (Dai et al. 2010: Fig. 25).
43. Front tibia row PD: 0, without well differentiated macrosetae (Fig. 4D); 1, with 3 or more well differentiated preapical macrosetae (Figs 4A-C).
44. Hind femur macrosetal formula: 0, 2+2+1; 1, 2+1+1; 2, 2+1; 3, 2+0; 4, 2+2.
45. Hind femur penultimate setal pair: 0, with setae subequal in size; 1, with posterior seta less than half length of anterior seta [score as ? if 0-1 penultimate seta present].
46. Hind tarsomere I: 0, without enlarged dorsoapical setae; 1, with at least 1 enlarged dorsoapical seta (usually a pair).
47. Hind tarsomere I row PV setae: 0, simple or absent; 1, cucullate (Dai & Dietrich 2015: Fig. 4D).

Male abdomen

48. Sternum II apodemes: 0, vestigial; 1, well developed, extended posterad past segment III.
49. Sternite VIII: 0, no longer than sternite VII; 1, distinctly longer than sternite VII.
50. Sternite VIII: 0, slightly produced apically; 1, acutely produced apically; 2, emarginate.
51. Genital capsule: 0, not or only slightly retracted into segment VII; 1, strongly retracted into segment VII, plates mostly or entirely concealed, long axis nearly vertical when everted.
52. Tergite IX: 0, short, bandlike, not continuous with pygofer lobe (Dai & Dietrich 2015: Fig. 5B); 1, long, continuous with pygofer lobe (Krishnankutty & Dietrich 2012: Fig. 28).
53. Pygofer macrosetae: 0, absent or poorly differentiated; 1, well differentiated (Fig. 5Q).
54. Pygofer: 0, without conspicuous row of setae near midlength of posteroventral margin; 1, with conspicuous row of widely spaced setae near midlength of posteroventral margin.

55. Pygofer margin: 0, without dense tuft of long, fine setae; 1, with dense tuft of long, fine setae.
56. Pygofer posteroventral marginal setae: 0, short, stout; 1, numerous long, fine setae in dense brush; 2, few short, fine, widely spaced setae (Fig. 5N) [score as ? if setae absent].
57. Pygofer: 0, without group of fine ventrolateral setae; 1, with group of long, fine ventrolateral setae (Viraktamath 2006: Fig. 60).
58. Pygofer anterodorsal margin: 0, entire; 1, emarginate near midlength (Fig. 5N).
59. Pygofer posteroventral margin: 0, convex (Figs 5M-P); 1, truncate or concave (Krishnankutty & Dietrich 2012: Fig. 27).
60. Pygofer anteroventral margin: 0, rounded, without projection; 1, with angulate projection.
61. Pygofer ventral appendage: 0, absent (Fig. 5N); 1, present (Figs 5M, O, P).
62. Pygofer ventral appendage: 0, elongate, curved dorsad in lateral view (Fig. 5M); 1, short, falcate, curved ventrad in lateral view (Figs 5O-P) [score as ? if appendage is absent]. The appendage of *Momoria* and *Baldriga* has setae and may not be homologous to that of *Pachyopsis*, etc.; the former may instead be homologous with the pseudostyles of *Grunchia*, etc.; more comparative study is needed.
63. Pygofer dorsal appendage: 0, absent; 1, present (Fig. 5Q).
64. Subgenital plate: 0, well developed (5M-Q); 1, strongly reduced or absent (Krishnankutty & Dietrich 2012: Fig. 29).
65. Subgenital plate macrosetae: 0, absent; 1, well differentiated.
66. Subgenital plates: 0, freely articulated to genital capsule and separate from each other; 1, fused to each other and genital capsule (Krishnankutty & Dietrich 2012: Fig. 29).
67. Subgenital plate shape: 0, digitiform (Figs 5O, P); 1, strongly expanded (Blocker 1975: Fig. 89); 2, flattened and depressed but not expanded (Fig. 5N).
68. Subgenital plate mesal margin: 0, not thickened; 1, thickened, forming pseudostyle (Blocker 1975: Fig. 89).
69. Subgenital plate: 0, without conspicuous long, fine setae; 1, with conspicuous long fine setae (Fig. 5Q).
70. Subgenital plate: 0, without stout apical setae; 1, with stout apical setae (Fig. 5N); 2, with row of submedial macrosetae.
71. Anal tube appendage: 0, absent; 1, present (Fig. 5P).
72. Connective: 0, well sclerotized; 1, membranous.
73. Connective: 0, platelike, with anterior lobe (Krishnankutty & Dietrich 2012: Fig. 16); 1, Y- or U-shaped (Krishnankutty & Dietrich 2012: Fig. 32); 2, straplike, linear (Dai et al. 2015: Fig. 13F) [score as ? if connective membranous].
74. Connective: 0, without median posterior stem (Krishnankutty & Dietrich 2012: Fig. 32); 1, with median posterior stem (Krishnankutty & Dietrich 2012: Fig. 16) [score as ? if connective membranous].
75. Style: 0, strongly sigmoid with prominent lateral lobe near base of apophysis (Krishnankutty & Dietrich 2012: Fig. 15); 1, linear, without lobe near base of apophysis (Krishnankutty & Dietrich 2012: Fig. 31) [score as ? if apophysis vestigial].
76. Style: 0, not serrate; 1, serrate (Dai & Dietrich 2012: Fig. 2J) [score as ? if apophysis vestigial].
77. Style: 0, without preapical tooth; 1, with preapical tooth or spine (Krishnankutty & Dietrich 2012: Fig. 15).
78. Style apophysis: 0, absent, or short (Linnavuori & Quartau 1975: Fig. 10i); 1, elongate (Fig 5O).
79. Style apex: 0, slender, acuminate (Dai et al. 2015: Fig. 13C); 1, broad [score as ? if apophysis vestigial].
80. Aedeagus: 0, articulated and closely adjacent to connective; 1, well separated from connective; 2, fused with connective [score as ? if connective membranous].

81. Aedeagus dorsal apodeme: 0, poorly developed; 1, well developed, Y- or T-shaped (Dai et al. 2015: Fig. 6D); 2, well developed, parallel-sided or tapered in posterior view (Dai et al. 2015: Fig. 13E).
82. Aedeagus apex: 0, entire (Dai & Dietrich 2015: Fig. 5F); 1, bifid (Krishnankutty & Dietrich 2012: Fig. 34).
83. Aedeagus paired distal processes: 0, absent; 1, present, preapical (Dai & Dietrich 2015: Fig. 5D); 2, present, apical.
84. Aedeagus basal process: 0, absent; 1, present, paired (Krishnankutty & Dietrich 2012: Fig. 21); 2, present, single.
85. Atrium: 0, not expanded; 1, strongly expanded laterad (Dai et al. 2010: Fig. 19).
86. Aedeagus preatrium: 0, absent or extended anterad; 1, extended posteroventrad at angle to shaft (Dai et al. 2015: Fig. 14C).
87. Intersegmental membrane between pygofer and anal tube: 0, membranous; 1, sclerotized and darkly pigmented.
88. Tergum IX: 0, truncate or emarginate; 1, triangular.
89. Ventral membrane of anal tube: 0, with few or no setae; 1, with numerous long setae (Fig. 5P).

Female genitalia

90. First valvulae dorsal sculpture: 0, strigate (Domahovski et al. 2014: Fig. 83); 1, areolate (Dai et al. 2015: Fig. 24C).
91. Second valvulae, dorsal margin: 0, with numerous irregular teeth distally; 1, with 2-3 prominent teeth (Dai et al. 2015: Fig. 24B); 2, without teeth (Dietrich 1993: Fig. 11).

Table S4. Morphological data matrix used in phylogenetic analysis

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	
<i>Xerophloea</i> sp.	1	2	0	1	1	0	1	0	0	0	0	0	0	1	0	?	1	0	0	1	0	0	0	2	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Neotartessus</i>	1	1	1	1	0	0	0	0	0	0	0	0	3	1	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Putoniessa</i> sp.	1	1	1	0	0	0	0	0	0	0	0	0	3	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
<i>Stenocotis</i> sp.	1	1	1	1	0	0	1	1	0	0	1	0	3	1	1	1	1	0	0	1	1	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0
<i>Hatigoria</i> sp.	1	2	0	1	1	0	1	0	1	0	0	0	1	0	0	?	0	0	0	0	0	0	0	2	0	0	1	0	0	1	1	0	0	0	0	0	0
<i>Bythonia</i> sp.	0	0	1	1	0	0	1	0	1	0	0	0	3	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0
<i>Lipokrisna</i> sp.	1	1	0	1	1	0	1	0	0	0	0	1	3	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	2	1	1	0	0	1	1	0	0
<i>Scaris</i> sp.	1	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	1	0	1	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Clinonella</i> sp.	1	1	0	1	0	0	0	1	0	0	0	0	0	1	1	0	1	0	1	0	1	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Polana</i> sp.	1	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Ponana</i> sp.	1	1	0	1	0	0	1	1	0	0	0	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Gyponana</i> sp.	1	1	0	1	0	0	1	1	0	0	0	0	0	1	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Prairiana</i> sp.	1	1	0	1	0	0	1	0	0	0	0	0	0	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Krisna</i> sp. 1	1	1	0	1	0	0	1	0	0	0	0	1	3	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	2	1	1	0	0	1	0	0	0
<i>Gessius</i> sp. 2	1	1	0	0	0	0	0	0	0	0	0	0	3	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Gessius</i> sp. 1	1	1	0	0	0	0	0	0	0	0	0	0	3	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Krisna</i> sp. 2	1	0	0	1	0	0	1	0	0	0	0	0	3	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
<i>Platyjassus</i> n.	1	1	0	1	1	1	1	0	0	0	0	0	0	1	0	?	1	0	1	0	0	1	0	0	0	0	0	0	2	1	1	0	0	1	1	0	0
<i>Platyjassus</i> sp.	1	1	0	1	1	1	1	0	0	0	0	0	0	1	0	?	1	0	0	0	0	0	0	3	0	0	0	1	2	1	1	0	0	0	1	0	0
<i>Platyjassus</i> n.	1	1	0	1	1	1	1	0	0	0	0	0	0	1	0	?	1	0	1	0	1	1	0	0	0	0	0	0	1	1	0	0	0	?	?	0	0
<i>Platyjassini</i> ge	1	1	0	1	0	0	1	0	0	0	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	2	1	1	0	0	1	0	0	0
<i>Platyjassini</i> ge	1	1	0	1	1	1	1	0	0	0	0	0	0	1	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	1	1	0	0	1	1	0	0
<i>Platyjassini</i> ge	1	1	0	1	1	1	1	0	0	0	0	1	0	1	1	1	1	0	0	0	1	0	0	0	0	0	0	0	2	1	1	0	0	?	?	0	0
<i>Selenomorphu</i>	1	1	1	1	0	0	1	0	0	0	0	0	3	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Pachyopsis</i> sp.	1	1	1	0	0	0	0	0	0	0	0	0	2	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0
<i>Scaroidana</i> sp.	1	1	1	0	0	0	0	0	0	0	0	0	2	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Linnavuoria</i> sp.	1	1	1	1	0	0	1	0	0	0	0	0	2	1	0	?	0	1	0	1	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0
<i>Trocnada</i> sp.	1	0	1	0	0	0	0	0	0	0	0	0	2	1	1	0	2	0	0	0	0	1	1	0	0	0	0	0	1	1	1	0	0	1	1	1	1
<i>Thalattoscopu</i>	0	0	1	0	0	0	1	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	1	1	1	1
<i>Batracomorph</i>	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	1	1	1	1	1
<i>Batracomorph</i>	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	1	1	1	1	1
<i>Batracomorph</i>	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	1	1	1	1

Table S4. Morphological data matrix used in phylogenetic analysis

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	
<i>Reuplemmeles</i>	1	1	0	1	1	0	1	0	0	0	0	1	3	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	1		
<i>Afroiaassus</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	1	0	0	0	0	0	1	1	1	0	1	1	1	1	
<i>Acacioiaassus</i> s	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	1	
<i>iaassus lanio</i>	0	0	1	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	1	1	1	
<i>Jassulus</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	?	1	0	0	0	0	0	1	0	0	1	0	0	1	1	1	0	0	0	?	1	
<i>Hyalojassus</i> p	0	0	0	0	0	0	0	0	1	0	0	0	2	1	1	1	1	1	0	0	0	0	1	0	0	1	1	1	1	1	1	0	0	0	1	1	
<i>Lamelliaassus</i> s	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	1	0	0	0	0	0	0	1	1	0	0	1	1	1	
<i>Trocanadella</i> s	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	2	0	0	0	0	0	1	0	0	0	0	0	1	1	1	0	0	0	1	1	
<i>Siniaassus</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	1	0	0	0	0	0	1	1	1	0	1	0	1	1	
<i>Neotrocnada</i> s	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	?	2	0	0	0	0	1	1	0	0	0	0	0	1	1	1	0	0	0	0	1	
Gen. nov. 1	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	1	0	0	0	1	1	1	1	1	0	1	0	1	1	
<i>Platyhyanna</i> sp	1	2	0	1	1	0	0	0	0	0	0	0	0	1	0	?	2	0	0	0	0	1	0	1	0	1	1	0	2	1	1	0	1	1	0	1	
<i>Webaskola</i> sp	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	1	0	0	1	1	1	1	1	0	1	1
<i>Momoria</i> sp.	0	0	0	0	0	0	0	0	0	1	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	1	1	0	1	1	1	1	1	0	1	1
<i>Grunchia</i> sp. r	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	2	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	1	0	1	1	
<i>Grunchia</i> gros	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	1	0	1	1	
<i>Grunchia</i> sp. r	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	1	0	1	1	
<i>Grunchia</i> sp. r	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	1	0	1	1	
<i>Penestragnia</i>	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	1	1	1	0	1	1
<i>Penestragnia</i>	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	1	1	1	0	1	1
<i>Jivena</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	1	0	1	1	

Table S4. Morphological data matrix used in phylc

	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	
<i>Reuplemmeles</i> sp.	1	1	0	0	1	1	1	0	0	1	0	1	1	0	1	0	1	0	0	?	1	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Afroiaassus</i> sp.	1	1	0	1	1	1	1	0	1	0	0	0	1	0	1	0	0	0	0	?	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Acacioiaassus</i> sp.	0	1	0	1	1	0	0	4	0	0	0	0	1	0	1	0	0	0	0	?	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>iaassus lanio</i>	0	1	0	1	1	0	1	2	?	0	1	0	1	0	1	0	0	0	0	?	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Jassulus</i> sp.	0	1	0	1	1	0	0	2	?	?	1	0	1	0	1	0	0	0	0	?	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Hyalojassus punctulatus</i>	0	1	0	1	1	0	1	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	1	0	0	?	0	0	0	0	0	0	0	0
<i>Lamelliaassus</i> sp.	1	1	0	1	1	1	1	0	1	0	0	0	1	0	1	1	1	1	0	?	0	0	1	0	0	?	0	0	0	2	1	0	1	
<i>Trocanadella</i> sp.	1	1	0	1	1	0	1	0	0	0	0	0	1	0	1	1	1	1	0	2	0	1	0	0	0	?	0	0	0	0	1	0	0	
<i>Siniaassus</i> sp.	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	1	1	0	0	2	0	1	0	0	0	?	0	0	0	2	1	0	0	
<i>Neotrocnada</i> sp.	0	1	0	1	1	0	0	2	?	0	1	0	1	0	1	1	0	0	0	0	0	1	0	0	1	1	0	1	0	1	?	0	0	
Gen. nov. 1	1	1	0	0	1	0	1	1	?	0	1	0	1	0	1	1	1	0	0	0	0	1	1	1	1	1	0	1	0	1	?	0	0	
<i>Platyhyanna</i> sp.	0	1	0	1	1	0	0	3	?	0	0	0	1	2	1	1	0	0	0	?	0	0	1	0	0	?	0	0	0	0	0	0	0	
<i>Webaskola</i> sp.	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	1	1	1	0	1	0	1	0	0	0	?	0	0	0	0	0	0	0	
<i>Momoria</i> sp.	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	1	1	1	0	0	0	1	1	0	1	1	0	0	0	0	1	0	0	
<i>Grunchia</i> sp. nov. 3	1	1	0	1	1	0	1	0	1	0	0	0	1	1	1	1	1	0	1	2	0	1	1	0	0	?	0	0	0	0	1	1	0	
<i>Grunchia grossa</i>	1	1	0	1	1	0	1	1	1	0	0	0	1	1	1	1	1	1	0	0	1	1	0	0	?	0	0	0	0	1	1	0		
<i>Grunchia</i> sp. nov. 1	1	1	0	1	1	0	1	0	1	0	0	0	1	1	1	1	0	1	0	0	0	1	1	0	0	?	0	0	0	0	1	1	0	
<i>Grunchia</i> sp. nov. 2	1	1	0	1	1	0	1	0	1	0	0	0	1	1	1	1	0	0	1	0	1	1	0	0	?	0	0	0	0	1	1	0		
<i>Penestrangania</i> sp.	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	1	1	0	0	?	0	1	0	0	0	?	1	0	0	0	1	1	0	
<i>Penestrangania robusta</i>	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	1	1	0	0	?	0	1	0	0	0	?	1	0	0	0	1	1	0	
<i>Jivena</i> sp.	1	1	0	1	1	0	1	0	1	0	0	0	1	1	1	1	0	1	1	2	0	1	0	0	0	?	0	0	0	0	?	1	1	

Table S4. Morphological data matrix used in phylogenetic analysis

	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91
<i>Reuplemmeles</i> sp.	1	0	0	1	1	0	0	0	1	0	0	2	0	2	0	0	0	0	0	?	0	1
<i>Afroiaassus</i> sp.	0	1	0	1	1	?	?	?	0	?	0	0	1	0	0	0	0	0	1	0	1	1
<i>Acacioiaassus</i> sp.	0	1	0	1	1	?	?	?	0	?	0	1	1	0	0	0	0	0	1	1	1	1
<i>iaassus lanio</i>	0	1	0	1	1	?	?	?	0	?	0	0	1	0	0	0	0	0	1	1	1	1
<i>Jassulus</i> sp.	1	0	0	1	1	?	?	?	0	?	0	0	0	0	0	0	0	0	1	0	?	?
<i>Hyalojassus punctulatus</i>	0	0	0	0	0	0	0	1	1	1	0	1	1	1	0	0	0	1	0	0	1	1
<i>Lamelliassus</i> sp.	0	0	1	?	?	1	0	0	1	0	?	2	1	0	0	0	0	1	0	0	1	1
<i>Trocanadella</i> sp.	0	0	1	?	?	0	0	1	1	2	?	0	0	0	0	0	0	0	0	0	1	1
<i>Siniassus</i> sp.	1	0	1	?	?	1	0	1	1	0	?	1	0	0	0	1	0	0	0	0	1	1
<i>Neotrocnada</i> sp.	0	0	0	1	0	0	1	1	1	1	0	0	1	0	0	0	0	0	0	0	?	?
Gen. nov. 1	0	0	1	?	?	1	0	0	1	0	?	1	0	0	?	0	0	0	0	0	1	1
<i>Platyhyanna</i> sp.	0	0	1	?	?	0	0	0	1	0	?	1	1	0	0	0	0	0	0	0	0	1
<i>Webaskola</i> sp.	1	0	0	1	0	0	0	1	1	1	1	0	0	0	0	0	0	1	0	0	1	1
<i>Momoria</i> sp.	0	0	0	1	0	1	0	0	1	1	1	1	0	0	0	1	0	1	0	0	1	1
<i>Grunchia</i> sp. nov. 3	1	0	1	?	?	1	1	0	1	0	?	0	1	0	0	1	0	0	0	0	1	1
<i>Grunchia grossa</i>	1	0	1	?	?	1	0	1	1	1	?	0	0	0	0	1	0	0	0	0	1	1
<i>Grunchia</i> sp. nov. 1	1	0	1	?	?	1	0	0	1	1	?	2	0	0	0	1	0	0	0	0	1	1
<i>Grunchia</i> sp. nov. 2	1	0	1	?	?	1	0	0	1	0	?	2	0	0	0	1	0	0	0	0	1	1
<i>Penestrangania</i> sp.	0	0	1	?	?	1	0	1	1	0	?	1	0	0	0	1	0	1	0	0	1	1
<i>Penestrangania robusta</i>	0	0	1	?	?	1	0	1	1	0	?	1	0	0	0	1	0	1	0	0	1	1
<i>Jivena</i> sp.	0	0	1	?	?	1	1	1	1	1	?	1	0	0	0	1	0	0	0	0	1	1

Table S5. Estimated node ages from BEAST analysis and inferred ancestral areas from RASP (BBM and DEC models) for the nodes labeled in fig. 2 and fig. 3 95% HPD confidence intervals are given in parentheses. Area: A-Nearctic; B- Neotropical; C- Africa; D- Madagascar; E-Asia; F- Australasia; G- Palearctic. Inferred ancestral area along with its marginal probabilities are listed

Node	Crown groups/Splits	Node age (MY)	Bayes Binary MCMC (BBM)	Lagrange (DEC)
1	Lipokrisna +Gyponini vs. rest	99.8 (81.6, 117.7)	B, 63.23; AB, 35.10	B, 78.34; AB 21.66
2	Gyponini crown age	24 (28.3, 66.2)	AB 97.60 B 1.87 A	AB, 52.16; B 47.84
3	Platyjassini vs. rest	94.8 (76.3, 113.4)	B, 71.94; D 10.80; BD 4.71	B, 83.14; BD 16.86
4	Platyjassini crown age	43.8 (22.9, 64.8)	D, 98.29; BD, 1.07	D, 73.40; BD 26.60
5	Selenomorphini crown age	75.3 (52.6, 97.9)	F, 48.68; B, 37.17	B, 63.92; BF 36.08
6	Krisnini clade crown age	46.1 (24.3, 67.6)	E, 98.6	E, 74.95; BE 25.05
7	Reuplemmelini clade + rest	64.2 (49.4, 78.8)	F, 94.36	BF, 58.27; EF 17.43; F 13.17; B11.13
8	Batracomorphus crown age	26.5 (13.1, 39.7)	CDEFG, 90.01	B, 70.03; E, 29.97
9	Hyalojassini crown age	38.6 (28.5, 48.8)	E, 67.56; B, 7.18; BE, 6.78	BE, 100.00
10	Hyalojassini [Oriental/New World genera split]	32.7 (23.5, 41.9)	B, 90.56; AB, 5.69	B, 100.00