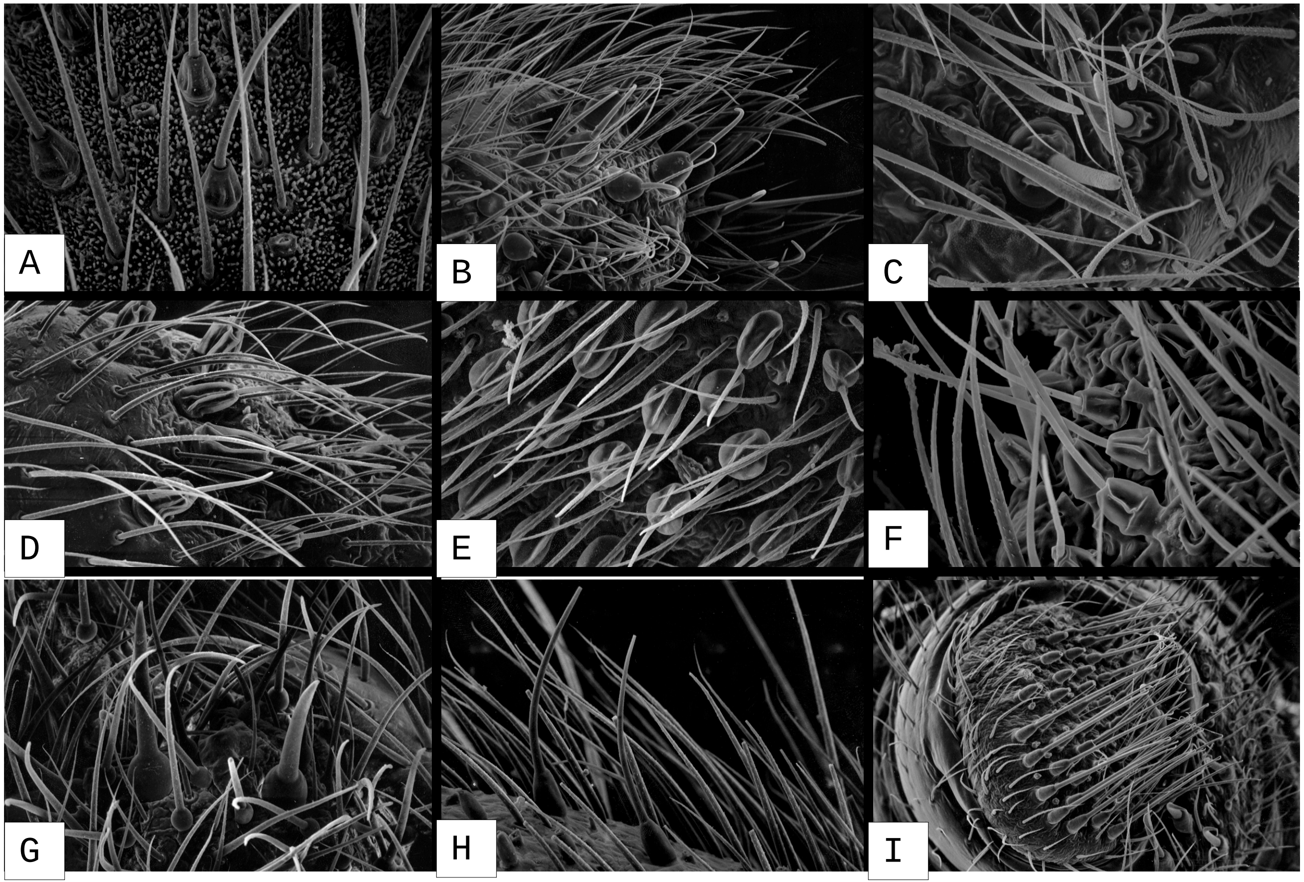


Figure 1. Posterior lateral spinneret spigot types for select rastelloid taxa. A. *Kiama lachrymoides,* B. *Cyrtauchenius luridus* Simon 1881, C. *Promyrmekiaphila gertschi*, D. *Acontius* sp., E. *Eucteniza rex*, F. *Apachella rothi*, G. *Rhytidicolus* sp., H. *Myrmekiaphila torreya*, I. *Ummidia* sp.

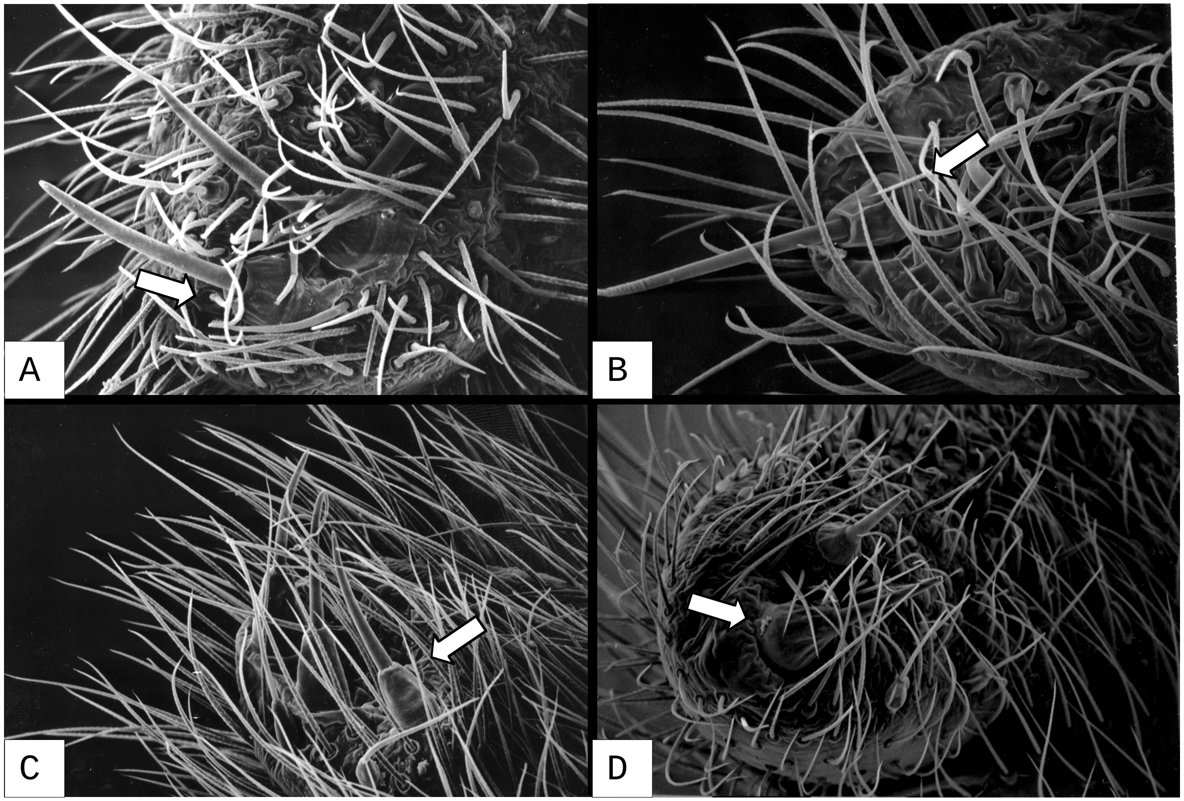


Figure 2. Silk spigots on apical most article of posterior lateral spinnerets for select euctenizid taxa. A. *Aptostichus hesperius*, B. *Apachella rothi*, C. *Entychides arizonica*, D. *Eucteniza rex*.

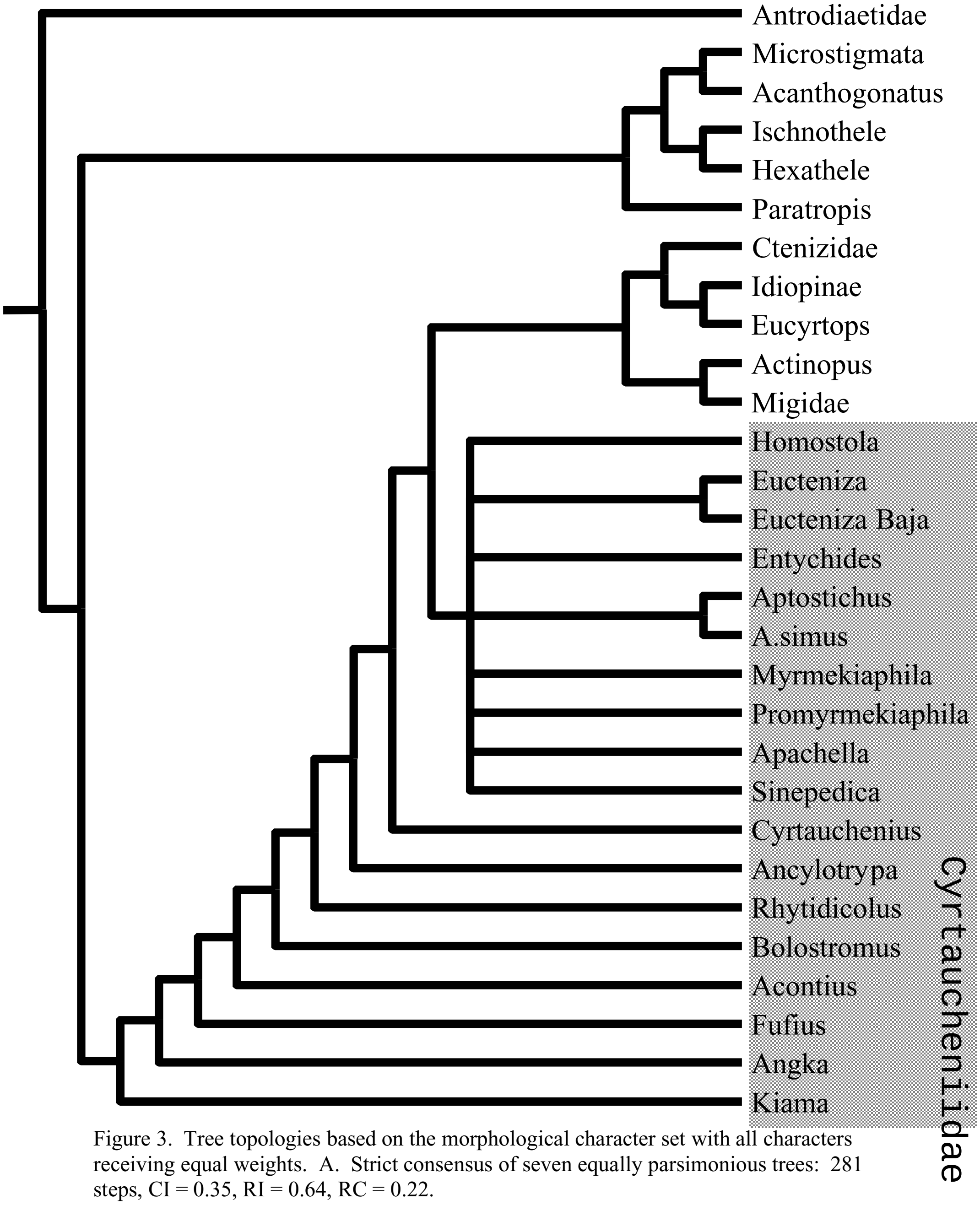


Figure 3. Tree topologies based on the morphological character set with all characters receiving equal weights. A. Strict consensus of seven equally parsimonious trees: 281 steps, CI = 0.35, RI = 0.64, RC = 0.22.

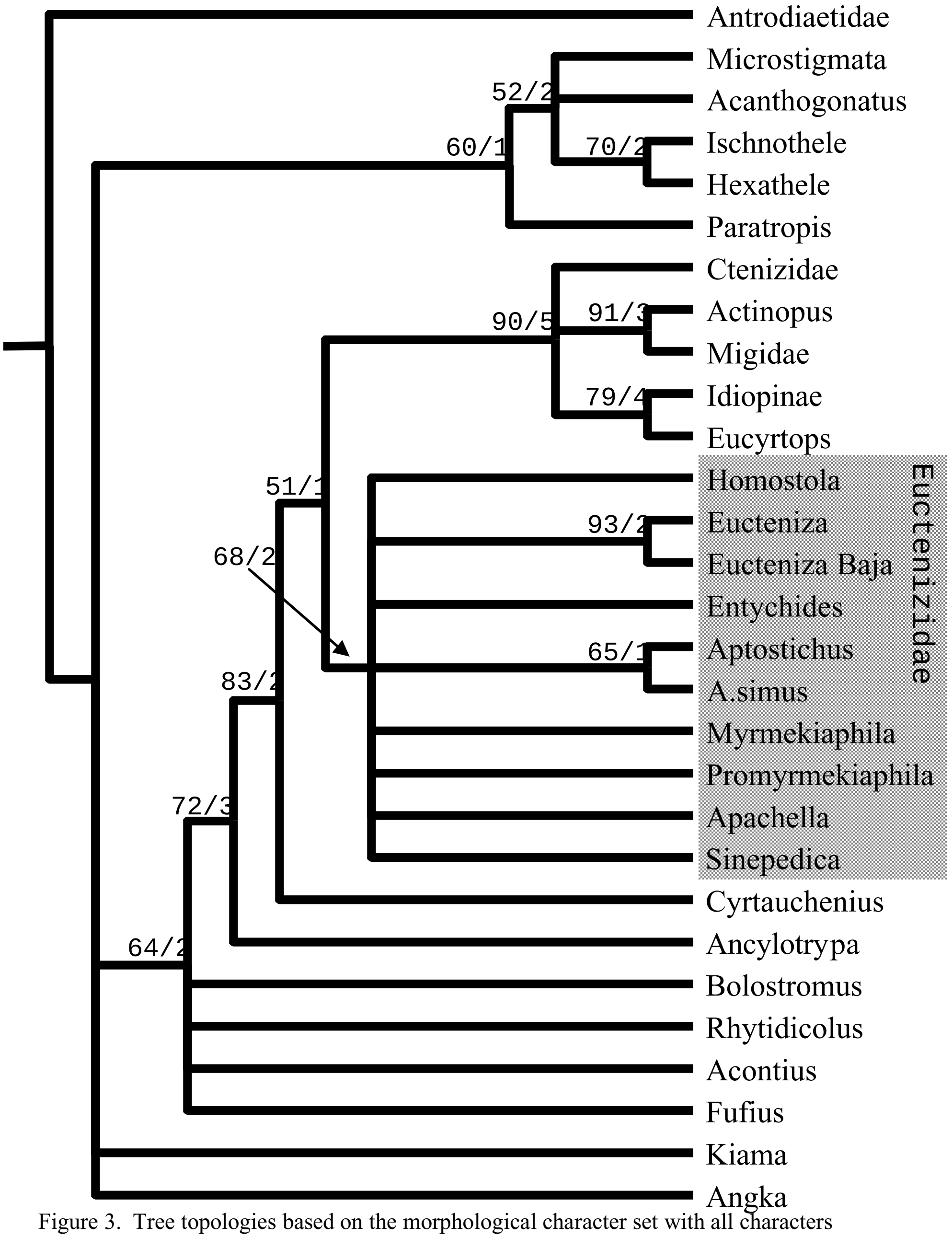


Figure 3. Tree topologies based on the morphological character set with all characters receiving equal weights. B. Fifty percent majority rule bootstrap consensus; bootstrap/decay values are given for those nodes with bootstrap values greater than 50%.

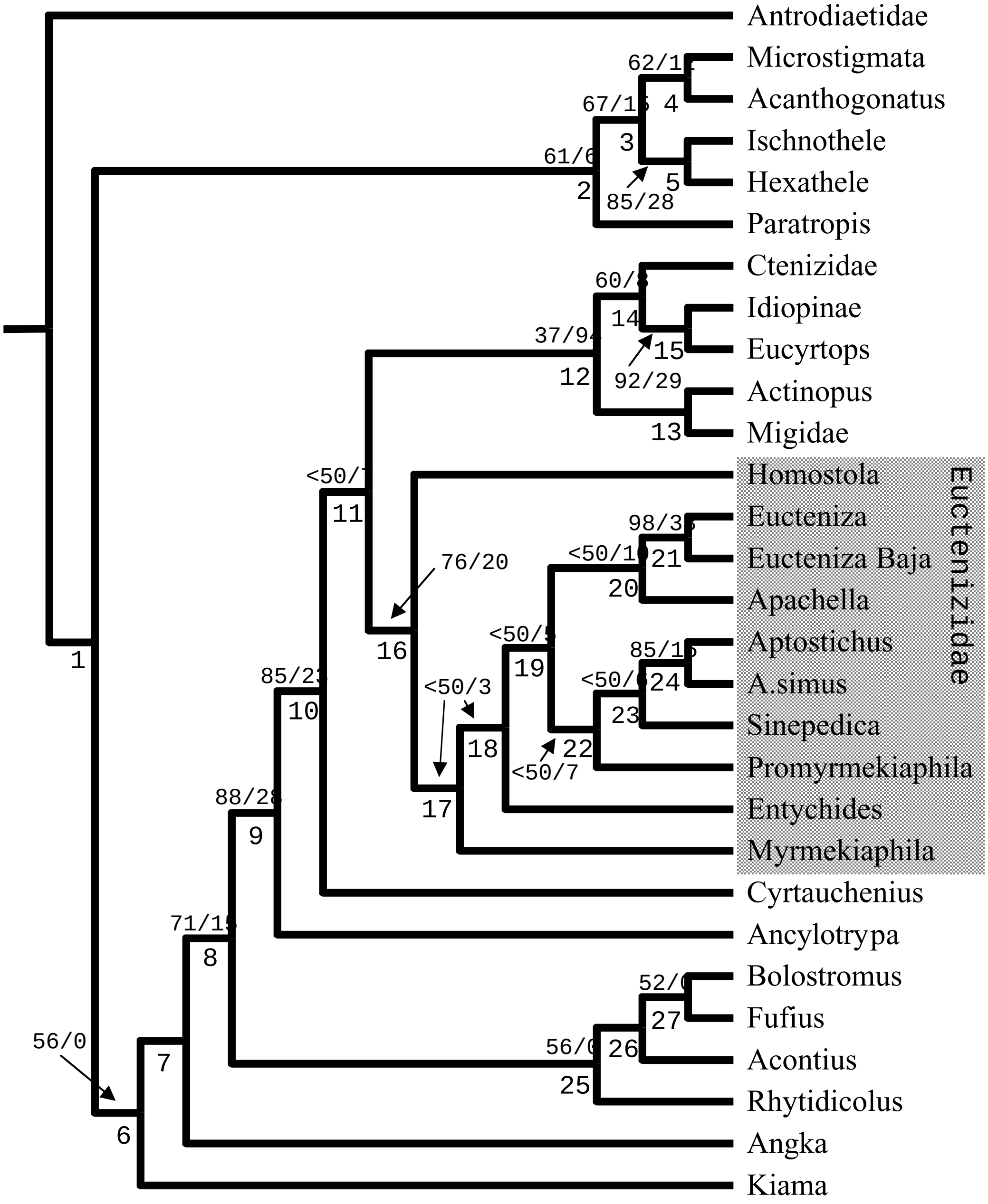
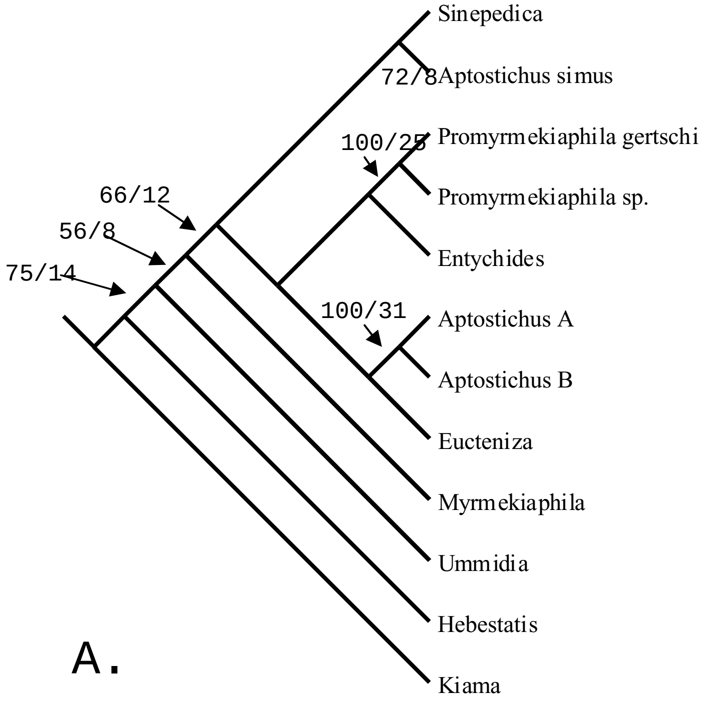


Figure 4. Tree topology based on morphological character set using implied weighting with k = 4 (283 steps, CI = 0.35, RI = 0.63, RC = 0.22, G fit = 50.45). Bootstrap/decay values are given for nodes with bootstrap values greater than 50% and/or decay values greater than 3 above the branch, branch numbers are given below.



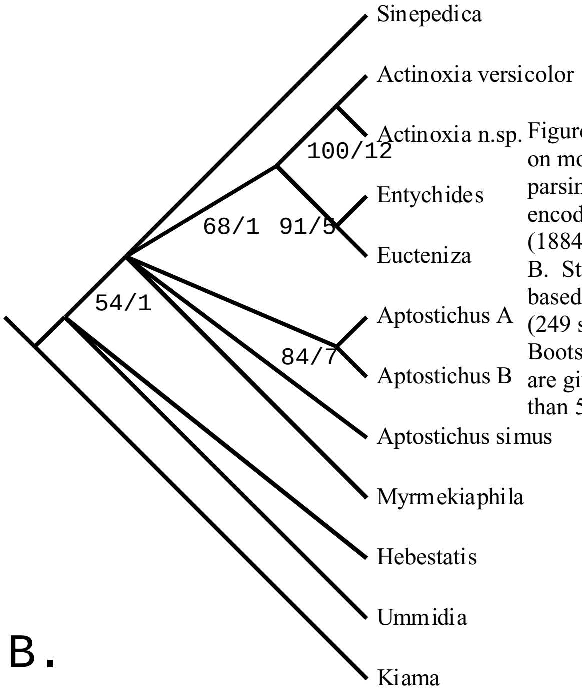


Figure 5. Euctenizid tree topologies based on molecular character set. A. Single most parsimonious tree based on mtDNA genes encoding for 16S rRNA and cytochrome oxidase I (1884 steps, CI = 0.54, RI = 0.32, RC = 0.18). B. Strict consensus of 4 most parsimonious trees based on the nuclear 28S rRNA encoding gene (249 steps, CI = 0.72, RI = 0.51, RC = 0.37). Bootstrap/decay values (above/below branch) are given for nodes with bootstrap values greater than 50% and/or decay values greater than 3.

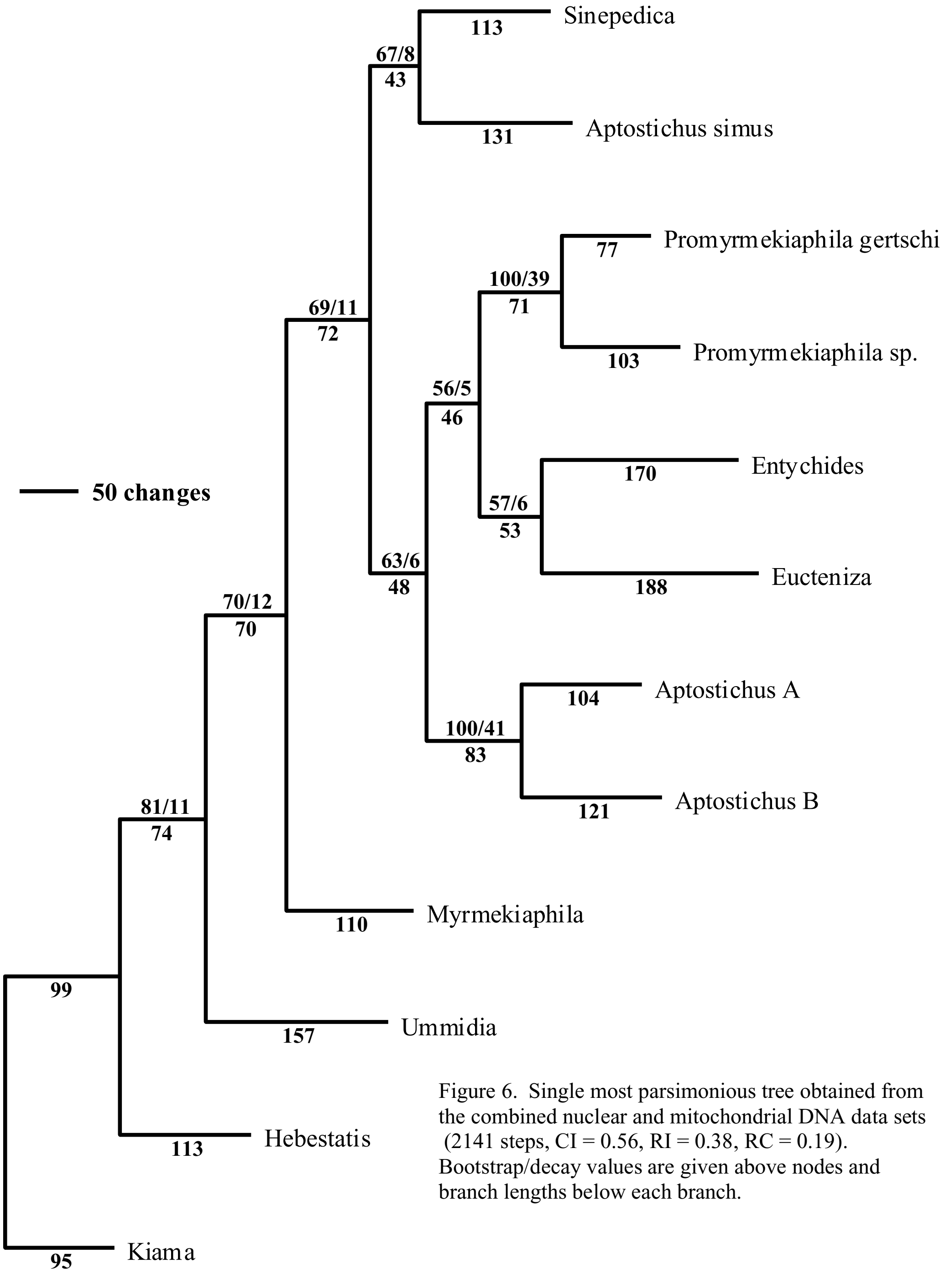


Figure 6. Single most parsimonious tree obtained from the combined nuclear and mitochondrial DNA data sets (2141 steps, CI = 0.56, RI = 0.38, RC = 0.19). Bootstrap/decay values are given above nodes and branch lengths below each branch.

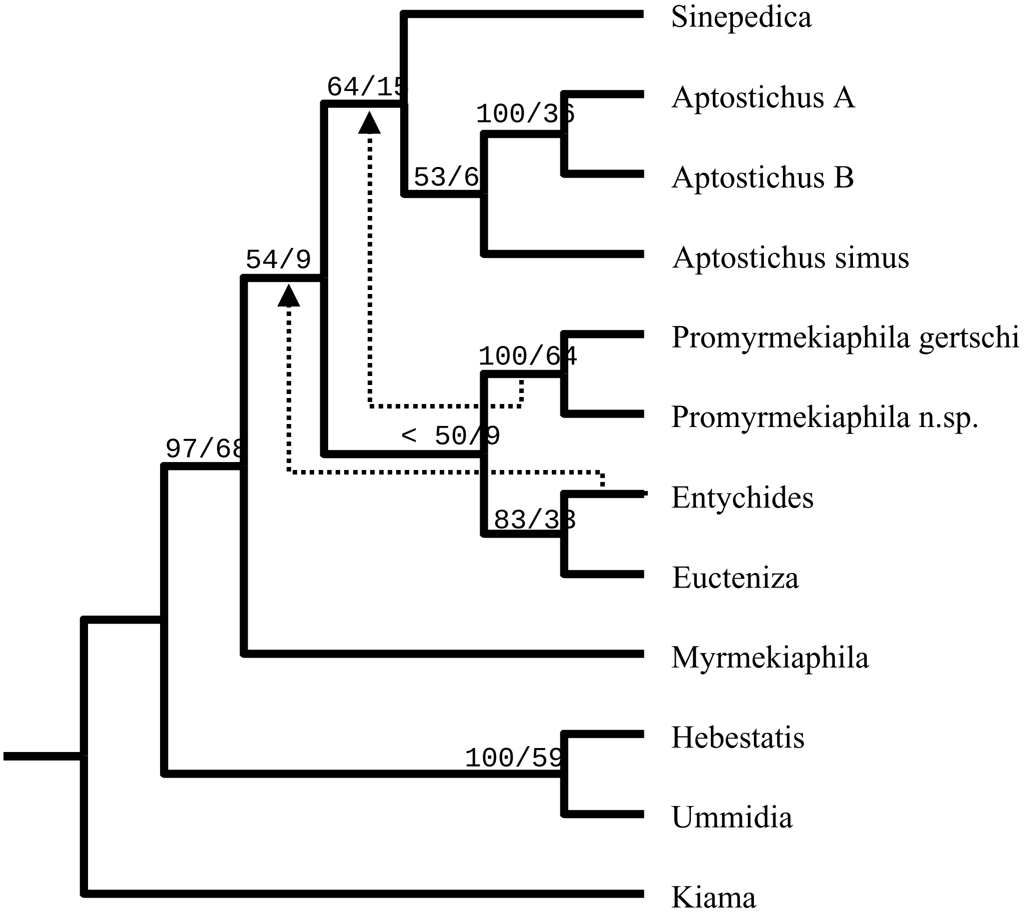


Figure 7. Single most parsimonious tree obtained for the combined morphological and molecular data sets with morphological characters up - weighted by 12 (3370 steps, CI = 0.60, RI = 0.49, RC = 0.29). Dashed lines indicate alternative placements of *Promyrmekiaphila* and *Entychides* as indicated in the morphological analysis. Bootstrap/decay values are given above nodes and branch lengths below each branch.

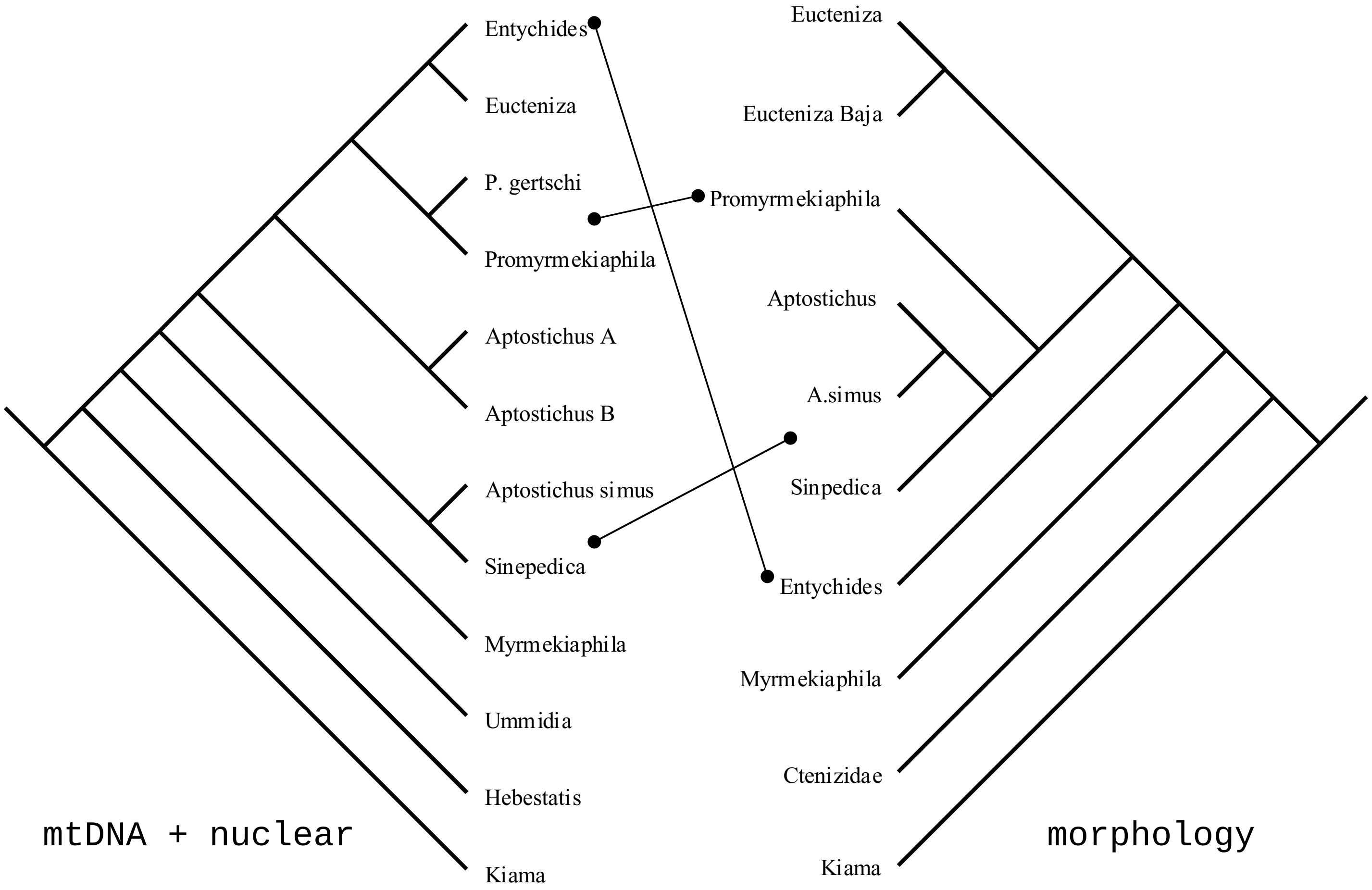


Figure 8. Comparison of euctenizid tree topologies based on the molecular and morphological data sets. Lines indicate taxon placements that disagree between the two.

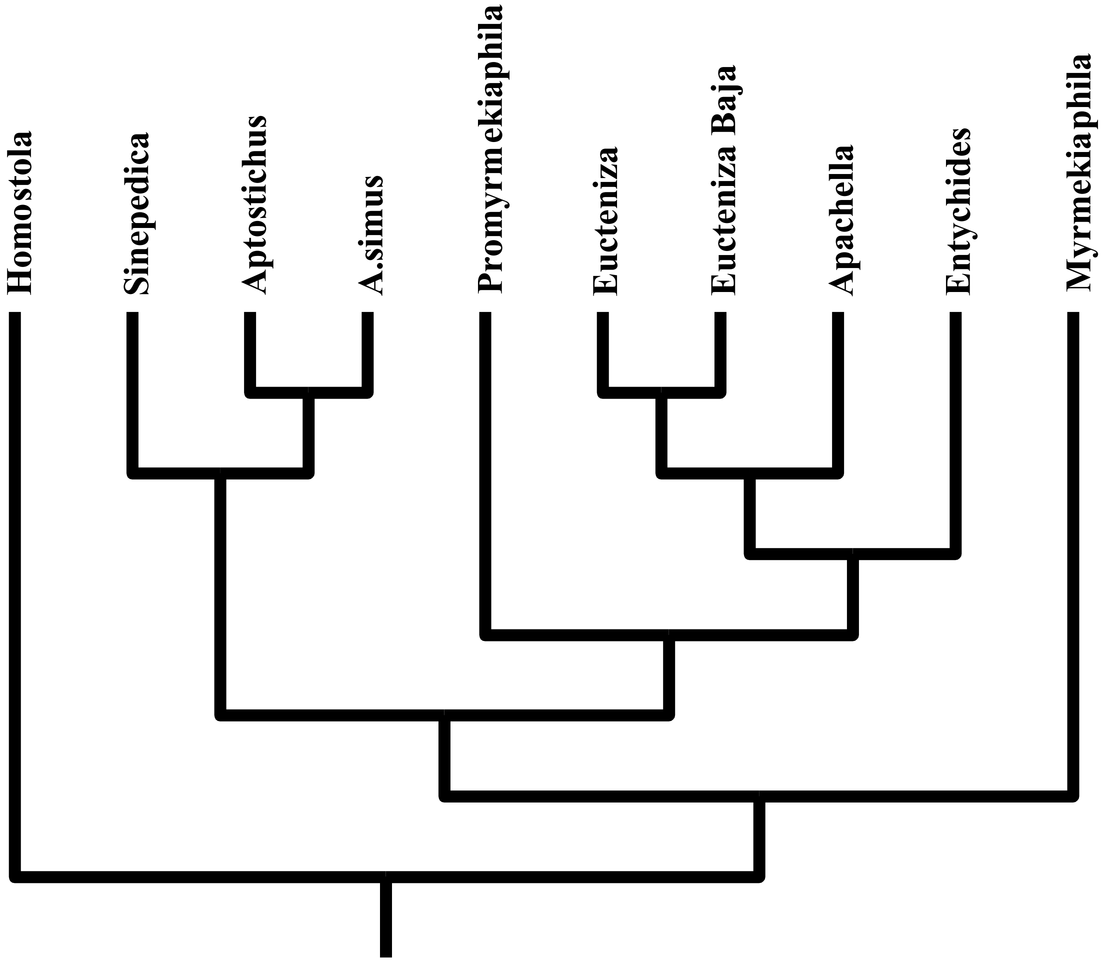


Figure 9. Composite phylogeny for the Euctenizidae based on the morphological and molecular data sets.

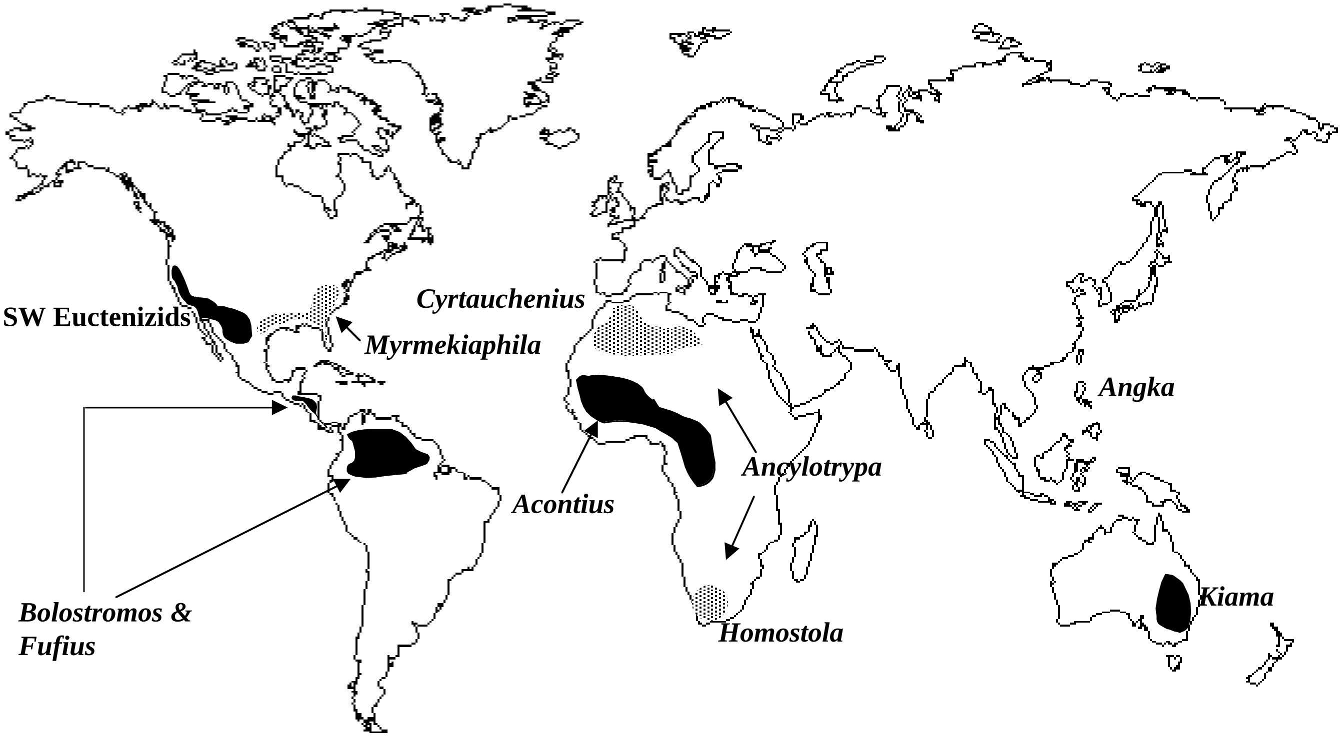


Figure 10. Generalized worldwide distribution for the basal rastelloid taxa.

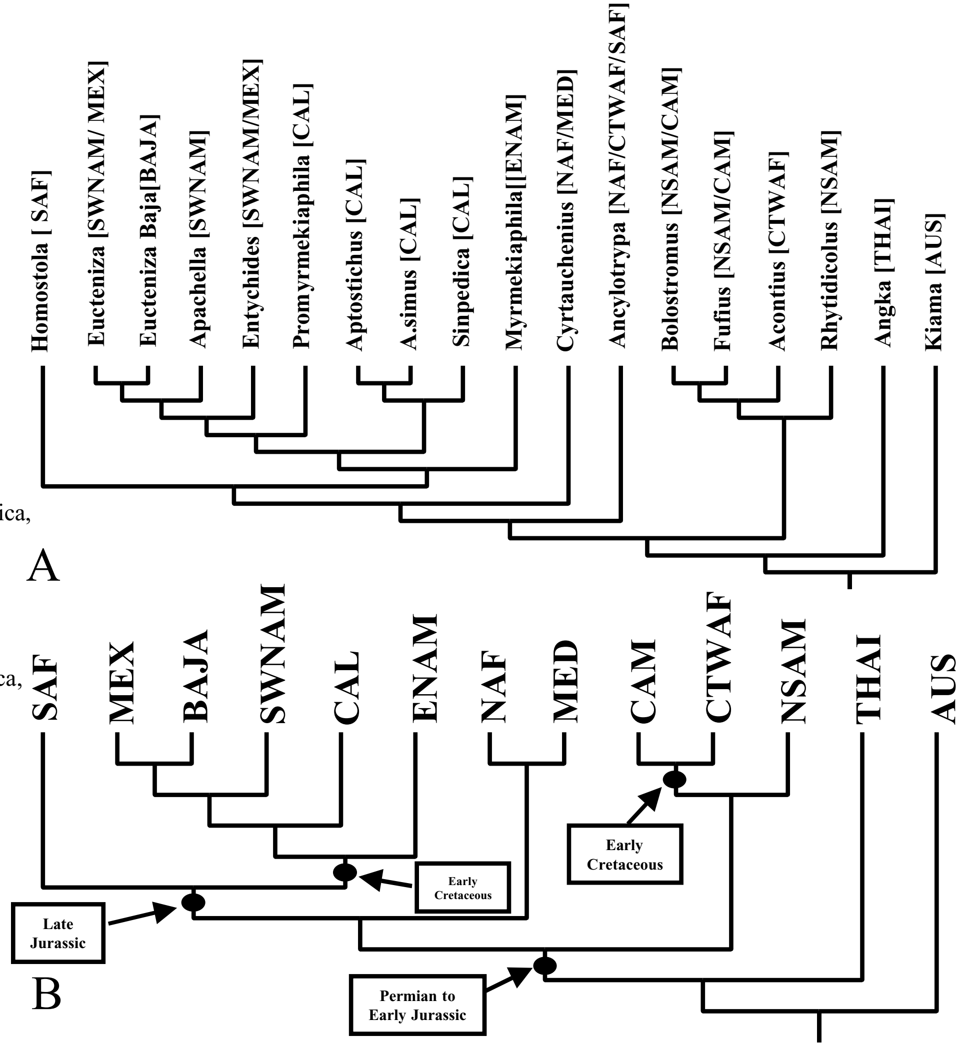


Figure 11. Taxon - Area cladograms used in analysis of biogeographic relationships. A. Taxon cladogram. B. Area cladogram.
SAF = South Africa,
MEX = Northern Mexico,
BAJA = Baja California,
SWNAM = Southwestern North America,
CAL = California,
ENAM = Eastern North America,
NAF = North Africa,
MED = Mediterranean,
CAM = Central America,
CTWAF = Central Tropical West Africa,
NSAM = Northern South America,
THAI = Thailand,
AUS = Australia.

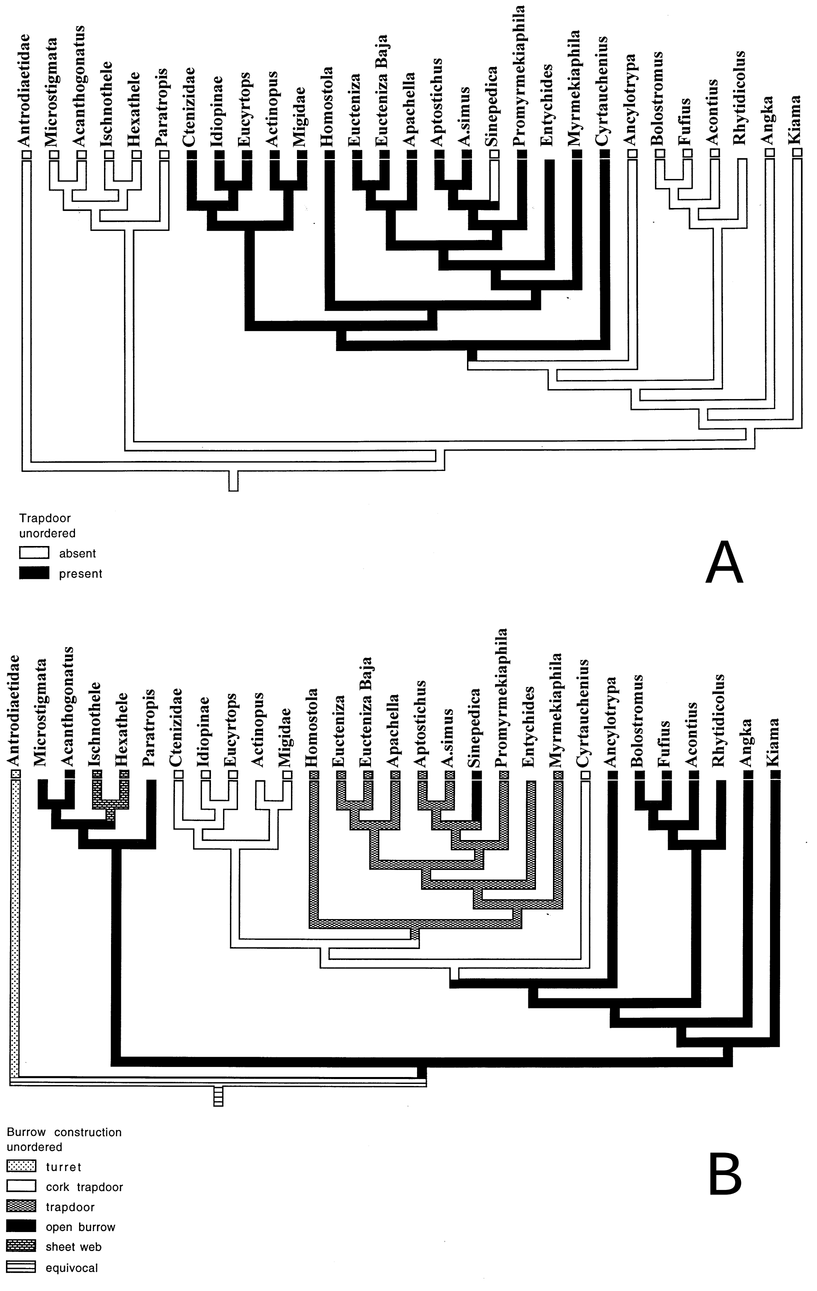


Figure 12. Trapdoor building behavior and burrow opening type character optimization on the preferred tree topology. A. The presence or absence of trapdoor building behavior. B. Type of burrow opening.

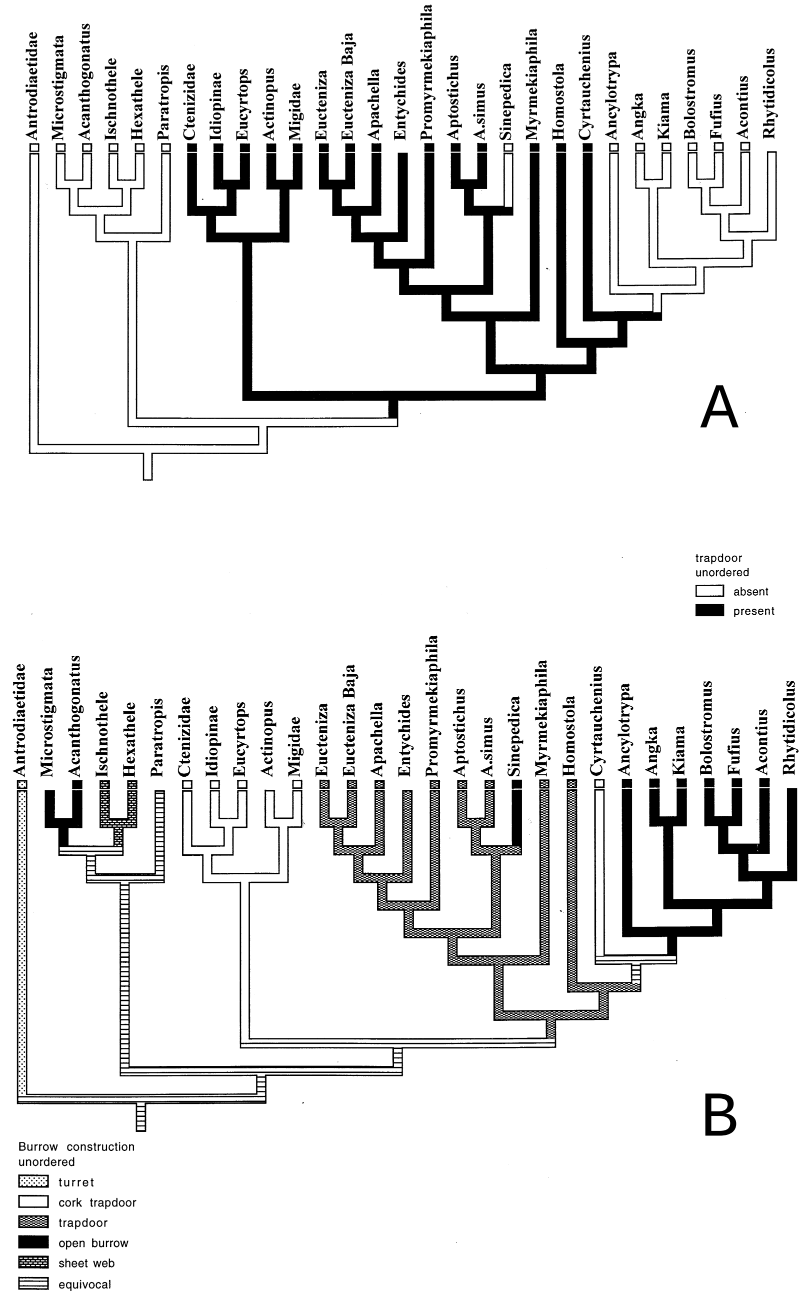


Figure 13. Trapdoor building behavior and burrow opening type character optimization on Raven's (1985) phylogeny. A. The presence or absence of trapdoor building behavior. B. Type of burrow opening.

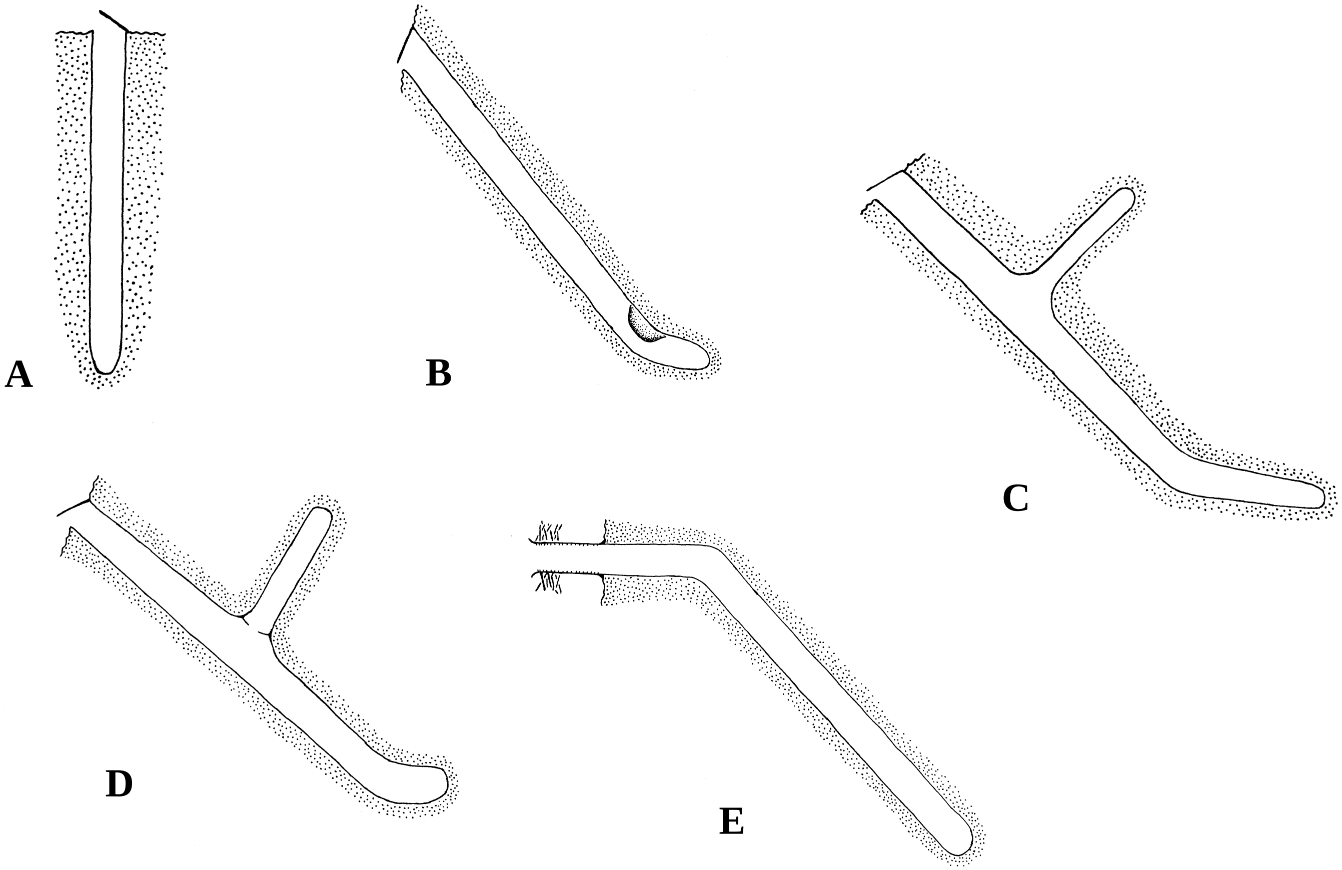


Figure 14. Summary of known euctenizid burrow types. A. *Eucteniza*. B. *Aptostichus* burrow with eggsac, C. *Aptostichus* burrow with side chamber, D. *Promyrmekiaphila*, E. *Sinepedica*.

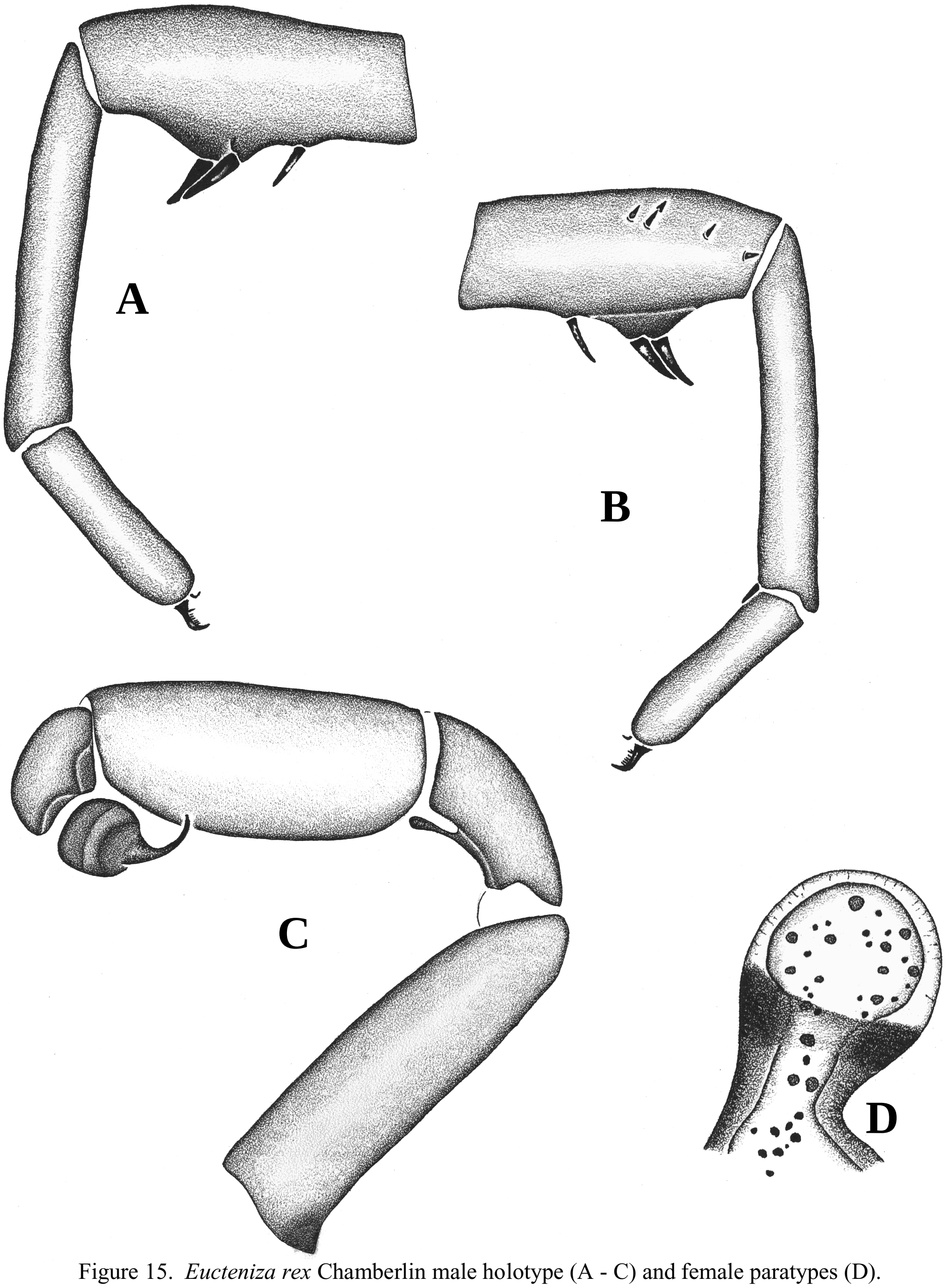


Figure 15. *Eucteniza rex* Chamberlin male holotype (A - C) and female paratypes (D). A. Retrolateral aspect of legI. B. Prolateral aspect of legI. C. Retrolateral aspect of pedipalp. D. Spermathecal receptula.

Figure 16. *Eucteniza rex* from Laredo Texas.

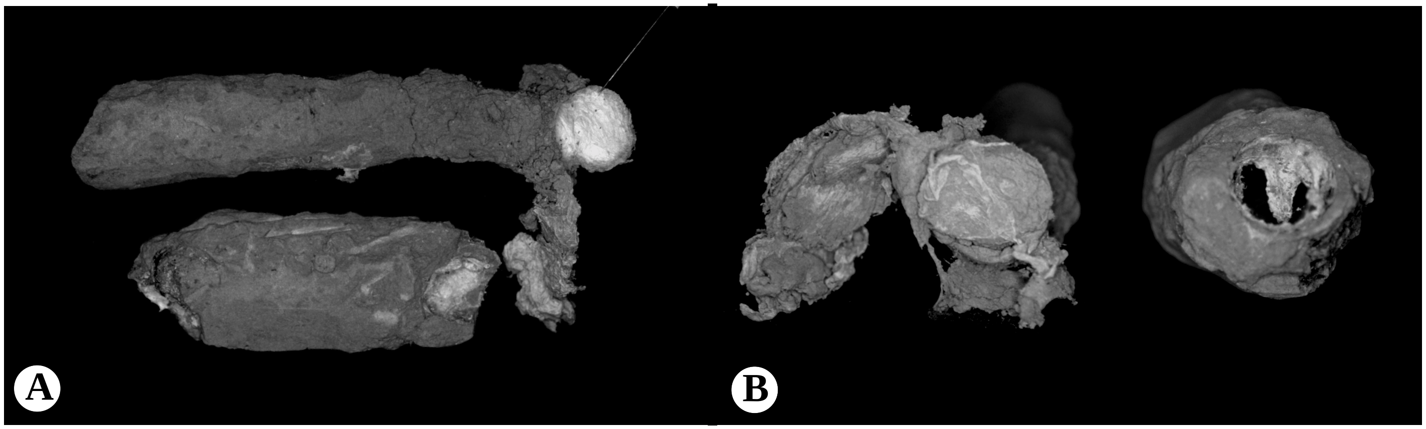


Figure 17. *Eucteniza rex* burrow from Laredo Texas excavated by W. Icenogle and bisected. A. Lateral view with trapdoor open, B. Top view with trapdoor closed.

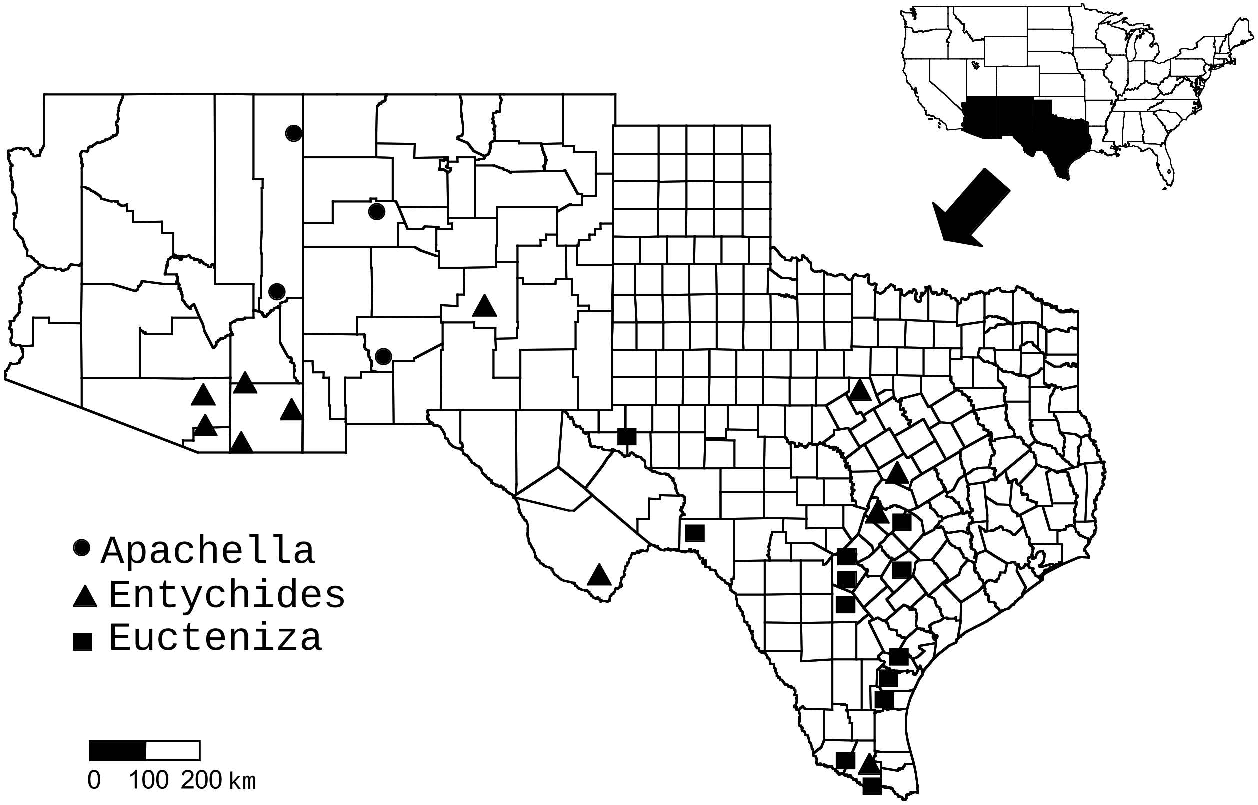


Figure 18. North American distribution map for *Apachella, Entychides,* and *Eucteniza*.

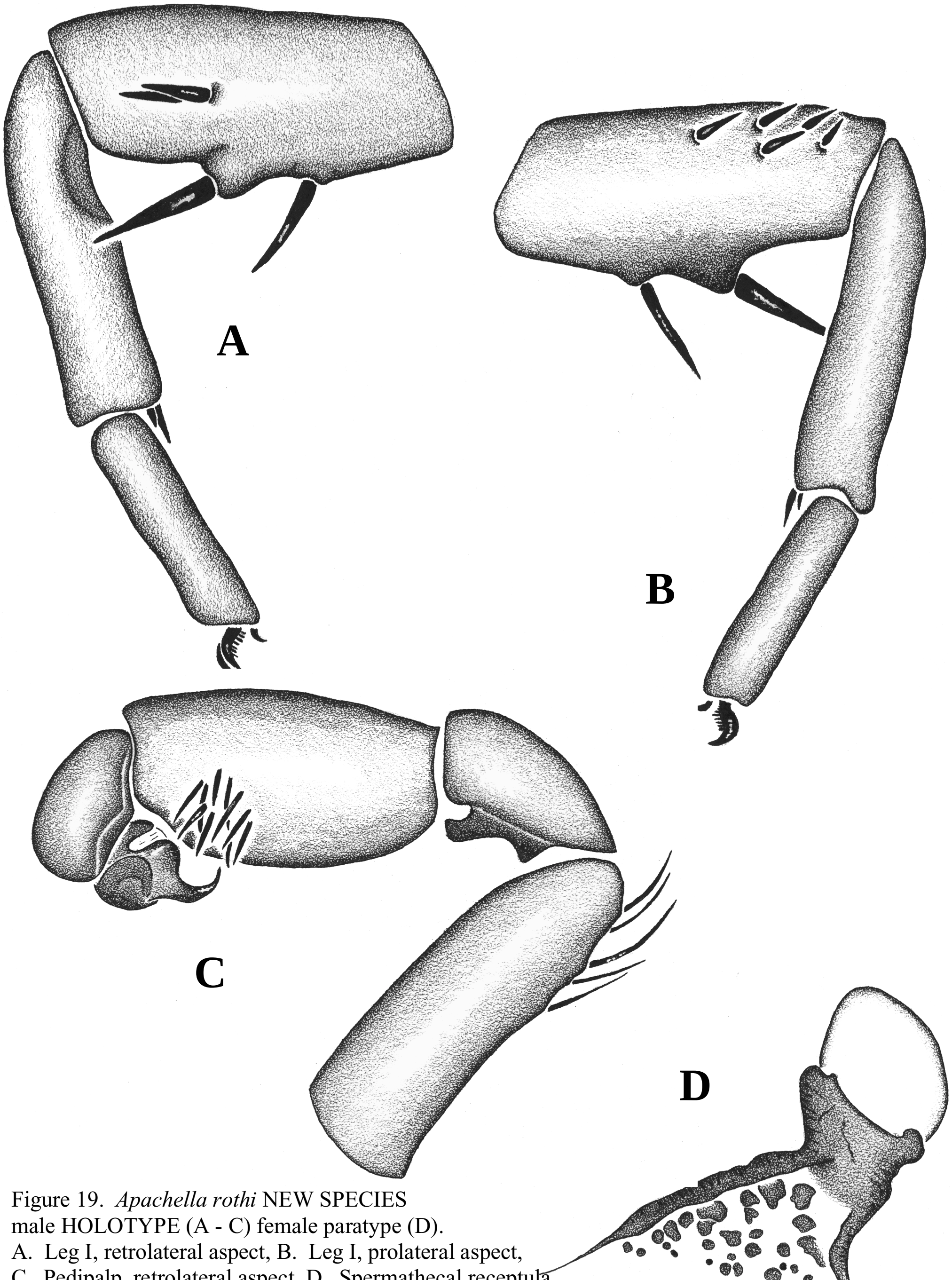


Figure 19. *Apachella rothi* NEW SPECIES
male HOLOTYPE (A - C) female paratype (D).
A. Leg I, retrolateral aspect, B. Leg I, prolateral aspect,
C. Pedipalp, retrolateral aspect, D. Spermathecal receptula.

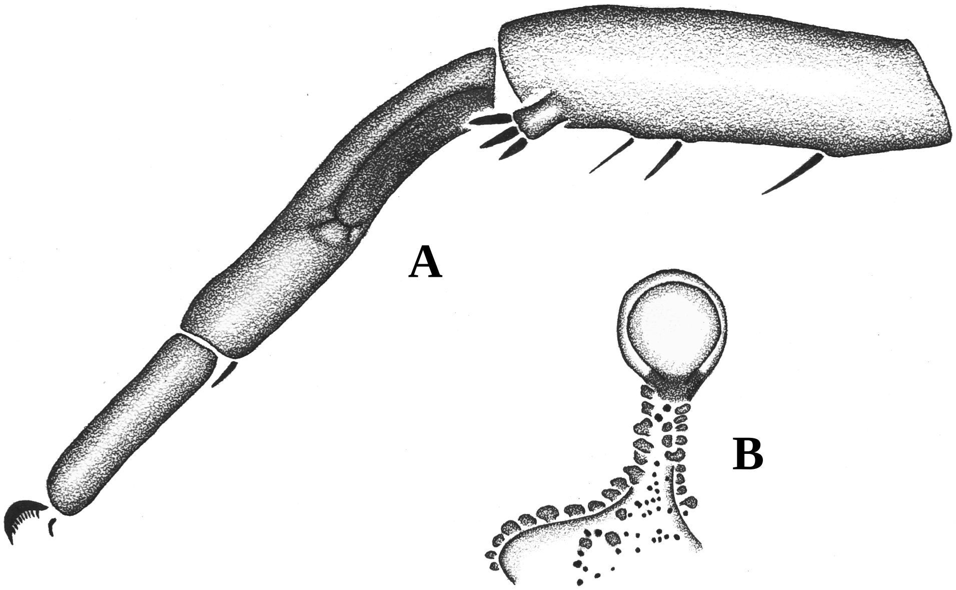


Figure 20. *Entychides arizonica* Gertsch and Mulaik from Cochise County, Arizona, 5 miles southwest of Portal (SWRS) in AMNH. A. Male leg I, retrolateral aspect. B. Spermathecal receptula.

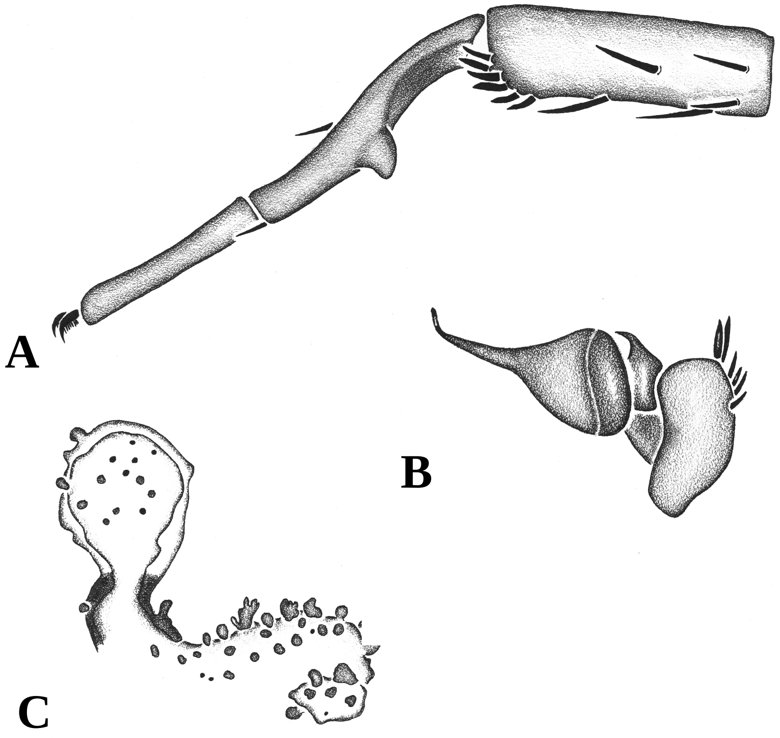


Figure 21. *Aptostichus atomarius* Simon from Los Angeles County, California, Chatsworth in CAS. A. Male leg I, retrolateral aspect. B. Cymbium and palpal bulb, retrolateral aspect. C. Spermathecal receptula.

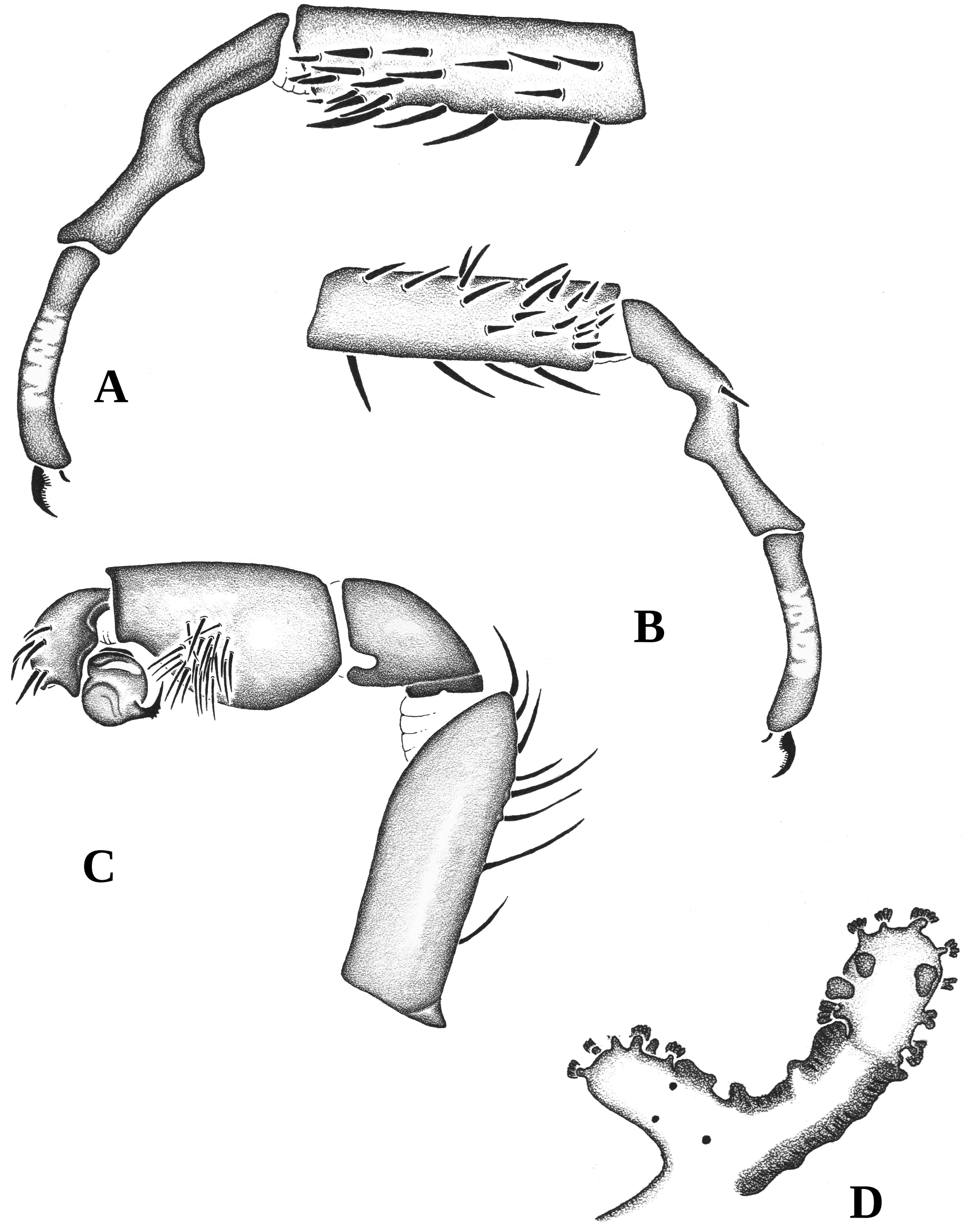


Figure 22. *Aptostichus simus* Gertsch, male from Los Angeles County, California, Playa del Rey State Beach (A - C), female from the type locality San Diego County, Silverstrand State Beach (D). A. Leg I, retrolateral aspect, B. Leg I, prolateral aspect, C. Pedipalp, retrolateral aspect. D. spermathecal receptula.

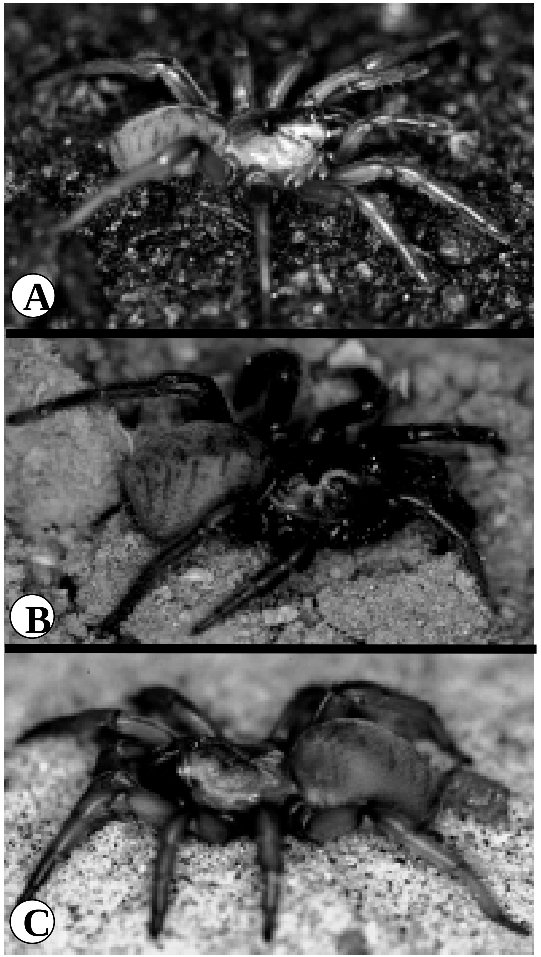


Figure 23. *Aptostichus* species. A. *Aptostichus atomarius*. B. *Aptostichus* n. sp. from Riverside County, California. C. *Aptostichus simus* from Silverstrand State Beach.

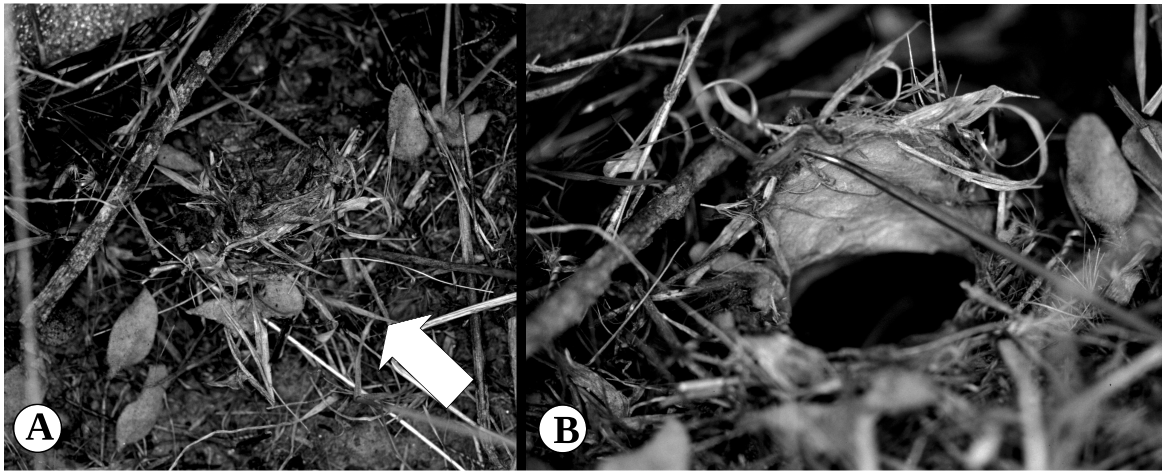


Figure 24. *Aptostichus* n. sp. burrow from Riverside County, Winchester, California. A. Burrow closed with error indicating its location. B Same burrow opened.

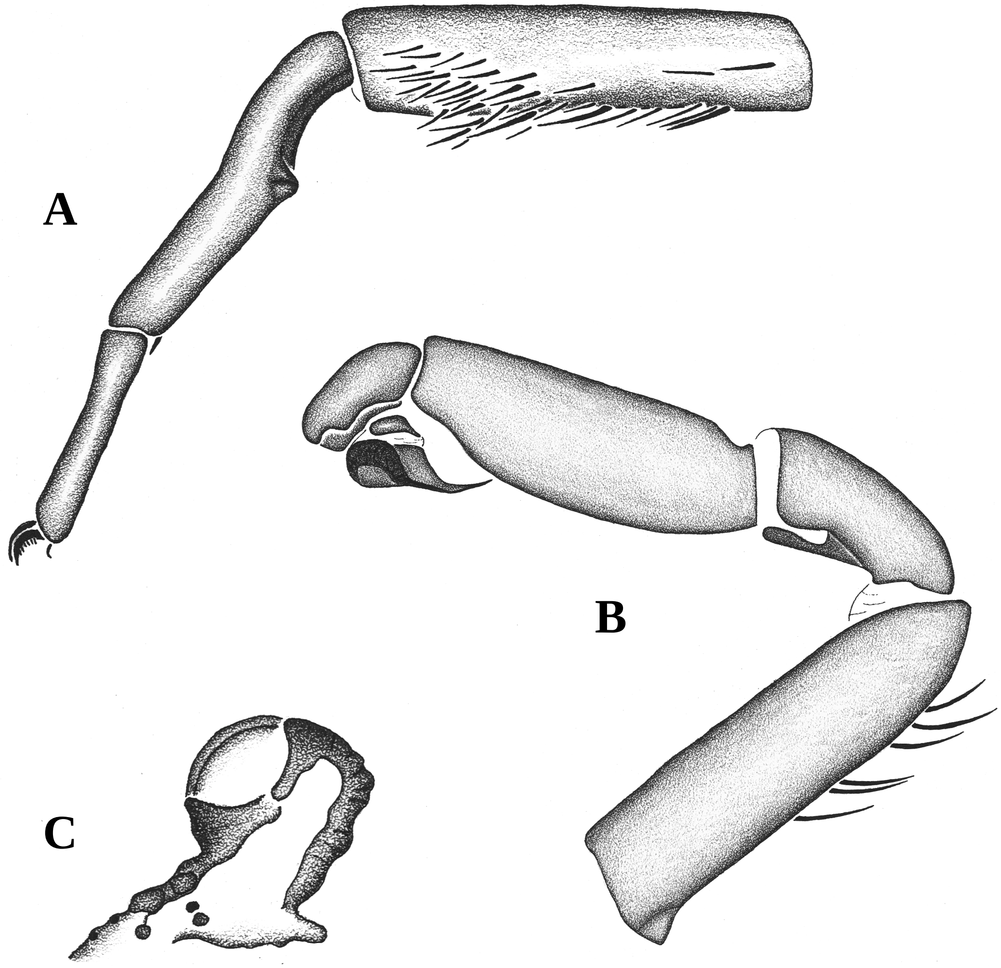


Figure 25. *Promyrmekiaphila gertschi* Schenkell from Santa Cruz County, Ben Lomond, California. A. Male leg I, retrolateral aspect. B. Pedipalp, retrolateral aspect. C. Spermathecal receptula.

Figure 26. *Promyrmekiaphila gertschi* from San Mateo County, California.

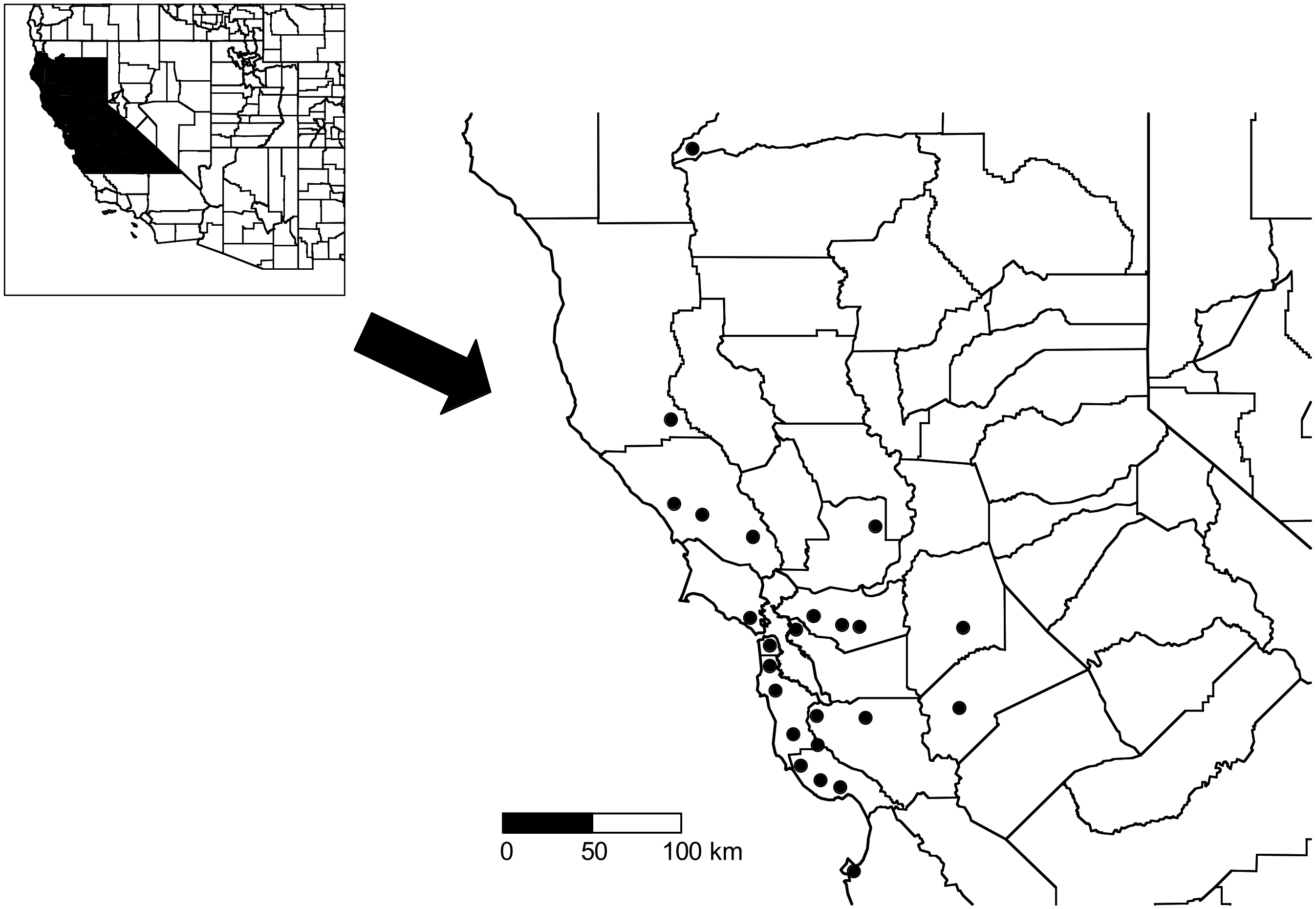


Figure 27. Distribution of *Promyrmekiaphila* in California.

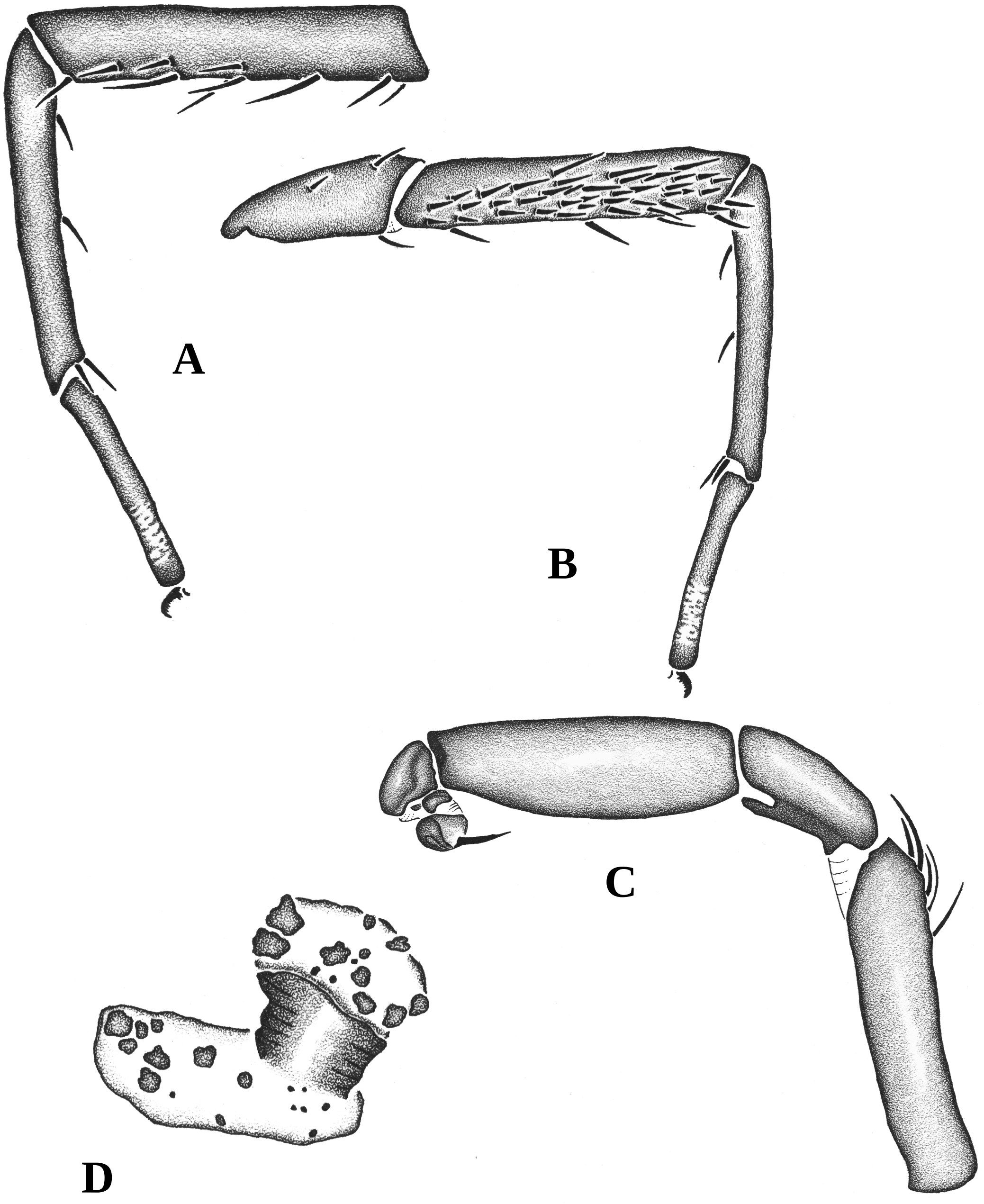


Figure 28. *Sinepedica topanga* male HOLOTYPE (A - C) and female paratype (D). A. Leg I, retrolateral aspect. B. Leg I, prolateral aspect. C. Pedipalp, retrolateral aspect. D. Spermathecal receptula.

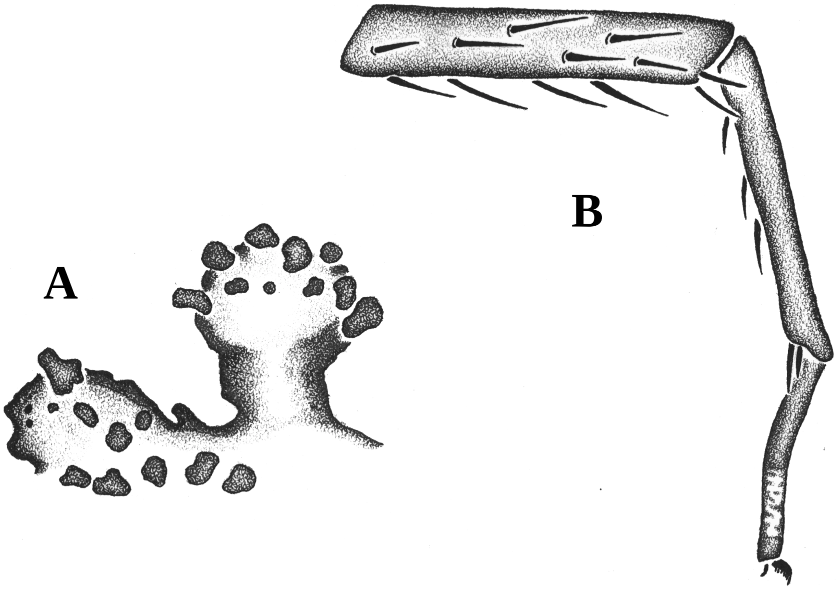


Figure 29. *Sinepedica schlingeri* female paratype and male HOLOTYPE. A. Spermathecal receptula. B. Male leg I, prolateral aspect.

Figure 30. *Sinepedica schlingeri* burrow opening from Orange County, California.

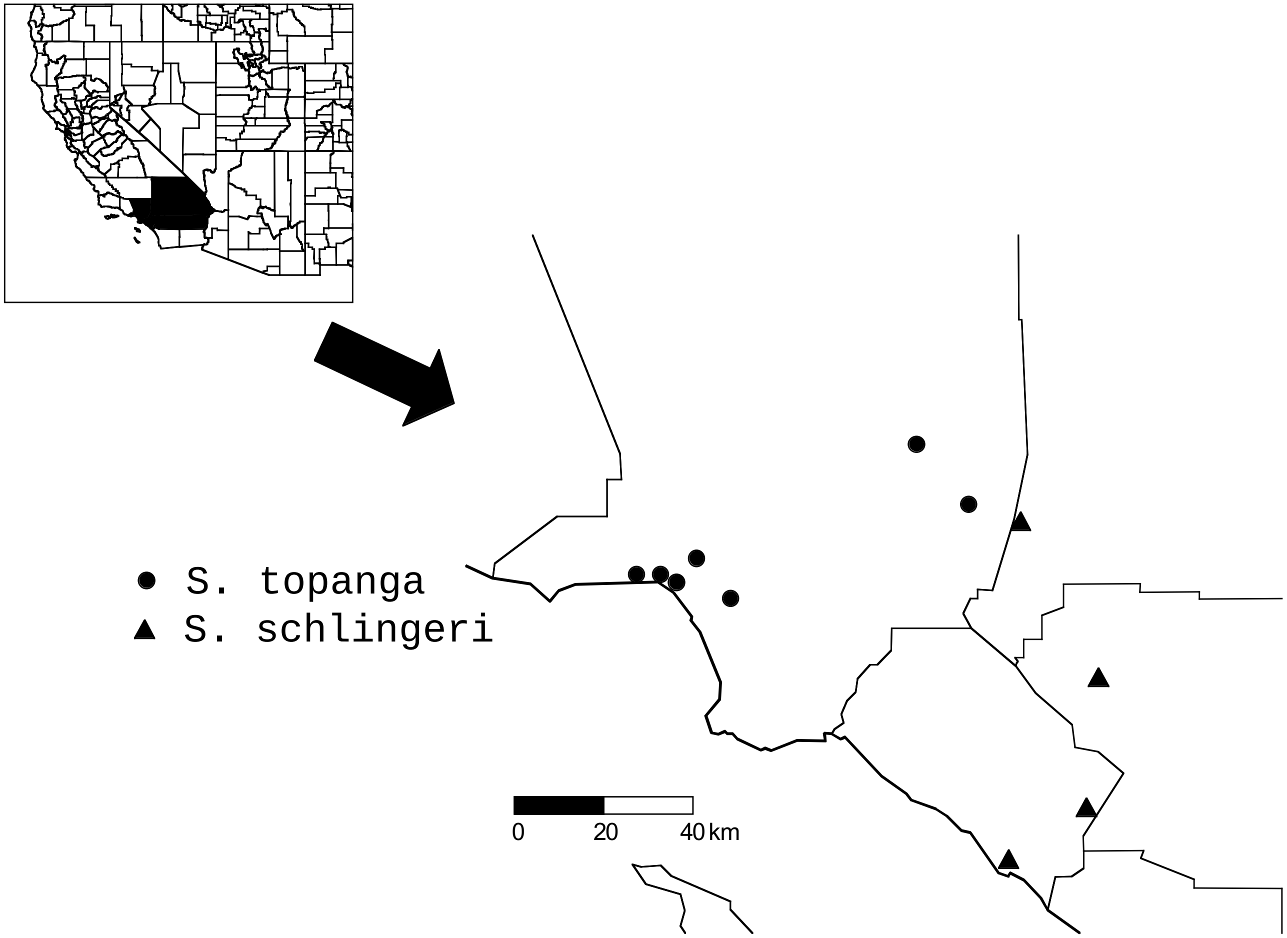


Figure 31. Distribution of *Sinepedica* in Southern California.

Table 1. Morphological data matrix.

	0	**10**	**20**	**30**	**40**	**50**	**60** **70**
	123456789	0123456789	0123456789	0123456789	0123456789	0123456789	012345678901
Antrodiaetus	010000000	2000200000	0000101000	0000012000	0000000001	1110000000	000100000000
Hexathele	101030000	2200121100	0000000010	1000013000	0000000010	0000000000	000100000004
Ischnothele	101050001	2200101100	0000101010	1001113010	0010000010	0001000000	000101000004
Acanthogonatus	102030000	220011211?	0000001000	1301110000	0010001000	0000000000	00010?000003
Microstigmata	102030000	2200112100	0000000000	1200010101	2???101000	0001000000	00010100000?
Paratropis	112030000	2000123000	00000002?0	0200010010	00?01101?0	0001000000	00010000000?
Domiothelina							
Ctenizidae	111120000	0011112021	0011000001	0200001010	2001000110	1000001110	000100000101
Migidae	100010010	0210023000	0111000001	0200011110	2100200111	0001000100	000101000101
Actinopus	010220010	0211213020	0111100001	0200011010	2101200111	1100001100	00000000010?
Idiopinae	110121000	0210013020	0011000001	0200001010	2011000111	1001000100	00010001110?
Eucyrtops	110121000	0210013020	0011000001	0202201000	2011000111	1001000100	00010001110?
Other rastelloids							
Angka	110121000	1000102000	0000000000	030111010?	0200?00000	0001000010	000001000003
Kiama	010121001	2000102000	0000000100	0300011101	0011000000	0000000010	000100000003
Cyrtauchenius	110220000	0211000020	0011000000	0302201000	1111000011	1000011000	000000000001
Acontius	110121000	1100202010	0100100100	1301110?00	0011000000	1000010000	000100000003
Ancylotrypa	110120000	0211002010	0010000000	1301110?00	1011000000	1000010000	000000000103
Bolostromos	110121000	1100202110	0110100000	0301110000	0011100000	1001011000	000000000003
Rhytidicolus	110120001	120021201?	01001??000	0?011?1100	0111000011	100?0110??	??? ??? ?0000?
Fufius	110111001	1100212100	0100100000	1301110?00	1011000000	2010000010	000100000003
Euctenizidae							
Homostola	011220000	0201121011	0010000000	0101111?10	1101010001	2010100000	000101000102
Myrmekiaphila	010220000	0211111021	0011000000	0101210010	1101010111	1010101010	000101100202
Aptostichus atomarius	111220101	0211112011	0011000000	0102210000	1111011001	1011101010	000101100212
Aptostichus simus	111211101	0211101011	0011011000	1102210000	1101011001	1011100010	000111100212
Sinpedica n. gen.	110230000	0211101011	0011011000	1102210000	1111011001	1010100000	000101000213
Eucteniza	010220000	0212123020	1011000000	0112201010	1111011001	1100101001	111100000102
Eucteniza Baja n.sp.	010220000	0212123020	1011010000	0112211000	1111?1?001	1100011001	11110100010?
Entychides	010220000	0212113021	1011000000	0112200000	1111010011	1000101010	00010000020?
Promyrmekiaphila	010220001	0211113021	0011000000	1102210000	1011011001	1010101010	000101000202
Apachella n.gen.	010230000	0211113011	0011000000	0102210000	1011011001	1000101001	100111000202

Table 2. List of unambiguous characters state changes for the major nodes for the preferred tree topology based on implied weighting (Fig. 4).

Node	**Characters and state changes**
Node 1	1: 0→1; 5: 0→2; **14**:2→1; **16**: 0→2; **24**: 1→0; **26**:1→0; 31: 0→2; **36**:2→0; **42**:0→1; **49**:1→0; **50**: 1→0; **51**:1→0; **52**:1→0
Node 2	**3**: 0→2; 5: 2→3; 15: 0→2 53: 0→1
Node 3	**2**: 1→0; **11**: 0→2; **17**: 0→1; **30**: 0→1; 65: 0→1
Node 4	**15**: 2→1; **46**: 0→1
Microstigmata	**37**: 0→1; **39**: 0→1; **40**: 0→2; **44**: 0→1
Acanthogonatus	**18**: 0→1; **26**: 0→1; 31: 2→3; **33**: 0→1; **34**: 0→1; 53: 1→0
Node 5	**3**: 2→1; **16**: 2→1; **28**: 0→1; 31: 2→0; **36**: 0→3; **48**: 0→1;
Ischnothele	**5**: 3→2; **9**: 0→1; 15: 2→0; **24**: 0→1; **26**: 0→1; **33**: 0→1; **34**: 0→1; **38**: 0→1
Hexathele	**42**: 1→0; 53: 1→0; 65: 1→0
Paratropis	**16**: 2→3; **27**: 0→2; **38**: 0→1; **44**: 0→1; **45**: 0→1; **47**: 0→1
Node 6 (Rastelloidina)	**4**: 0→1; 6: 0→1; 31: 2→3; **33**: 0→1; 37: 0→1; 43: 0→1; 58: 0→1
Node 7	**10**: 2→1; **34**: 0→1; **63**: 1→0
Node 8	6: 1→0; **11**: 0→2; 14: 1→0; **18**: 0→1; 37: 0→1; **50**: 0→1; **55**: 0→1; 58: 1→0
Node 9	**10**: 1→0; **12**: 0→1; **13**: 0→1; **22**: 0→1; **40**: 0→1; 69: 0→1
Node 10	**4**: 1→2; 16: 2→1; **18**: 1→2; **23**: 0→1; 34: 1→2; **36**: 0→1; **41**: 0→1; **48**: 0→1; **49**: 0→1; 56: 0→1; **71**: 3→1
Node 11	**15**: 0→1; 16: 0→1; 31: 3→1; **38**: 0→1; **42**: 1→0; **55**: 1→0; 63: 0→1;

Table 2a. continued

Branch	**Characters and state changes**
Node 12 (Domiothelina)	16: 1→3; **29**: 0→1; 31: 1→2; **33**: 1→0; **34**: 2→0; **40**: 1→2; **47**: 0→1; **57**: 0→1
Node 13 (Migoidea)	**8**: 0→1; **21**: 0→1; **24**: 0→1; **44**: 0→2;
Ctenizidae	**3**: 0→1; **11**: 2→1; **14**: 0→1; 16: 3→2; **19**: 0→1; **49**: 1→0; **58**: 0→1;
Node 15	**6**: 0→1; **13**: 1→0; **42**: 0→1; **53**: 0→1 56: 1→0; **67**: 0→1; **68**: 0→1
Eucyrtops	**33**: 0→2; **34**: 0→2; **38**: 1→0
Actinopus	**1**: 1→0; **14**: 0→2; **51**: 0→1; **63**: 1→0
Migidae	**2**: 1→0; **4**: 2→0; **5**: 2→1; **13**: 1→0; **15**: 1→2; **18**: 2→0; **37**: 0→1; **43**: 1→0; **50**: 1→0; **53**: 0→1; 56: 1→0; **65**: 0→1
Node 16 (Euctenizidae)	**1**: 1→0; **14**: 0→1 **19**: 0→1; **45**: 0→1; 52: 0→1; **54**: 0→1; **65**: 0→1; **71**: 1→2
Homostola	**3**: 0→1; **12**: 1→0; **15**: 1→2; **18**: 2→1; **23**: 1→0; 34: 2→1; **48**: 1→0; **50**: 1→2 56: 1→0
Node 17 (Euctenizinae)	**36**: 1→0; **58**: 0→1; **69**: 1→2;
Node 18	16: 1→3; **33**: 1→2; **38**: 1→0; **42**: 0→1; 52: 1→0;
Node 19	**46**: 0→1; **48**: 1→0
Node 20	**58**: 1→0; **59**: 0→1; **60**: 0→1
Node 21	**13**: 1→2; **19**: 1→0 **20**: 0→1; **32**: 0→1; **36**: 0→1; **51**: 0→1; **61**: 1→0; **62**: 0→1; **69**: 2→1
Eucteniza	**15**: 1→2; **35**: 1→0; **38**: 0→1; **65**: 1→0
Eucteniza n.sp.Baja	**25**: 0→1; **54**: 1→0; **55**: 0→1
Apachella.	**5**: 2→3; **18**: 2→1; **41**: 1→0; **64**: 0→1
Node 22	9: 0→1; **30**: 0→1; 52: 0→1

Table 2b. continued

Branch	Characters and state changes
Node 23	**1**: 0→1; **15**: 1→0; **16**: 3→1; **18**: 2→1; 25: 0→1; 26: 0→1; 56: 1→0
Node 24 *Aptostichus*	**3**:0→1; **7**: 0→1; **53**: 0→1; **66**: 0→1; **70**: 0→1
Aptostichus	**15**: 0→1; **16**: 1→2; 25: 1→0; 26: 1→0; **30**: 1→0; 56: 1→0
Aptostichus simus	**5**: 2→1; **6**: 0→1; **42**: 1→0; **64**: 0→1
Sinpedica	**5**: 2→3; 9: 1→0; **58**: 1→0; **71**: 2→3
Promyrmekiaphila	**41**: 1→0
Entychides	**13**: 1→2; **20**: 0→1; **32**: 0→1; **35**: 1→0; **65**: 1→0
Myrmekiaphila	**47**: 0→1; **66**: 0→1
Cyrtauchenius	**33**: 1→2; **35**: 1→0; 69: 1→0
Ancylotrypa	**30**: 0→1
Node 25 (Aporoptychinae)	14: 0→2; **21**: 0→1; **24**: 0→1; **63**: 0→1
Node 26	6: 0→1; **11**: 2→1; 30: 0→1;
Node 27	**17**: 0→1; **44**: 0→1
Bolostromus	**22**: 0→1; 30: 1→0; **53**: 0→1 **56**: 0→1; 63: 1→0;
Fufius	**5**: 2→1; **9**: 0→1; **15**: 0→1; **18**: 1→0; **35**: 1→0; **41**: 0→1;**50**: 1→2; **55**: 1→0; **58**: 0→1;
Acontius	**27**: 0→1
Rhytidicolus	**9**: 0→1; **15**: 0→1; 37: 0→1; **41**: 0→1; **48**: 0→1; **49**: 0→1; **56**: 0→1
Angka	**41**: 0→2; **42**: 1→0; 43: 1→0; **53**: 0→1; **65**: 0→1
Kiama	1: 1→0; **9**: 0→1; **27**: 0→1; **36**: 0→1; **39**: 0→1;

Table 3. Sample of published spider phylogenetic studies. Expected CI values are based on Sanderson & Donoghues' (1989) regression equation:

$CI = 0.90 - 0.022(\# \text{ taxa}) + 0.000213(\# \text{ taxa})^2$

Source	**# Taxa**	**CI**	**Expected CI**
Mygalomorphae			
Goloboff (1993)	42	0.39	0.35
Coyle (1994)	11	0.69	0.68
Coyle (1995)	25	0.75	0.48
Goloboff (1995)[1]	84	0.44	n/a
Miller & Coyle (1996)	16	0.71	0.6
Bond & Opell (this study)	29	0.34	0.44
Araneomorphae			
Coddington (1989)	19	0.68	0.55
Catley (1994)	11	0.86	0.68
Griswold (1993)	8	0.63	0.73
Griswold (1994)	10	0.9	0.7
Hormiga (1994)	16	0.73	0.6
Hormiga (1994)	31	0.71	0.42
Bond & Opell (1997)	20	0.84	0.55
Sierwald (1997)	14	0.72	0.63
Scharff & Coddington (1997)	57	0.35	0.33

[1] CI was not published and was therefore estimated by us. No expected value because it exceeds the limits of the function; included for comparison.