

Supplementary Tables and Figures

A Rearrangement of the Mitochondrial Genes of Centipedes (Arthropoda, Myriapoda) with a Phylogenetic Analysis

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Table S1. GenBank accession numbers for taxa used in this study.

Taxon	Species	Accession No.	References
Chilopoda	<i>Lithobius forficatus</i>	NC_002629	[1]
	<i>Bothropolys</i> sp.	NC_009458	[2]
	<i>Cermatobius longicornis</i>	NC_021403	[3]
	<i>Scutigera coleoptrata</i>	NC_005870	[4]
	<i>Scolopendra dehaani</i>	KY947341	[5]
	<i>Scolopendra mutilans</i>	MN317390	[6]
	<i>Scolopendra subspinipes</i>	MN642577	this study
	<i>Scolopocryptops</i> sp.	KC200076	[7]
	<i>Strigamia maritima</i>	NC_026557	[8]
	<i>Mecistocephalus marmoratus</i>	KX774322	this study
	<i>Scolopendra morsitans</i>	MW810062	[27]
	<i>Scolopocryptops</i> sp.	KC200076	[28]
Diplopoda	<i>Narceus annularus</i>	NC_003343	[9]
	<i>Thyropygus</i> sp.	NC_003344	[9]
	<i>Antrokoreana gracilipes</i>	NC_010221	[10]
	<i>Abacion magnum</i>	NC_021932	[11]
	<i>Brachycybe lecontii</i>	NC_021934	[11]
	<i>Appalachioria falcifera</i>	NC_021933	[11]
	<i>Asiomorpha coarctata</i>	KU721885	[12]
Symphyla	<i>Xystodesmus</i> sp.	KU721886	[12]
	<i>Scutigera</i> sp.	NC_008453	[13]
Pauropoda	<i>Symphylella</i> sp.	NC_011572	[14]
	<i>Pauropus longiramus</i>	NC_016676	[15]
Chelicerata	<i>Pauropus longiramus</i>	NC_016676	[15]
	<i>Achella bituberculata</i>	NC_009724	[16]
	<i>Calisoga longitemsis</i>	NC_010780	[17]
	<i>Limulus polyphemus</i>	NC_003057	[18]
	<i>Tachyleus tridentatus</i>	NC_012574	[19]
Crustacea	<i>Phalangium opilio</i>	NC_010766	[17]
	<i>Penaeus monodon</i>	NC_002184	[20]
	<i>Hutchinsoniella macracantha</i>	NC_005937	[21]
Hexapoda	<i>Petrobius brevistylis</i>	NC_007688	[22]
	<i>Thermobia domestica</i>	NC_006080	[23]
	<i>Drosophila yakuba</i>	NC_001322	[24]
	<i>Japyx solifugus</i>	NC_007214	[25]
Onychophora	<i>Epiperipatus biolleyi</i>	NC_009082	[13]
Priapulida	<i>Priapulus caudatus</i>	NC_008557	[26]

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Table S2. Optimal partition strategy and evolutionary models used in phylogenetic analyses.

Dataset	Subset	Best Model	Sites	Partiotion Names
AA	1	MTART+I+G+F	646	atp8, atp6, nad3, nad2, nad6
	2	MTART+I+G	493	cox1
	3	MTART+I+G	452	cox3, cox2
	4	MTART+I+G	322	cob
	5	MTART+I+G+F	1,024	nad5, nad4, nad1, nad4L
PCG12RNA	1	GTR+I+G	721	cox2_pos1, cox1_pos1
	2	GTR+I+G	504	cox1_pos2
	3	TVM+I+G	293	nad1_pos1
	4	GTR+I+G	377	nad4L_pos2, nad1_pos2
	5	GTR+I+G	1,065	cox2_pos2, cob_pos2, cox3_pos2, atp6_pos2
	6	GTR+I+G	559	atp8_pos1, nad6_pos1, nad3_pos1, nad2_pos1
	7	TVM+I+G	559	atp8_pos2, nad6_pos2, nad2_pos2, nad3_pos2
	8	GTR+I+G	848	atp6_pos1, cox3_pos1, cob_pos1
	9	GTR+I+G	1027	nad4L_pos1, nad5_pos1, nad4_pos1
	10	GTR+I+G	943	nad4_pos2, nad5_pos2
	11	GTR+I+G	1,647	rrnL, rrnS
PCGRNA	1	GTR+I+G	721	cox2_pos1, cox1_pos1
	2	GTR+I+G	504	cox1_pos2
	3	GTR +G	1,347	cox2_pos3, cox1_pos3, cox3_pos3, cob_pos3
	4	TVM+I+G	908	rrnS, nad1_pos1
	5	GTR+I+G	377	nad1_pos2, nad4L_pos2
	6	TVM+G	1,320	nad4_pos3, nad4L_pos3, nad5_pos3, nad1_pos3
	7	GTR+I+G	1,065	cox2_pos2, cob_pos2, atp6_pos2, cox3_pos2
	8	GTR+I+G	781	nad3_pos1, nad2_pos1, atp6_pos1, nad6_pos1, atp8_pos1
	9	TVM+I+G	559	atp8_pos2, nad6_pos2, nad3_pos2, nad2_pos2
	10	GTR+G	781	nad2_pos3, nad3_pos3, atp6_pos3, nad6_pos3, atp8_pos3
	11	GTR+I+G	626	cob_pos1, cox3_pos1
	12	GTR+I+G	1,027	nad4L_pos1, nad5_pos1, nad4_pos1
	13	GTR+I+G	943	nad5_pos2, nad4_pos2
	14	GTR+I+G	1,032	rrnL

Table S3. Mitochondrial genomes Organization of *Scolopendra subspinipes*.

Gene	Strand	Location	Length	Start /Stop Codon	Intergenic Nucleotides
<i>trnI</i>	F	1-61	61		-2
<i>trnQ</i>	R	60-129	70		-3
<i>trnM</i>	F	127-194	68		-1
<i>nad2</i>	F	194-1,163	970	ATT/T--	0
<i>trnW</i>	F	1,164-1242	79		-27
<i>trnC</i>	R	1,216-1,277	62		-4
<i>trnY</i>	R	1,274-1,334	61		-6
<i>cox1</i>	F	1,299-2,864	1,566	TTA/TAA	3
<i>cox2</i>	F	2,868-3,539	672	ATG/TAA	-7
<i>trnK</i>	F	3,538-3,604	67		0
<i>trnD</i>	F	3,604-3,664	61		-1
<i>atp8</i>	F	3,664-3,819	156	ATT/TAA	-7
<i>atp6</i>	F	3,816-4,479	667	ATA/T--	0
<i>cox3</i>	F	4,480-5262	783	ATG/TAA	4
<i>trnG</i>	F	5,267-5,330	64		-1
<i>nad3</i>	F	5,330-5,678	349	ATA/T--	0
<i>trnA</i>	F	5,679-5,740	62		6
<i>trnR</i>	F	5,747-5,806	60		1
<i>trnN</i>	F	5,808-5,863	56		-3
<i>trnS1</i>	F	5,861-5,912	52		-1
<i>trnE</i>	F	5,912-5,975	64		-5
<i>trnF</i>	R	5,971-6,031	61		2
<i>nad5</i>	R	6,034-7,732	1,699	TTA/TAA	1
<i>trnH</i>	R	7,734-7,794	61		1
<i>nad4</i>	R	7,794-9,125	1,332	ATG/T	-7
<i>nad4L</i>	R	9,119-9,403	285	ATA/TAA	7
<i>trnT</i>	F	9,411-9,472	62		-2
<i>trnP</i>	R	9,471-9,528	58		2
<i>nad6</i>	F	9,525-9,998	474	ATT/TAA	47
<i>cob</i>	F	10,044-11,155	1,112	ATG/TAA	0
<i>trnS2</i>	F	11,156-11,221	66		1
<i>nad1</i>	R	11,223-12,140	918	ATT/TAG	1
<i>trnL2</i>	R	12,142-12,203	62		-9
<i>trnL1</i>	R	12,195-12,254	60		0
<i>rrnL</i>	R	12,255-13,398	1,144		0
<i>trnV</i>	F	13,399-13,458	60		0
<i>rrnS</i>	R	13,459-13,918	460		0
CR	F	13,919-14,637	719		0

Table S4. Mitochondrial genomes Organization of *Mecistocephalus marmoratus*.

Gene	Strand	Location	Length	Start /Stop Codon	Intergenic Nucleotides
<i>cox1</i>	F	1-1,536	1,536	ATA/TAA	0
<i>cox2</i>	F	1,536-2,216	681	ATG/TAA	-1
<i>trnK</i>	F	2,215-2,279	65		-2
<i>trnD</i>	F	2,281-2,342	62		1
<i>atp8</i>	F	2,343-2,498	156	ATT/TAA	0
<i>atp6</i>	F	2,492-3,160	669	ATG/TAA	-7
<i>cox3</i>	F	3,160-3,945	786	ATG/TAA	-1
<i>trnG</i>	F	3,945-4,005	61		-1
<i>trnA</i>	F	4,006-4,065	60		0
<i>trnR</i>	F	4,067-4,124	58		1
<i>trnS1</i>	F	4,129-4,187	59		4
<i>trnE</i>	F	4,195-4,251	57		7
<i>trnT</i>	F	4,255-4,306	52		3
<i>nad6</i>	F	4,311-4,814	504	ATA/TAA	4
<i>cob</i>	F	4,818-5,954	1,137	ATG/TAA	3
<i>trnS2</i>	R	5,954-6,024	71		-1
<i>trnQ</i>	F	6,023-6,091	69		-2
<i>trnM</i>	F	6,083-6,147	65		-9
<i>nad2</i>	F	6,148-7,137	990	ATC/TAA	0
<i>trnW</i>	F	7,136-7,201	66		-2
<i>nad3</i>	F	7,208-7,561	354	ATG/TAA	6
<i>trnN</i>	F	7,561-7,633	73		-1
<i>trnF</i>	R	7,627-7,689	63		-7
<i>nad5</i>	R	7,688-9,382	1,695	ATT/TAA	-2
<i>trnH</i>	R	9,390-9,451	62		7
<i>nad4</i>	R	9,452-10,775	1,324	ATG/T--	0
<i>nad4L</i>	R	10,769-11,047	279	ATT/TAG	-7
<i>trnP</i>	R	11,051-11,111	61		3
<i>nad1</i>	R	11,112-12,036	925	ATA/T--	0
<i>trnL2</i>	R	12,038-12,099	62		1
<i>rrnL</i>	R	12,100-13,414	1,315		0
<i>trnV</i>	R	13,415-13,481	67		0
<i>rrnS</i>	R	13,482-14,246	765		0
<i>trnL1</i>	R	14,247-14,317	71		0
CR	F	14,318-15,080	766		0
<i>trnC</i>	F	15,084-15,137	54		0
<i>trnY</i>	R	15,145-15,209	65		7
<i>trnI</i>	F	15,211-15,277	67		1

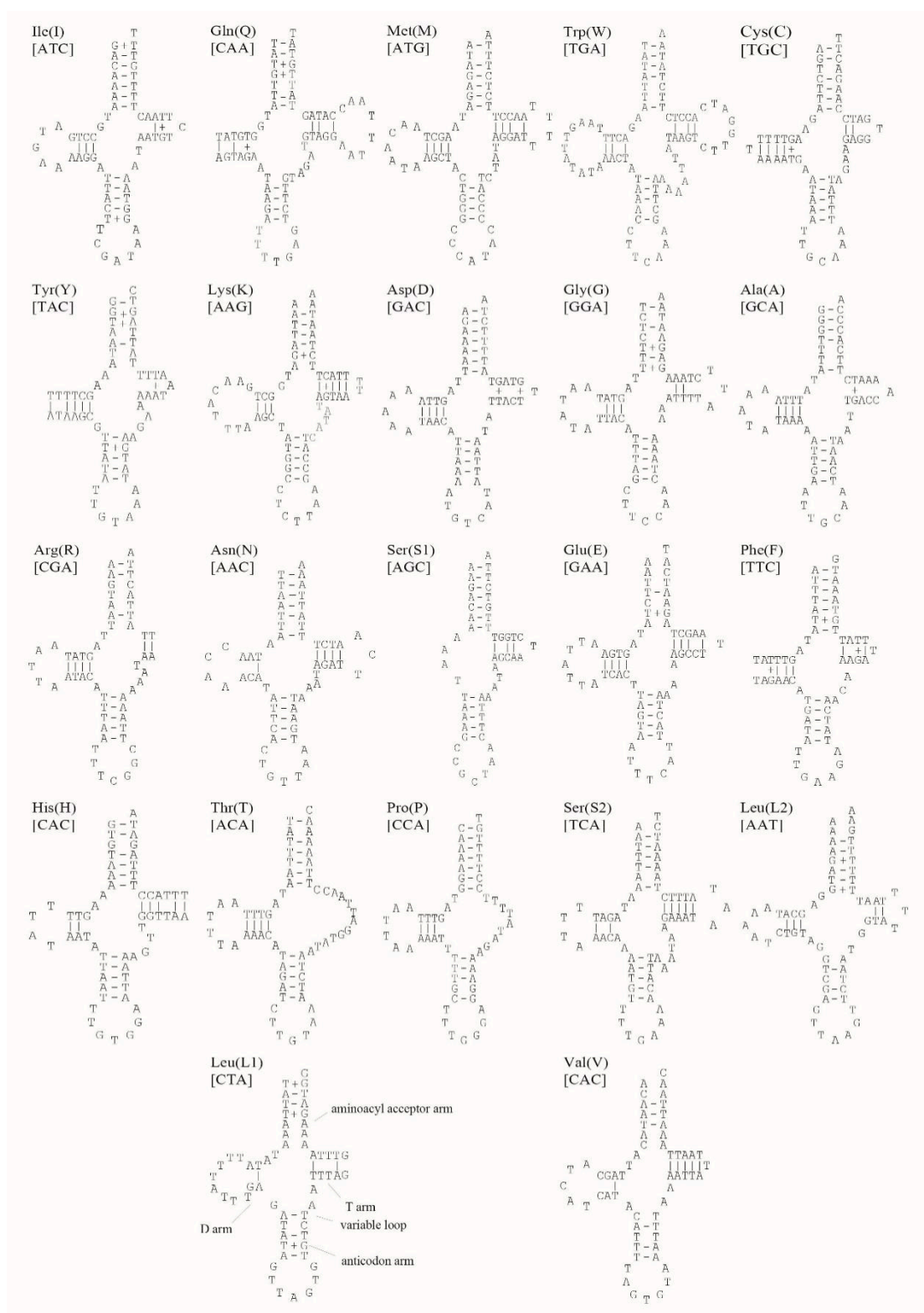


Figure S1. Predicted secondary structure of the 22 tRNAs in the *Scolopendra subspinipes* mitogenome Dashes (–) indicate Watson–Crick base pairing.

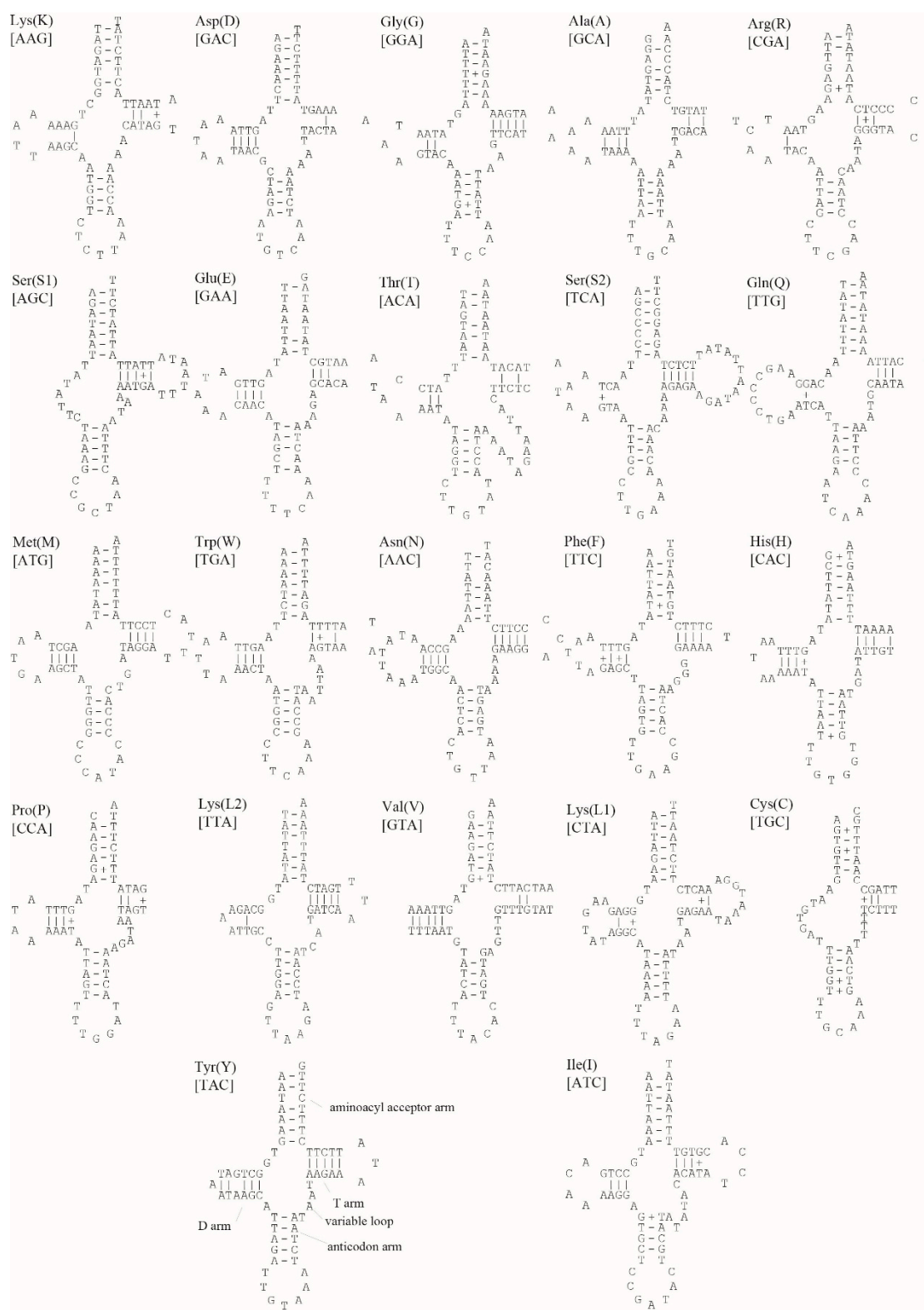


Figure S2. Predicted secondary structure of the 22 tRNAs in the *Mecistocephalus marmoratus* mitogenome Dashes (-) indicate Watson-Crick base pairing.