

Table S1. Collection information of specimens in the present study.

Name	Locality	Time	Collector
<i>V. nigricans</i>	Huayang ancient town, hanzhongyang, shaanxi	23, July 2018	Hu Li
<i>K. angustiabdomena</i>	Huayang ancient town, hanzhongyang, shaanxi	25, July 2018	Hu Li

Note: *V. nigricans* indicates *Volucella nigricans* and *K. angustiabdomena* indicates *Korinchia angustiabdomena*

Table S2. List of mitochondrial genomes used for the phylogenetic analysis in this study.

	family	Species	NCBI No.	References
	Phoridae	<i>Megaselia scalaris</i>	NC_023794	[1]
	Tephritidae	<i>Anastrepha fraterculus</i>	NC_034912	[2]
		<i>Bactrocera arecae</i>	NC_028327	[3]
		<i>Ceratitis capitata</i>	AJ242872	[4]
		<i>Dacus longicornis</i>	NC_032690	[5]
		<i>Neoceratitis asiatica</i>	MF434829	[6]
		<i>Zeugodacus scutellatus</i>	MF358969	[7]
	Drosophilidae	<i>Drosophila melanogaster</i>	NC_024511	[8]
		<i>Drosophila incompta</i>	NC_025936	[9]
	Sepsidae	<i>Nemopoda mamaevi</i>	NC_026866	[10]
	Muscidae	<i>Musca domestica</i>	NC_024855	[11]
		<i>Haematobia irritans</i>	NC_007102	
		<i>Muscina stabulans</i>	NC_026292	
		<i>Hydrotaea chalcogaster</i>	NC_041089	[12]
		<i>Graphomya rufitibia</i>	NC_038210	[13]
		<i>Scathophaga stercoraria</i>	NC_024856	[14]
	Calliphoridae	<i>Chrysomya nigripes</i>	NC_028412	
		<i>Aldrichina grahami</i>	NC_026996	
		<i>Cochliomyia hominivorax</i>	NC_002660	[15]
		<i>Calliphora vomitoria</i>	NC_028411	
ingroups		<i>Phormia regina</i>	NC_026668	[16]
		<i>Lucilia porphyrina</i>	NC_019637	
		<i>Hemipyrellia ligurriens</i>	NC_019638	[17]
		<i>Chrysomya saffranea</i>	NC_019635	
	Oestridae	<i>Dermatobia hominis</i>	NC_006378	
		<i>Gasterophilus pecorum</i>	NC_029812	[18]
		<i>Gasterophilus intestinalis</i>	NC_029834	[19]
		<i>Hypoderma lineatum</i>	NC_013932	[20]
	Sarcophagidae	<i>Sarcophaga impatiens</i>	NC_017605	[21]
		<i>Ravinia pernix</i>	NC_026196	
		<i>Peckia australis</i>	NC_041078	[22]
	Lauxaniidae	<i>Pachycerina decemlineata</i>	NC_034923	[23]
		<i>Cestrotus liui</i>	NC_034922	
	Syrphidae	<i>Ocyptamus sativus</i>	KT272862	[24]
		<i>Simosyrphus grandicornis</i>	NC_008754	[25]
		<i>Episyrrhus balteatus</i>	NC_036481	[26]
		<i>Eupeodes corollae</i>	NC_036482	
		<i>Volucella nigricans</i>	MK870079	This study
		<i>Korinchia angustiabdomena</i>	MK870078	This study
		<i>Eristalis tenax</i>	NC_041143	
outgroups	Tabanidae	<i>Cydistomyia duplonotata</i>	NC_008756	

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Table S3. Partition strategies and evolutionary models used in ML analysis.

Dataset	Subset	Best Model	Score	Partition names
PCG12RNA 7 partitions	1	TIM2+F+I+G4	31812.155	cox1_pos1, cox2_pos1, cox3_pos1, cob_pos1, atp6_pos1
	2	TVM+F+R3	12536.897	atp6_pos2, cob_pos2, cox1_pos2, cox2_pos2, cox3_pos2
	3	GTR+F+I+G4	22812.410	ad6_pos1, nad3_pos1, atp8_pos1, nad2_pos1
	4	TVM+F+I+G4	12633.906	nad6_pos2, atp8_pos2, nad2_pos2, nad3_pos2
	5	GTR+F+I+G4	31527.481	nad4_pos1, nad5_pos1, nad1_pos1, nad4l_pos1
	6	GTR+F+R4	18576.627	nad4_pos2, nad4l_pos2, nad5_pos2, nad1_pos2
	7	GTR+F+R4	44215.658	rrnS, rrnL
PCGRNA 10 partitions	1	GTR+F+I+G4	31924.912	cox1_pos1, cox3_pos1, cox2_pos1, cob_pos1, atp6_pos1
	2	TVM+F+R3	12712.388	atp6_pos2, cob_pos2, cox1_pos2, cox3_pos2, cox2_pos2
	3	TPM3u+F+R5	100584.070	cob_pos3, nad3_pos3, cox3_pos3, cox2_pos3, nad6_pos3, atp8_pos3, cox1_pos3, atp6_pos3
	4	GTR+F+I+G4	22932.849	nad6_pos1, nad3_pos1, atp8_pos1, nad2_pos1
	5	TVM+F+I+G4	12841.048	atp8_pos2, nad2_pos2, nad3_pos2, nad6_pos2
	6	GTR+F+I+G4	31849.066	nad4_pos1, nad5_pos1, nad1_pos1, nad4l_pos1
	7	GTR+F+R4	18823.436	nad4_pos2, nad4l_pos2, nad1_pos2, nad5_pos2
	8	TIM3+F+R5	69354.080	nad4l_pos3, nad5_pos3, nad4_pos3, nad1_pos3
	9	TPM3u+F+I+G4	18334.308	nad2_pos3
	10	GTR+F+R4	44519.431	rrnL, rrnS
AA 4 partitions	1	mtART+R4	13560.661	atp6, nad1
	2	mtMet+F+R5	33559.415	nad3, atp8, nad6, nad2
	3	mtZOA+R4	29086.044	cox2, cox3, cox1, cob
	4	mtInv+R5	41596.083	nad5, nad4, nad4l

Table S4. Organization of the *Korinchia angustiabdomena* mitogenome.

Name	Direction	Location	Size(bp)	Anti / Start/ Stop codon	IN
<i>tRNA-I</i>	F	1-66	66	30-32 GAT	
<i>tRNA-Q</i>	R	64-132	69	102-100 TTG	-3
<i>tRNA-M</i>	F	140-208	69	170-172 CAT	7
<i>ND2</i>	F	209-1231	1023	ATT/TAA	0
<i>tRNA-W</i>	F	1230-1297	68	1260-1262 TCA	-2
<i>tRNA-C</i>	R	1290-1354	65	1325-1323 GCA	-8
<i>tRNA-Y</i>	R	1371-1436	66	1405-1403 GTA	16
<i>COX1</i>	F	1447-2973	1527	ATA/TAA	10
<i>tRNA-L1</i>	F	2969-3033	65	2998-3000 TAA	-5
<i>COX2</i>	F	3037-3720	684	ATG/TAA	3
<i>tRNA-K</i>	F	3722-3792	71	3752-3754 CTT	1
<i>tRNA-D</i>	F	3871-3938	68	3902-3904 GTC	78
<i>ATP8</i>	F	3939-4100	162	ATT/TAA	0
<i>ATP6</i>	F	4097-4771	675	ATA/TAA	-4
<i>COX3</i>	F	4771-5559	789	ATG/TAA	-1
<i>tRNA-G</i>	F	5566-5630	65	5595-5597 TCC	6
<i>ND3</i>	F	5631-5984	354	ATT/TAA	0
<i>tRNA-A</i>	F	5990-6056	67	6020-6022 TGC	5
<i>tRNA-R</i>	F	6056-6118	63	6085-6087 TCG	-1
<i>tRNA-N</i>	F	6120-6186	67	6151-6153 GTT	1
<i>tRNA-S1</i>	F	6187-6253	67	6212-6214 GCT	0
<i>tRNA-E</i>	F	6255-6320	66	6285-6287 TTC	1
<i>tRNA-F</i>	R	6341-6406	66	6374-6372 GAA	20
<i>ND5</i>	R	6407-8141	1735	ATT/T--	0
<i>tRNA-H</i>	R	8139-8204	66	8174-8172 GTG	-3
<i>ND4</i>	R	8209-9549	1341	ATG/TAA	4
<i>ND4L</i>	R	9543-9839	297	ATG/TAA	-7
<i>tRNA-T</i>	F	9842-9906	65	9872-9874 TGT	2
<i>tRNA-P</i>	R	9907-9973	67	9943-9941 TGG	0
<i>ND6</i>	F	9976-10500	525	ATT/TAA	2
<i>Cytb</i>	F	10504-11640	1137	ATG/TAA	3
<i>tRNA-S2</i>	F	11643-11710	68	11672-11674 TGA	2
<i>ND1</i>	R	11727-12665	939	ATA/TAG	16
<i>tRNA-L2</i>	R	12676-12740	65	12711-12709 TAG	10
<i>16S</i>	R	12741-14078	1338		0
<i>tRNA-V</i>	R	14079-14150	72	14117-14115 TAC	0
<i>12S</i>	R	14151-14947	797		0
CR		14948-16473	1526		0

NOTE: IN (Intergenic nucleotides): indicates gap nucleotides (positive value) or overlapped nucleotides (negative value) between two adjacent genes. CR means Control Region.

Table S5. Organization of the *Volucella nigricans* mitogenome.

Name	Direction	Location	Size(bp)	Anti / Start/ Stop codon	IN
<i>tRNA-I</i>	F	1-66	66	30-32 GAT	0
<i>tRNA-Q</i>	R	81-149	69	119-117 TTG	14
<i>tRNA-M</i>	F	149-217	69	179-181 CAT	-1
<i>ND2</i>	F	218-1237	1,020	ATT/TAA	0
<i>tRNA-W</i>	F	1235-1304	70	1266-1268 TCA	-3
<i>tRNA-C</i>	R	1296-1360	65	1331-1329 GCA	-9
<i>tRNA-Y</i>	R	1372-1437	66	1406-1404 GTA	11
<i>COX1</i>	F	1472-2977	1,506	ATT/TAA	34
<i>tRNA-L1</i>	F	2973-3038	66	3002-3004 TAA	-5
<i>COX2</i>	F	3048-3731	684	ATG/TAA	9
<i>tRNA-K</i>	F	3732-3802	71	3762-3764 CTT	0
<i>tRNA-D</i>	F	3803-3869	67	3834-3836 GTC	0
<i>ATP8</i>	F	3870-4031	162	ATT/TAA	0
<i>ATP6</i>	F	4028-4702	675	ATA/TAA	-4
<i>COX3</i>	F	4702-5490	789	ATG/TAA	-1
<i>tRNA-G</i>	F	5502-5568	67	5531-5533 TCC	11
<i>ND3</i>	F	5566-5922	357	ATA/TAA	-3
<i>tRNA-A</i>	F	5925-5991	67	5955-5957 TGC	2
<i>tRNA-R</i>	F	5991-6053	63	6020-6022 TCG	-1
<i>tRNA-N</i>	F	6060-6126	67	6090-6092 GTT	6
<i>tRNA-SI</i>	F	6127-6193	67	6152-6154 GCT	0
<i>tRNA-E</i>	F	6195-6259	65	6225-6227 TTC	1
<i>tRNA-F</i>	R	6281-6347	67	6315-6313 GAA	21
<i>ND5</i>	R	6348-8085	1,738	ATT/T--	0
<i>tRNA-H</i>	R	8083-8148	66	8115-8113 GTG	-3
<i>ND4</i>	R	8149-9489	1,341	ATG/TAA	0
<i>ND4L</i>	R	9483-9779	297	ATG/TAA	-7
<i>tRNA-T</i>	F	9782-9847	66	9812-9814 TGT	2
<i>tRNA-P</i>	R	9848-9913	66	9883-9881 TGG	0
<i>ND6</i>	F	9916-10440	525	ATT/TAA	2
<i>Cytb</i>	F	10440-11576	1,137	ATG/TAA	-1
<i>tRNA-S2</i>	F	11584-11651	68	11613-11615 TGA	7
<i>ND1</i>	R	11672-12610	939	ATA/TAA	20
<i>tRNA-L2</i>	R	12621-12685	65	12656-12654 TAG	10
<i>I6S</i>	R	12686-14023	1,338		0
<i>tRNA-V</i>	R	14024-14095	72	14062-14060 TAC	0
<i>I2S</i>	R	14096-14881	786		0
CR		14882-15724	843		0

NOTE: IN (Intergenic nucleotides): indicates gap nucleotides (positive value) or overlapped nucleotides (negative value) between two adjacent genes. CR means Control Region.

Table S6. Nucleotide compositions, AT- and GC-skew in rRNAs of sequenced Syphidae mitochondrial genomes.

Species	16S								12S							
	Length	A	T	G	C	AT	AT Skew	GC Skew	Length	A	T	G	C	AT	AT Skew	GC Skew
<i>Korinchia angustiabdomena</i>	1338	43.3	40.8	5.4	10.5	84.2	0.03	-0.32	787	43	39.4	5.9	11.7	82.4	0.04	-0.33
<i>Volucella nigricans</i>	1338	43.7	40.7	5.4	10.2	84.5	0.04	-0.31	786	42	40.1	6.1	11.8	82.1	0.02	-0.32
<i>Ocyptamus sativus</i>	1314	42.7	41.7	5.5	10.1	84.4	0.01	-0.29	778	41.8	41	6.2	11.1	82.8	0.01	-0.28
<i>Simosyrphus grandicornis</i>	1339	43	42	5.3	9.7	85	0.01	-0.29	804	42.2	41.7	5.8	10.3	83.8	0.01	-0.28
<i>Episyrrhus balteatus</i>	1338	42.8	41.8	5.5	9.9	84.6	0.01	-0.29	804	42.2	41.8	5.8	10.2	84	0.00	-0.28
<i>Eupeodes corollae</i>	1334	43.4	41.4	5.3	9.9	84.8	0.02	-0.30	795	42.3	40.9	5.9	10.9	83.1	0.02	-0.30
<i>Eristalis tenax</i>	1340	42.6	41.1	5.6	10.7	83.7	0.02	-0.31	792	42.2	40.5	5.9	11.4	82.7	0.02	-0.32
mean	1334	43.1	41.4	5.4	10.1	84.5	0.02	-0.30	792	42.2	40.8	5.9	11.1	83.0	0.02	-0.30

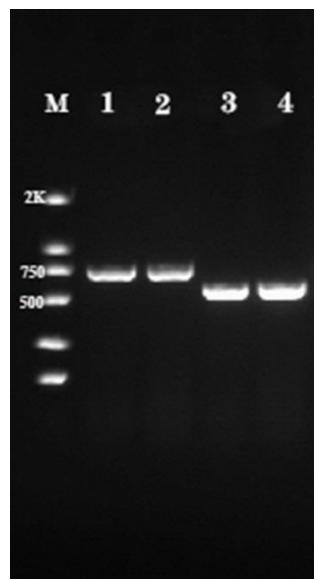


Figure S1. An agarose gel showing the bands of PCR fragments of *COX1* (1–2) and *12s* rRNA (3–4). M: Marker; 1, 3: *Korinchia angustiabdomena*; 2, 4: *Volucella nigricans*.