

Table S1. Mitogenome sequences of the order Siphonaptera used for phylogenetic analysis in the present study.

	Order	Superfamily	Family	subfamily	Species	Size (bp)	GenBank number	References
Outgroup	Mecoptera		Boreidae		<i>Boreus elegans</i>	16,803	HQ696579	25
Ingroup	Siphonaptera	Pulicoidea	Pulicidae	Pulicinae	<i>Ctenocephalides felis</i>	20,873	MT594468	26
					<i>Ctenocephalides felis felis</i>	20,911	MW420044	27
					<i>Ctenocephalides canis</i>	15,609	MW234554	28
					<i>Pulex irritans</i>	20,337	MW745784	28
					<i>Xenopsylla cheopis</i>	18,902	MW310242	29
					<i>Ctenocephalides orientis</i>	22,189	NC073009	30
					<i>Hystrihopsyllaweida qinlingensis</i>	17,173	NC042380	31
					<i>Stenischia humilis</i>	15,617	NC073020	22
					<i>Stenischia montanis yunlongensis</i>	15,651	OR780663	unpublished
					<i>Ctenophthalmus quadratus</i>	15,938	NC072692	22
					<i>Ctenophthalmus yunnanus</i>	15,801	OR780664	unpublished
				Ctenophthalminae	<i>Neopsylla specialis</i>	16,820	NC073019	21
					<i>Stenoponia polyspina</i>	14,933	OR834393	unpublished
					<i>Aviostivaliusklossibispiniformi</i>	16,593	OR774970	unpublished
			Pygiopsyllidae	Stivallinae	<i>Dorcadia ioffi</i>	16,785	NC036066	32
					<i>Ceratophyllus wui</i>	18,081	NC040301	33
		Vermipsylloidea	Vermipsyllidae	Vermipsyllinae	<i>Jellisonia amadoi</i>	17,031	NC022710	34
					<i>Macrostylophora euteles</i>	16,027	OR774969	unpublished
		Ceratophylloidea	Ceratophyllidae	Ceratophyllinae	<i>Citellophilus tesquorum</i>	15,345	NC088096	unpublished
					<i>Ceratophyllus anisus</i>	15,875	NC073017	35
					<i>Frontopsylla spadix</i>	15,085	NC073018	21
					<i>Frontopsylladiqingensis</i>	15,878	OR780662	unpublished
					<i>Leptopsylla segnis</i>	15,785	NC072691	35
					<i>Paradoxopsyllus custodis</i>	15,375	OQ627398	unpublished
			Leptopsyllidae	Leptopsyllinae				

Table S2. Optimal partitioning scheme and substitution model for datasets used in ML analysis.

Dataset	Subset Partitions	Best Model
PCGRNA gene partition	P1: (<i>ATP6</i>)	GTR+F+I+G4
	P2: (<i>ATP8</i>)	TIM3+F+I+G4
	P3: (<i>COX1</i>)	GTR+F+I+G4
	P4: (<i>COX2</i>)	GTR+F+I+G4
	P5: (<i>COX3</i>)	GTR+F+I+G4
	P6: (<i>CYTB</i>)	GTR+F+I+G4
	P7: (<i>ND1</i>)	TIM+F+I+G4
	P8: (<i>ND2</i>)	GTR+F+I+G4
	P9: (<i>ND3</i>)	GTR+F+I+G4
	P10: (<i>ND4</i>)	GTR+F+I+G4
	P11: (<i>ND4L</i>)	GTR+F+I+G4
	P12: (<i>ND5</i>)	TIM+F+I+I+R3
	P13: (<i>ND6</i>)	GTR+F+I+G4
	P14: (<i>rrnS</i>)	GTR+F+I+G4
	P15: (<i>rrnL</i>)	GTR+F+I+G4
PCGRNA codon partition	P1: (<i>ATP6_codon1</i> , <i>CYTB_codon1</i> , <i>COX1_codon1</i> , <i>COX2_codon1</i> , <i>COX3_codon1</i> , <i>ND3_codon1</i> , <i>ND6_codon2</i>)	GTR+F+I+G4
	P2: (<i>ATP6_codon2</i> , <i>CYTB_codon2</i> , <i>COX1_codon2</i> , <i>COX2_codon2</i> , <i>COX3_codon2</i> , <i>ND1_codon2</i> , <i>ND2_codon2</i> , <i>ND3_codon2</i> , <i>ND4L_codon2</i> , <i>ND4_codon2</i> , <i>ND5_codon2</i>)	GTR+F+R3
	P3: (<i>ATP6_codon3</i> , <i>CYTB_codon3</i> , <i>COX1_codon3</i> , <i>COX2_codon3</i> , <i>COX3_codon3</i> , <i>ND2_codon3</i> , <i>ND3_codon3</i> , <i>ND6_codon3</i>)	TIM2+F+I+I+R5
	P4: (<i>ATP8_codon1</i> , <i>ATP8_codon2</i> , <i>ND2_codon1</i> , <i>ND6_codon1</i>)	TIM2+F+I+G4
	P5: (<i>ATP8_codon3</i>)	K3Pu+F+G4
	P6: (<i>ND1_codon1</i> , <i>ND4L_codon1</i> , <i>ND4_codon1</i> , <i>ND5_codon1</i> , <i>rrnL</i> , <i>rrnS</i>)	GTR+F+I+G4
	P7: (<i>ND1_codon3</i> , <i>ND4L_codon3</i> , <i>ND4_codon3</i> , <i>ND5_codon3</i>)	GTR+F+I+I+R5
PCG12RNA gene partition	P1: (<i>ATP6</i>)	TVM+F+I+G4
	P2: (<i>ATP8</i>)	TIM3+F+I+I+R2
	P3: (<i>COX1</i>)	GTR+F+I+G4
	P4: (<i>COX2</i>)	GTR+F+I+G4
	P5: (<i>COX3</i>)	TVM+F+I+G4
	P6: (<i>CYTB</i>)	TVM+F+I+G4
	P7: (<i>ND1</i>)	TVM+F+I+G4
	P8: (<i>ND2</i>)	TVM+F+G4
	P9: (<i>ND3</i>)	TVM+F+I+G4
	P10: (<i>ND4</i>)	TVM+F+I+G4
	P11: (<i>ND4L</i>)	TVM+F+G4
	P12: (<i>ND5</i>)	TVM+F+I+G4
	P13: (<i>ND6</i>)	TIM+F+G4
	P14: (<i>rrnS</i>)	GTR+F+I+G4
	P15: (<i>rrnL</i>)	GTR+F+I+G4

PCG12RNA codon partition	P1: (<i>ATP6_codon1</i> , <i>CYTB_codon1</i> , <i>COX3_codon1</i> , <i>ND3_codon1</i> , <i>ND4L_codon1</i> , <i>ND4_codon1</i> , <i>ND5_codon1</i> , <i>ND6_codon2</i>)	GTR+F+I+G4
	P2: (<i>ATP6_codon2</i> , <i>CYTB_codon2</i> , <i>COX1_codon2</i> , <i>COX2_codon2</i> , <i>COX3_codon2</i> , <i>ND1_codon2</i> , <i>ND2_codon2</i> , <i>ND3_codon2</i> , <i>ND4L_codon2</i> , <i>ND4_codon2</i> , <i>ND5_codon2</i>)	GTR+F+R3
	P3: (<i>ATP8_codon1</i> , <i>ATP8_codonB</i> , <i>ND2_codon1</i> , <i>ND6_codon1</i>)	TIM2+F+I+G4
	P4: (<i>COX1_codon1</i> , <i>COX2_codon1</i>)	GTR+F+G4
	P5: (<i>ND1_codon</i> , <i>rrnL</i> , <i>rrnS</i>)	GTR+F+I+G4

Table S3. Optimal partitioning scheme and substitution model for datasets used in BI analysis.

Dataset	Subset Partitions	Best Model
PCGRNA gene partition	P1: (<i>ATP6</i>)	GTR+F+I+G4
	P2: (<i>ATP8</i>)	GTR+F+I+G4
	P3: (<i>COX1</i>)	GTR+F+I+G4
	P4: (<i>COX2</i>)	GTR+F+I+G4
	P5: (<i>COX3</i>)	GTR+F+I+G4
	P6: (<i>CYTB</i>)	GTR+F+I+G4
	P7: (<i>ND1</i>)	GTR+F+I+G4
	P8: (<i>ND2</i>)	GTR+F+I+G4
	P9: (<i>ND3</i>)	GTR+F+I+G4
	P10: (<i>ND4</i>)	GTR+F+I+G4
	P11: (<i>ND4L</i>)	GTR+F+I+G4
	P12: (<i>ND5</i>)	GTR+F+I+G4
	P13: (<i>ND6</i>)	GTR+F+I+G4
	P14: (<i>rrnS</i>)	GTR+F+I+G4
	P15: (<i>rrnL</i>)	GTR+F+I+G4
PCGRNA codon partition	P1: (<i>ATP6_codon1</i> , <i>CYTB_codon1</i> , <i>COX1_codon1</i> , <i>COX2_codon1</i> , <i>COX3_codon1</i> , <i>ND3_codon1</i> , <i>ND6_codon2</i>)	GTR+F+I+G4
	P2: (<i>ATP6_codon2</i> , <i>CYTB_codon2</i> , <i>COX1_codon2</i> , <i>COX2_codon2</i> , <i>COX3_codon2</i> , <i>ND1_codon2</i> , <i>ND2_codon2</i> , <i>ND3_codon2</i> , <i>ND4L_codon2</i> , <i>ND4_codon2</i> , <i>ND5_codon2</i>)	GTR+F+I+G4
	P3: (<i>ATP6_codon3</i> , <i>COX2_codon3</i> , <i>ND2_codon3</i>)	HKY+F+I+G4
	P4: (<i>ATP8_codon1</i> , <i>ATP8_codon2</i> , <i>ND2_codon1</i> , <i>ND6_codon1</i>)	GTR+F+I+G4
	P5: (<i>ATP8_codon3</i> , <i>CYTB_codon3</i> , <i>COX1_codon3</i> , <i>COX3_codon3</i> , <i>ND3_codon3</i> , <i>ND6_codon3</i>)	GTR+F+G4
	P6: (<i>COX1_codon1</i> , <i>COX2_codon1</i>)	GTR+F+G4
	P7: (<i>ND1_codon1</i> , <i>ND4L_codon1</i> , <i>ND4_codon1</i> , <i>ND5_codon1</i> , <i>rrnL</i> , <i>rrnS</i>)	GTR+F+I+G4
	P8:(<i>ND1_codon3</i> , <i>ND4L_codon3</i>)	GTR+F+G4
	P9:(<i>ND4_codon3</i> , <i>ND5_codon3</i>)	GTR+F+I+G4
PCG12RNA gene partition	P1: (<i>ATP6</i>)	GTR+F+I+G4
	P2: (<i>ATP8</i>)	F81+F+I+G4
	P3: (<i>COX1</i>)	GTR+F+I+G4
	P4: (<i>COX2</i>)	GTR+F+I+G4
	P5: (<i>COX3</i>)	GTR+F+I+G4
	P6: (<i>CYTB</i>)	GTR+F+I+G4
	P7: (<i>ND1</i>)	GTR+F+I+G4
	P8: (<i>ND2</i>)	GTR+F+G4
	P9: (<i>ND3</i>)	GTR+F+G4
	P10: (<i>ND4</i>)	GTR+F+I+G4
	P11: (<i>ND4L</i>)	GTR+F+I+G4
	P12: (<i>ND5</i>)	GTR+F+I+G4
	P13: (<i>ND6</i>)	GTR+F+G4
	P14: (<i>rrnS</i>)	GTR+F+I+G4
	P15: (<i>rrnL</i>)	GTR+F+I+G4
PCG12RNA codon partition	P1: (<i>ATP6_codon1</i> , <i>CYTB_codon1</i> , <i>COX3_codon1</i> , <i>ND3_codon1</i> , <i>ND4L_codon1</i> , <i>ND4_codon1</i> , <i>ND5_codon1</i> , <i>ND6_codon2</i>)	GTR+F+I+G4
	P2: (<i>ATP6_codon2</i> , <i>CYTB_codon2</i> , <i>COX1_codon2</i> , <i>COX2_codon2</i> , <i>COX3_codon2</i> , <i>ND1_codon2</i> , <i>ND2_codon2</i> , <i>ND3_codon2</i> , <i>ND4L_codon2</i> , <i>ND4_codon2</i> , <i>ND5_codon2</i>)	GTR+F+I+G4
	P3: (<i>ATP8_codon1</i> , <i>ATP8_codon2</i> , <i>ND2_codon1</i> , <i>ND6_codon1</i>)	GTR+F+I+G4
	P4: (<i>COX1_codon1</i> , <i>COX2_codon1</i>)	GTR+F+G4
	P5: (<i>ND1_codon1</i> , <i>rrnL</i> , <i>rrnS</i>)	GTR+F+I+G4