

Table S1. Mitogenomic organization of nine Fulgoridae mitochondrial genomes.
Dichoptera sp. (D.); *Limois* sp. (L.); *Neocalathous huangshanana* (N.).

| Gene | Position | | Size (bp) | Codon | | Strand |
|------------------|-------------------|-------------------|----------------|-------------|-------------|--------|
| | From | To | | Start | Stop | |
| D./L./N. | | | | | | |
| <i>trnI</i> | 1/1/1 | 63/65/63 | 63/65/63 | | | +/+/+ |
| <i>trnQ</i> | 66/72/72 | 134/140/414 | 69/69/70 | | | -/-/- |
| <i>trnM</i> | 134/140/141 | 197/204/204 | 64/65 | | | +/+/+ |
| <i>nad2</i> | 198/205/205 | 1163/1167/1143 | 966/963/939 | ATT/ATT/ATT | TAA/TAA/TAA | +/+/+ |
| <i>trnW</i> | 1162/1174/1202 | 1229/1236/1269 | 68/63/68 | | | +/+/+ |
| <i>trnC</i> | 1222/1229/1262 | 1287/1290/1329 | 66/62/68 | | | -/-/- |
| <i>trnY</i> | 1290/1293/1332 | 1351/1356/1394 | 62/64/63 | | | -/-/- |
| <i>cox1</i> | 1357/1360/1409 | 2895/2899/2947 | 1539/1539/1539 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnL2</i> | 2891/2895/2943 | 2958/2959/3009 | 68/65/67 | | | +/+/+ |
| <i>cox2</i> | 2959/2960/3010 | 3630/3631/3684 | 672/672/675 | ATA/ATA/ATA | TAA/TAA/TAA | +/+/+ |
| <i>trnK</i> | 3637/3639/3694 | 3708/3709/3764 | 72/71/71 | | | +/+/+ |
| <i>trnD</i> | 3713/3710/3765 | 3774/3772/3827 | 62/63/63 | | | +/+/+ |
| <i>atp8</i> | 3775/3773/3828 | 3930/3931/3986 | 156/159/159 | ATT/ATT/ATC | TAA/TAA/TAA | +/+/+ |
| <i>atp6</i> | 3924/3925/3980 | 4575/4576/4631 | 652/652/652 | ATG/ATG/ATG | T/T/T | +/+/+ |
| <i>cox3</i> | 4576/4577/4632 | 5356/5359/5414 | 781/783/783 | ATG/ATG/ATG | T/TAA/TAA | +/+/+ |
| <i>trnG</i> | 5357/5361/5422 | 5417/5425/5485 | 61/65/64 | | | +/+/+ |
| <i>nad3</i> | 5418/5426/5486 | 5765/5773/5833 | 348/348/348 | ATT/ATT/ATA | TAA/TAA/TAA | +/+/+ |
| <i>trnA</i> | 5766/5795/5837 | 5830/5858/5900 | 65/64/64 | | | +/+/+ |
| <i>trnR</i> | 5831/5861/5901 | 5891/5922/5960 | 61/62/60 | | | +/+/+ |
| <i>trnN</i> | 5894/5828/5963 | 5962/5991/6029 | 69/64/67 | | | +/+/+ |
| <i>trnS1</i> | 5962/5991/6030 | 6021/6048/6087 | 60/58/67 | | | +/+/+ |
| <i>trnE</i> | 6021/6050/6092 | 6076/6113/6152 | 56/64/61 | | | +/+/+ |
| <i>trnF</i> | 6083/6112/6151 | 6149/6176/6215 | 67/65/65 | | | -/-/- |
| <i>nad5</i> | 6144/6167/6206 | 7805/7837/7879 | 1662/1671/1674 | ATT/ATG/ATA | TAA/TAG/TAG | -/-/- |
| <i>trnH</i> | 7817/7838/7893 | 7879/7899/7955 | 63/62/63 | | | -/-/- |
| <i>nad4</i> | 7870/7890/7937 | 9204/9224/9268 | 1335/1335/1332 | ATG/ATG/ATT | TAG/TAG/TAA | -/-/- |
| <i>nad4L</i> | 9198/9218/9274 | 9473/9493/9549 | 276/276/276 | ATG/ATG/ATG | TAA/TAG/TAA | -/-/- |
| <i>trnT</i> | 9480/9502/9569 | 9544/9567/9632 | 65/66/64 | | | +/+/+ |
| <i>trnP</i> | 9550/9575/9636 | 9613/9638/9698 | 64/64/61 | | | -/-/- |
| <i>nad6</i> | 9618/9646/9698 | 10112/10140/10192 | 495/495/495 | ATA/ATT/ATT | TAA/TAA/TAA | +/+/+ |
| <i>cytb</i> | 10119/10133/10203 | 11240/11251/11327 | 1122/1119/1125 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnS2</i> | 11240/11251/11353 | 11302/11312/11414 | 63/62/62 | | | +/+/+ |
| <i>nad1</i> | 11305/11306/11426 | 12247/12250/12358 | 943/945/933 | ATG/ATG/ATG | T/TAA/TAA | -/-/- |
| <i>trnL1</i> | 12249/12252/12360 | 12314/12314/12422 | 66/64/63 | | | -/-/- |
| <i>rrnL</i> | 12315/12315/12423 | 13532/13527/13635 | 1218/1213/1213 | | | -/-/- |
| <i>trnV</i> | 13533/13528/13636 | 13600/13591/13696 | 68/64/61 | | | -/-/- |
| <i>rrnS</i> | 13601/13592/13697 | 14334/14323/14428 | 734/732/732 | | | -/-/- |
| A +T-rich region | 14335/14324/14429 | 15803/15957/16510 | 1469/1634/2082 | | | +/+/+ |

Table S2. Mitogenomic organization of nine Fulgoridae mitochondrial genomes.
Penthicodes atomaria (Pea.); *Penthicodes caja* (Pec.); *Penthicodes variegata* (Pev.).

| Gene | Position | | Size (bp) | Codon | | Strand |
|-----------------------|-------------------|-------------------|----------------|-------------|-------------|--------|
| | From | To | | Start | Stop | |
| <i>Pea./Pec./Pev.</i> | | | | | | |
| <i>trnI</i> | 1/1/1 | 64/64/64 | 64/64/64 | | | +/+/+ |
| <i>trnQ</i> | 81/77/77 | 149/145/145 | 69/69/69 | | | -/-/- |
| <i>trnM</i> | 149/145/145 | 212/210/210 | 64/66/66 | | | +/+/+ |
| <i>nad2</i> | 219/217/211 | 1184/1182/1179 | 966/966/969 | ATA/ATA/ATT | TAA/TAA/TAA | +/+/+ |
| <i>trnW</i> | 1194/1188/1228 | 1256/1251/1291 | 63/64/64 | | | +/+/+ |
| <i>trnC</i> | 1249/1244/1284 | 1311/1303/1344 | 63/60/61 | | | -/-/- |
| <i>trnY</i> | 1318/1311/1356 | 1379/1373/1420 | 62/63/65 | | | -/-/- |
| <i>cox1</i> | 1385/1390/1426 | 2923/2925/2961 | 1539/1536/1536 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnL2</i> | 2924/2929/2964 | 2987/2995/3027 | 64/67/64 | | | +/+/+ |
| <i>cox2</i> | 2988/2996/3028 | 3659/3670/3702 | 672/675/675 | ATA/ATA/ATA | TAA/TAA/TAA | +/+/+ |
| <i>trnK</i> | 3665/3673/3705 | 3734/3743/3774 | 70/71/70 | | | +/+/+ |
| <i>trnD</i> | 3735/3744/3775 | 3796/3808/3840 | 62/65/66 | | | +/+/+ |
| <i>atp8</i> | 3797/3809/3841 | 3958/3964/3996 | 162/156/156 | ATT/ATT/ATT | TAA/TAA/TAA | +/+/+ |
| <i>atp6</i> | 3952/3958/3990 | 4603/4609/4641 | 652/652/652 | ATG/ATG/ATG | T/T/T | +/+/+ |
| <i>cox3</i> | 4604/4610/4642 | 5386/5392/5424 | 783/783/783 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnG</i> | 5407/5414/5441 | 5469/5477/5504 | 63/64/64 | | | +/+/+ |
| <i>nad3</i> | 5470/5478/5505 | 5817/5825/5852 | 348/348/348 | ATT/ATT/ATT | TAG/TAA/TAA | +/+/+ |
| <i>trnA</i> | 5816/5843/5876 | 5883/5907/5943 | 68/65/68 | | | +/+/+ |
| <i>trnR</i> | 5887/5913/5968 | 5949/5978/6030 | 63/66/63 | | | +/+/+ |
| <i>trnN</i> | 5954/5987/6041 | 6016/6053/6105 | 63/67/65 | | | +/+/+ |
| <i>trnS1</i> | 6017/6054/6106 | 6073/6113/6163 | 57/60/58 | | | +/+/+ |
| <i>trnE</i> | 6076/6116/6166 | 6137/6180/6232 | 62/65/67 | | | +/+/+ |
| <i>trnF</i> | 6136/6179/6237 | 6199/6243/6302 | 64/65/66 | | | -/-/- |
| <i>nad5</i> | 6194/6241/6300 | 7867/7912/7971 | 1674/1672/1672 | ATG/ATG/ATG | TAG/T/T | -/-/- |
| <i>trnH</i> | 7868/7898/7972 | 7930/7961/8034 | 63/64/63 | | | -/-/- |
| <i>nad4</i> | 7921/7967/8082 | 9261/9301/9359 | 1341/1335/1335 | ATG/ATG/ATT | TAG/TAG/TAG | -/-/- |
| <i>nad4L</i> | 9255/9307/9359 | 9530/9582/9634 | 276/276/276 | ATG/ATG/ATG | TAG/TAA/TAA | -/-/- |
| <i>trnT</i> | 9545/9590/9643 | 9611/9655/9776 | 67/66/64 | | | +/+/+ |
| <i>trnP</i> | 9614/9663/9713 | 9676/9726/9776 | 63/64/64 | | | -/-/- |
| <i>nad6</i> | 9678/9758/9778 | 10181/10258/10281 | 504/501/504 | ATA/ATC/ATT | TAA/TAA/TAA | +/+/+ |
| <i>cytb</i> | 10174/10239/10274 | 11292/11357/11395 | 1119/1119/1122 | ATG/ATG/ATG | TAG/TAA/TAG | +/+/+ |
| <i>trnS2</i> | 11291/11343/11394 | 11352/11409/11456 | 62/67/63 | | | +/+/+ |
| <i>nad1</i> | 11346/11418/11450 | 12269/12353/12370 | 924/936/921 | ATA/ATG/ATT | TAA/TAA/TAA | -/-/- |
| <i>trnL1</i> | 12298/12340/12402 | 12360/12403/12465 | 63/64/64 | | | -/-/- |
| <i>rrnL</i> | 12361/12404/12466 | 13575/13624/13689 | 1215/1221/1224 | | | -/-/- |
| <i>trnV</i> | 13576/13625/13690 | 13635/13686/13751 | 60/62/62 | | | -/-/- |
| <i>rrnS</i> | 13636/13687/13752 | 14365/14442/14487 | 730/756/736 | | | -/-/- |
| A +T-rich region | 14366/14443/14488 | 16093/16040/15814 | 1728/1598/1327 | | | +/+/+ |

Table S3. Mitogenomic organization of nine Fulgoridae mitochondrial genomes.
Pyrops clavatus (Pyc.); *Pyrops lathburii* (Pyl.) and *Pyrops spinolae* (Pys.).

| Gene | Position | | Size (bp) | Codon | | Strand |
|-----------------------|-------------------|-------------------|----------------|-------------|-------------|--------|
| | From | To | | Start | Stop | |
| <i>Pyc./Pyl./Pys.</i> | | | | | | |
| <i>trnI</i> | 1/1/1 | 64/64/64 | 64/64/64 | | | +/+/+ |
| <i>trnQ</i> | 71/71/71 | 140/140/140 | 70/70/70 | | | -/-/- |
| <i>trnM</i> | 140/141/140 | 203/204/203 | 64/64/64 | | | +/+/+ |
| <i>nad2</i> | 210/205/204 | 1178/1170/1172 | 969/966/969 | ATA/ATT/ATT | TAA/TAA/TAA | +/+/+ |
| <i>trnW</i> | 1211/1193/1201 | 1280/1262/1269 | 70/70/69 | | | +/+/+ |
| <i>trnC</i> | 1273/1255/1262 | 1337/1322/1329 | 65/68/68 | | | -/-/- |
| <i>trnY</i> | 1338/1323/1330 | 1400/1385/1392 | 63/63/63 | | | -/-/- |
| <i>cox1</i> | 1408/1397/1407 | 2946/2935/2945 | 1539/1539/1539 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnL2</i> | 2942/2931/2941 | 3008/2996/3006 | 67/66/66 | | | +/+/+ |
| <i>cox2</i> | 3009/2997/3007 | 3683/3671/3681 | 675/675/675 | ATA/ATA/ATA | TAA/TAA/TAA | +/+/+ |
| <i>trnK</i> | 3686/3674/3684 | 3756/3744/3754 | 71/71/71 | | | +/+/+ |
| <i>trnD</i> | 3758/3745/3755 | 3820/3807/3817 | 63/63/63 | | | +/+/+ |
| <i>atp8</i> | 3821/3808/3818 | 3976/3966/3979 | 156/159/162 | ATT/ATT/ATC | TAA/TAA/TAA | +/+/+ |
| <i>atp6</i> | 3970/3960/3973 | 4621/4611/4624 | 652/652/652 | ATG/GTG/ATG | T/T/T | +/+/+ |
| <i>cox3</i> | 4622/4612/4625 | 5404/5394/5407 | 783/783/783 | ATG/ATG/ATG | TAA/TAA/TAA | +/+/+ |
| <i>trnG</i> | 5413/5401/5408 | 5474/5463/5471 | 62/63/64 | | | +/+/+ |
| <i>nad3</i> | 5475/5464/5472 | 5822/5811/5819 | 348/348/348 | ATA/ATT/ATT | TAA/TAA/TAG | +/+/+ |
| <i>trnA</i> | 5850/5839/5846 | 5915/5909/5912 | 66/71/67 | | | +/+/+ |
| <i>trnR</i> | 5921/5916/5920 | 5982/5979/5981 | 62/61/62 | | | +/+/+ |
| <i>trnN</i> | 5985/5979/5984 | 6048/6043/6049 | 64/65/66 | | | +/+/+ |
| <i>trnS1</i> | 6048/6043/6049 | 6106/6101/6108 | 59/59/60 | | | +/+/+ |
| <i>trnE</i> | 6112/6105/6112 | 6172/6165/6173 | 61/61/62 | | | +/+/+ |
| <i>trnF</i> | 6171/6164/6172 | 6234/6227/6235 | 64/64/64 | | | -/-/- |
| <i>nad5</i> | 6229/6218/6221 | 7902/7888/7894 | 1674/1671/1674 | ATA/ATC/ATA | TAG/TAG/TAA | -/-/- |
| <i>trnH</i> | 7916/7905/7908 | 7975/7965/7968 | 60/61/61 | | | -/-/- |
| <i>nad4</i> | 7966/7956/7959 | 9300/9290/9293 | 1335/1335/1335 | ATG/ATG/ATG | TAG/TAG/TAG | -/-/- |
| <i>nad4L</i> | 9294/9284/9287 | 9566/9559/9562 | 273/273/276 | ATT/ATG/ATG | TAG/TAA/TAG | -/-/- |
| <i>trnT</i> | 9608/9600/9599 | 9671/9669/9666 | 64/70/68 | | | +/+/+ |
| <i>trnP</i> | 9677/9673/9670 | 9737/9733/9731 | 61/61/62 | | | -/-/- |
| <i>nad6</i> | 9739/9735/9733 | 10233/10229/10227 | 495/495/495 | ATT/ATT/ATC | TAA/TAA/TAA | +/+/+ |
| <i>cytb</i> | 10249/10245/10243 | 11367/11363/11361 | 1119/1119/1119 | ATA/ATA/ATA | TAA/TAA/TAA | +/+/+ |
| <i>trnS2</i> | 11367/11363/11361 | 11428/11424/11422 | 62/62/62 | | | +/+/+ |
| <i>nad1</i> | 11439/11423/11432 | 12371/12364/12364 | 933/942/933 | ATG/GTG/ATG | TAA/TAA/TAA | -/-/- |
| <i>trnL1</i> | 12373/12366/12366 | 12435/12428/12428 | 63/63/63 | | | -/-/- |
| <i>rrnL</i> | 12436/12429/12429 | 13645/13640/13640 | 1210/1212/1212 | | | -/-/- |
| <i>trnV</i> | 13646/13641/13641 | 13705/13701/13701 | 60/61/61 | | | -/-/- |
| <i>rrnS</i> | 13706/13702/13702 | 14443/14432/14433 | 738/731/732 | | | -/-/- |
| A +T-rich region | 14444/14433/14434 | 16054/16104/16028 | 1611/1672/1595 | | | +/+/+ |

Table S4. Start and stop codons usage of nine Fulgoridae mitogenomes.

| Gene | Start Codon / Stop Codon | | | | | | | | |
|--------------|--------------------------|-----------|-----------|-------------|-------------|-------------|-------------|-------------|-------------|
| | <i>D.</i> | <i>L.</i> | <i>N.</i> | <i>Pea.</i> | <i>Pec.</i> | <i>Pev.</i> | <i>Pyc.</i> | <i>Pyl.</i> | <i>Pys.</i> |
| <i>nad2</i> | ATT/TAA | ATT/TAA | ATT/TAA | ATA/TAA | ATA/TAA | ATT/TAA | ATA/TAA | ATT/TAA | ATT/TAA |
| <i>cox1</i> | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA |
| <i>cox2</i> | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA | ATA/TAA |
| <i>atp8</i> | ATT/TAA | ATT/TAA | ATC/TAA | ATT/TAA | ATT/TAA | ATT/TAA | ATT/TAA | ATT/TAA | ATC/TAA |
| <i>atp6</i> | ATG/T | ATG/T | ATG/T | ATG/T | ATG/T | ATG/T | ATG/T | GTG/T | ATG/T |
| <i>cox3</i> | ATG/TAA | ATG/TAA | ATG/T | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA | ATG/TAA |
| <i>nad3</i> | ATT/TAA | ATT/TAA | ATA/TAA | ATT/TAG | ATT/TAA | ATT/TAA | ATA/TAA | ATT/TAA | ATT/TAG |
| <i>nad5</i> | ATT/TAA | ATG/TAG | ATA/TAG | ATG/TAG | ATG/T | ATG/T | ATA/TAG | ATC/TAG | ATA/TAA |
| <i>nad4</i> | ATG/TAG | ATG/TAG | ATT/TAA | ATG/TAG | ATG/TAG | ATT/TAG | ATG/TAG | ATG/TAG | ATG/TAG |
| <i>nad4L</i> | ATG/TAA | ATG/TAA | ATG/TAG | ATG/TAG | ATG/TAA | ATG/TAA | ATT/TAG | ATG/TAA | ATG/TAG |
| <i>nad6</i> | ATA/TAA | ATT/TAA | ATT/TAA | ATA/TAA | ATC/TAA | ATT/TAA | ATT/TAA | ATT/TAA | ATC/TAA |
| <i>cytb</i> | ATG/TAA | ATG/TAA | ATG/TAG | ATG/TAA | ATG/TAA | ATG/TAG | ATA/TAA | ATA/TAA | ATA/TAA |
| <i>nad1</i> | ATG/TAA | ATG/TAA | ATG/T | ATA/TAA | ATG/TAA | ATT/TAA | ATG/TAA | GTG/TAA | ATG/TAA |

Table S5. Best partitioning scheme and models used in this study.

| Data matrix | Subset Partitions | Best Model |
|-------------|---|------------|
| ML | P1: (<i>cox3_codon1</i> , <i>atp6_codon1</i> , <i>cox2_codon1</i> , <i>cytb_codon1</i>) | GTR+I+G |
| | P2: (<i>cox3_codon2</i> , <i>atp6_codon2</i> , <i>cox2_codon2</i> , <i>cytb_codon2</i>) | TVM+I+G |
| | P3: (<i>nad6_codon3</i> , <i>atp6_codon3</i>) | TRN+G |
| | P4: (<i>nad2_codon1</i> , <i>nad3_codon1</i> , <i>nad6_codon1</i> , <i>atp8_codon1</i>) | TIM+I+G |
| | P5: (<i>nad2_codon2</i> , <i>nad3_codon2</i> , <i>atp8_codon2</i> , <i>nad6_codon2</i>) | TVM+I+G |
| | P6: (<i>atp8_codon3</i> , <i>cox2_codon3</i> , <i>cox3_codon3</i> , <i>nad3_codon3</i>) | TIM+G |
| | P7: (<i>cox1_codon1</i>) | GTR+I+G |
| | P8: (<i>cox1_codon2</i>) | TVM+I+G |
| | P9: (<i>cox1_codon3</i> , <i>cytb_codon3</i>) | GTR+I+G |
| | P10: (<i>nad1_codon1</i> , <i>nad4L_codon1</i> , <i>nad5_codon1</i> , <i>nad4_codon1</i>) | GTR+I+G |
| | P11: (<i>nad4L_codon2</i> , <i>nad1_codon2</i> , <i>nad5_codon2</i> , <i>nad4_codon2</i>) | GTR+I+G |
| | P12: (<i>nad1_codon3</i>) | HKY+G |
| | P13: (<i>nad2_codon3</i>) | TIM+G |
| | P14: (<i>nad5_codon3</i> , <i>nad4L_codon3</i> , <i>nad4_codon3</i>) | HKY+G |
| | P15: (<i>rrnL</i> , <i>rrnS</i>) | GTR+I+G |
| BI | P1: (<i>cox3_codon1</i> , <i>atp6_codon1</i> , <i>cox2_codon1</i> , <i>cytb_codon1</i>) | GTR+I+G |
| | P2: (<i>cox2_codon2</i> , <i>cytb_codon2</i> , <i>cox3_codon2</i> , <i>atp6_codon2</i>) | GTR+I+G |
| | P3: (<i>nad6_codon3</i> , <i>atp6_codon3</i> , <i>atp8_codon3</i>) | GTR+G |
| | P4: (<i>nad2_codon1</i> , <i>atp8_codon1</i> , <i>nad3_codon1</i> , <i>nad6_codon1</i>) | GTR+I+G |
| | P5: (<i>nad2_codon2</i> , <i>nad3_codon2</i> , <i>atp8_codon2</i> , <i>nad6_codon2</i>) | GTR+I+G |
| | P6: (<i>cox1_codon1</i>) | GTR+I+G |
| | P7: (<i>cox1_codon2</i>) | GTR+I+G |
| | P8: (<i>cytb_codon3</i> , <i>cox1_codon3</i>) | GTR+I+G |
| | P9: (<i>nad3_codon3</i> , <i>cox2_codon3</i> , <i>cox3_codon3</i>) | GTR+G |
| | P10: (<i>nad1_codon1</i> , <i>nad5_codon1</i> , <i>nad4_codon1</i> , <i>nad4L_codon1</i>) | GTR+I+G |
| | P11: (<i>nad4L_codon2</i> , <i>nad1_codon2</i> , <i>nad5_codon2</i> , <i>nad4_codon2</i>) | GTR+I+G |
| | P12: (<i>nad1_codon3</i>) | HKY+G |
| | P13: (<i>nad2_codon3</i>) | GTR+G |
| | P14: (<i>nad5_codon3</i> , <i>nad4_codon3</i> , <i>nad4L_codon3</i>) | HKY+G |
| | P15: (<i>rrnL</i> , <i>rrnS</i>) | GTR+I+G |