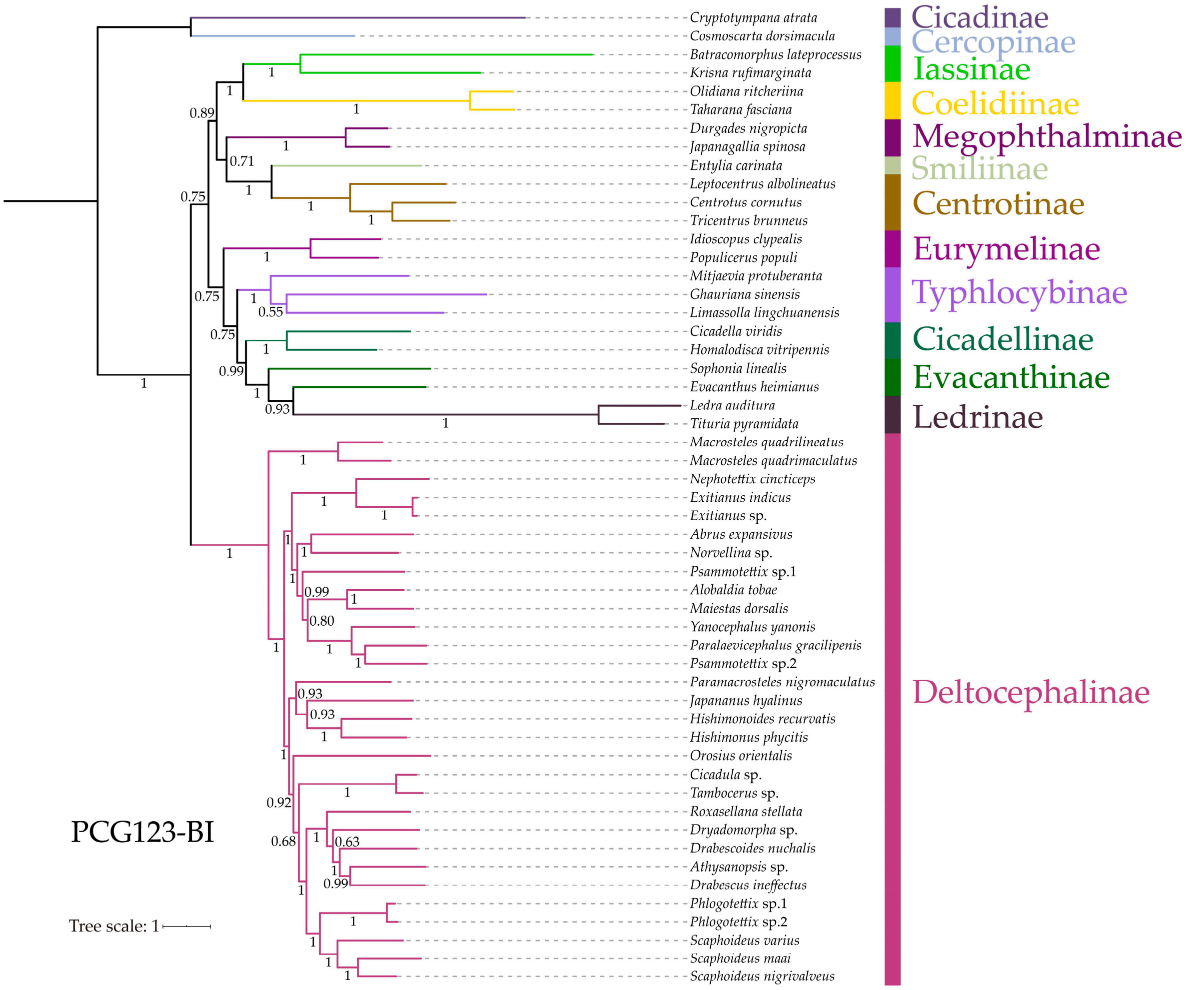

**Figure S1.** Phylogenetic tree inferred from BI method based on PCG123 dataset. Numbers on branches are posterior probabilities (PP).

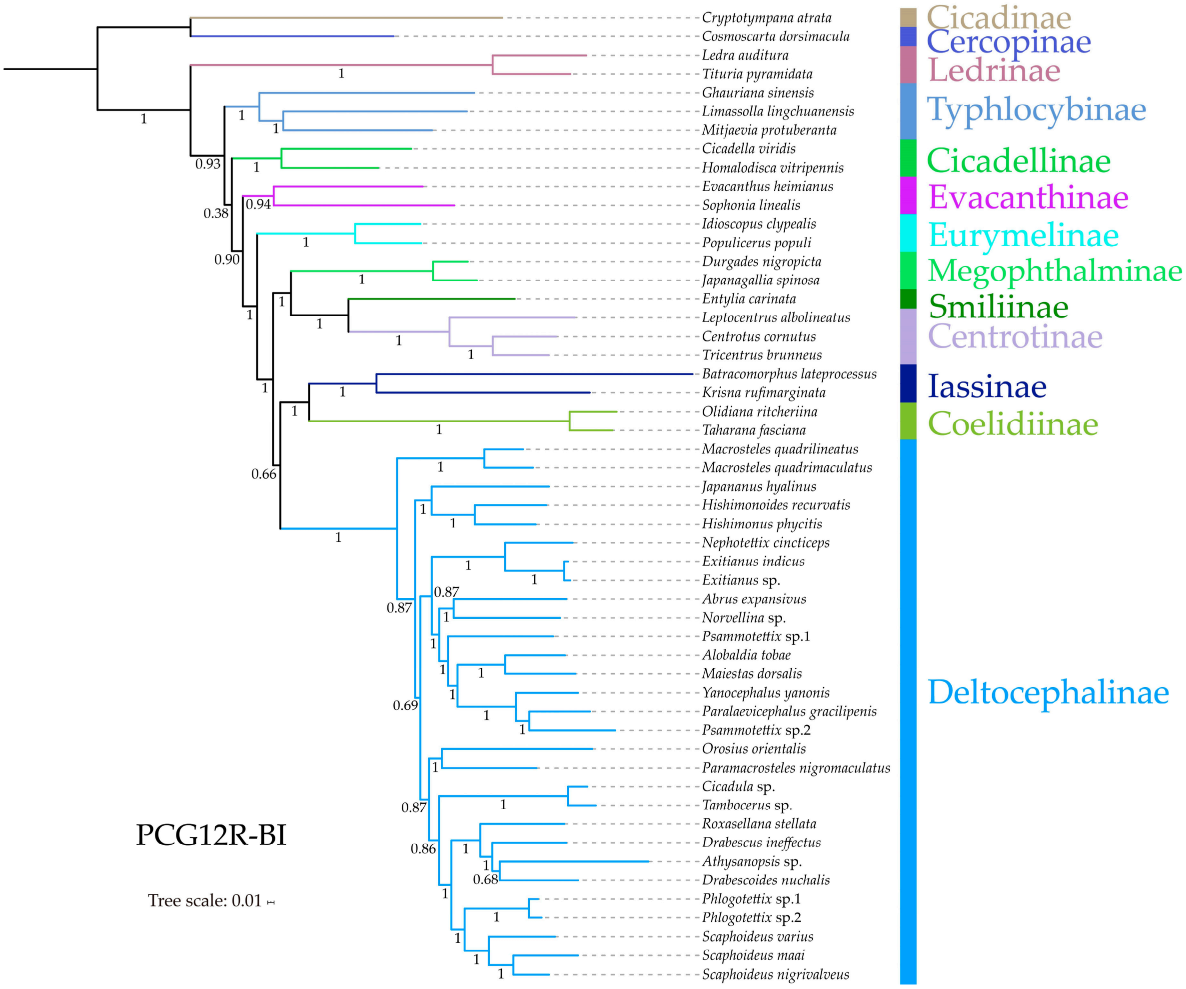

**Figure S2.** Phylogenetic tree inferred from BI method based on PCG12R dataset. Numbers on branches are posterior probabilities (PP).

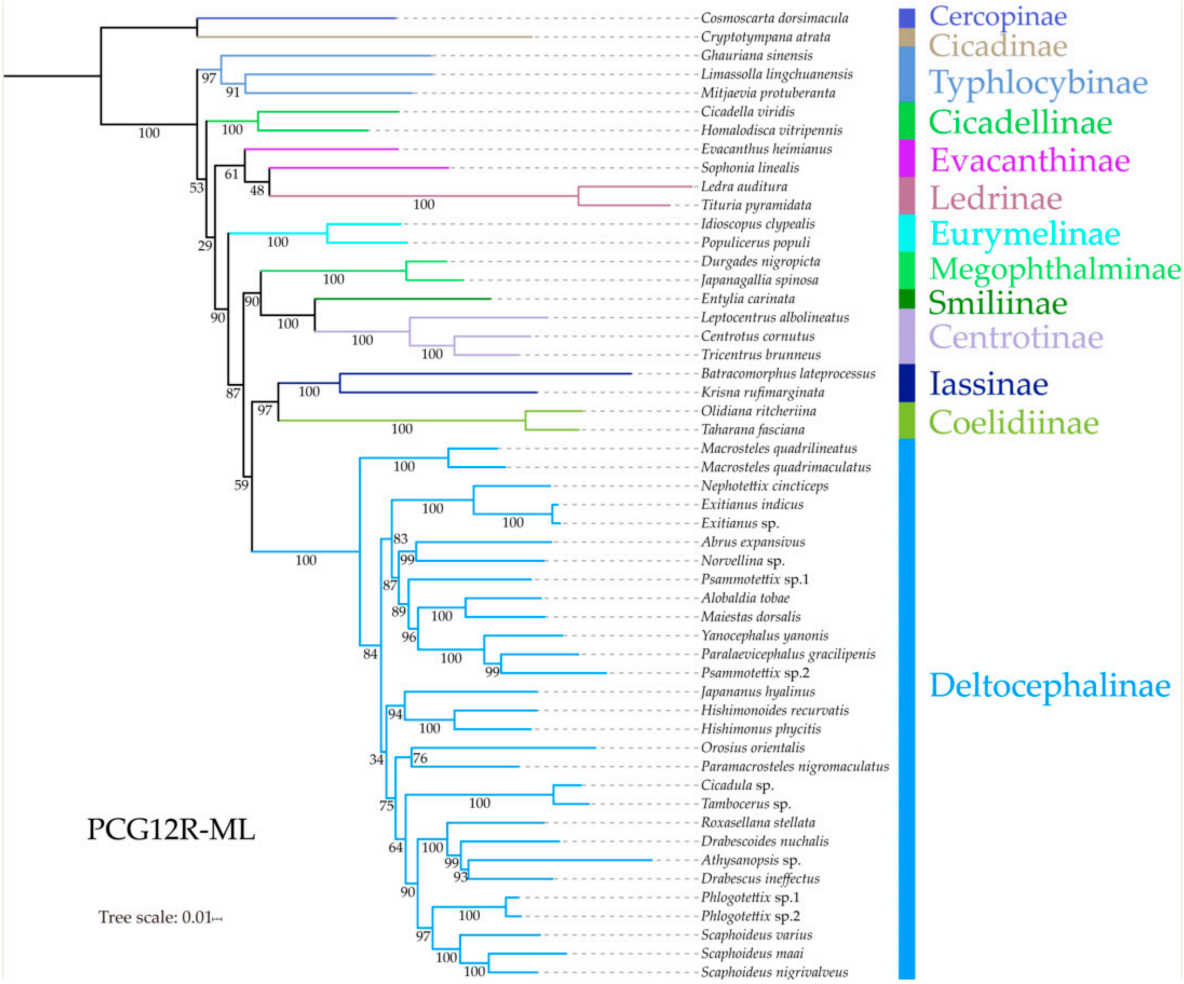

**Figure S3.** Phylogenetic tree inferred from ML method based on PCG12R dataset. Numbers on branches are bootstrap support values (BS).

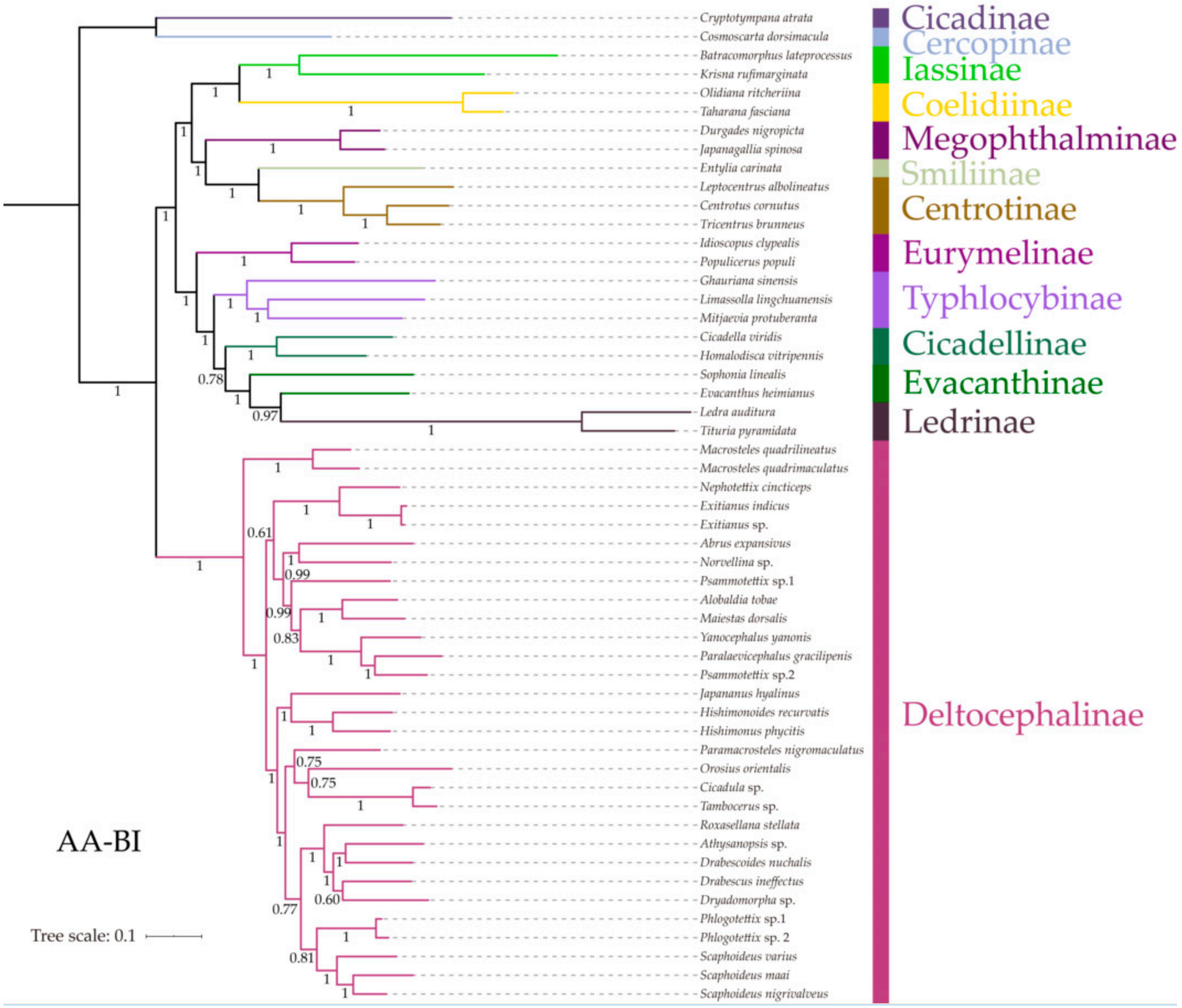

**Figure S4.** Phylogenetic tree inferred from BI method based on amino acid sequences. Numbers on branches are posterior probabilities (PP).

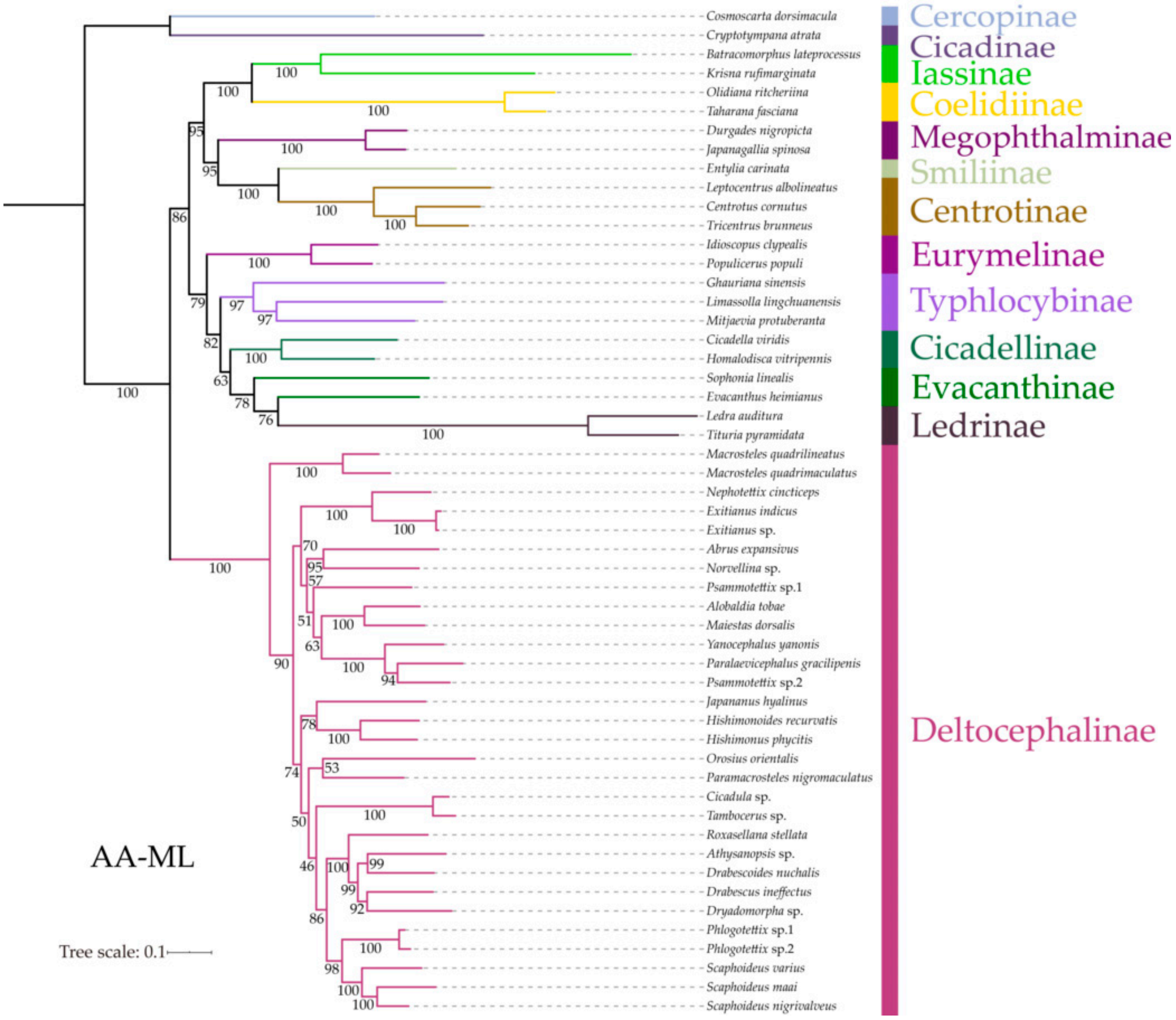

**Figure S5.** Phylogenetic tree inferred from ML method based on amino acid sequences. Numbers on branches are bootstrap support values (BS).

**Table S1.** Mitogenomic organization of *Drabescus ineffectus* and *Roxasellana stellata*.

| Gene. | Position | | Size (bp) | Intergenic Nucleotides | Codon | | Strand |
|---|---|---|---|---|---|---|---|
| | From | To | | | Start | Stop | |
| *trnI* | 1 / 1 | 66 / 70 | 66 / 70 | | | | J / J |
| *trnQ* | 64 / 68 | 132 / 136 | 69 / 69 | −3 / −3 | | | N / N |
| *trnM* | 142 / 143 | 206 / 206 | 65 / 64 | 9 / 6 | | | J / J |
| *nad2* | 207 / 207 | 1178 / 1178 | 972 / 972 | 0 / 0 | ATG/ATG | TAA / TAA | J / J |
| *trnW* | 1177 / 1177 | 1244 / 1249 | 68 / 73 | −2 / −2 | | | J / J |
| *trnC* | 1237 / 1242 | 1299 / 1309 | 63 / 68 | −8 / −8 | | | N / N |
| *trnY* | 1319 / 1325 | 1381 / 1386 | 63 / 62 | 19 / 15 | | | N / N |
| *cox1* | 1402 / 1404 | 2937 / 2939 | 1536 / 1536 | 20 / 17 | ATG / ATG | TAA / TAA | J / J |
| *trnL2* | 2943 / 2944 | 3005 / 3005 | 63 / 62 | 5 / 4 | | | J / J |
| *cox2* | 3006 / 3006 | 3690 / 3687 | 685 / 682 | 0 / 0 | ATA / ATA | T / T | J / J |
| *trnK* | 3691 / 3688 | 3760 / 3758 | 70 / 71 | 0 / 0 | | | J / J |
| *trnD* | 3761 / 3768 | 3829 / 3829 | 69 / 62 | 0 / 9 | | | J / J |
| *atp8* | 3830 / 3830 | 3982 / 3982 | 153 / 153 | 0 / 0 | ATA / ATC | TAA / TAA | J / J |
| *atp6* | 3976 / 3976 | 4629 / 4629 | 654 / 654 | −7 / −7 | ATG / ATG | TAA / TAA | J / J |
| *cox3* | 4631 / 4632 | 5410 / 5414 | 780/783 | 1 / 2 | ATG / ATG | TAG / TAA | J / J |
| *trnG* | 5413 / 5424 | 5476 / 5485 | 64 / 62 | 2 / 9 | | | J / J |
| *nad3* | 5477 / 5486 | 5830 / 5839 | 354 / 354 | 0 / 0 | ATT / ATT | TAG / TAA | J / J |
| *trnA* | 5830 / 5845 | 5891 / 5905 | 62 / 61 | −1 / 5 | | | J / J |
| *trnR* | 5895 / 5906 | 5956 / 5969 | 62 / 64 | 3 / 0 | | | J / J |
| *trnN* | 5956 / 5970 | 6020 / 6035 | 65 / 66 | −1 / 0 | | | J / J |
| *trnS1* | 6020 / 6035 | 6086 / 6100 | 67 / 66 | −1 / −1 | | | J / J |
| *trnE* | 6089 / 6098 | 6154 / 6160 | 66 / 63 | 2 / −3 | | | J / J |
| *trnF* | 6153 / 6161 | 6219 / 6224 | 67 / 64 | −2 / 0 | | | N / N |
| *nad5* | 6221 / 6227 | 7897 / 7900 | 1677 / 1674 | 1 / 2 | ATT / TTG | TAA / TAA | N / N |
| *trnH* | 7895 / 7901 | 7957 / 7965 | 63 / 65 | -3 / 0 | | | N / N |
| *nad4* | 7958 / 7967 | 9269 / 9275 | 1312 / 1309 | 0 / 1 | ATG / ATG | T / T | N / N |
| *nad4L* | 9263 / 9269 | 9538 / 9544 | 276 / 276 | −7 / −7 | ATA / ATT | TAA / TAA | N / N |
| *trnT* | 9541 / 9547 | 9604 / 9610 | 64 / 64 | 2 / 2 | | | J / J |
| *trnP* | 9605 / 9611 | 9671 / 9677 | 67 / 67 | 0 / 0 | | | N / N |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| *nad6* | 9674 / 9680 | 10162 / 10156 | 489 / 477 | 2 / 2 | ATT / ATA | TAA / TAA | J / J |
| *cytb* | 10155 / 10160 | 11291 / 11296 | 1137 / 1137 | −8 / 3 | ATG / ATG | TAA / TAA | J / J |
| *trnS2* | 11292 / 11296 | 11358 / 11359 | 67 / 64 | 0 / −1 | | | J / J |
| *nad1* | 11361 / 11364 | 12293 / 12291 | 933 / 928 | 2 / 4 | ATT / ATA | TAG / T | N / N |
| *trnL1* | 12294 / 12292 | 12357 / 12358 | 64 / 67 | 0 / 0 | | | N / N |
| *rrnL* | 12358 / 12359 | 13577 / 13568 | 1220 / 1210 | 0 / 0 | | | N / N |
| *trnV* | 13578 / 13569 | 13642 / 13635 | 65 / 67 | 0 / 0 | | | N / N |
| *rrnS* | 13643 / 13636 | 14363 / 14378 | 721/ 743 | 0 / 0 | | | N / N |
| CR | 14364 / 14379 | 15744 / 15361 | 1381 / 983 | 0 / 0 | | | |

**Table S2.** Nucleotide composition of the mitogenomes of *Drabescus ineffectus* and *Roxasellana stellata*.

| **Feature** | **Size (bp)** | **A%** | **C%** | **G%** | **T%** | **AT%** | **GC %** | **AT-skew** | **GC-skew** |
|---|---|---|---|---|---|---|---|---|---|
| | | | | *Drabescus ineffectus* | | | | | |
| Whole genome | 15744 | 41.7 | 13 | 9.9 | 35.4 | 77.1 | 22.9 | 0.081 | −0.133 |
| PCGs | 10956 | 33 | 12.2 | 12.4 | 42.4 | 75.4 | 24.6 | −0.124 | 0.009 |
| 1st codon position | 3652 | 36.8 | 11.4 | 16.7 | 35 | 71.9 | 28.1 | 0.024 | 0.187 |
| 2nd codon position | 3652 | 20.7 | 17.6 | 13.7 | 48 | 68.7 | 31.3 | −0.397 | −0.126 |
| 3rd codon position | 3652 | 41.6 | 7.4 | 6.8 | 44.2 | 85.8 | 14.2 | −0.030 | −0.048 |
| tRNAs | 1439 | 39.3 | 9.2 | 13.4 | 38.2 | 77.4 | 22.6 | 0.014 | 0.188 |
| rRNAs | 1941 | 35.2 | 7.5 | 12.5 | 44.8 | 80 | 20 | −0.120 | 0.247 |
| CR | 1381 | 41.8 | 7.7 | 7.0 | 43.5 | 85.3 | 14.7 | −0.020 | −0.054 |
| | | | | *Roxasellana stellata* | | | | | |
| Whole genome | 15361 | 41.4 | 14 | 9.9 | 34.6 | 76 | 24 | 0.089 | −0.17 |
| PCGs | 10932 | 33.9 | 12.5 | 12.2 | 41.4 | 75.3 | 24.7 | −0.099 | −0.013 |
| 1st codon position | 3644 | 36.9 | 11.4 | 16.5 | 35.3 | 72.1 | 27.9 | 0.022 | 0.184 |
| 2nd codon position | 3644 | 21 | 17.3 | 14 | 47.7 | 68.7 | 31.3 | −0.39 | −0.105 |
| 3rd codon position | 3644 | 43.9 | 8.9 | 6.1 | 41 | 84.9 | 15.1 | 0.034 | −0.185 |
| tRNAs | 1441 | 38.6 | 10 | 13.5 | 37.9 | 76.5 | 23.5 | 0.009 | 0.15 |
| rRNAs | 1953 | 36.3 | 7.2 | 12.4 | 44.1 | 80.4 | 19.6 | −0.098 | 0.264 |
| CR | 983 | 38.3 | 12 | 13.2 | 36.2 | 74.7 | 25.3 | 0.027 | 0.048 |

**Table S3.** Nucleotide compositions in regions of the Drabescini mitochondrial genomes.

| **Species** | **Whole genome** | | **AT-skew** | **GC-skew** | **PCGs** | | **tRNAs** | | **rRNAs** | | **CR** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Size(bp)** | **AT %** | | | **Size(bp)** | **AT %** | **Size(bp)** | **AT %** | **Size(bp)** | **AT %** | **Size(bp)** | **AT %** |
| *Drabescoides nuchalis* | 15309 | 75.6 | 0.099 | −0.175 | 10932 | 74.6 | 1480 | 77.1 | 1937 | 79 | 956 | 77.3 |
| *Drabescus ineffectus* | 15744 | 77.1 | 0.081 | −0.133 | 10956 | 75.4 | 1439 | 77.4 | 1941 | 80 | 1381 | 85.3 |
| *Roxasellana stellata* | 15361 | 76 | 0.089 | −0.17 | 10932 | 75.3 | 1441 | 76.5 | 1953 | 80.4 | 983 | 74.7 |
| *Athysanopsis* sp. | 14573 | 73.6 | 0.134 | −0.219 | 10938 | 73.2 | 1446 | 75.1 | 1821 | 78.3 | 200 | 73.5 |
| *Dryadomorpha* sp. | 12297 | 73.4 | 0.109 | −0.117 | 10656 | 73.7 | 1304 | 74.2 | – | – | 240 | 87.5 |

**Table S4.** Best partitioning scheme and nucleotide substitution models for different datasets selected by PartitionFinder.

| Data Matrix | Subset Partitions | Model |
|---|---|---|
| PCG123-BI | 1. *atp6*_pos1 | GTR + I + G |
| | 2. *nad6*_pos2, *nad3*_pos2, *atp6*_pos2, *atp8*_pos2, *nad2*_pos2 | GTR + I + G |
| | 3. *cox3*_pos3, *cytb*_pos3, *nad6*_pos3, *nad3*_pos3, *atp8*_pos3, *cox2*_pos3, *atp6*_pos3 | GTR + I + G |
| | 4. *atp8*_pos1, *nad6*_pos1, *nad2*_pos1, *nad3*_pos1 | GTR + I + G |
| | 5. *cytb*_pos1, *cox1*_pos1 | GTR + I + G |
| | 6. *cox1*_pos2, *cox3*_pos2, *cox2*_pos2, *cytb*_pos2 | GTR + I + G |
| | 7. *cox1*_pos3 | HKY + I + G |
| | 8. *nad1*_pos1, *cox3*_pos1, *cox2*_pos1 | GTR + I + G |
| | 9. *nad1*_pos2, *nad4*_pos2, *nad4L*_pos2, *nad5*_pos2 | GTR + I + G |
| | 10. *nad1*_pos3 | HKY + I + G |
| | 11. *nad2*_pos3 | GTR + G |
| | 12. *nad4L*_pos1, *nad4*_pos1, *nad5*_pos1 | GTR + I + G |
| | 13. *nad4*_pos3, *nad5*_pos3, *nad4L*_pos3 | HKY + I + G |
| PCG123-ML | 1. *atp6*_pos1 | GTR + I + G |
| | 2. *cox2*_pos2, *atp6*_pos2, *cytb*_pos2, *cox3*_pos2 | TVM + I + G |
| | 3. *nad3*_pos3, *atp8*_pos3, *atp6*_pos3, *cox1*_pos3, *cox2*_pos3 | K81UF + I + G |
| | 4. *atp8*_pos1, *nad6*_pos1, *nad2*_pos1, *nad3*_pos1 | GTR + I + G |
| | 5. *atp8*_pos2, *nad3*_pos2, *nad2*_pos2, *nad6*_pos2 | TVM + I + G |
| | 6. *cytb*_pos1, *cox1*_pos1 | GTR + I + G |
| | 7. *cox1*_pos2 | TVM + I + G |
| | 8. *nad1*_pos1, *cox3*_pos1, *cox2*_pos1 | GTR + I + G |
| | 9. *cox3*_pos3, *cytb*_pos3, *nad6*_pos3 | GTR + G |
| | 10. *nad1*_pos2, *nad4*_pos2, *nad4L*_pos2, *nad5*_pos2 | GTR + I + G |
| | 11. *nad1*_pos3, *nad4*_pos3, *nad5*_pos3, *nad4L*_pos3 | TIM + I + G |
| | 12. *nad2*_pos3 | TRN + G |
| | 13. *nad4*_pos1, *nad5*_pos1, *nad4L*_pos1 | GTR + I + G |
| PCG12R-BI | 1. *nad3*, *atp6*, *atp8*, *nad6*, nad2 | GTR + I + G |
| | 2. *cox1* | GTR + I + G |
| | 3. *cytb*, *cox2*, *cox3* | GTR + I + G |
| | 4. *nad1*, *nad4*, *nad4L*, *nad5* | GTR + I + G |

| | | |
|---|---|---|
| | 5. *rrnL*, *rrnS* | GTR + I + G |
| PCG12R-ML | 1. *nad2*, *nad6*, *nad3*, *apt6* | GTR + I + G |
| | 2. *atp8* | TRN + I + G |
| | 3. *cox1* | GTR + I + G |
| | 4. *cytb*, *cox3*, *cox2* | GTR + I + G |
| | 5. *nad1*, *nad4*, *nad5*, *nad4L* | TVM + I + G |
| | 6. *rrnL*, *rrnS* | GTR + I + G |
| AA-BI | 1. *cytb*, *nad1*, *cox2*, *atp6*, *cox3*, *atp8* | MTREV + I + G |
| | 2. *cox1* | MTREV + I + G |
| | 3. *nad2* | MTREV+ I + G |
| | 4. *nad6*, *nad3*, *nad4L* | MTREV + I + G |
| | 5. *nad4*, *nad5* | MTREV + I + G |
| AA-ML | 1. *atp8, cox2, cytb*, *nad6*, *nad3*, *atp6*, *nad2*, *cox3* | MTART + I + G + F |
| | 2. *cox1* | MTART + I + G |
| | 3. *nad4l*, *nad1*, *nad5*, *nad4* | MTART + I + G + F |