

# Complete Mitochondrial Genome of *Eurostus validus*

## Supplementary materials

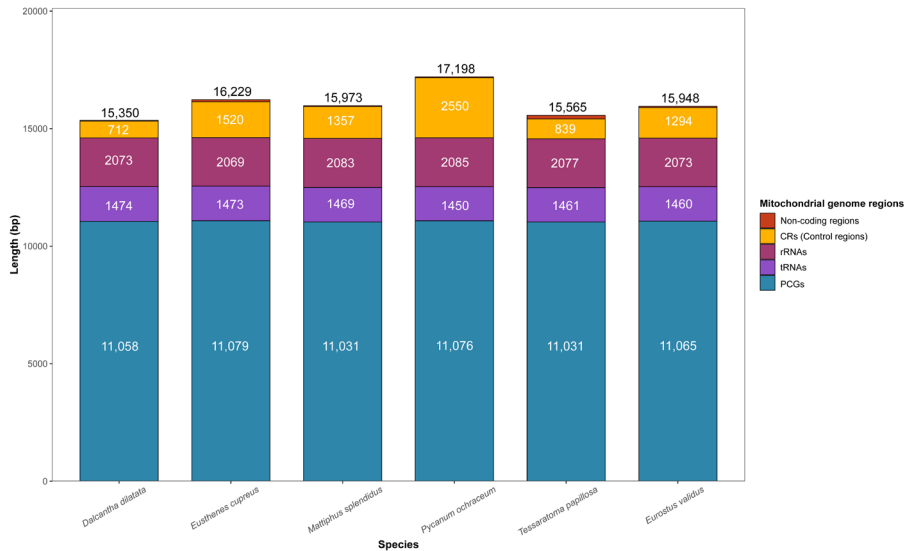


Figure S1. Lengths of different regions in the six Tessaratomidae mitogenomes.

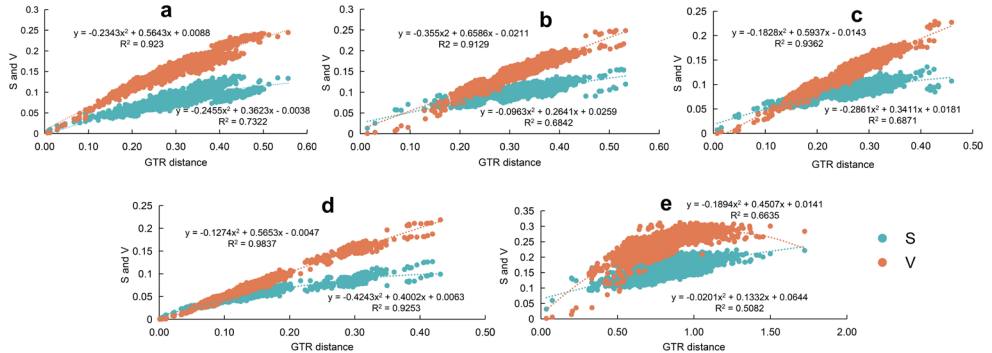


Figure S2. Substitution saturation plots of PCGs and rRNAs in the 74 Pentatomoidea mitogenomes. S represents the transition rate, and V represents the transversion rate. a) rRNAs. b) All sites of PCGs. c) The first site of PCGs. d) The second site of PCGs. e) The third site of PCGs.

Table S1. Complete mitogenomes used in this study.

| Superfamily   | Family           | Species                          | Accession number |
|---------------|------------------|----------------------------------|------------------|
| Pentatomoidea | Tessaratomidae   | <i>Eurostus validus</i>          | This study       |
|               |                  | <i>Dalcantha dilatata</i>        | JQ910981         |
|               |                  | <i>Eusthenes cupreus</i>         | JQ910983         |
|               |                  | <i>Mattiphus splendidus</i>      | MN496304         |
|               |                  | <i>Pycanum ochraceum</i>         | MW899159         |
|               |                  | <i>Tessaratomya papillosa</i>    | KY069965         |
|               | Acanthosomatidae | <i>Acanthosoma labiduroides</i>  | JQ743670         |
|               |                  | <i>Acanthosoma murreeanum</i>    | PQ723361         |
|               |                  | <i>Anaxandra taurina</i>         | MF497709         |
|               |                  | <i>Sastrapta edessoides</i>      | JQ743676         |
|               |                  | <i>Sastrapta esakii</i>          | MW847247         |
|               | Cydnidae         | <i>Adrisa magna</i>              | KU053339         |
|               |                  | <i>Aethus nigratus</i>           | MW847231         |
|               |                  | <i>Cydnidae</i> sp.              | MH643815         |
|               |                  | <i>Geotomus</i> sp.              | MF535442         |
|               |                  | <i>Macroscytus subaeneus</i>     | MW847241         |
|               | Pentatomidae     | <i>Scoparipes salvazai</i>       | MF614955         |
|               |                  | <i>Aeschrocoris tuberculatus</i> | OP526367         |
|               |                  | <i>Aeschrocoris ceylonicus</i>   | OP526368         |
|               |                  | <i>Anaxilax musgravei</i>        | MW679031         |
|               |                  | <i>Brachymna tenuis</i>          | MF497711         |
|               |                  | <i>Carbula sinica</i>            | KY069964         |
|               |                  | <i>Catacanthus incarnatus</i>    | MF497716         |
|               |                  | <i>Castryx obscurus</i>          | MF497717         |
|               |                  | <i>Dalpada cinctipes</i>         | MW847236         |
|               |                  | <i>Dolycoris baccarum</i>        | KJ507135         |
|               |                  | <i>Erthesina fullo</i>           | MW206767         |
|               |                  | <i>Eurydema oleracea</i>         | MG584835         |
|               |                  | <i>Eurydema qinlingensis</i>     | MG584836         |
|               |                  | <i>Eysarcoris rosaceus</i>       | MT165687         |
|               |                  | <i>Eysarcoris montivagus</i>     | MW846867         |
|               |                  | <i>Eysarcoris annamita</i>       | MW852483         |
|               |                  | <i>Glaucias dorsalis</i>         | MW847239         |
|               |                  | <i>Halyomorpha halys</i>         | FJ685650         |
|               |                  | <i>Hippotiscus dorsalis</i>      | MW847240         |
|               |                  | <i>Hoplistodera incisa</i>       | MF620037         |
|               |                  | <i>Menida violacea</i>           | MK617948         |
|               |                  | <i>Neojurtina typica</i>         | MW847243         |
|               |                  | <i>Nezara viridula</i>           | EF208087         |
|               |                  | <i>Palomena viridissima</i>      | MT242599         |
|               |                  | <i>Pentatoma semiannulata</i>    | MT985377         |
|               |                  | <i>Pentatoma rufipes</i>         | MT861131         |
|               |                  | <i>Pentatoma metallifera</i>     | MW847244         |
|               |                  | <i>Placosternum urus</i>         | MF497730         |
|               |                  | <i>Plautia fimbriata</i>         | MF497731         |
|               |                  | <i>Plautia crossota</i>          | MK757497         |
|               |                  | <i>Plautia lushanica</i>         | MW847245         |

# Complete Mitochondrial Genome of *Eurostus validus*

Table continued

| Superfamily  | Family        | Species                        | Accession number |
|--------------|---------------|--------------------------------|------------------|
|              |               | <i>Priassus spiniger</i>       | OK546352         |
|              |               | <i>Tholosanus proximus</i>     | NC063300         |
|              |               | <i>Zicrona caerulea</i>        | MK759656         |
|              | Plataspidae   | <i>Brachyplatys subaeneus</i>  | MW847232         |
|              |               | <i>Calacta lugubris</i>        | MW847233         |
|              |               | <i>Coptosoma variegatum</i>    | OP123035         |
|              |               | <i>Megacopta horvathi</i>      | OP123029         |
|              |               | <i>Megacopta lobata</i>        | OP123031         |
|              |               | <i>Megacopta cribraria</i>     | JF288758         |
|              | Scutelleridae | <i>Cantao ocellatus</i>        | MF497713         |
|              |               | <i>Chrysocoris stollii</i>     | MT740321         |
|              |               | <i>Eurygaster testudinaria</i> | MK251112         |
|              |               | <i>Hyperoncus lateritius</i>   | PV769133         |
|              |               | <i>Lamprocoris</i> sp.         | JQ743674         |
|              |               | <i>Poecilocoris nepalensis</i> | JQ743675         |
|              |               | <i>Scutellera amethystina</i>  | PQ668634         |
|              | Dinidoridae   | <i>Coridius chinensis</i>      | JQ739179         |
|              |               | <i>Coridius brunneus</i>       | MW899158         |
|              |               | <i>Cyclopelta parva</i>        | PV423521         |
|              |               | <i>Eumenotes</i> sp.           | MW847237         |
|              |               | <i>Eumenotes pacao</i>         | PV423523         |
|              |               | <i>Megymenum brevicorne</i>    | JQ739181         |
|              |               | <i>Megymenum gracilicorne</i>  | LC670767         |
|              | Urostylididae | <i>Urochela quadrinotata</i>   | JQ743678         |
|              |               | <i>Urolabida</i> sp.           | MF497734         |
|              |               | <i>Urolabida histrionica</i>   | MW847249         |
|              |               | <i>Urostylis flavoannulata</i> | KY069970         |
| Aradoidea    | Aradidae      | <i>Aradus compar</i>           | JQ780818         |
|              |               | <i>Aneurus similis</i>         | JQ780816         |
| Membracoidea | Cicadellidae  | <i>Idioscopus nitidulus</i>    | KR024406         |
|              |               | <i>Nephotettix cincticeps</i>  | KP749836         |
| Lygaeoidea   | Geocoridae    | <i>Geocoris pallidipennis</i>  | MW619657         |

Table S2. AT content in different genomic regions of six Tessaratomidae species.

|        | <i>Dalcantha dilatata</i> | <i>Eusthenes cupreus</i> | <i>Mattiphus splendidus</i> | <i>Pycanum ochraceum</i> | <i>Tessaratoma papillosa</i> | <i>Eurostus validus</i> |
|--------|---------------------------|--------------------------|-----------------------------|--------------------------|------------------------------|-------------------------|
| PCG123 | 75                        | 73.6                     | 71.8                        | 72.7                     | 74.6                         | 72.3                    |
| PCG12  | 68.7                      | 66.95                    | 67                          | 67.45                    | 68.35                        | 66.84                   |
| PCG3   | 87.7                      | 86.7                     | 81.4                        | 83.2                     | 87.2                         | 83.22                   |
| rRNAs  | 78.9                      | 76                       | 75.5                        | 76.3                     | 77.7                         | 76.17                   |
| tRNAs  | 78                        | 75                       | 74.7                        | 75.2                     | 76                           | 74.66                   |
| mitDNA | 75.7                      | 74.1                     | 72.7                        | 73.6                     | 75.1                         | 73.13                   |
| CR     | 73.96                     | 73.47                    | 72.05                       | 74.67                    | 74.24                        | 72.47                   |

Table S3. AT-skew and GC-skew values of different genomic regions in six Tessaratomidae species.

|                              | AT-skew |       |      |        |       |       |       | GC-skew |       |       |       |       |        |        |
|------------------------------|---------|-------|------|--------|-------|-------|-------|---------|-------|-------|-------|-------|--------|--------|
|                              | PCG123  | PCG12 | PCG3 | rRNA   | tRNA  | mtDNA | CR    | PCG123  | PCG12 | PCG3  | rRNA  | tRNA  | mtDNA  | CR     |
| <i>Dalcantha dilatata</i>    | -0.1    | -0.16 | 0    | -0.166 | 0.056 | 0.138 | 0.087 | 0.01    | 0.06  | -0.21 | 0.267 | 0.096 | -0.115 | -0.258 |
| <i>Eurostus validus</i>      | -0.11   | -0.18 | 0    | -0.17  | 0.02  | 0.14  | -0.01 | 0       | 0.06  | -0.22 | 0.22  | 0.12  | -0.13  | -0.281 |
| <i>Eusthenes cupreus</i>     | -0.1    | -0.18 | 0.01 | -0.171 | 0.018 | 0.133 | 0.09  | 0.01    | 0.06  | -0.25 | 0.213 | 0.117 | -0.103 | -0.217 |
| <i>Mattiphus splendidus</i>  | -0.09   | -0.18 | 0.05 | -0.192 | 0.03  | 0.158 | 0.006 | -0.03   | 0.03  | -0.25 | 0.198 | 0.118 | -0.129 | 0.276  |
| <i>Pycanum ochraceum</i>     | -0.1    | -0.17 | 0.01 | -0.164 | 0     | 0.14  | -0.10 | -0.01   | 0.05  | -0.24 | 0.216 | 0.139 | -0.133 | 0.169  |
| <i>Tessaratoma papillosa</i> | -0.1    | -0.18 | 0.03 | -0.163 | 0     | 0.129 | -0.11 | 0.04    | 0.08  | -0.15 | 0.246 | 0.134 | -0.129 | 0.196  |

Table S4. Relative amino acid usage (%) in PCGs of six Tessaratomidae species.

|                              | Ala  | Arg  | Asn  | Asp  | Cys  | Gln  | Glu  | Gly  | His  | Ile   | Leu   | Lys  | Met   | Phe  | Pro  | Ser   | Thr  | Trp  | Tyr  |
|------------------------------|------|------|------|------|------|------|------|------|------|-------|-------|------|-------|------|------|-------|------|------|------|
| <i>Dalcantha dilatata</i>    | 3.92 | 1.47 | 5.06 | 1.88 | 1.25 | 1.69 | 2.37 | 5.6  | 1.93 | 10.17 | 13.57 | 2.75 | 10.36 | 8.19 | 3.59 | 9.6   | 4.52 | 2.72 | 4.84 |
| <i>Eurostus validus</i>      | 4.27 | 1.5  | 4.68 | 1.9  | 1.06 | 1.63 | 2.37 | 6.04 | 2.04 | 10.25 | 13.7  | 2.66 | 8.18  | 8.27 | 3.75 | 9.54  | 5.25 | 2.69 | 4.7  |
| <i>Eusthenes cupreus</i>     | 4.32 | 1.49 | 4.83 | 1.95 | 1.06 | 1.68 | 2.36 | 5.89 | 1.98 | 10.07 | 13.6  | 2.72 | 8.25  | 8.28 | 3.75 | 9.53  | 5.24 | 2.69 | 4.7  |
| <i>Mattiphus splendidus</i>  | 3.9  | 1.45 | 4.69 | 1.91 | 1.17 | 1.66 | 2.24 | 5.73 | 1.94 | 9.79  | 13.94 | 2.73 | 8.78  | 8.24 | 3.74 | 10.23 | 5.21 | 2.65 | 4.53 |
| <i>Pycanum ochraceum</i>     | 3.8  | 1.44 | 4.7  | 1.96 | 1.11 | 1.63 | 2.39 | 5.81 | 2.01 | 10.48 | 13.58 | 2.66 | 8.85  | 8.58 | 3.69 | 10.1  | 4.92 | 2.74 | 4.48 |
| <i>Tessaratoma papillosa</i> | 3.82 | 1.5  | 4.75 | 1.94 | 1.23 | 1.66 | 2.35 | 5.81 | 1.91 | 9.96  | 13.53 | 2.67 | 9.38  | 8.37 | 3.66 | 9.52  | 5.16 | 2.73 | 4.88 |

Table S5. Codon number and RSCU in the mitogenome of *Eurostus validus*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 232   | 1.53 | UCU(S) | 103   | 2.35 | UAU(Y) | 143   | 1.67 | UGU(C) | 33    | 1.69 |
| UUC(F) | 72    | 0.47 | UCC(S) | 12    | 0.27 | UAC(Y) | 28    | 0.33 | UGC(C) | 6     | 0.31 |
| UUA(L) | 327   | 3.89 | UCA(S) | 93    | 2.12 | UAA(*) | 0     | 0    | UGA(W) | 87    | 1.76 |
| UUG(L) | 52    | 0.62 | UCG(S) | 6     | 0.14 | UAG(*) | 0     | 0    | UGG(W) | 12    | 0.24 |
| CUU(L) | 47    | 0.56 | CCU(P) | 64    | 1.86 | CAU(H) | 38    | 1.01 | CGU(R) | 17    | 1.24 |
| CUC(L) | 9     | 0.11 | CCC(P) | 22    | 0.64 | CAC(H) | 37    | 0.99 | CGC(R) | 1     | 0.07 |
| CUA(L) | 60    | 0.71 | CCA(P) | 50    | 1.45 | CAA(Q) | 44    | 1.47 | CGA(R) | 34    | 2.47 |
| CUG(L) | 9     | 0.11 | CCG(P) | 2     | 0.06 | CAG(Q) | 16    | 0.53 | CGG(R) | 3     | 0.22 |
| AUU(I) | 306   | 1.62 | ACU(T) | 80    | 1.66 | AAU(N) | 141   | 1.64 | AGU(S) | 44    | 1    |
| AUC(I) | 71    | 0.38 | ACC(T) | 27    | 0.56 | AAC(N) | 31    | 0.36 | AGC(S) | 6     | 0.14 |
| AUA(M) | 266   | 1.77 | ACA(T) | 82    | 1.7  | AAA(K) | 67    | 1.37 | AGA(S) | 87    | 1.98 |
| AUG(M) | 35    | 0.23 | ACG(T) | 4     | 0.08 | AAG(K) | 31    | 0.63 | AGG(S) | 0     | 0    |
| GUU(V) | 84    | 1.66 | GCU(A) | 64    | 1.63 | GAU(D) | 53    | 1.51 | GGU(G) | 87    | 1.57 |
| GUC(V) | 11    | 0.22 | GCC(A) | 20    | 0.51 | GAC(D) | 17    | 0.49 | GGC(G) | 6     | 0.11 |
| GUA(V) | 94    | 1.85 | GCA(A) | 66    | 1.68 | GAA(E) | 71    | 1.63 | GGA(G) | 95    | 1.71 |
| GUG(V) | 14    | 0.28 | GCG(A) | 7     | 0.18 | GAG(E) | 16    | 0.37 | GGG(G) | 34    | 0.61 |

# Complete Mitochondrial Genome of *Eurostus validus*

Table S6. Codon number and RSCU in the mitogenome of *Eusthenes cupreus*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 243   | 1.59 | UCU(S) | 95    | 2.17 | UAU(Y) | 154   | 1.78 | UGU(C) | 31    | 1.59 |
| UUC(F) | 62    | 0.41 | UCC(S) | 14    | 0.32 | UAC(Y) | 19    | 0.22 | UGC(C) | 8     | 0.41 |
| UUA(L) | 350   | 4.19 | UCA(S) | 99    | 2.26 | UAA(*) | 0     | 0    | UGA(W) | 96    | 1.94 |
| UUG(L) | 34    | 0.41 | UCG(S) | 2     | 0.05 | UAG(*) | 0     | 0    | UGG(W) | 3     | 0.06 |
| CUU(L) | 59    | 0.71 | CCU(P) | 68    | 1.97 | CAU(H) | 50    | 1.37 | CGU(R) | 17    | 1.24 |
| CUC(L) | 5     | 0.06 | CCC(P) | 21    | 0.61 | CAC(H) | 23    | 0.63 | CGC(R) | 3     | 0.22 |
| CUA(L) | 47    | 0.56 | CCA(P) | 47    | 1.36 | CAA(Q) | 52    | 1.68 | CGA(R) | 28    | 2.04 |
| CUG(L) | 6     | 0.07 | CCG(P) | 2     | 0.06 | CAG(Q) | 10    | 0.32 | CGG(R) | 7     | 0.51 |
| AUU(I) | 312   | 1.68 | ACU(T) | 80    | 1.66 | AAU(N) | 155   | 1.74 | AGU(S) | 40    | 0.91 |
| AUC(I) | 59    | 0.32 | ACC(T) | 23    | 0.48 | AAC(N) | 23    | 0.26 | AGC(S) | 3     | 0.07 |
| AUA(M) | 268   | 1.76 | ACA(T) | 87    | 1.8  | AAA(K) | 76    | 1.52 | AGA(S) | 98    | 2.23 |
| AUG(M) | 36    | 0.24 | ACG(T) | 3     | 0.06 | AAG(K) | 24    | 0.48 | AGG(S) | 0     | 0    |
| GUU(V) | 85    | 1.65 | GCU(A) | 69    | 1.74 | GAU(D) | 62    | 1.72 | GGU(G) | 69    | 1.27 |
| GUC(V) | 12    | 0.23 | GCC(A) | 11    | 0.28 | GAC(D) | 10    | 0.28 | GGC(G) | 8     | 0.15 |
| GUA(V) | 100   | 1.94 | GCA(A) | 78    | 1.96 | GAA(E) | 69    | 1.59 | GGA(G) | 112   | 2.06 |
| GUG(V) | 9     | 0.17 | GCG(A) | 1     | 0.03 | GAG(E) | 18    | 0.41 | GGG(G) | 28    | 0.52 |

Table S7. Codon number and RSCU in the mitogenome of *Dalcantha dilatata*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 249   | 1.65 | UCU(S) | 92    | 2.08 | UAU(Y) | 158   | 1.78 | UGU(C) | 42    | 1.83 |
| UUC(F) | 52    | 0.35 | UCC(S) | 18    | 0.41 | UAC(Y) | 20    | 0.22 | UGC(C) | 4     | 0.17 |
| UUA(L) | 337   | 4.05 | UCA(S) | 95    | 2.15 | UAA(*) | 0     | 0    | UGA(W) | 96    | 1.92 |
| UUG(L) | 45    | 0.54 | UCG(S) | 4     | 0.09 | UAG(*) | 0     | 0    | UGG(W) | 4     | 0.08 |
| CUU(L) | 51    | 0.61 | CCU(P) | 72    | 2.18 | CAU(H) | 56    | 1.58 | CGU(R) | 18    | 1.33 |
| CUC(L) | 5     | 0.06 | CCC(P) | 18    | 0.55 | CAC(H) | 15    | 0.42 | CGC(R) | 2     | 0.15 |
| CUA(L) | 57    | 0.69 | CCA(P) | 39    | 1.18 | CAA(Q) | 54    | 1.74 | CGA(R) | 33    | 2.44 |
| CUG(L) | 4     | 0.05 | CCG(P) | 3     | 0.09 | CAG(Q) | 8     | 0.26 | CGG(R) | 1     | 0.07 |
| AUU(I) | 320   | 1.71 | ACU(T) | 77    | 1.86 | AAU(N) | 167   | 1.8  | AGU(S) | 49    | 1.11 |
| AUC(I) | 54    | 0.29 | ACC(T) | 17    | 0.41 | AAC(N) | 19    | 0.2  | AGC(S) | 3     | 0.07 |
| AUA(M) | 343   | 1.8  | ACA(T) | 72    | 1.73 | AAA(K) | 77    | 1.52 | AGA(S) | 92    | 2.08 |
| AUG(M) | 38    | 0.2  | ACG(T) | 0     | 0    | AAG(K) | 24    | 0.48 | AGG(S) | 0     | 0    |
| GUU(V) | 70    | 1.69 | GCU(A) | 63    | 1.75 | GAU(D) | 58    | 1.68 | GGU(G) | 64    | 1.24 |
| GUC(V) | 3     | 0.07 | GCC(A) | 21    | 0.58 | GAC(D) | 11    | 0.32 | GGC(G) | 11    | 0.21 |
| GUA(V) | 89    | 2.14 | GCA(A) | 58    | 1.61 | GAA(E) | 72    | 1.66 | GGA(G) | 105   | 2.04 |
| GUG(V) | 4     | 0.1  | GCG(A) | 2     | 0.06 | GAG(E) | 15    | 0.34 | GGG(G) | 26    | 0.5  |

Table S8. Codon number and RSCU in the mitogenome of *Mattiphus splendidus*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 227   | 1.5  | UCU(S) | 117   | 2.5  | UAU(Y) | 127   | 1.53 | UGU(C) | 36    | 1.67 |
| UUC(F) | 75    | 0.5  | UCC(S) | 18    | 0.38 | UAC(Y) | 39    | 0.47 | UGC(C) | 7     | 0.33 |
| UUA(L) | 323   | 3.79 | UCA(S) | 90    | 1.92 | UAA(*) | 0     | 0    | UGA(W) | 89    | 1.84 |
| UUG(L) | 36    | 0.42 | UCG(S) | 5     | 0.11 | UAG(*) | 0     | 0    | UGG(W) | 8     | 0.16 |
| CUU(L) | 45    | 0.53 | CCU(P) | 70    | 2.04 | CAU(H) | 45    | 1.27 | CGU(R) | 10    | 0.75 |
| CUC(L) | 11    | 0.13 | CCC(P) | 15    | 0.44 | CAC(H) | 26    | 0.73 | CGC(R) | 6     | 0.45 |
| CUA(L) | 82    | 0.96 | CCA(P) | 50    | 1.46 | CAA(Q) | 46    | 1.51 | CGA(R) | 32    | 2.42 |
| CUG(L) | 14    | 0.16 | CCG(P) | 2     | 0.06 | CAG(Q) | 15    | 0.49 | CGG(R) | 5     | 0.38 |
| AUU(I) | 267   | 1.49 | ACU(T) | 76    | 1.59 | AAU(N) | 136   | 1.58 | AGU(S) | 36    | 0.77 |
| AUC(I) | 92    | 0.51 | ACC(T) | 27    | 0.57 | AAC(N) | 36    | 0.42 | AGC(S) | 11    | 0.23 |

Table continued

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| AUA(M) | 275   | 1.71 | ACA(T) | 86    | 1.8  | AAA(K) | 74    | 1.48 | AGA(S) | 92    | 1.96 |
| AUG(M) | 47    | 0.29 | ACG(T) | 2     | 0.04 | AAG(K) | 26    | 0.52 | AGG(S) | 6     | 0.13 |
| GUU(V) | 69    | 1.37 | GCU(A) | 52    | 1.45 | GAU(D) | 51    | 1.46 | GGU(G) | 55    | 1.05 |
| GUC(V) | 18    | 0.36 | GCC(A) | 16    | 0.45 | GAC(D) | 19    | 0.54 | GGC(G) | 11    | 0.21 |
| GUA(V) | 95    | 1.89 | GCA(A) | 69    | 1.93 | GAA(E) | 60    | 1.46 | GGA(G) | 101   | 1.92 |
| GUG(V) | 19    | 0.38 | GCG(A) | 6     | 0.17 | GAG(E) | 22    | 0.54 | GGG(G) | 43    | 0.82 |

Table S9. Codon number and RSCU in the mitogenome of *Pycnanum ochraceum*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 238   | 1.51 | UCU(S) | 106   | 2.28 | UAU(Y) | 134   | 1.62 | UGU(C) | 29    | 1.41 |
| UUC(F) | 78    | 0.49 | UCC(S) | 19    | 0.41 | UAC(Y) | 31    | 0.38 | UGC(C) | 12    | 0.59 |
| UUA(L) | 315   | 3.78 | UCA(S) | 87    | 1.87 | UAA(*) | 0     | 0    | UGA(W) | 87    | 1.72 |
| UUG(L) | 43    | 0.52 | UCG(S) | 7     | 0.15 | UAG(*) | 0     | 0    | UGG(W) | 14    | 0.28 |
| CUU(L) | 51    | 0.61 | CCU(P) | 64    | 1.88 | CAU(H) | 46    | 1.24 | CGU(R) | 16    | 1.21 |
| CUC(L) | 17    | 0.2  | CCC(P) | 18    | 0.53 | CAC(H) | 28    | 0.76 | CGC(R) | 0     | 0    |
| CUA(L) | 68    | 0.82 | CCA(P) | 53    | 1.56 | CAA(Q) | 50    | 1.67 | CGA(R) | 28    | 2.11 |
| CUG(L) | 6     | 0.07 | CCG(P) | 1     | 0.03 | CAG(Q) | 10    | 0.33 | CGG(R) | 9     | 0.68 |
| AUU(I) | 310   | 1.61 | ACU(T) | 68    | 1.5  | AAU(N) | 149   | 1.72 | AGU(S) | 41    | 0.88 |
| AUC(I) | 76    | 0.39 | ACC(T) | 21    | 0.46 | AAC(N) | 24    | 0.28 | AGC(S) | 11    | 0.24 |
| AUA(M) | 288   | 1.77 | ACA(T) | 90    | 1.99 | AAA(K) | 75    | 1.53 | AGA(S) | 90    | 1.94 |
| AUG(M) | 38    | 0.23 | ACG(T) | 2     | 0.04 | AAG(K) | 23    | 0.47 | AGG(S) | 11    | 0.24 |
| GUU(V) | 74    | 1.59 | GCU(A) | 62    | 1.77 | GAU(D) | 57    | 1.58 | GGU(G) | 70    | 1.31 |
| GUC(V) | 10    | 0.22 | GCC(A) | 19    | 0.54 | GAC(D) | 15    | 0.42 | GGC(G) | 4     | 0.07 |
| GUA(V) | 84    | 1.81 | GCA(A) | 55    | 1.57 | GAA(E) | 70    | 1.59 | GGA(G) | 110   | 2.06 |
| GUG(V) | 18    | 0.39 | GCG(A) | 4     | 0.11 | GAG(E) | 18    | 0.41 | GGG(G) | 30    | 0.56 |

Table S10. Codon number and RSCU in the mitogenome of *Tessaratomya papillosa*.

| Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU | Codon  | Count | RSCU |
|--------|-------|------|--------|-------|------|--------|-------|------|--------|-------|------|
| UUU(F) | 248   | 1.62 | UCU(S) | 98    | 2.25 | UAU(Y) | 154   | 1.72 | UGU(C) | 39    | 1.73 |
| UUC(F) | 59    | 0.38 | UCC(S) | 8     | 0.18 | UAC(Y) | 25    | 0.28 | UGC(C) | 6     | 0.27 |
| UUA(L) | 369   | 4.46 | UCA(S) | 101   | 2.32 | UAA(*) | 0     | 0    | UGA(W) | 95    | 1.9  |
| UUG(L) | 45    | 0.54 | UCG(S) | 0     | 0    | UAG(*) | 0     | 0    | UGG(W) | 5     | 0.1  |
| CUU(L) | 38    | 0.46 | CCU(P) | 62    | 1.85 | CAU(H) | 50    | 1.43 | CGU(R) | 15    | 1.09 |
| CUC(L) | 7     | 0.08 | CCC(P) | 14    | 0.42 | CAC(H) | 20    | 0.57 | CGC(R) | 2     | 0.15 |
| CUA(L) | 32    | 0.39 | CCA(P) | 56    | 1.67 | CAA(Q) | 56    | 1.84 | CGA(R) | 36    | 2.62 |
| CUG(L) | 5     | 0.06 | CCG(P) | 2     | 0.06 | CAG(Q) | 5     | 0.16 | CGG(R) | 2     | 0.15 |
| AUU(I) | 309   | 1.69 | ACU(T) | 82    | 1.74 | AAU(N) | 155   | 1.78 | AGU(S) | 43    | 0.99 |
| AUC(I) | 56    | 0.31 | ACC(T) | 13    | 0.28 | AAC(N) | 19    | 0.22 | AGC(S) | 2     | 0.05 |
| AUA(M) | 302   | 1.76 | ACA(T) | 94    | 1.99 | AAA(K) | 84    | 1.71 | AGA(S) | 93    | 2.13 |
| AUG(M) | 42    | 0.24 | ACG(T) | 0     | 0    | AAG(K) | 14    | 0.29 | AGG(S) | 4     | 0.09 |
| GUU(V) | 74    | 1.56 | GCU(A) | 55    | 1.57 | GAU(D) | 59    | 1.66 | GGU(G) | 68    | 1.28 |
| GUC(V) | 5     | 0.11 | GCC(A) | 11    | 0.31 | GAC(D) | 12    | 0.34 | GGC(G) | 9     | 0.17 |
| GUA(V) | 96    | 2.02 | GCA(A) | 70    | 2    | GAA(E) | 66    | 1.53 | GGA(G) | 99    | 1.86 |
| GUG(V) | 15    | 0.32 | GCG(A) | 4     | 0.11 | GAG(E) | 20    | 0.47 | GGG(G) | 37    | 0.69 |

### Complete Mitochondrial Genome of *Eurostus validus*

Table S11. Nucleotide diversity (Pi), non-synonymous substitution rate (Ka), synonymous substitution rate (Ks), and Ka/Ks ratios for the 13 PCGs across 74 Pentatomoidea species.

| Gene  | Average Pi value | Ka    | Ka/Ks | Ks    |
|-------|------------------|-------|-------|-------|
| atp6  | 0.2615           | 0.21  | 0.23  | 0.915 |
| atp8  | 0.4160           | 0.512 | 0.734 | 0.698 |
| cox1  | 0.1766           | 0.067 | 0.066 | 1.01  |
| cox2  | 0.2174           | 0.149 | 0.533 | 0.938 |
| cox3  | 0.2156           | 0.127 | 0.124 | 1.026 |
| cytb  | 0.2164           | 0.126 | 0.107 | 1.18  |
| nad1  | 0.2168           | 0.176 | 0.232 | 0.758 |
| nad2  | 0.3100           | 0.334 | 0.422 | 0.19  |
| nad3  | 0.2405           | 0.214 | 0.17  | 1.25  |
| nad4  | 0.2813           | 0.290 | 0.421 | 0.689 |
| nad4L | 0.2623           | 0.248 | 0.32  | 0.771 |
| nad5  | 0.2763           | 0.279 | 0.397 | 0.701 |
| nad6  | 0.3187           | 0.332 | 0.372 | 0.892 |

Table S12. GC content at the first and second codon positions (GC12), the third codon position (GC3), and the effective number of codons (ENC) of PCGs in species from different families of Pentatomoidea.

| Species                          | GC12  | GC3   | ENC    | Family           |
|----------------------------------|-------|-------|--------|------------------|
| <i>Acanthosoma labiduroides</i>  | 0.315 | 0.152 | 37.983 | Acanthosomatidae |
| <i>Acanthosoma murreeanum</i>    | 0.320 | 0.176 | 39.396 | Acanthosomatidae |
| <i>Adrisa magna</i>              | 0.344 | 0.220 | 42.314 | Cydnidae         |
| <i>Aeschrocoris ceylonicus</i>   | 0.322 | 0.174 | 38.392 | Pentatomidae     |
| <i>Aeschrocoris tuberculatus</i> | 0.326 | 0.158 | 37.133 | Pentatomidae     |
| <i>Aethus nigrinus</i>           | 0.331 | 0.185 | 39.979 | Cydnidae         |
| <i>Anaxandra taurina</i>         | 0.309 | 0.135 | 36.369 | Acanthosomatidae |
| <i>Anaxilaus musgravei</i>       | 0.301 | 0.107 | 33.825 | Pentatomidae     |
| <i>Brachymna tenuis</i>          | 0.299 | 0.092 | 33.143 | Pentatomidae     |
| <i>Brachyplatys subaeneus</i>    | 0.318 | 0.141 | 36.564 | Plataspidae      |
| <i>Calacta lugubris</i>          | 0.340 | 0.224 | 41.716 | Plataspidae      |
| <i>Cantao ocellatus</i>          | 0.321 | 0.147 | 36.846 | Scutelleridae    |
| <i>Carbula sinica</i>            | 0.304 | 0.107 | 34.494 | Pentatomidae     |
| <i>Catacanthus incarnatus</i>    | 0.304 | 0.108 | 34.093 | Pentatomidae     |
| <i>Caystrus obscurus</i>         | 0.300 | 0.117 | 35.027 | Pentatomidae     |
| <i>Chrysocoris stollii</i>       | 0.318 | 0.126 | 36.202 | Scutelleridae    |
| <i>Coptosoma variegatum</i>      | 0.333 | 0.192 | 40.088 | Plataspidae      |
| <i>Coridius brunneus</i>         | 0.315 | 0.133 | 35.820 | Dinidoridae      |
| <i>Coridius chinensis</i>        | 0.320 | 0.121 | 35.309 | Dinidoridae      |
| <i>Cyclopelta parva</i>          | 0.313 | 0.150 | 37.641 | Dinidoridae      |
| <i>Cydnidae</i> sp.              | 0.319 | 0.170 | 38.833 | Cydnidae         |
| <i>Dalcantia dilatata</i>        | 0.314 | 0.123 | 35.658 | Tessaratomidae   |
| <i>Dalpada cinctipes</i>         | 0.298 | 0.099 | 33.173 | Pentatomidae     |
| <i>Dolycoris baccarum</i>        | 0.330 | 0.166 | 39.358 | Pentatomidae     |
| <i>Erthesina fullo</i>           | 0.314 | 0.157 | 37.487 | Pentatomidae     |
| <i>Eumenotes pacao</i>           | 0.318 | 0.161 | 38.847 | Dinidoridae      |
| <i>Eumenotes</i> sp.             | 0.318 | 0.161 | 38.631 | Dinidoridae      |
| <i>Eurostus validus</i>          | 0.316 | 0.171 | 50.571 | Tessaratomidae   |
| <i>Eurydema oleracea</i>         | 0.309 | 0.120 | 35.093 | Pentatomidae     |
| <i>Eurydema qinlingensis</i>     | 0.295 | 0.096 | 33.612 | Pentatomidae     |
| <i>Eurygaster testudinaria</i>   | 0.342 | 0.255 | 44.153 | Scutelleridae    |
| <i>Eusthenes cupreus</i>         | 0.331 | 0.132 | 36.927 | Tessaratomidae   |

Table continued

| Species                        | GC12  | GC3   | ENC    | Family           |
|--------------------------------|-------|-------|--------|------------------|
| <i>Eysarcoris annamita</i>     | 0.305 | 0.125 | 35.727 | Pentatomidae     |
| <i>Eysarcoris montivagus</i>   | 0.321 | 0.162 | 39.193 | Pentatomidae     |
| <i>Eysarcoris rosaceus</i>     | 0.313 | 0.135 | 36.412 | Pentatomidae     |
| <i>Geotomus</i> sp.            | 0.325 | 0.165 | 38.686 | Cydnidae         |
| <i>Glaucias dorsalis</i>       | 0.319 | 0.170 | 38.622 | Pentatomidae     |
| <i>Halyomorpha halys</i>       | 0.302 | 0.126 | 35.680 | Pentatomidae     |
| <i>Hippotiscus dorsalis</i>    | 0.299 | 0.117 | 34.512 | Pentatomidae     |
| <i>Hoplistodera incisa</i>     | 0.317 | 0.140 | 36.683 | Pentatomidae     |
| <i>Hyperoncus lateritius</i>   | 0.334 | 0.169 | 38.449 | Scutelleridae    |
| <i>Lamprocoris</i> sp.         | 0.287 | 0.217 | 41.124 | Scutelleridae    |
| <i>Macroscytus subaeneus</i>   | 0.337 | 0.194 | 40.712 | Cydnidae         |
| <i>Mattiphus splendidus</i>    | 0.331 | 0.186 | 39.854 | Tessaratomidae   |
| <i>Megacopta cribraria</i>     | 0.345 | 0.247 | 45.188 | Plataspidae      |
| <i>Megacopta horvathi</i>      | 0.345 | 0.243 | 43.576 | Plataspidae      |
| <i>Megacopta lobata</i>        | 0.329 | 0.222 | 42.388 | Plataspidae      |
| <i>Megymenum brevicorne</i>    | 0.327 | 0.181 | 40.002 | Dinidoridae      |
| <i>Megymenum gracilicorne</i>  | 0.327 | 0.179 | 39.793 | Dinidoridae      |
| <i>Menida violacea</i>         | 0.309 | 0.132 | 35.948 | Pentatomidae     |
| <i>Neojurtina typica</i>       | 0.327 | 0.173 | 38.813 | Pentatomidae     |
| <i>Nezara viridula</i>         | 0.305 | 0.111 | 34.177 | Pentatomidae     |
| <i>Palomena viridissima</i>    | 0.305 | 0.120 | 35.296 | Pentatomidae     |
| <i>Pentatoma metallifera</i>   | 0.299 | 0.103 | 34.491 | Pentatomidae     |
| <i>Pentatoma rufipes</i>       | 0.300 | 0.088 | 33.073 | Pentatomidae     |
| <i>Pentatoma semiannulata</i>  | 0.299 | 0.091 | 33.337 | Pentatomidae     |
| <i>Placosternum urus</i>       | 0.294 | 0.084 | 32.200 | Pentatomidae     |
| <i>Plautia crossota</i>        | 0.318 | 0.159 | 37.464 | Pentatomidae     |
| <i>Plautia fimbriata</i>       | 0.313 | 0.135 | 35.329 | Pentatomidae     |
| <i>Plautia lushanica</i>       | 0.302 | 0.093 | 33.107 | Pentatomidae     |
| <i>Poecilocoris nepalensis</i> | 0.302 | 0.101 | 33.907 | Scutelleridae    |
| <i>Priassus spiniger</i>       | 0.302 | 0.097 | 33.395 | Pentatomidae     |
| <i>Pycanum ochraceum</i>       | 0.326 | 0.168 | 39.174 | Tessaratomidae   |
| <i>Sastragala edessoides</i>   | 0.318 | 0.159 | 37.957 | Acanthosomatidae |
| <i>Sastragala esakii</i>       | 0.311 | 0.146 | 36.939 | Acanthosomatidae |
| <i>Scaptocoris castanea</i>    | 0.359 | 0.241 | 43.968 | Cydnidae         |
| <i>Scoparipes salvazai</i>     | 0.364 | 0.281 | 46.254 | Cydnidae         |
| <i>Scutellera amethystina</i>  | 0.320 | 0.171 | 38.619 | Scutelleridae    |
| <i>Tessaratomia papillosa</i>  | 0.317 | 0.128 | 35.301 | Tessaratomidae   |
| <i>Tholosanus proximus</i>     | 0.306 | 0.113 | 35.102 | Pentatomidae     |
| <i>Urochela quadrinotata</i>   | 0.309 | 0.160 | 37.833 | Urostylididae    |
| <i>Urolabida histrionica</i>   | 0.325 | 0.192 | 39.803 | Urostylididae    |
| <i>Urolabida</i> sp.           | 0.315 | 0.153 | 38.293 | Urostylididae    |
| <i>Urostylis flavoannulata</i> | 0.310 | 0.160 | 37.552 | Urostylididae    |
| <i>Zicrona caerulea</i>        | 0.309 | 0.090 | 32.977 | Pentatomidae     |