

Table S1. Nucleotide characteristics of the mitogenome of *Penthe kochi*.

| | Size (bp) | A | T | G | C | A + T | G + C | AT-skew | GC-skew |
|-------------|-----------|--------|--------|--------|--------|--------|--------|---------|---------|
| Full genome | 16,719 | 40.97% | 39.63% | 7.70% | 11.69% | 80.60% | 19.40% | 0.02 | -0.21 |
| PCGs | 11,130 | 34.14% | 44.85% | 10.46% | 10.55% | 78.99% | 21.01% | -0.14 | -0.0043 |
| rRNAs | 2020 | 39.50% | 43.02% | 11.63% | 5.84% | 82.52% | 17.48% | -0.04 | 0.33 |
| tRNAs | 1416 | 41.24% | 38.84% | 11.44% | 8.47% | 80.08% | 19.92% | 0.03 | 0.15 |
| CR | 2119 | 45.73% | 41.81% | 3.78% | 8.68% | 87.54% | 12.46% | 0.04 | -0.39 |

CR = A + T rich region.

Table S2. The codon count and RSCU of the mitogenome of *Penthe kochi*.

| Codon | Count | RSCU | Codon | Count | RSCU | Codon | Count | RSCU |
|---------|-------|------|--------|-------|------|---------|-------|------|
| UUU(F) | 311 | 1.83 | CCC(P) | 5 | 0.16 | AAA(K) | 95 | 1.73 |
| UUC(F) | 28 | 0.17 | CCA(P) | 43 | 1.39 | AAG(K) | 15 | 0.27 |
| UUA(L2) | 508 | 5.13 | CCG(P) | 0 | 0 | GAU(D) | 55 | 1.72 |
| UUG(L2) | 14 | 0.14 | ACU(T) | 86 | 2.18 | GAC(D) | 9 | 0.28 |
| CUU(L1) | 40 | 0.4 | ACC(T) | 6 | 0.15 | GAA(E) | 74 | 1.9 |
| CUC(L1) | 3 | 0.03 | ACA(T) | 65 | 1.65 | GAG(E) | 4 | 0.1 |
| CUA(L1) | 29 | 0.29 | ACG(T) | 1 | 0.03 | UGU(C) | 32 | 1.83 |
| CUG(L1) | 0 | 0 | GCU(A) | 74 | 2.45 | UGC(C) | 3 | 0.17 |
| AUU(I) | 429 | 1.91 | GCC(A) | 6 | 0.2 | UAG(W) | 86 | 1.91 |
| AUC(I) | 21 | 0.09 | GCA(A) | 41 | 1.36 | UGG(W) | 4 | 0.09 |
| AUA(M) | 253 | 1.89 | GCG(A) | 0 | 0 | CGU(R) | 18 | 1.31 |
| AUG(M) | 15 | 0.11 | UAU(Y) | 139 | 1.74 | CGC(R) | 0 | 0 |
| GUU(V) | 77 | 2.11 | UAC(Y) | 21 | 0.26 | CGA(R) | 36 | 2.62 |
| GUC(V) | 5 | 0.14 | UAA | 0 | 0 | CGG(R) | 1 | 0.07 |
| GUA(V) | 61 | 1.67 | UAG | 0 | 0 | AUG(S1) | 13 | 0.29 |
| GUG(V) | 3 | 0.08 | CAU(H) | 63 | 1.8 | AGC(S1) | 1 | 0.02 |
| UCU(S2) | 125 | 2.82 | CAC(H) | 7 | 0.2 | AGA(S1) | 99 | 2.24 |
| UCC(S2) | 15 | 0.34 | CAA(Q) | 61 | 1.94 | AGG(S1) | 1 | 0.02 |
| UCA(S2) | 99 | 2.24 | CAG(Q) | 2 | 0.06 | GGU(G) | 44 | 0.93 |
| UCG(S2) | 1 | 0.02 | AAU(N) | 214 | 1.86 | GGC(G) | 1 | 0.02 |
| CCU(P) | 76 | 2.45 | AAC(N) | 16 | 0.14 | GGA(G) | 127 | 2.67 |
| | | | | | | GGG(G) | 18 | 0.38 |

Table S3. The length of 13 PCGs in Tetratomidae species.

| | nd2 | cox1 | cox2 | atp8 | atp6 | cox3 | nad3 | nad5 | nad4 | nad4L | nad6 | cytb | nad1 |
|--------------------|------|------|------|------|------|------|------|------|------|-------|------|------|------|
| <i>P. kochi</i> | 1008 | 1534 | 688 | 156 | 672 | 789 | 354 | 1713 | 1333 | 288 | 507 | 1137 | 951 |
| <i>T. fungorum</i> | 996 | 1543 | 682 | 156 | 672 | 786 | 354 | 1645 | 1333 | 264 | 498 | 1128 | 948 |

Table S4. The nonsynonymous (Ka) and synonymous (Ks) of the mitogenome of *Penthe kochi*.

| | nd2 | cox1 | cox2 | atp8 | atp6 | cox3 | nad3 | nad5 | nad4 | nad4L | nad6 | cytb | nad1 |
|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Ka | 0.2731 | 0.7 | 0.0838 | 0.2714 | 0.1148 | 0.1294 | 0.1725 | 0.2585 | 0.2039 | 0.2130 | 0.3334 | 0.1213 | 0.1294 |
| Ks | 0.8885 | 0.9200 | 0.6765 | 0.5021 | 0.8625 | 0.8024 | 0.7654 | 0.0742 | 0.5341 | 0.4598 | 0.4643 | 0.7477 | 0.4304 |
| Ka/Ks | 0.3074 | 0.0761 | 0.1234 | 0.5405 | 0.1331 | 0.1613 | 0.2254 | 3.4839 | 0.3818 | 0.4634 | 0.7181 | 0.1622 | 0.3007 |

Table S5. The A+T content of Tetratomidae mitogenome.

| | Full genome | PCGs | rRNAs | tRNAs | CR |
|--------------------|-------------|--------|--------|--------|--------|
| <i>P. kochi</i> | 80.60% | 78.99% | 82.52% | 80.08% | 87.54% |
| <i>T. fungorum</i> | 77.77% | 76.13% | 82.88% | 80.11% | 87.55% |

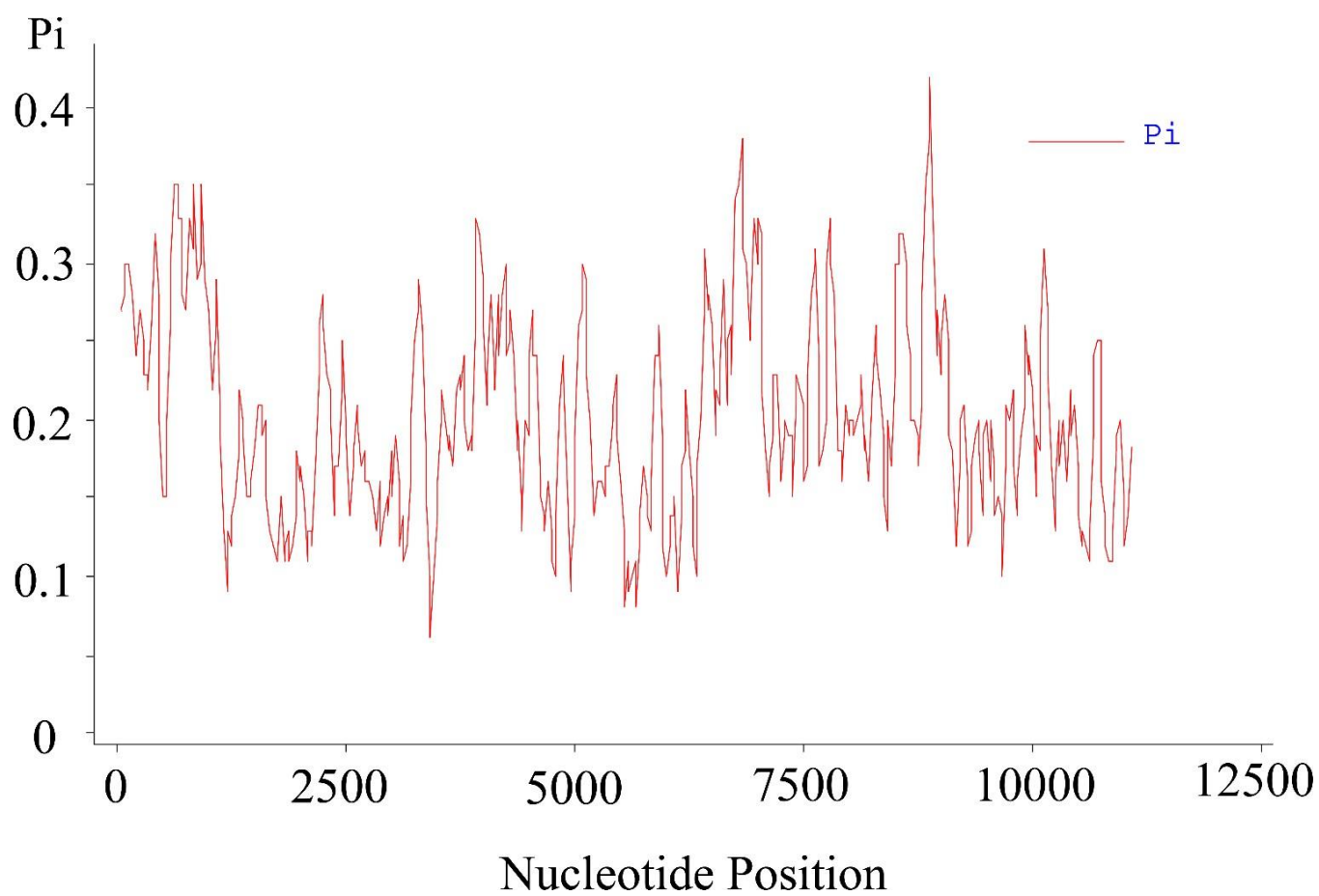


Figure S1. The nucleotide diversity of 13 PCGs of *Penthe kochi*.