**Table S1. Some pairs of PCR primers were designed to amplify overlapping segments of the entire mitochondrial genomes of *C. fasciata.***

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| **Primer Name** | **Primer Sequence** | **Tm°** |
| F1 | 5’-TAGGTGGGCTGCCACCAATACTAGC- 3’ | 54.73 |
| R1 | 5’-TGTTCCTACTATTCCAGCTCA - 3’ | 49.53 |
| F2 | 5’- GAATGAAATCAAGGAGCACTT - 3’ | 49.51 |
| R2 | 5’- GATTCTGGTTGAGGTGAG - 3’ | 54.00 |
| F3 | 5’- CTCACCTCAACCAGAATC - 3’ | 54.00 |
| R3 | 5’-TCTAATATGGCTTCTCCTCC - 3’ | 58.00 |
| F4 | 5’- ATTTATCCTATCAAGATAA - 3’ | 46.00 |
| R4 | 5’- CATGAGATAGGTTCCTCTG - 3’ | 56.00 |
| F5 | 5’- TTGAATTAGAAGATCAACCAGC - 3’ | 50.97 |
| R5 | 5’- ACATGATCTGAGTTCAGACCGG - 3’ | 51.02 |
| F6 | 5’- AGGGTATCTAATCCTAGTCT - 3’ | 56.00 |
| R6 | 5’- AAGTTTTATTCTTGCTTA - 3’ | 44.00 |
| F7 | 5’- AAGTCTTTAATTGCTTATTCTTC - 3’ | 52.26 |
| R7 | 5’- GAAATTGGAGCTTCAACATGAGC - 3’ | 52.33 |
| F8 | 5’- CGAGGTAAAGTACCACGAACCCA- 3’ | 52.37 |
| R8 | 5’- GTTGCTTTTTTAACTTTAATGGAGCG - 3’ | 55.68 |
| F9 | 5’- CCATTTGAATGTGGATTTGACCC - 3’ | 52.33 |
| R9 | 5’-TCATTTATATTATTAACAGTAA - 3’ | 50.87 |
| F10 | 5’- ACCCAAAGCTCCCTCACAAAC - 3’ | 49.57 |
| R10 | 5’- CCTAGTAATGATCCAAGGTTTCA - 3’ | 52.31 |
| F11 | 5’- CACATTCAACCAGAATGATA - 3’ | 54.00 |
| R11 | 5’- AACCGGACACCTTTTGATTTTGC - 3’ | 52.33 |
| F12 | 5’- AATCAAGCTAATGGGTTCATACCC - 3’ | 53.55 |
| R12 | 5’- ATAACTTTGAAGGTTATTAGTTT - 3’ | 52.24 |
| F13 | 5’- GGACTGGGATTAGAGGGAC - 3’ | 60.00 |
| R13 | 5’- TGACATGAGAAGAAGGGTT - 3’ | 54.00 |
| F14 | 5’ATAAAGATAGATATGGAACAC - 3’ | 49.47 |
| R14 | 5’ TATGGGAATAAACGAGAGTAA -3’ | 49.49 |