

ABSTRACT

Rasbora are freshwater fishes that belongs to Cyprinidae family whereby most of its member share similar morphology which makes them difficult to be differentiated between species. In this study, both the morphometry analysis and mitochondrial DNA approach were used to resolve the phylogenetic relationship between these species. The complete sequence of mt-genome for *R. argyrotaenia*, *R. myersi*, *R. sarawakensis* and *Rasbora* sp. were 16,574 bp, 16,581 bp, 16,709 bp and 16,518 bp respectively. The structure of all study species mtDNA was characterized using bioinformatics analysis. *Rasbora* mt-genome comprises of a standard set of 22 tRNAs, two rRNAs, 13 PCGs and two typical non-coding regions. The AT-skew and GC-skew values in the whole genome of *Rasbora* were 0.141 and -0.268 respectively, revealing that the H-strand had the amount of C and A were more prevalent. All the tRNA genes could be folded into cloverleaf secondary structures, while the secondary structure of Ser^(AGY) lacked a D arm (DHU stem). By comparing *Rasbora* genome sequence with the recognition sites in teleost species, five conserved sequence blocks were identified in the control region. The common conserved motif sequence of origin of L-strand replication were also identified. The phylogenetic analyses were based on the concatenated of nucleotide sequence and amino acid sequence from 13 PCGs. The phylogenetic position of *R. argyrotaenia*, *R. myersi*, *R. sarawakensis* and *Rasbora* sp. were evaluated from the Maximum likelihood trees. Overall, this study enriches the knowledge of *Rasbora* mt-genomes while partially resolving the ambiguity of the phylogenetic relationships of *Rasbora* taxonomy.

Keywords: *Rasbora argyrotaenia*, *Rasbora myersi*, *Rasbora sarawakensis*, mitochondrial DNA, phylogenetic analysis

DNA Mitokondria Rasbora Lengkap: Pencirian Mitogenom dan Implikasi Filogenetik

ABSTRAK

Rasbora adalah ikan air tawar yang termasuk dalam keluarga Cyprinidae di mana kebanyakan ahlinya berkongsi morfologi yang sama yang membuat mereka sukar dibezakan antara spesies. Dalam kajian ini, kedua-dua analisis morfometri dan pendekatan mitokondria DNA digunakan untuk menyelesaikan hubungan filogenetik antara spesies ini. Urutan lengkap mt-genom untuk *R. argyrotaenia*, *R. myersi*, *R. sarawakensis* dan *Rasbora sp.* adalah 16,574 bp, 16,581 bp, 16,709 bp dan 16,518 bp masing-masing. Struktur mtDNA untuk semua spesies di bawah kajian disenaraikan dengan analisa bioinformatik. Mt-genome *Rasbora* terdiri daripada set standard 22 tRNAs, dua rRNAs, 13 PCGs dan dua kawasan tidak berkod khas. Nilai AT-skew dan GC-skew dalam seluruh mt-genom *Rasbora* adalah 0.141 dan -0.268 masing-masing, mendedahkan bahawa H-strand mempunyai jumlah C dan A secara lebih lazim. Semua gen tRNA boleh dilipat ke dalam struktur sekunder cloverleaf, sementara struktur sekunder Ser (AGY) tidak mempunyai lengan D (batang DHU). Dengan membandingkan urutan mt-genom *Rasbora* dengan tapak pengiktirafan dalam spesies teleost, lima blok urutan dipulih telah dikenal pasti di rantau kawalan. Urutan motif umum yang dipelihara dari asal replikasi L-strand juga dikenalpasti. Analisis filogenetik adalah berdasarkan urutan-urutan nukleotida dan urutan asid amino dari 13 PCGs. Kedudukan filogenetik *R. argyrotaenia*, *R. myersi*, *R. sarawakensis* dan *Rasbora sp.* telah dinilai dari pokok Maximum Likelihood. Keseluruhannya, kajian ini memperkaya pengetahuan tentang mt-genome *Rasbora* serta menyelesaikan sebahagian keaburan hubungan filogenetik taxonomi *Rasbora*.

Kata kunci: *Rasbora argyrotaenia*, *Rasbora myersi*, *Rasbora sarawakensis*, mitokondria DNA, analisis filogenetik