Dicystostelium intermedium sp. n. is a member of dictyostelids, the highly diverse group of unicellular eukaryotes with a unique life cycle, including a social cycle. Despite the high diversity of dictyostelids, only five species’ complete mitochondrial genome sequences were reported. This study aimed to add the D. intermedium mitochondrial genome sequence to the list. The size of this genome is 58,627 bp, with 73.99% A/T, containing 62 genes located on one strand: 41 protein-coding genes, three ribosomal RNA genes, and 18 transfer RNA genes. The 41 protein-coding genes comprised 18 oxidative phosphorylation-related, 16 ribosomal, and seven hypothetical protein-coding genes. The cox1/2 and rnl gene contained introns, similar to other species of Dictyostelium. The phylogenetic tree built based on 34 protein sequences could be separated into five subclades and the dictyostelids order: Dictyosteliales and Acytosteliales.
evolutionary model. The maximum likelihood (ML) phylogeny was built by the RAxML (Silvestro and Michalak 2012) with 1000 bootstrap replicates.

The total length of Dictyostelium intermedium mitogenome is 58,627 bp (TPA: BK014289), comprising 45.30% A, 28.69% T, 17.02% G, and 8.99% C. This mitogenome contains 18 oxidative phosphorylation (OXPHOS) related PCGs, 16 ribosomal PCGs, seven hypothetical PCGs, three rRNA genes, and 18 tRNA genes. The cox1/2 and rnl genes contained 3 and 2 introns, respectively. These genes are located on one strand. By revising the potential function of 11 hypothetical PCGs in the previously reported dictyostelids mitogenomes by blastx, 18 OXPHOS related PCGs, 18 ribosomal PCGs, and three rRNA genes have commonly been found. The paralogs of rps3 and rps11 gene could not be identified on the D. intermedium mitogenome; however, due to the conserved position across the previously reported five species, the two mitogenome regions located next to rps3 and rps11 gene possibly carrying these paralogs. The arrangement of non-hypothetical PCGs and all rRNA genes of Dictyostelium is similar to that found in D. discoideum and D. citrinum, but not D. purpureum (Heidel and Glöckner 2008). Therefore, the mitochondrial genome of D. intermedium has size, content, and arrangement, similar to other species of Dictyostelium.

Amino acid sequences translated from 34 mitochondrial genes were retrieved from seven species, including A. castellanii. The maximum likelihood phylogeny was built based on the LG substitution model and a gamma correction for rate variation across sites with empirical frequencies (LG + G + F), as shown in Figure 1. This phylogeny presented two monophyletic clades: one contained only Dictyostelium, and another contained Heterostelium and Cavenderia, which corresponded to two orders: Dictyosteliales and Acytosteliales (Sheikh et al. 2018). The common ancestor of dictyostelids was placed between these two clades. The topology of this phylogenetic tree corresponded well with mitochondrial genome phylogeny (Heidel and Glöckner 2008), 18S rRNA gene phylogeny (Sheikh et al. 2018), and nuclear PCGs phylogeny (Schilde et al. 2019). Therefore, this phylogeny supported the monophyletic group of Dictyostelium and dictyostelids’ ancestor’s position between Dictyosteliales and Acytosteliales.

**Disclosure statement**

No potential competing interest was reported by the author(s).

**Funding**

This work was supported by the Graduate School, Kasetsart University, and the Kasetsart University Research and Development Institute (KURDI) under [Grant FF(KU)13.64].

**ORCID**

Kamonchat Prommarit http://orcid.org/0000-0002-0112-1299

**Data availability statement**

The complete mitogenome sequence of Dictyostelium intermedium is available in the Third Party Annotation Section of the DDBJ/ENA/GenBank (https://www.ncbi.nlm.nih.gov) databases under the accession number TPA: BK014289. While waiting for the availability of the updated sequence record, the mapping results supporting the replacement of Ns in the sequence and the updated sequence are available upon request. This data was derived from the 454 short-read whole-genome sequence data of D. intermedium submitted by the Baylor College of Medicine Human Genome Sequencing Center (BCM-HGSC) and stored in the ENA database at https://www.ebi.ac.uk/ena/browser/home, accession number SRR037009-17.

**References**

Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. Cambridge, United Kingdom: Babraham Bioinformatics, Babraham Institute.

Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL. 2009. BLAST+: architecture and applications. BMC Bioinformatics. 10(1):421.

Cavender JC. 1976. Cellular slime molds of Southeast Asia. I. Description of new species. Am J Bot. 63(1):60–70.

Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32(5):1792–1797.

Heidel AJ, Glöckner G. 2008. Mitochondrial genome evolution in the social amoebae. Mol Biol Evol. 25(7):1440–1450.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.

Lagesen K, Hallin P, Redland EA, Staerfeldt HH, Rognés T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. 35(9):3100–3108.

Larsson A. 2014. AllView: a fast and lightweight alignment viewer and editor for large datasets. Bioinformatics. 30(22):3276–3278.

Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. ArXiv. 1303.

Lowe TM, Chan PP. 2016. tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res. 44(W1): W54–W57.

Nylander J. 2011. Catfasta2phyml.pl. [accessed 2014 May 15]. Available from http://www.abc.se/~nylander/catfasta2phyml/.

Romeralo M, Escalante R, Baldauf SL. 2012. Evolution and diversity of dictyostelid social Amoebae. Protist. 163(3):327–343.
Schilde C, Lawal HM, Kin K, Shibano-Hayakawa I, Inouye K, Schaap P. 2019. A well supported multi gene phylogeny of 52 dictyostelia. Mol Phylogenet Evol. 134:66–73.
Sheikh S, Thulin M, Cavender JC, Escalante R, Kawakami S-I, Lado C, Landolt JC, Nanjundiah V, Queller DC, Strassmann JE, et al. 2018. A new classification of the dictyostelids. Protist. 169(1):1–28.
Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. Org Divers Evol. 12(4):335–337.
Souvorov A, Landsman D, Lipman DJ, Church DM, Benson DA, Maglott DR, Sequeira E, Yaschenko E, Schuler GD, Starchenko G, et al. 2008. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 36(Database issue): D13–D21.
Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol. 13(6):e1005595.