

Short communication

DNA Barcoding for *Diophrys quadrinucleata* (Ciliophora: Euplotia) from South Korea

Kyu-Seok Chae¹, Gi-Sik Min^{1,*}

¹Department of Biological Sciences and Bioengineering, Inha University, Incheon 22212, Korea

ABSTRACT

One marine ciliate, *Diophrys quadrinucleata* Zhang *et al.*, 2020 was newly recorded from South Korea in this study. We provided morphological diagnosis and images of the Korean *D. quadrinucleata* population. We determined the small subunit ribosomal DNA (SSU rDNA) and cytochrome oxidase subunit I (CO1) sequence data of *D. quadrinucleata*, and then the sequences were compared with other *Diophrys* species. Intra-specific variation between the Korean and type (Chinese) populations was identical in the SSU rDNA, while the inter-specific variations between seven *Diophrys* species were 0.3–3.8% in the SSU rDNA and 12.6–18.2% in the CO1. In this study, we obtained 18S and CO1 data from species with identified morphology. As the importance of securing 18S and CO1 based on morphology increases in current studies, this study will contribute to ciliate studies.

Keywords: CO1, Hypotrichia, morphology, seawater, SSU rDNA

INTRODUCTION

The genus *Diophrys* Foissner et al., 1991 currently comprises 11 species, this genus is mainly characterized by the combined features of the oral area with the conspicuous adoral zone of membranelles and separate paroral and endoral membranes, five frontal, two ventral, five transverse and one or two left marginal cirri, and three caudal cirri (Zhang et al., 2020). Recently, three *Diophrys* species have been recorded in South Korea: *D. appendiculata* (Ehrenberg, 1838) Schewiakoff, 1893; *D. oligothrix* Borror, 1965; and *D. scutum* (Dujardin, 1841) Kahl, 1932 (Kwon and Shin, 2006; Kwon et al., 2008; Jung et al., 2017). In this study, we found an unrecorded *Diophrys* species, *D. quadrinucleata* Zhang et al., 2020, in South Korea.

Small subunit ribosomal DNA (SSU rDNA) has been commonly used for phylogenetic studies of ciliates, but the approach based on SSU rDNA could mislead the understanding of ciliate evolution (Dunthorn et al., 2011). Therefore, several barcode studies have been conducted recently, and the suitability of cytochrome c oxidase subunit 1 (CO1) barcodes has been proven in some Oligohymenophorea and Spirotrichea species (Barth et al., 2006; Lynn and Strüder-Kypke, 2006; Chantangsi and Lynn, 2008; Gentekaki and Lynn, 2009; Jung et al., 2011; Kher et al., 2011; Tarcz et al., 2012, 2013, 2014; Zhao et al., 2013, 2016; Song et al., 2014; Park et al., 2018).

Seawater samples were collected in November 2020. For sample collection, depth of 30 cm of sand was dug in Eulwang-ri Beach, and seawater was collected there. The water temperature was approximately 3.5° C, and the salinity was 27.7%. Specimens were maintained in the laboratory as raw cultures for one to two weeks at 4°C and 20°C, and rice grains were used to promote the growth of bacteria as food for the ciliates. Raw cultures were microscopically observed in vivo (Leica DM2500; Wetzlar, Germany) from \times 50 to \times 1,000 magnification. Cell staining was performed to use Procedure A method described by Foissner (2014). Classification and terminology are according to Zhang et al. (2020) and Lynn (2008).

DNA extract, polymerase chain reaction (PCR) amplification and sequencing were performed according to the methods of Jung et al. (2012) and Park et al. (2018). Amplification of the nuclear 18S rDNA gene was performed using the forward primer EukA (5'-AAC CTG GTT GAT CCT GCC AGT-3') and reverse primer EukB (5'-TGA TCC TTC TGC AGG TTC ACC TAC-3') (Medlin et al., 1988). PCR amplification of CO1 was performed using the ciliate specific CO1 primers, CiCO1 Fv2 (5'-GWT GRG CKA TGA TYA CAC C-3') and

***To whom correspondence should be addressed** Tel: 82-32-860-7692, Fax: 82-32-874-6737 E-mail: mingisik@inha.ac.kr

[©] This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/ licenses/by-nc/3.0/) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.



Fig. 1. Photomicrographs of *Diophrys quadrinucleata* from live (A, B), after protargol impregnation (C–E). A, B, Ventral views showing cirral pattern; C, D, Ventral and dorsal view; E, Arrows and arrowheads indicate macronuclear nodules and micronuclei, respectively. Scale bars: A, C=50 µm, E=10 µm.

CiCO1 Rv2 (5'-ACC ATR TAC ATA TGA TGW CC-3') (Park et al., 2018). The 18S and CO1 sequences of *D. quadrinucleata* and other *Diophrys* species retrieved from GenBank were aligned using BioEdit (Hall, 1999), and the pairwise distances and number of nucleotide differences were calculated using MEGA 11 (Tamura et al., 2021).

RESULTS AND DISCUSSION

Phylum Ciliophora Doflein, 1901 Class Spirotrichea Bütschli, 1889 Subclass Hypotrichia Stein, 1859 Order Euplotida Small & Lynn, 1985 Family Uronychiidae Jankowski, 1975 Genus *Diophrys* Dujardin, 1840

Diophrys quadrinucleata Zhang et al., 2020 (Fig. 1) *Diophrys quadrinucleata* Zhang et al., 2020: 979, fig. 2.

Material examined. Seawater sample (27.7‰) from Eurwang-dong, Incheon-si, Korea (37°26′50″N, 126°22′9.5″E), on Nov 2020.

Diagnosis. Size about $80-110 \times 50-70 \,\mu\text{m}$ in vivo; body elliptical, greyish; 27–39 adoral zone membranelles; 4 macronuclear nodules; 2 or 3 micronuclei; 5 frontal cirri; 2 ventral cirri; 5 transverse cirri; 1 left marginal cirrus; 5 dorsal kineties; 3 caudal cirri.

Distribution. China and Korea.

Remarks. *Diophrys quadrinucleata* differs from other *Diophrys* species by the number of macronuclear nodules (4 vs. 2 or 7–23) (Zhang et al., 2020). The Korean population of *Diophrys quadrinucleata* morphologically corresponds to the type population by the number of frontal cirri, ventral cirri, marginal cirri, transverse cirri, caudal cirri, and dorsal kineties (Zhang et al., 2020).

Voncher slides. One slide with protargol-impregnated specimens was deposited at the National Institute of Biological Resources (NIBRPR0000111058).

The alignment length of the two 18S rDNA sequence (Gen-Bank accession No. OP070164, OP070165) of the Korean *D. quadrinucleata* population and seven *Diophrys* species was 1,613 bp. The intra-specific variation of *D. quadrinucleata* was identical. Inter-specific variation in *D. quadrinucleata* and other congeners was 0.3–3.8% (Table 1).

The alignment length of the four CO1 sequences (GenBank accession No. OP096457–OP096460) the Korean *D. quadrinucleata* population (26.3% GC content) and the three species in the genetic comparison was 476 bp. The intra-specific variation of *D. quadrinucleata* were identical. Inter-specific variation in between *D. quadrinucleata* and *D. scutum* was 11.1–13.9% (Table 2). Inter-specific variation in between *D. quadrinucleata* was 14.3%. Inter-specific variation in between *D. quadrinucleata* and *D. oligothrix* was 17.5–17.7%. Inter-generic variations within the genus *Diophrys* were in the range of 11.1–17.7%. In a previous study, intra- and inter-specific variations in CO1 sequences of genus *Diophrys* were 0.00–4.54% and 13.49–22.01% (Park et

Table 1. The number of nucleotides differences (abov	ve the diagor	al) and pi	airwise dist	ances (belo	ow the diag	jonal) betv	veen selecte	ed Diophrys	s 18S rDNA	A sequence	S	
	1.		2.	3.	4.		5.	.9	7.		8.	9.
1. Diophrys quadrinucleata OP070164, OP070165			0	4	23		39	42	43		59	59
2. Diophrys quadrinucleata MT109370	0.000			4	23		39	42	43		59	59
3. Diophrys apoligothrix JF694038	0.003	0.0	003		25		39	42	43		61	61
4. Diophrys scutum MT109372	0.015	0.0	015	0.016			46	47	51		62	62
5. Diophrys oligothrix MG603603	0.025	0.0	025	0.025	0.029	-		7	10		56	56
6. Diophrys blakeneyensis JN172996	0.027	0.0	027	0.027	0.030	0	.004		15		58	58
7. Diophrys appendiculata MG603601	0.027	0.0	027	0.027	0.033	0	.006	0.009			53	53
8. Diophrys appendiculata AY004773	0.038	0.0	038	0.039	0.040	0	.036	0.037	0.034			0
9. Diophrys parappendiculata EU267928	0.038	0.0	038	0.039	0.040	0	.036	0.037	0.034	4	.000	
	1.	2.	Э.	4.	5.	6.	7.	8.	9.	10.	11.	12.
1. Diophrys quadrinucleata OP096457-OP096460		53	53	54	54	54	59	66	68	83	84	84
2. Diophrys scutum MG594861	0.111		1	2	2	2	20	55	81	87	87	87
3. Diophrys scutum MG594860	0.111	0.002		1	1	1	20	56	82	88	88	88
4. Diophrys scutum MG594858	0.113	0.004	0.002		0	0	21	57	83	89	89	89
5. Diophrys scutum MG594859	0.113	0.004	0.002	0.000		0	21	57	83	89	89	89
6. Diophrys scutum MG594857	0.113	0.004	0.002	0.000	0.000		21	57	83	89	89	89
7. Diophrys scutum MG594862	0.124	0.042	0.042	0.044	0.044	0.044		61	83	85	85	85
8. Diophrys scutum MG594863	0.139	0.116	0.118	0.120	0.120	0.120	0.128		75	88	89	89
9. Diophrys appendiculata MG594867	0.143	0.170	0.172	0.174	0.174	0.174	0.174	0.158		84	85	85
10. Diophrys oligothrix MG594866	0.175	0.183	0.185	0.187	0.187	0.187	0.179	0.185	0.177		1	Ч
11. Diophrys oligothrix MG594864	0.177	0.183	0.185	0.187	0.187	0.187	0.179	0.187	0.179	0.002		0
12. Diophrys oligothrix MG594865	0.177	0.183	0.185	0.187	0.187	0.187	0.179	0.187	0.179	0.002	0.000	

Kyu-Seok Chae, Gi-Sik Min

al., 2018), respectively. The results of this study overlap with previous studies and show that the CO1 barcode is effective in distinguishing *D. quadrinucleata* from other species in the genus *Diophrys*. Therefore, additional studies involving CO1 barcodes show that they could be effective to resolve the discrepancy between morphology and DNA taxonomy. Currently, most ciliate studies provide only morphology and 18S rDNA, so it is necessary to obtain CO1 to avoid misleading phylogenetic studies. However, CO1 and morphology must be provided together. Therefore, the importance of a study that provides 18S rDNA and CO1 together based on a fully identified individual such as this study will increase in the future, and this study will be helpful.

ORCID

Kyu-Seok Chae: https://orcid.org/0000-0002-9289-7059 Gi-Sik Min: https://orcid.org/0000-0003-2739-3978

CONFLICTS OF INTEREST

Gi-Sik Min, a contributing editor of the Animal Systematics, Evolution and Diversity, was not involved in the editorial evaluation or decision to publish this article. Remaining author has declared no conflicts of interest.

ACKNOWLEDGMENTS

This study was supported by research funds from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202102203).

REFERENCES

- Barth D, Krenek S, Fokin SI, Berendonk TU, 2006. Intraspecific genetic variation in *Paramecium* revealed by mitochondrial cytochrome c oxidase I sequences. Journal of Eukaryotic Microbiology, 53:20-25. https://doi.org/10.1111/j.1550-7408.2005.00068.x
- Chantangsi C, Lynn DH, 2008. Phylogenetic relationships within the genus *Tetrahymena* inferred from the cytochrome c oxidase subunit 1 and the small subunit ribosomal RNA genes. Molecular Phylogenetics and Evolution, 49:979-987. https://doi.org/10.1016/j.ympev.2008.09.017
- Dunthorn M, Foissner W, Katz LA, 2011. Expanding character sampling for ciliate phylogenetic inference using mitochondrial SSU-rDNA as a molecular marker. Protist, 162:85-99.

https://doi.org/10.1016/j.protis.2010.06.003

- Foissner W, 2014. An update of 'basic light and scanning electronmicroscopic methods for taxonomic studies of ciliated protozoa'. International Journal of Systematic and Evolutionary Microbiology, 64:271-292. https://doi.org/10.1099/ ijs.0.057893-0
- Gentekaki E, Lynn DH, 2009. High-level genetic diversity but no population structure inferred from nuclear and mitochondrial markers of the peritrichous ciliate *Carchesium polypinum* in the Grand River Basin (North America). Applied and Environmental Microbiology, 75:3187-3195. https://doi. org/10.1128/AEM.00178-09
- Hall T, 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series, 41:95-98.
- Jung JH, Park MH, Kim SY, Choi JM, Min GS, Kim YO, 2017. Checklist of Korean ciliates (Protozoa: Ciliophora). Journal of Species Research, 6:241-257.
- Jung JH, Park KM, Min GS, 2012. Morphology, morphogenesis, and molecular phylogeny of a new brackish water ciliate, *Pseudourostyla cristatoides* n. sp., from Songjiho lagoon on the coast of East Sea, South Korea. Zootaxa, 3334:42-54. https://doi.org/10.11646/zootaxa.3334.1.3
- Jung SJ, Im EY, Strüder-Kypke MC, Kitamura SI, Woo PTK, 2011. Small subunit ribosomal RNA and mitochondrial cytochrome c oxidase subunit 1 gene sequences of 21 strains of the parasitic scuticociliate *Miamiensis avidus* (Ciliophora, Scuticociliatia). Parasitology Research, 108:1153-1161. https://doi.org/10.1007/s00436-010-2157-7
- Kher CP, Doerder FP, Cooper J, Ikonomi P, Achilles-Day U, Küpper FC, Lynn DH, 2011. Barcoding *Tetrahymena*: discriminating species and identifying unknowns using the cytochrome c oxidase subunit I (cox1) barcode. Protist, 162:2-13. https://doi.org/10.1016/j.protis.2010.03.004
- Kwon CB, Lee ES, Shin MK, 2008. Redescriptions of *Diophrys* appendiculata and *D. scutum* (Ciliophora: Spirotrichea: Uronychiidae) new to Korea. Korean Journal of Systematic Zoology, 24:191-197.
- Kwon CB, Shin MK, 2006. Redescription of previously unknown euplotine ciliates, *Euplotes charon* and *Diophrys oligothrix* (Ciliophora: Spirotrichea: Euplotida), from Korea. Korean Journal of Systematic Zoology, 22:29-35.
- Lynn DH, Strüder-Kypke MC, 2006. Species of *Tetrahymena* identical by small subunit rRNA. gene sequences are discriminated by mitochondrial cytochrome c oxidase I gene sequences. Journal of Eukaryotic Microbiology, 53:385-387. https://doi.org/10.1111/j.1550-7408.2006.00116.x
- Lynn HD, 2008. The ciliated protozoa: characterization, classification and guide to the literature. Springer, New York, pp. 1-605.
- Medlin L, Elwood HJ, Stickel S, Sogin ML, 1988. The characterization of enzymatically amplified eukaryotic 16S-like rR-NA-coding regions. Gene, 71:491-499.
- Park MH, Jung JH, Jo E, Park KM, Baek YS, Kim SJ, Min GS, 2018. Utility of mitochondrial CO1 sequences for species

discrimination of Spirotrichea ciliates (Protozoa, Ciliophora). Mitochondrial DNA Part A, DNA Mapping, Sequencing, and Analysis, 30:148-155. https://doi.org/10.1080/2470 1394.2018.1464563

- Song W, Li J, Liu W, Al-Rasheid KAS, Hu X, Lin X, 2014. Taxonomy and molecular phylogeny of four *Strombidium* species, including description of *S. pseudostylifer* sp. nov. (Ciliophora, Oligotrichia). Systematics and Biodiversity, 13:76-92. https://doi.org/10.1080/14772000.2014.970674
- Tamura K, Stecher G, Kumar S, 2021. MEGA11: molecular evolutionary genetics analysis version 11. Molecular Biology and Evolution, 38:3022-3027. https://doi.org/10.1093/ molbev/msab120
- Tarcz S, Potekhin A, Rautian M, Przyboś E, 2012 Variation in ribosomal and mitochondrial DNA sequences demonstrates the existence of intraspecific groups in *Paramecium multimicronucleatum* (Ciliophora, Oligohymenophorea). Molecular Phylogenetics and Evolution, 63:500-509. https://doi. org/10.1016/j.ympev.2012.01.024
- Tarcz S, Przyboś E, Surmacz M, 2013. An assessment of haplotype variation in ribosomal and mitochondrial DNA fragments suggests incomplete lineage sorting in some species of the *Paramecium aurelia* complex (Ciliophora, Protozoa). Molecular Phylogenetics and Evolution, 67:255-265. https:// doi.org/10.1016/j.ympev.2013.01.016

- Tarcz S, Rautian M, Potekhin A, Sawka N, Beliavskaya A, Kiselev A, Nekrasova I, Przyboś E, 2014. *Paramecium putrinum* (Ciliophora, Protozoa): the first insight into the variation of two DNA fragments - Molecular support for the existence of cryptic species. Molecular Phylogenetics and Evolution, 73:140-145. https://doi.org/10.1016/j.ympev.2014.01.019
- Zhang C, Huang J, Ye T, Lu B, Chen X, 2020. The morphology and phylogeny of three *Diophrys* ciliates collected from the subtropical waters of China, including a new species (Ciliophora; Euplotia). Journal of Ocean University of China, 19:975-987. https://doi.org/10.1007/s11802-020-4536-8
- Zhao Y, Gentekaki E, Yi Z, Lin X, 2013. Genetic differentiation of the mitochondrial cytochrome oxidase c subunit I gene in genus *Paramecium* (Protista, Ciliophora). PLoS ONE, 8:e77044. https://doi.org/10.1371/journal.pone.0077044
- Zhao Y, Yi Z, Gentekaki E, Zhan A, Al-Farraj SA, Song W, 2016. Utility of combining morphological characters, nuclear and mitochondrial genes: an attempt to resolve the conflicts of species identification for ciliated protists. Molecular Phylogenetics and Evolution, 94:718-729. https://doi.org/10.1016/ j.ympev.2015.10.017

Received May 10, 2022 Revised August 26, 2022 Accepted September 2, 2022