Korean J. Limnol. 40 (3) : 387~394 (2007)

Nuclear SSU and Plastid *rbc*L Genes and Ultrastructure of *Mallomonas caudata* (Synurophyceae) from Korea

Kim, Han-soon, Woongghi Shin[1] and Sung Min Boo[1,*]

(Department of Biology, Kyungpook National University, Daegu 702-701,
[1]Department of Biology, Chungnam National University, Daejeon 305-764, Korea)

Despite geographic barriers such as oceans, many freshwater algal species inhabit different continents of the world. A unicellular freshwater alga, *Mallomonas caudata*, commonly occurring in Asia, Europe, and America of the northern Hemisphere, is closely related to human life such as monitoring blooms and detecting changes in climates. In order to demonstrate its occurrence in Korea and to infer its phylogeny, we sequenced nuclear SSU and plastid *rbc*L genes from isolates collected in six different reservoirs. We have also investigated transmission electron microscopy of the Korean isolates. SSU sequences of the species from Korea and USA were almost identical, having pair-wise divergences of 0.06% in SSU and 0.45% in *rbc*L. Both gene trees revealed that the species was clearly separated from other species of the genus, while the genus was not monophyletic. Rhizoplasts are composed of microfibrils organised in striated rootlets attached to the multilayered plate of basal bodies and arranged on the surface of the nucleus at their distal ends. The rhizoplast constitutes a basal body-nucleus connector similar to that of typical Synurophyceae. The results that *Mallomonas* was not supported by both SSU and *rbc*L data sets require a further study with additional taxon sampling.

Key words : *Mallomonas caudata*, phylogeny, *rbc*L, SSU rDNA, stramenopiles, rhizoplast, ultrastructure

INTRODUCTION

Mallomonas Perty is a unicellular freshwater genus with approximately 183 species that occurs commonly worldwide (Rezacova and Neustupa, 2007). The genus is an important component of biomass as well as contributes species diversity of the phytoplankton community in the lakes and water reservoirs (Kristiansen, 1975; Takahashi, 1978). Some species of the genus form very dense blooms (Kristiansen, 1971; Hoffmann and Wille, 1992; Kim and Hwang, 2001), which negatively affected tastes and odour of potable water (Clasen and Bernhardt, 1982). The genus is characterized by unicellular system and an amour of silica scales and bristles with one to two bilobed chloroplasts, and two parallel flagella, one of which is much reduced in the majority of species (Siver, 1991; Wee, 1997). The siliceous cell covering consists of individual plates known as scales that are imbricated and arranged in a very precise manner (Takahashi, 1978; Asmund and Kristiansen, 1986; Siver and Glew, 1990). Classification of *Mallomonas* is exclusively based on the morphology and scanning electron microscopy of siliceous scales and bristles (Kristiansen, 1979; Wee, 1982; Asmund and Kristiansen, 1986). However, there are difficulties in their identification because some species showed a transitional scale

* Corresponding author: Tel: +82-42-821-6555, Fax: +82-42-822-9690, E-mail: smboo@cnu.ac.kr

structure in natural samples and scales in a single clonal culture sometimes varied according to cultured conditions (Siver, 1987; Martin-Wagenmann and Gutowski, 1995; Lee and Kim, 2007). To date, approximately 32 species of *Mallomonas* are reported to occur in Korea (Kristiansen *et al.*, 1990; Kim, 1995, 1997; Kim *et al.*, 1995), but little is known on molecular systematics of the species.

Mallomonas caudata Ivanoff is the most common and widespread species in the family Synurophyceae (Asmund and Kristiansen, 1986; Siver, 1991). It is an ovoid to spindle shaped and small alga, usually not exceeding 60 μm in length and 25 μm in width, covered with distinctive scales and bristles (Takahashi, 1978; Siver, 1991; Kim, 1997). It was first reported in Russia (Ivanoff, 1899), followed by northern Europe (Asmund and Kristiansen, 1986) and north America (Wujek, 1978). The species also occurs in Korea (Kim, 1997; Kristiansen *et al.*, 1990), Japan (Takahashi, 1978), and China (Hu and Wei, 2006). The species sometimes predominates almost all over the year or its populations show an abrupt maximum and decline in summer in a metalimnetic water (Hoffman and Wille, 1992). The ultrastructure of the species from Kansas, USA was investigated by Wujek (1978). However, despite its common occurrence in the northern Hemisphere and its ecological importance in freshwater algal community, classification and phylogeny of *M. caudata* is still least attended.

In order to identify the species and deciphering its phylogenetic relationships, nuclear ribosomal SSU and plastid *rbc*L sequences from six samples collected in Korea were analyzed here. Although both genes are commonly used markers in systematic of algae, there is a SSU data from a single strain of *M. caudata* (Lavau *et al.*, 1997). We also investigated transmission electron microscopy (TEM) of the isolates of the species from Korea, in addition to previous study on the isolates from Kansas, USA, by Wujek (1978). The present endeavor provides basic information on *Mallomonas caudata* in order to use it as a model species for understanding evolutionary biology because of its common occurrence in the world's most aquatic freshwater bodies and its relatively large size within the Synurophyceae.

MATERIALS AND METHODS

Sampling and growth of cells

The six strains of *Mallomonas caudata* were isolated from six different reservoirs in Korea during April to November, 2004. Details of the collection sites and environmental conditions are provided in Table 1. All the isolates were grown in DY III medium (Lehman, 1976) buffered to pH 7. The unialgal culture was maintained at 15±1 °C with illumination of 100 μmol m^{-2} s^{-1} of cool white fluorescent light at a 14 : 10 h light-dark cycle.

DNA extraction and sequencing

Live cells in a culture tube of each strain were used for DNA extraction. Extraction buffer was added directly into tubes of live cells and following procedures were as described, according to the manufacturer's protocols, in the Qiagen Plant mini kit (Qiagen GmbH, Hilden, Germany).

Polymerase chain reaction (PCR) amplifications of nuclear ribosomal DNA small subunit (SSU) and plastid *rbc*L were performed with a thermocycler (BioRad, California, USA) and a TaKaRa ExTaq reaction kit (Takara Shuzo, Shiga, Japan). Primers for PCR and DNA sequencing were SR1, SR4, SR9, and SR12 for SSU (Nakayama *et al.*, 1996) and NDrbcL2 and NDrbcL9 for *rbc*L (Daugbjerg and Andersen, 1997).

A total reaction mixture (25 μL) consisted of extracted DNA 2 μL containing 0.5~1.0 μg DNA,

Table 1. List and collection information of samples used in the present study.

Strain (code)	pH	Temperature (°C)	EC (μS cm^{-1})	Sampling date	Isolation site
M. caudata (JCMC)	7.2	13.8	117.4	Sep-02	Jinchon Swamp (128°26′N, 35°43′E)
M. caudata (GSC)	8.0	20.3	76.3	Sep-03	Gongsan-dam (128°39′E, 35°56′N)
M. caudata (GCMC)	8.0	20.3	76.3	Sep-03	Kachang-dam (128°37′E, 35°48′N)
M. caudata (DGC)	7.8	13.9	218.0	Apr-04	Daegok Reservoir (128°39′N, 35°57′E)
M. caudata (AKC)	7.0	11.1	97.5	Nov-04	Angae Reservoir (129°28′N, 36°00′E)
M. caudata (MYC)	6.6	16.0	39.0	Nov-04	Miryang-dam (128°57′N, 35°28′E)

10X ExTaq buffer (Mg^{2+} free) 2.5 μL, $MgCl_2$ (25 mM) 1.5 μL, dNTPs 2.0 μL, and Taq polymerase 0.1 μL (Takara ExTaq). The thermal profile for PCR amplification included: 95°C for 4 min for initial denaturation, followed by 34 cycles at 95 °C for 1 min; 50~48°C for 1 min, 72°C for 2 min. The amplification was terminated with a final extension at 72°C for 6 min. PCR products were purified using High Pure™ PCR Product Purification Kit (Roche Diagnostics GmbH, Mannheim, Germany) according to the manufacturer's protocols. Cycle sequencing reactions were performed using ABI Prism BigDye Terminator Cycle Sequencing ready Reaction Kit (PE Applied Biosystems, Foster City, CA, USA) and analyzed on an ABI PRISM™ 377 DNA Sequencer (Applied Biosystems, Foster City, CA, USA) at the Center for Research Facilities, Chungnam National University, Daejeon, Korea. Sequences were assembled and edited using Sequence Navigator version 1.0.1 (Applied Biosystems, Foster City, CA, USA). All the gene sequence data analyzed here are lodged with GenBank under the Accession Numbers EF469638-EF469643 for SSU and EF469644-EF469649 for *rbc*L.

The complete alignments of 25 strains for SSU and 21 taxa for *rbc*L were collated with the multiple sequences editing program, SeqPup. Multiple alignments were done with selected GenBank sequences. The sequences with ambiguities were coded as missing data. There were no gaps found in all four alignments. Maximum likelihood (ML) analyses of the SSU and *rbc*L data were performed using PAUP* and a best-fitting evolution model. The model of sequence evolution was chosen based on results from the successive approximation method. Tree likelihoods were estimated using a heuristic search with 100 random-addition-sequence replicates, and TBR branch swapping. To test the stability of nodes, maximum likelihood and parsimony bootstrap analyses were performed with 500 replicates.

Maximum parsimony (MP) analyses were conducted using PAUP*. All heuristic searches were performed with 1,000 replicates, employed the random-addition of sequences, retained only the best tree, held 10 trees at each step, used TBR branch swapping, collapsed zero-length branches, and used MULTREES. Bootstrap support values were calculated using 1,000 replicates with the following options selected: heuristic search; TBR branch swapping; collapse of zero-length branches; and random-sequence-addition with one replicate.

Ultrastructure under transmission electron microscopy

Live cells were observed under a light microscope (Nikon Eclipse 80i, Nikon Co., Japan) equipped with differential interference contrast (DIC) optics. Images were saved on hard drive of a computer with DS-5M (Nikon Co., Japan) photomicrographic system attached to the microscope.

For the TEM, cells were fixed in 2.5% glutaraldehde in culture medium for 1.5 to 2 h. Then, cells were centrifuged, and the pellet was agarized. After several medium rinses, the cells were postfixed in 1% osmium tetroxide with deionized water. Dehydration was accomplished using a graded ethanol series (50%, 60%, 70%, 80%, 90%, and 100% ethanol, followed by two 100% ethanol steps). The material was embedded in Spurr's low-viscosity resin (Spurr 1969). Sections were obtained with a RMC MT-XL ultramicrotome (Boeckeler Instruments Inc., USA) and poststained with 3% aqueous uranyl acetate followed by lead citrate. Stained sections were observed under a JEOL-1010 electron microscope (Jeol Ltd., Japan).

RESULTS

Molecular phylogeny

The SSU sequences determined in the present study were of 1821 nucleotides for *Mallomonas caudata* and its putative relatives. The 25 aligned SSU sequences had 98 variable sites (5.4 %) and 160 parsimoniously informative sites (8.8%). Within the species, samples from Korea and USA differed by up to 5 bp (0.3% pairwise divergence). However, samples collected within Korea differed by one bp (0.06% pairwise divergence). *M. caudata* and its close relative, *M. matvienkoae*, differed by up to 20 bp (1.2% pairwise divergence). In the phylogenetic tree of the SSU data, all six samples of *M. caudata* produced a strongly supported clade. However, the genus was not monophyletic (Fig. 1).

The *rbc*L sequences determined in the present study were of 1080 nucleotides for *Mallomonas caudata* and its putative relatives. The 21 aligned *rbc*L sequences had 73 variable sites (6.7%)

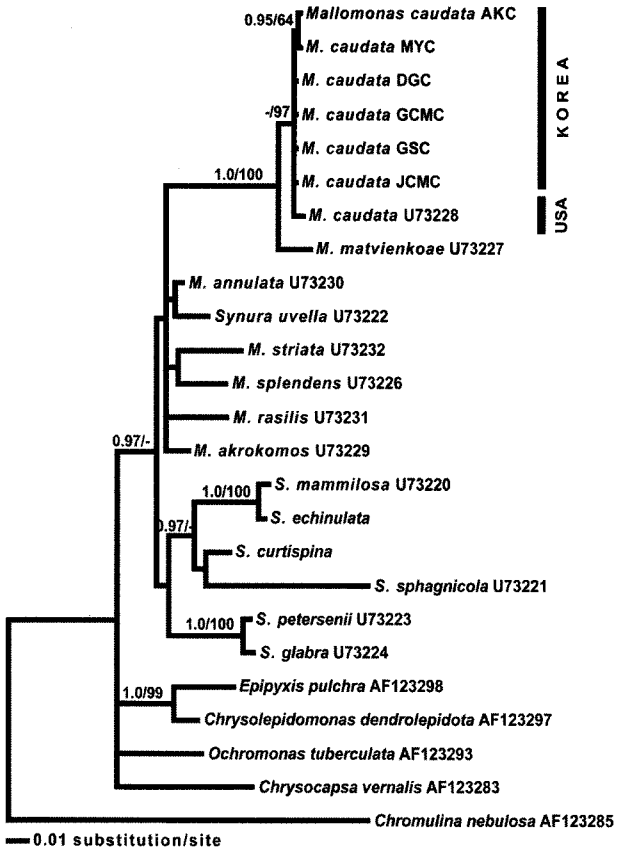

Fig. 1. ML tree of nuclear SSU sequences from *Mallomonas caudata* and putative relatives. Numbers near each clade refer to maximum likelihood and parsimony bootstrap values. Bars represent nodes with support values < 50%.

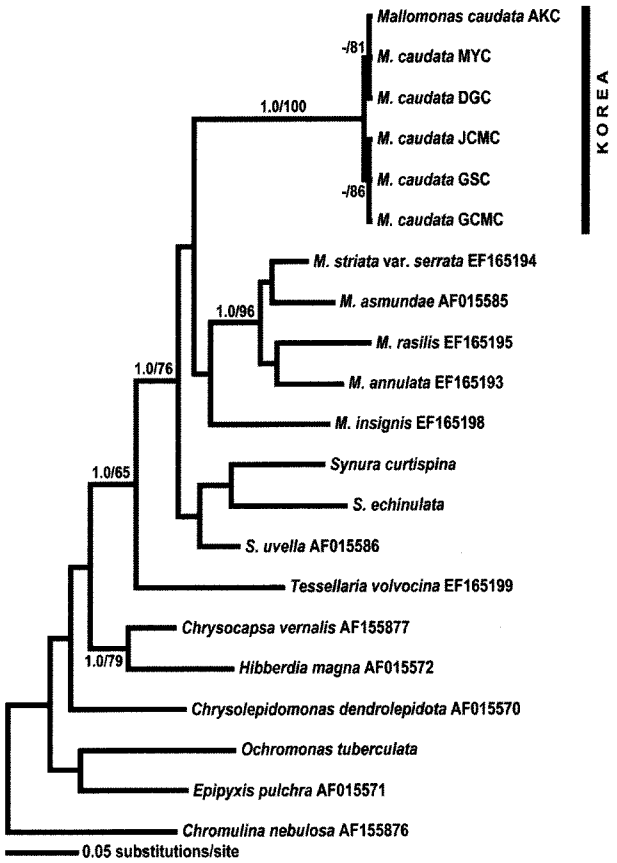

Fig. 2. ML tree of plastid *rbc*L sequences from *Mallomonas caudata* and putative relatives. Numbers near each clade refer to maximum likelihood and parsimony bootstrap values. Bars represent nodes with support values < 50%.

and 304 parsimoniously informative sites (28.0%). Within *M. caudata*, samples from Korea and USA differed by up to 5 bp (0.45% pairwise divergence). *M. caudata* and its close relative, *M. asumundiae*, differed by at least 149 bp (15% pairwise divergence). In the phylogenetic tree of the *rbc*L data, all six samples of *M. caudata* produced a strongly supported clade. However, the genus was not monophyletic (Fig. 2).

Ultrastructure

Mallomonas caudata is an ovoid to spindle shaped, unicellalur alga, which remains covered with distinctive body scales and bristles (Fig. 3A). Under scanning electron microscope, body scales have a large elongated or circular pore in the center of the posterior end of the scale. Bristles are serrated on one side with minute teeth (Fig. 3B).

Cells are surrounded by body scales under TEM (Fig. 4A). The nucleus is placed in the center of the cell, but anteriorly at the longitudinal section (Fig. 4B). The nucleus is connected to the anteriorly inserted basal bodies by a rhizoplast (Fig. 4C-D). The connecting structures are fibrous roots that are distinct with extension from the basal body to the anterior part of the nucleus. These roots are composed of striated rootlets with covered part of the anterior surface of the nucleus (Fig. 4C-D). The microfibrillar and periodic structures of the rootlets of the rhizoplast are lined with nucleus and attached to a plate on the proximal section of the basal body at the top of the cell (Fig. 4E). There is a conspicuous incomplete collar of granular material around the fibres of the basal body-nucleus connector (Fig. 4D).

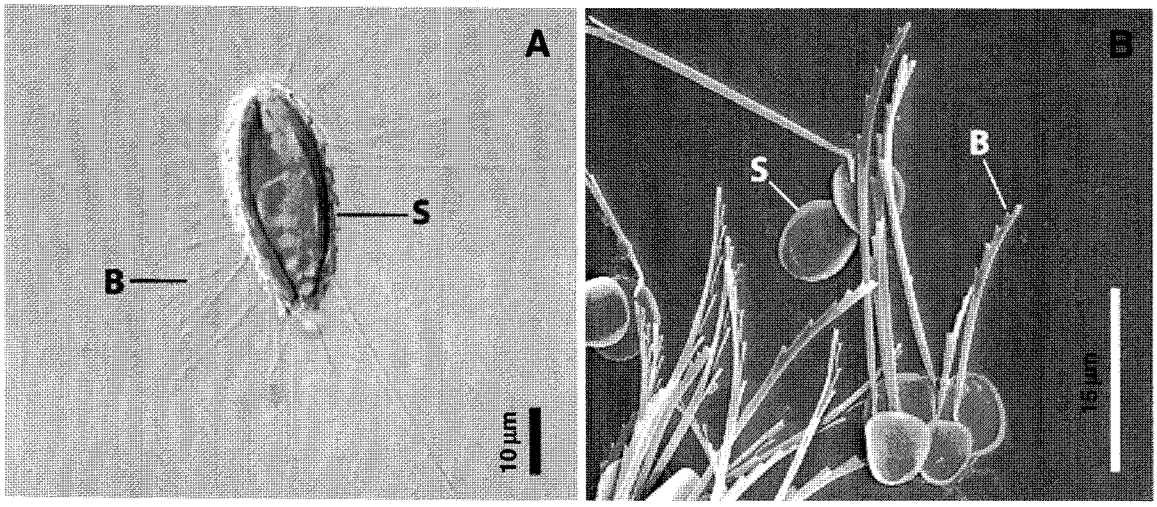

Fig. 3. *Mallomonas caudata.* A. Morphology of cell showing bristles (B) and scales (S) under light microscope. B. Detailed morphology of bristles (B) and scales (S) under scanning electron microscope.

DISCUSSION

Nuclear SSU and plastid *rbc*L data of *Mallomonas caudata* strains from Korea clearly show that this cosmopolitan planktonic species is genetically homogeneous. However, pairwise divergence of SSU sequences of samples between Korea and USA is higher than those of samples collected in Korea. Cosmopolitan species are often assemblages of diverge genetic lineages, as in *Synura petersenii* (Wee *et al.*, 2001). Additional studies using samples from Europe and USA will show the genetic variations among the allopatric populations of *Mallomonas.*

Protein-coding *rbc*L region is usually more variable than ribosomal SSU region in stramenopiles such as brown algae reported by us earlier (Boo *et al.*, 1999). Pairwise divergence of SSU sequences between *M. caudata* and *M. matvienkoae* ranged up to 1.2%. The sister relationship between these two species was also strongly supported in the phylogenetic tree. Lack of dome scales in both species is proposed as a plesiomorphic character of *Mallomonas* (Asmund and Kristiansen, 1986; Lavau *et al.*, 1997).

Morphology of *Mallomonas caudata* isolated from Korea is very similar to that of the species present in freshwater bodies of USA and Europe (Asmund and Kristiansen, 1986; Siver, 1991). Ultrastructure of the scales and bristles of the strains isolated from different reservoirs is very similar and recognizable difference lacked between specimens from Korea and Europe. The large pore in the center of the posterior end of the scale is mostly elongated shape and rarely observed as circular.

TEM studies of *Mallomonas caudata* have shown the existence of striated roots, named rhizoplast, attached to the basal bodies. These structures are present in the Synurophyceae (Andersen, 1991) but are more prominent in the *Mallomonas* species (Brugerolle and Mignot, 2003). The rhizoplast is composed of microfibrils organized in striated rootlets attached to the multilayered plate of basal bodies and arranged on the surface of the nucleus at their distal ends. According to the ultrastructural studies, the rhizoplast of Synurophyceae constitutes a basal body-nucleus connector, typical to *Synura* (Andersen, 1985). The semicircular collar of granular material surrounding the rhizoplast is found in *M. caudata*, as reported in *M. fastigiata* (Brugerolle and Mignot, 2003). In this structure, *Mallomonas* is different from *Synura uvella*, which has naked rhizoplasts (Andersen, 1985). However, overall ultrastructure of the specimens of *M. caudata* from Korea is very similar to that of the cells from Texas, USA (Wujek, 1978).

Although cladistic analysis of scale morphology supported the monophyly of the genus, *Mallomanas* was divided into different groups in previous SSU data (Lavau *et al.*, 1997). In our study of SSU data, the genus was polyphyletic, dividing into

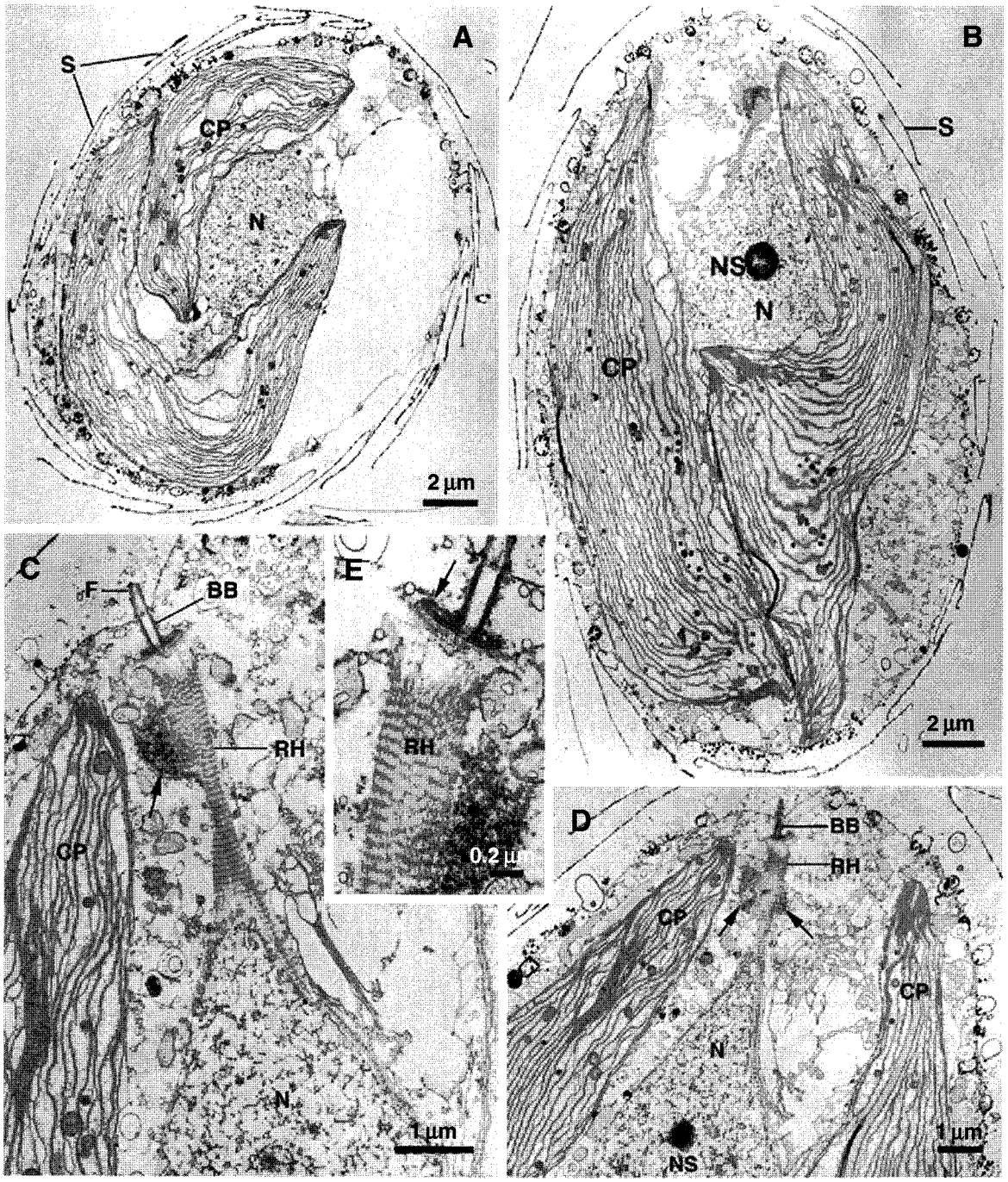

Fig. 4. Ultrastructure of *Mallomonas caudata* under transmission electron microscope. A. Cross section showing chloroplast (CP), nucleus (N), and scale (S) covering the cell. B. Longitudinal section showing nucleolus (NS), nucleus (N), chloroplast (CP), and scale. C-D. Serial sections showing basal body (BB), semicircular collar (arrows), and rhizoplast (RH) connecting between the basal body (BB) and nucleus (N). E. High magnification of the basal body region showing the microfibrillar and periodic structure of the rhizoplast (RH) attached to a plate (arrow).

several groups. In *rbc*L data, the strong clade existed among *M. annulata*, *M. asmundiae*, *M. rasilis* and *M. striata* excluded *M. caudata* and *M. insignis*. The results imply that the current concept regarding *Mallomonas*, based on the nature of flagella and the colonial vs unicellular

nature (see review of Wee, 1997), should be reconsidered. The additional samplings of the genus from allover the world's aquatic bodies would give a better resolution on the phylogeny of *Mallomonas* with highlights on the classification of the genus.

ACKNOWLEDGEMENT

We acknowledge Dr. R.K. Asthana for reading the first draft. This study was supported by a grant from the Basic Research Program of the Korea Science & Engineering Foundation to H.S. Kim and by the Korean Science and Engineering Foundation (KOSEF) grant funded by the Korea Government (RO5-2003-000-10956-0).

LITERATURE CITED

Andersen, R.A. 1985. The flagellar apparatus of the golden alga *Synura uvella*: Four absolute orientations. *Protoplasma* **128**: 94-106.

Andersen, R.A. 1991. The cytoskeleton of chromophyte algae. *Protoplasma* **164**: 143-159.

Asmund, B. and J. Kristiansen. 1986. The genus *Mallomonas* (Chrysophyceae). *Opera Bot.* **85**: 1-128.

Boo, S.M., W.J. Lee, H.S. Yoon, A. Kato and H. Kawai. 1999. Molecular phylogeny of the Laminariales (Phaeophyceae) inferred from small subunit ribosomal DNA sequences. *Phycol. Res.* **47**: 109-114.

Brugerolle, G. and J.-P. Mignot. 2003. The rhizoplast of chrysomonads, a basal body-nucleus connector that polarizes the dividing spindle. *Protoplasma* **222**: 13-21.

Clasen, J. and H. Bernhardt. 1982. A bloom of the Chrysophyceae *Synura uvella* in the Wahnbach reservoir as indication for the release of phosphates from the sediment. *Arch Hydrobiol. Beih.* **18**: 61-68.

Daugbjerg, N. and R.A. Andersen. 1997. Phylogenetic analyses of the *rbc*L sequences from haptophytes and heterokont algae suggest their chloroplasts are unrelated. *Mol. Biol. Evol.* **14**: 1242-1251.

Hoffmann, L. and E. Wille. 1992. Occurrence of a metalimnetic summer peak of *Mallomonas caudata* (Synruophyceae). *Nord. J. Bot.* **12**: 465-469.

Hu, H. and Y. Wie. 2006. The freshwater algae of China: systematics, taxonomy, and ecology. Science Press, Peking. 1023p.

Ivanoff, L. 1899. Beitrag zur kenntniss der Morphologie und Systematik der Chrysomonaden. *Bull. Acad. Imp. Sci. St. Petersbourg* **4**: 247-262.

Kim, H.S. 1995. Morphological notes on the scales and bristles of *Mallomonas trummensis* new to Korea and *Mallomonas* sp. (Mallomonadaceae, Synurophyceae). *Korean J. Phycol.* **10**: 77-80.

Kim, H.S. 1997. Silica-scaled chrysophytes (Synurophyceae) in several reservoirs, swamps and a highland pond from Changnyong County, Korea. *Algae* **12**: 1-10.

Kim, H.S. and K.J. Hwang. 2001. Occurrence and seasonal changes of silica-scaled chrysophytes in Kachang Dam Reservoir. *Algae* **16**: 421-27.

Kim, H.S., E. Takahashi and J. Chung. 1995. Morphologic and taxonomic studies on scale-bearing Chrysophyta from Naktong River Estuary Lake, Pusan, in Korea. *Korean J. Limnol.* **28**: 87-99.

Kristiansen, J. 1971. A *Mallomonas* bloom in a Bulgarian mountain lake. *Nova Hedwigia* **21**: 877-882.

Kristiansen, J. 1975. Chrysophyceae from alberta and british columbia. *Syesis* **8**: 97-108.

Kristiansen, J. 1979. Problems in classification and identification of Synurophyceae (Chrysophyceae). *Schweiz, Z. Hydrobiol.* **40**: 310-319.

Kristiansen, J. 1986. The ultrastructural basis of chrysophyte systematics and phylogeny. *Crit. Rev. Plant Sci.* **4**: 149-211.

Kristiansen, J., D. Tong and K. Olrik. 1990. Silica-scaled chrysophytes from Korea, a preliminary study. *Nord. J. Bot.* **9**: 685-691.

Lavau S., G. Saunders and R. Wetherbee. 1997. A phylogenetic analysis of the Synurophyceae using molecular data and scale case morphology. *J. Phycol.* **33**: 135-151.

Lee, K.L. and H.S. Kim. 2007. Growth characteristics of three synurophytes (*Mallomonas* species) at different temperatures and pH. *Nova Hedwigia* **84**: 227-240.

Lehman, J.T. 1976. Ecological and nutritional studies on *Dinobryon* Ehrenb.: seasonal periodicity and the phosphate toxicity problem. *Limnol. Oceanogr.* **21**: 646-58.

Martin-Wagenmann, B. and A. Gutowski. 1995. Scale morphology and growth characteristics of clones of *Synura petersenii* (Synurophyceae) at different temperatures.-In: Sandgren, C.D., J.P. Smol and J. Kristiansen (eds): Chrysophyte algae: 345-360. Cambridge University Press, Cambridge.

Nakayama, T., S. Watanabe, K. Mitsui, S. Uchida and I. Inouye. 1996. The phylogenetic relationships between Chlamydomonadales and Chlorococcales inferred from the 18S rDNA sequence data. *Phycol. Res.* **44**: 47-55.

Rezacova, M. and J. Neustupa. 2007. Distribution of the genus *Mallomonas* (Synurophyceae)- ubiquitous dispersal in microorganisms evaluated. *Protist* **158**: 29-37.

Ronquist, F. and J.P. Huelsenbeck. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**: 1572-1574.

Siver, P.A. 1987. The distribution and variation of *Synura* species (Chrysophyceae) in Connecticut, USA. *Nord. J. Bot.* **7**: 107-116.
Siver, P.A. 1991. The Biology of Mallomonas: Morphology, Taxonomy and Ecology. Kluwer Academic Publ., Dordrecht. 230p.
Siver, P.A. and J.R. Glew. 1990. The arrangement of scales and bristles on *Mallomonas* (Chrysophyceae): a proposed mechanism for the formation of the cell covering. *Can. J. Bot.* **68**: 374-80.
Soudek, D. Jr. and G.G.C. Robinson. 1983. Electrophoretic analysis of the species and population structure of the diatom *Asterionella formosa*. *Can. J. Bot.* **61**: 418-433.
Spurr, A.R. 1969. A low-viscosity epoxy resin-embedding medium for electron microscopy. *J. Ultrast. Res.* **26**: 31-43.
Takahashi, E. 1978. Electron Microscopical Studies of the Synuraceae (Chrysophyceae) in Japan: Taxonomy and Ecology. Tokai University Press, Tokyo. 194p.
Wee, J.L. 1982. Studies on the Synuraceae (Chrysophyceae) of Iowa. *Bibl. Phycol.* **62**: 1-183. J. Cramer, Braunschweig, Germany.
Wee, J.L. 1997. Scale biogenesis in synurophycean protists: phylogenetic implications. *CRC Rev. Plant Sci.* **16**: 497-534.
Wee, J.L., L.D. Fasone, A. Sattler, W. Starks and D.L. Hurley. 2001. ITS/5. 8S DNA sequence variation in 15 isolates of *Synura petersenii* Korshikov (Synurophyceae). *Nova Hedwigia Beiheft* **122**: 245-258.
Wujek, D.E. 1978. Ultrastructure of flagellated chrysophytes. III. *Mallomonas caudata*. *Trans. Kansas Acad. Sci.* **81**: 327-335.

(Manuscript received 3 July 2007,
Revision accepted 13 August 2007)

<국문적요>

한국산 *Mallomonas caudata* (Synurophyceae)의 미세구조, 핵 SSU 그리고 색소체 *rbc*L 유전자

김 한 순 · 신 웅 기[1] · 부 성 민[1,*]

(경북대학교 생물학과, [1]충남대학교 생물학과)

해양 같은 지리적 장벽에도 불구하고, 많은 담수조류는 세계의 다른 대륙에 서식하고 있다. 단세포 담수조류, *Mallomonas caudata*는 북반구의 미국, 유럽, 및 아시아에서 흔하며, 기후변화 감지나 수화현상 감시 같은 인간생활에 밀접하게 관련되어 있다. 본 종의 계통과 국내출현을 설명하기 위해 여섯 군데의 저수지에서 채집된 균주로부터 엽록체 *rbc*L과 핵 SSU 유전자를 염기서열 분석하였다. 또한, 한국산 균주의 전자현미경적 구조를 조사하였다. 한국과 미국산 종의 SSU 염기서열은 0.06%가, *rbc*L은 0.45%의 차이로 거의 동일하였다. 두 유전자를 이용한 계통수에서 본 종은 속의 다른 종들과 분명히 분리되지만, 단계통군은 아니었다. 근형질은 기저체의 다층판에 부착된 가로무늬의 microfibril들로 구성되어 있었으며, microfibril들의 끝은 핵의 표면 위에 배열되어 있었다. 이 근형질은 Synurophyceae에서 전형적으로 보이는 기저체-핵 연결자이다. *Mallomonas*가 SSU와 *rbc*L자료에 의해 지지되지 않는 결과는 분류군 추가와 함께 좀더 연구되어야 할 것으로 사료된다.