

18S Ribosomal RNA Gene Phylogeny of a Colonial Volvoclean Lineage (*Tetrabaenaceae-Goniaceae-Volvocaceae*, *Volvocales*, *Chlorophyceae*) and Its Close Relatives

Takashi NAKADA^{a,b,*}, Takuro ITO^{a,b} and Masaru TOMITA^{a,b}

^aInstitute for Advanced Biosciences, Keio University, Kakuganji, Tsuruoka, Yamagata, 997-0052 JAPAN;

^bSystems Biology Program, Graduate School of Media and Governance, Keio University, Fujisawa, Kanagawa, 252-0882 JAPAN;

*Corresponding author: naktak@ttck.keio.ac.jp

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The lineage of colonial green algae consisting of *Tetrabaenaceae*, *Goniaceae*, and *Volvocaceae* (TGV-clade) belongs to the clade *Reinhardtinia* within *Volvocales* (*Chlorophyceae*). *Reinhardtinia* is closely related to some species in the unicellular genera *Chlamydomonas* and *Vitreochlamys*. Although 18S *r*RNA gene sequences are preferred phylogenetic markers for many volvoclean species, phylogenetic relationships among the TGV-clade and its relatives have been examined mainly based on chloroplast genes and ITS2 sequences. To determine the candidate unicellular sister, 18S *r*RNA gene sequences of 41 species of the TGV-clade and its relatives were newly determined, and single and 6-gene phylogenetic analyses performed. No unicellular sister was determined by 18S *r*RNA gene analyses, but 6 unicellular clades and 11 ribospecies were recognized as candidates. Five of the candidate lineages and 27 taxa of the TGV-clade were examined by 6-gene phylogeny, revealing one clade including *Chlamydomonas reinhardtii*, *Chlamydomonas debaryana*, and *Vitreochlamys ordinata* to be more closely related than that containing *Vitreochlamys aulata* and *Vitreochlamys pinguis*.

Key words: 18S *r*RNA, colonial, green algae, molecular phylogeny, unicellular, *Volvocales*.

Tetrabaenaceae, *Goniaceae*, and *Volvocaceae* constitute a colonial green algal clade (TGV-clade) within *Volvocales* (*Chlorophyceae*), and include simple to complex colonial forms (e.g., Nozaki 2003a, Nozaki et al. 2014, Nakada and Nozaki 2015). *Tetrabaenaceae* includes undifferentiated 4-celled genera (*Tetrabaena*, *Basichlamys*), *Goniaceae* undifferentiated 8- to 128-celled genera (*Gonium*, *Astrephomene*), and *Volvocaceae* both undifferentiated and differentiated (with somatic and reproductive

cells) 8- to 50,000-celled genera (*Pandorina*, *Volvulina*, *Platydorina*, *Colemanosphaera*, *Yamagishiella*, *Eudorina*, *Pleodorina*, and *Volvox*). Only colonies of *Volvocaceae* have a shared colonial envelope.

Within *Volvocales*, the TGV-clade belongs to the clade *Reinhardtinia* (Nakada et al. 2008, 2010a). To understand the evolutionary origin of coloniality of the TGV-clade, determination of its unicellular sister is first required. Previous phylogenetic analyses showed that the TGV-clade is more closely related to some species

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仲田崇志^{a,b}, 伊藤卓朗^{a,b}, 富田 勝^{a,b}: 群体性オオヒゲマワリ系統 (緑藻綱, オオヒゲマワリ目, テトラバエナ科・ヒラタヒゲマワリ科・オオヒゲマワリ科) および近縁種の 18S リボソーム RNA 遺伝子系統

テトラバエナ科, ヒラタヒゲマワリ科, オオヒゲマワリ科からなる群体性系統 (TGV 系統群) は *Reinhardtinia* 系統群 (緑藻綱, オオヒゲマワリ目) に属し, 単細胞性のコナミドリムシ属 (*Chlamydomonas*) や *Vitreochlamys* のいくつかの種と近縁である. TGV 系統群と近縁種では葉緑体遺伝子や ITS2 配列が系統解析に使われていたが, TGV 系統群の姉妹群は特定されていなかった. そこで本研究では TGV 系統群と近縁種 41 種について 18S rRNA 遺伝子配列を新たに決定し, 系統解析に用いた. 18S rRNA 遺伝子の解析では TGV 系

統群の姉妹群は特定されず, その候補として 6 系統群と 11 種が見出された. この内 5 系統群/種と主な TGV 系統群について 6 遺伝子系統解析を行ったところ, コナミドリムシ (*Chlamydomonas reinhardtii*), *Chlamydomonas debaryana*, *Vitreochlamys ordinata* を含む単系統群が, *Vitreochlamys aulata* と *Vitreochlamys pinguis* よりも TGV 系統群に近いことが示唆された.

^a慶應義塾大学先端生命科学研究所,

^b慶應義塾大学大学院政策・メディア研究科)