

Comparative genomics of photosynthetic and non-photosynthetic *Cryptomonas* (Cryptophyta) species.

Goro Tanifuji¹, Ryoma Kamikawa², Christa E. Moore³, Tyler Mills³, Naoko T. Onodera³, John M. Archibald³, Yuji Inagaki⁴, Tetsuo Hashimoto⁵

1. Department of Zoology, National Museum of Nature and Science, Ibaraki, Japan
2. Graduate School of Human and Environmental Studies, Kyoto University, Kyoto, Japan
3. Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, Canada
4. Center for Computational Sciences, University of Tsukuba, Ibaraki, Japan
5. Graduate School of Life and Environmental Sciences, University of Tsukuba, Ibaraki, Japan

The loss of photosynthesis has occurred multiple times in eukaryotic lineages and the remaining non-photosynthetic plastids take essential roles other than photosynthesis such as fatty acid, isoprenoid, and amino acid biosyntheses. The unicellular algal genus *Cryptomonas* (Cryptophyta) contains both photosynthetic and non-photosynthetic members, the latter having lost the photosynthetic ability on at least three separate occasions. In order to elucidate the evolutionary process underlying the loss of photosynthesis in *Cryptomonas*, we sequenced the plastid genomes of two non-photosynthetic strains, *Cryptomonas* sp. CCAC1634B and SAG977-2f, and compared them to the previously sequenced plastid genome of the non-photosynthetic *C. paramecium* CCAP977/2a. Also, the plastid genome of photosynthetic *Cryptomonas curvata* CCAP979/52 was sequenced as reference. The genome sizes of non-photosynthetic plastids are 106,661 bp, 80,503 bp and 77,717 bp in SAG977-2f, CCAC1634B and CCAP977/2a, respectively. Although the most of photosynthesis related genes such as *psa* and *psb* gene families were disappeared from the non-photosynthetic plastid genomes, a few pseudogenes retained in SAG977-2f. While the gene order of the photosynthetic plastids is roughly common among Cryptophyte genera, the genome rearrangements are seen in the smaller genomes of the non-photosynthetic plastid genomes more frequently. Intriguingly, the light-independent protochlorophyllide reductase comprising of *chlB*, *L* and *N* retain in SAG977-2f, CCAC1634B despite the loss of photosynthesis. On the other hand, while CCAP977/2a maintain rubisco related genes including *rbcL*, *rbcS* and *cbbX*, the other two non-photosynthetic strains lost the rubisco proteins. In addition, we present the draft nuclear genome sequences of two non-photosynthetic *Cryptomonas* strains, CCAC 1634B and CCAP977/2a. We discuss the evolutionally mechanisms of loss of photosynthesis and the divergence of non-photosynthetic plastids in *Cryptomonas*.