

<b>Thesis Title</b>	Comparative Genomic Analysis Illustrates Evolutionary Dynamics of Multi-subunit Tethering Complexes Across Green Algal Diversity
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## **ABSTRACT**

Green algae are the prevalent group of photosynthetic eukaryotes. Although a vast majority of them carry out oxygenic photosynthesis, certain species can also at times transition into mixotrophs, free living heterotrophs, or even parasites. The physical characteristics of green algae are highly diverse – they vary greatly in size, shape, color, and habitat. Nonetheless, all of them share the immense cellular complexity, a key constituent of which is the complex web of interacting membrane-bound organelles, collectively known as the endomembrane system. It is strictly controlled by an array of proteins, such as tethering factors. Among them are the multi-subunit tethering complexes (MTCs), which promote the initial interaction between a vesicle and its destination organelle. The aims of this study are to compare the multi-subunit tethering complexes in various green algae and study their evolutionary dynamic across the diversity of Chlorophyta. Our results reveal that while green algae carry a generally conserved and unduplicated complement of MTCs, some intriguing variation exists. Notably, we identified incomplete sets of TRAPP<sub>II</sub>, exocyst, and HOPS/CORVET components in all Mamiellophyceae, and what is more, not a single subunit of Dsl1 has been found in *Cymbomonas*

*tetramitiformis*. As absence of Dsl1 have been correlated with having unusual peroxisomes, we searched for peroxisome biogenesis machinery, finding very few components in *Cymbomonas*, suggestive of peroxisomal lack. Overall, we demonstrate conservation of MTCs across green algae with some notable taxon-specific losses possibly indicative of unusual endomembrane systems.

**Keywords:** Multi-subunit Tethering Complexes, Exocyst, TRAPP II, Dsl1, Peroxisome, membrane-trafficking, Prototheca, Cymbomonas

