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Using *Symbiodinium* as a Model for Dinoflagellate Genome Structures

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Dinoflagellates have some of the largest genomes of any eukaryote and their genes can be both highly repetitive and highly duplicated. Additionally, few dinoflagellate genomes have been sequenced and even less have been accurately annotated. As a result, our current understanding of how a dinoflagellate's genome is structured is limited. *Symbiodinium*, on the other hand, has one of the smaller genomes among dinoflagellate species, eleven of which have been published to NCBI, making it a useful model for dinoflagellate genetic studies.

Symbiodinium is a dinoflagellate species of particular ecological interest due to its symbiotic relationship with coral. It was recently discovered that various species of *Symbiodinium* are capable of producing different toxins. However, why and when these toxins are produced, as well as whether they have any effect on the cnidarian host, is relatively unknown. To understand what effect toxin production may have on the coral-symbiont relationship, scientists must first attempt to understand how *Symbiodinium*'s genes are structured so they can be best manipulated at the molecular level.

In this study, we present our efforts to identify multiple genes including the triple KS gene— a protein thought to be involved in toxin production in dinoflagellates— in the *Symbiodinium* genome. We used Illumina and PacBio transcriptomic data from *Symbiodinium tridacnidorum* CCMP2592 and compared it to Illumina genomic data from the same species and strain. The results will ultimately allow us to better understand how dinoflagellate genes, especially those involved in toxin production, are regulated and what sort of genetic engineering tools are viable for future studies.