**Objective:**

The goals of the project I am currently working are **1)** to quantitatively differentiate between red and orange color morphs in *Montipora capitata*, **2)** monitor their physiological responses to varied light conditions over time, and **3)** see if there are any genetic markers that suggest that these color morphs are genetically distinguishable.

**Project Summary:**

This project is essentially a follow-up experiment to Innis et al., 2018. In this study they found that the main drivers between color morph prevalence and dominant Symbiodiniaceae clade was depth/light environment. I wanted to expand upon this by being able to quantitatively identify between the color morphs and to try to identify any other distinguishing factors between these color morphs.

In this experiment I took 13 colonies (6 identified as Red/Brown, and 7 identified as Orange) of opportunity from the coral nursery, fragmented each of these colonies into four fragments, and exposed them to four different light treatments (control – same depth they were found at, shallow (high light), shade, and deep) for 8 weeks. Using weekly photos and bimonthly biopsies of each fragment, color, protein concentration, and zoox density data was acquired through ImageJ, BCA protein assays, and cell counts. These biopsies also produced material for CTAB DNA extractions which we are hoping to get qPCR data from.

To achieve objective #1 we are using color, protein concentration, zoox count, and clade community composition data to identify physiological and colormetric differences between the color morphs. To achieve object #2 we are using the same data throughout all timepoints with biopsy data (t= 0, 2, 4 and 7 weeks) to monitor their physiological responses to the light treatments. And lastly to achieve objective #3 we will be mining pooled sequence data that Zack Foresman has on a manuscript he is currently working on to see if there are genetic markers to distinguish between the color morphs.

**qPCR Rationale:**

For this experiment qPCR data would help establish initial clade community composition in each of the color morph colonies and provide yet another distinguishing factor between colormorphs. Additionally, qPCR data would allow us to see how the clade community compositions change over time under the four light treatments throughout time. My goals are to use qPCR to try to **1)** corroborate the findings from Innis et al., 2018, with color morph identity and dominate clade type (96.9% Clade C dominated were Brown/Red morphs, 75.5% D dominated were Orange morphs) and **2)** correlate colormetric data to clade community composition. For example, are the red channels significantly higher in colonies that have high proportions of D1a in them than those dominated by C31?

The qPCR data is a fundamental part of this project and hopefully will elucidate the relationship between color and dominate clade type in a quantitative way. I would be testing timepoints 0 and 7 weeks first to essentially see if there is a difference at all between the first and last sampling points. This would be 65 samples total but if there is potentially an interesting story of clade community change, I may try to run the remaining sampling points (t = 2 and 4 - an additional 104 samples, 52 per timepoint).