STX [Species] Report

Name:

**Instructions:** Please create a folder including all high-resolution plots and text files referenced in this report. Make sure your folder includes the following files (note that your filenames will contain your species abbreviation, not “STX”):

**From TACC:**

1. qualRanks
2. alignmentRates
3. idxstats
4. dd.pdf
5. hctree.pdf
6. bams.qc
7. bams.nr
8. STX1.ibsMat
9. STX2.ibsMat
10. STX.res
11. STX \_k2.qopt
12. STX \_k3.qopt

**From STX\_popstructure.R:**

1. STX\_IBS\_dendrogram.png
2. STX\_IBS\_heatmap.png
3. STX \_relate\_dendrogram.png
4. STX \_relate\_heatmap.png
5. STX \_admix\_k2.png
6. STX \_IBS\_capscale.txt
7. STX \_PCoA\_admix.tiff
8. STX \_cluster1
9. STX\_cluster2
10. STX \_admix\_k3.png

**From STX\_spatial.R:**

1. STX\_scatterpie.tiff
2. STX\_tess3r.tiff

**From STX\_Environment.R:**

1. STX\_IBD.tiff
2. STX\_PCoA\_depth.tiff
3. STX\_PCoA\_env.tiff
4. STX\_PCoA\_lat.tiff
5. STX\_PCoA\_lon.tiff
6. STX\_gf\_boxplot.tiff
7. STX\_gf\_barchart.tiff
8. Map of adaptive communities

*\*Do not include gradient forest plots if model does not converge.*

You can zip the folder and email with your report to Kristina at kblack@utexas.edu.

**Background:**

Include some background about your species for the introduction of the manuscript.

What kind of taxa is your species? (Family? Common name?)

Where is your species found?

What is your species’ reproductive strategy: (ex. spawner or brooder?)

Is your species threatened or endangered? If so, please cite the source.

Read some of the other scientific literature on your species to answer the following questions:

Are there cryptic genetic lineages? If so, where and how many?

Have any unique adaptations been found? (i.e. to depth, heat, etc.)

Are there any previous studies on this species in the Virgin Islands? If so, what did they find?

**Methods:**

How many samples did you start with? (ex. ls \*fastq | wc -l)

What was your quality cutoff for qualRanks?

How many samples passed quality filtering? (ex. wc -l bams.qc)

How many sites were retained after quality filtering? (ex. tail a1.e\*)

How many samples were retained after removing clones? (ex. wc -l bams.nr)

How many sites were retained after removing clones? (ex. tail a2.e\*)

**Results:**

**Figure 1:** Paste your dd.pdf here and explain observations in each plot.

**Figure 2:** Paste your hctree.pdf here and explain observations in this plot.

**Figure 3:** Paste your IBS dendrogram and heatmap together here and explain observations in each plot.

**Figure 4:** Paste your relatedness dendrogram and heatmap together here and explain observations in each plot.

**Figure 5:** Paste your admixture barplots for k=2 and k-3 together here and explain observations in each plot.

**Figure 6:** Paste your PCoA colored by admixture here and explain observations in this plot.

**Figure 7:** Paste your scatterpie and tess3r maps here and explain observations in each plot.

**Figure 8:** Paste your isolation by distance plot here and explain observations in this plot.

**Figure 9:** Paste your PCoAs colored by depth, longitude, latitude, and any environmental variables that show a nice gradient. Explain whether there are any noticeable trends in each plot.

**Figure 10:** Paste your gradient forest boxplot, barchart, and map here (if your model converged). Explain observations in each plot.

**Discussion:**

First discuss the population structure you observed in your species in St. Croix, then discuss any environmental adaptation you believe is going on:

How many genetic clusters do you believe there are here? Are there many clones or siblings?

Do your genetic clusters (aka “admixture groups”) separate in geographic space? Could they be isolated by distance?

Do you think that separation of your clusters is associated with environmental differences across the seascape? If so, with which environmental variable? What evidence supports your claim (which of your plots point you to this conclusion)?

Is there any previous literature that found associations between your species and this environmental variable? What about any other coral species?

If you don’t think your clusters are driven by environmental adaptation, then what else might be causing genetic differentiation?

What future experiment or samples would you need to explore your hypothesis?