**RNA Extractions and Sequencing**

RNA was extracted from a small fragment (~3-5 μg) of tissue and skeleton using the RNAaqueous Kit with DNAse step kit (Life Technologies AM1914). Each fragment was first ground in a 2 mL microcentrifuge tube with 800 μL of Lysis Buffer for 2 minutes. Next, the tube was centrifuged on an AccuSpin Micro (Fisher Scientific) after witch 700 μL of the supernatant were removed and placed in a new tube along with 700 μl of 64% Ethanol solution. This solution was then passed through the column provided with the kit and washed with the wash one solution and twice with the wash two solution. The column was spun dry for 2 minutes and RNA eluted with 50 μL elution solution. Potential contaminating DNA was removed from samples by mixing 25 μL final extract with 2.95 μL of Master Mix and 1.6 μL DNase solution. This mixture was incubated at 37 °C for 1 hour and then incubated at room temperature for 2 minutes with 2.95 μL inactivation reagent. The final extract (~30 μL) was then passed to a new tube and stored at -80°C.

**cDNA Library Prep and Sequencing**

Following extraction the three replicates from each species and colony within a treatment were pooled for RNA library sequencing, due to budgetary constraints (n = 4-5 per treatment and species).Quality of combined extracts was assessed at the University of Texas at Arlington Genomics Core facility using an Agilent BioAnalyzer 2100. Samples with RIN numbers (quality values) higher than 8 were processed for cDNA library creation using an Illumina TruSeq RNA with Poly-A selection libraries kit (Illumina). Pooled samples were then sent to the University of Texas Southwestern Medical Center Genomics Core facility where library construction and sequencing occurred. Samples were sequenced in two separate lines with 20 samples each. The second lane was completed with samples from a separate project.

**Transcriptome Assembly and RNA-seq analysis**

Following sequencing, RNA-seq libraries were sorted and the quality of reads was assessed. The Trimmomatic v. 3 software package was used to remove adaptors and low quality reads (Lohse et al. 2012). Non-host sequences were filtered out using methods described in [1]. Alignments were performed using BLAT (parameters: 90% identity and e-value < 0.000001). Duplicate hits were removed and coral-only sequences were identified using cdbfasta/dcbyank (<http://sourceforge.net/projects/cdbfasta/>). For three of the four species studied, a new reference transcriptome was composed from the sequences libraries. Libraries for *P. strigosa*, *P. asteroides*, and *P. porties* were each assembled *de novo* into transcriptomes using the Trinity software package [2, 3]. The existing *O. faveolata* reference transcriptome was used for analyses of that species’ reads [1].

The Cufflinks software package, v. 2.2.1, was used to conduct differential expression analyses [4]. Analyses were run separately for each species. Read counts for each transcript within a species were obtained by aligning coral only reads to either the newly generated reference transcriptomes (for *P. strigosa*, *P. asteroides*, and *P. porties*), or the existing reference transcriptome in the case of *O. faveolata* [1]. Default parameters were used for this step. Next, normalized expression values were generated in the Cuffdiff package with the default parameters [4]. Average log2fold change per transcript was estimated by comparing normalized expression values between treatments within a species.Significantly differentially expressed transcripts were identified based on log2fold change(adjusted p < 0.05) across treatments.

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