**QPX gene ontology in response to heat stress: Questions, Proteins, eXamples**

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**Keywords:**

**Abstract**

**Introduction**

QPX, clams,

Temperature (mucus and cell) –hypothesis? We hypothesize that altered biochemical pathways will be associated with changes in temperature? Specifically we are interested in virulence factors, mucus production, cell growth and responses to heat stress. HELP!

Virulence factors and QPX and methods to id

**Methods**

BLURB about how QPX was grown/ strain, etc.

We used ILUMINA (LOCATION) to create an mRNA sequence library for QPX at each of the two temperature treatments (10**°**C and 21**°**C). This created ~400 million reads. The resulting libraries were trimmed using XX stringency and a *de novo* assembly was performed using both libraries in CLC () (bubble size? And stringency x?). This resulted in a backbone consisting of 11,271 contigs.

Gene annotation

The contigs from our *de novo* assembly were annotated by BLASTx against the Swis Prot database (). The annotation was delimited with a maximum e-value of 10-5 and limited to a single hit per contig. Gene ontologies and GO SLIM ontologies were assigned to Swiss Prot accession numbers for the annotated contigs.

Differential Expression

RNA-Seq was performed by comparing contigs from each library against the *de novo* backbone using CLC bio (??). Genes with more than a 2-fold difference in expression were were annotated using the previously annotated backbone. Enrichment analyses were performed in DAVID (v. 6.7 Available from http://david.abcc.ncifcrf.gov/) to compare gene ontologies for the differentially expressed genes against the entire QPX transcriptome. Gene ontologies (GO-Fat) for biological processes that were enriched (p < 0.05) were visualized using Revigo ().

**Results**

Gene discovery section (ASHTON) (Tables and graphs)

Differential Expression

Summary

Several GO pathways in detail

Virulence factors or other factors? (Table?)

**Discussion**

**Conclusions**

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**References**

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