



Gene expression profiling in the ovary of Queen conch (*Strombus gigas*) exposed to environments with high tributyltin in the British Virgin Islands

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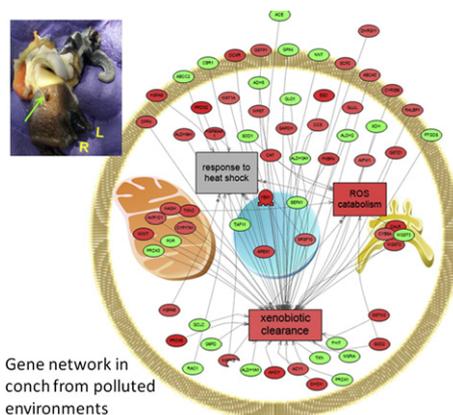
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HIGHLIGHTS

- ▶ British Virgin Islands experience heavy pollution from boating activity.
- ▶ Reproduction of endangered Queen conch is threatened.
- ▶ Microarray analysis showed that cell proliferation and oxidative stress were impacted at polluted sites.
- ▶ General metabolism, immune, lipid metabolism, and stress were also affected in polluted environments.
- ▶ Polluted sites differed in transcriptome profiles, suggesting other factors that TBT regulating gene expression.

GRAPHICAL ABSTRACT



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ABSTRACT

Queen conch (*Strombus gigas*) are listed in CITES Appendix II. Populations may be declining due to anthropogenic inputs that include pollutants from boating activity. In the British Virgin Islands (BVI), some conch exhibit imposex, a condition in which male external genitalia are present in female conch. Previous studies suggest that tributyltin (TBT), an antifouling chemical used in boat paint, is correlated to increased incidence of imposex although the mechanisms leading to imposex are not known. The present study utilized a Queen conch microarray to measure the response of the ovarian transcriptome in conch inhabiting polluted environments with high TBT levels in the BVI. The polluted sites, Road Harbour (RH) and Trellis Bay (TB), are areas with high boating activity while the reference sites, Guana Island (GI) and Anegada (AN), are areas with low boating activity. There were 754 and 898 probes differentially expressed in the ovary of conch collected at RH and TB respectively compared to conch collected at GI. Of the genes that were differentially expressed at both sites, >10% were shared suggesting that these sites have additional environmental factors influencing gene expression patterns. Functional enrichment analysis showed that the biological processes of cell proliferation, translation, and oxidative stress were over-represented in the polluted sites. Gene set enrichment analysis revealed that transcripts involved in the biological processes of general metabolism,

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