Environmental epigenetics: Non-traditional molecular tools for effects assessment.

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Background

- Nutrients and many other chemical contaminants are reaching the natural ecosystems at unprecedented rates. Molecular approaches could improve monitoring tools to evaluate impacts of contaminants in ecosystems, assessing responses occurring before effects.
- Responses to environmental stress require changes in gene expression. Epigenetic mechanisms, are dynamic, heritable and highly responsive, modulating changes in gene expression in response to environmental cues.

Approach

Two species, two stressors

Eastern oyster (Crassostrea virginica)
Staghorn coral (Acropora cervicornis)

Marine Toxins

Nutrients

Lab experiments
Field experiments

DNA methylation.
Histone variant expression.
Histone post-translational modifications.

Results

Eastern oyster

- Global DNA methylation reduced during exposure to marine toxins.
- H2A.X phosphorylation (γH2A.X) increases during exposure to marine toxins, potentially linked to epigenetic maintenance of genomic integrity.

Staghorn coral

- Rapid reduction in global DNA methylation upon exposure to nutrient stress.
- H2A.X phosphorylation (γH2A.X) displays a dynamic response, increasing early in the exposure to all nutrients and being impaired in the nitrogen only treatment (phosphorus starvation syndrome). H2A.X gene expression is increased 3 days after nitrogen only exposure probably as a compensatory mechanism.

Conclusions

Our results support the role of different types of epigenetic mechanisms (histone variants and DNA methylation) during responses to environmental stressors in non-model organisms. Among those, H2A.X phosphorylation seems to play a key role in the epigenetic maintenance of genome integrity. Complementary, the observed reduction in DNA methylation is consistent with the activation of genes specifically involved in responses to the stressors studied. This work opens a new exciting perspectives for the coral management and restoration.

Acknowledgments.

This material is based upon work supported by the National Science Foundation under Grant No. HRD-1547798. This NSF Grant was awarded to Florida International University as part of the Centers of Research Excellence in Science and Technology (CREST) Program. We thank the support of the Coral Restoration Foundation and Rockery Bay National Estuarine Research Reserve. “Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.”
