

# Epigenetic Landscapes in the Pacific Oyster (*Crassostrea gigas*)

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## Project Summary

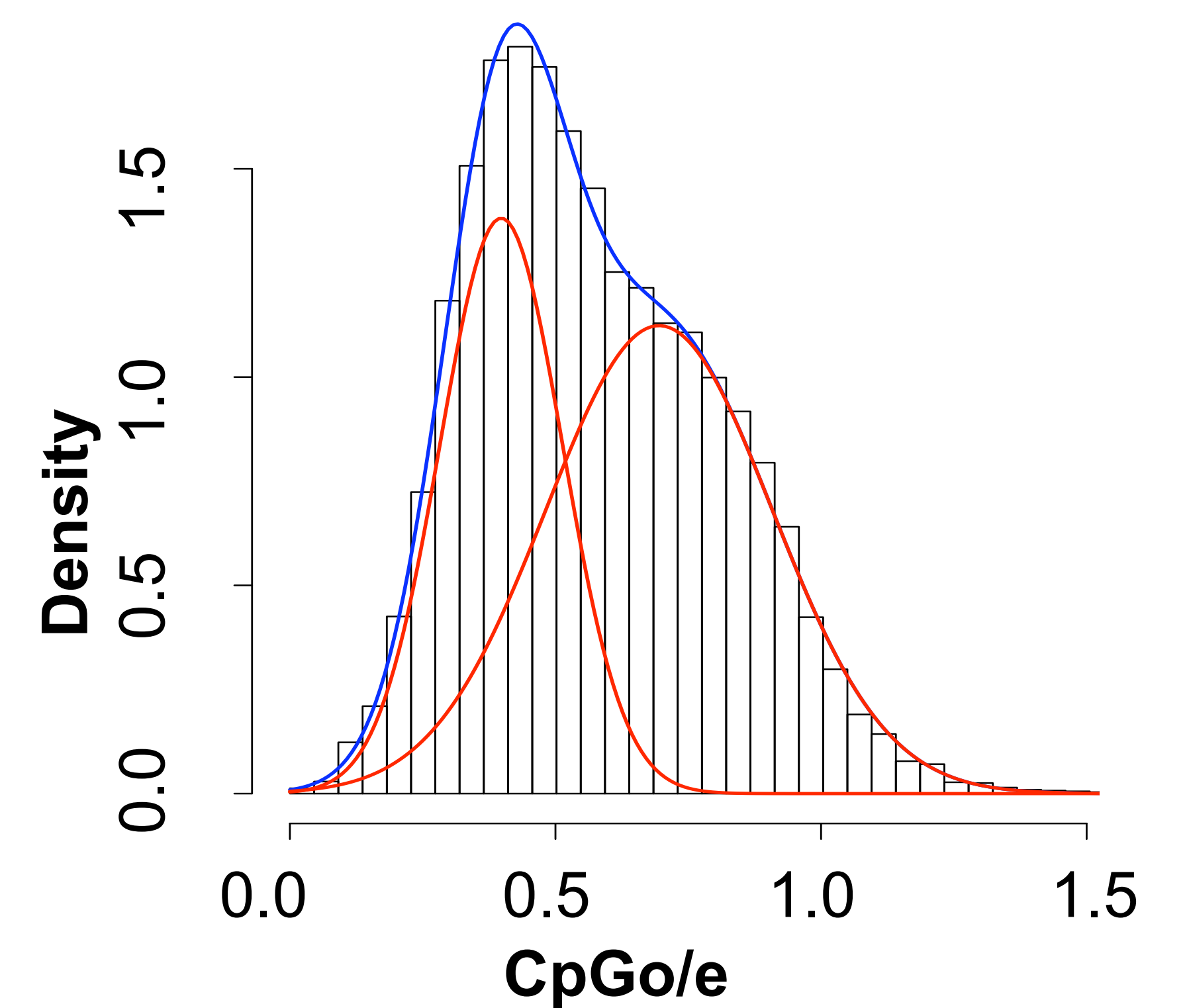
DNA methylation is an epigenetic mechanism with important regulatory functions in animals. This mechanism has been well studied in mammals; however, there are limited data on invertebrates, particularly molluscs. This study provides the first investigation into the functional role of DNA methylation in a mollusc.

### Specific Research Objectives

- Characterize the distribution of DNA methylation in the Pacific oyster (*Crassostrea gigas*) genome
- Investigate potential functions of DNA methylation in oysters

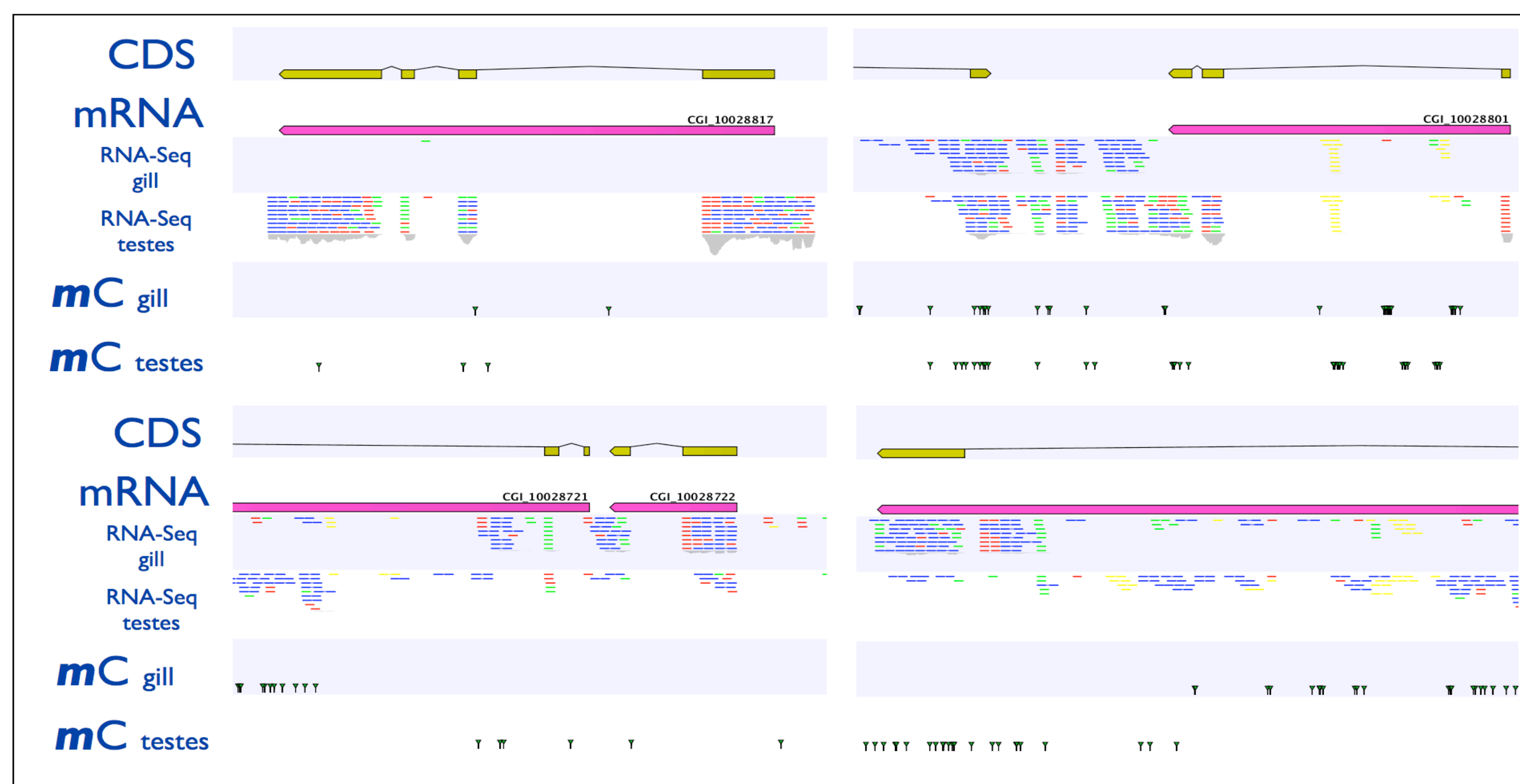
## Bimodal Distribution of CpG Methylation

The ratio of observed to expected CpG dinucleotides (CpGo/e) was used to predict methylation status in the *C. gigas* transcriptome. Regions of DNA with a low CpGo/e are predicted to be methylated, whereas regions with a high CpGo/e (~1) are predicted to be unmethylated. For this analysis, a CpGo/e was calculated for 12,210 sequences in GigasDatabase, a non-redundant *C. gigas* contig database. The bimodal distribution of the contigs indicates there are two populations of genes in *C. gigas*, those that are highly methylated (low CpGo/e) and those that are less methylated (high CpGo/e).



Probability density function of CpGo/e for 12,210 *C. gigas* contigs.

## Tissue Specific DNA Methylation Patterns in the Pacific Oyster



- DNA methylation is distributed throughout the genome in gill tissue of *C. gigas*: approximately half of the methylation is found in intra-genic regions, 18% is found in exons.
- DNA methylation patterns vary between tissues: 35% of analyzed CG dinucleotides are significantly less methylated in testes compared to gill.
- Differentially methylated regions are frequently associated with 'expressed' portions of the genome, but are not necessarily associated with differential gene expression.
- Methylation data features are available at: [genefish.wikispaces.com/crassostreome](http://genefish.wikispaces.com/crassostreome)

## Implications and Future Directions

Results of this investigation suggest that DNA methylation has important regulatory functions in *Crassostrea gigas*, particularly in gene families involved in stress and environmental response. We are currently investigating relationships between the environment, DNA methylation, and control of gene expression to better understand these processes.

### Aquaculture and Hybrid Vigor

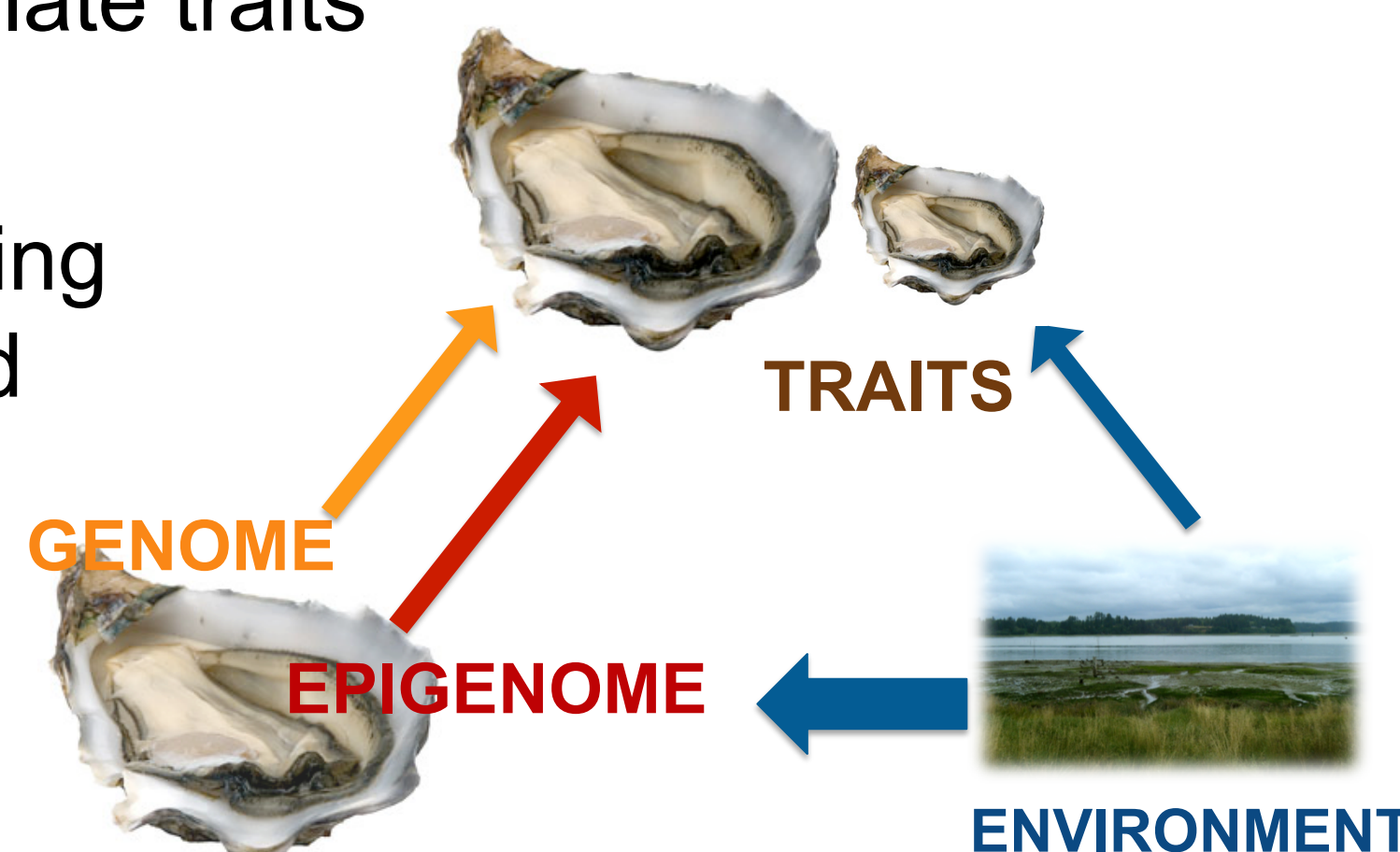
Understanding the role of DNA methylation in oyster development could increase the ability to predict and manipulate traits in hatchery settings.

Genetic models have not succeeded in explaining phenomena such as inbreeding depression and hybrid vigor in oysters; it is likely that epigenetic mechanisms are involved.

### Invertebrate Gene Regulation

DNA methylation is confined to exonic regions in invertebrate genomes; however, the mechanism of regulation by intragenic methylation is unclear.

By combining high-resolution bisulfite sequencing and gene expression analyses we will examine this relationship in the oyster.



### Environmental Change

DNA methylation patterns can be disrupted by a wide range of environmental compounds, and in some cases these disruptions can be passed on to multiple generations.

We are examining the effects of environmental perturbations on DNA methylation in oysters with an emphasis on:

- Contamination in estuarine environments
- The role of epigenetics in the evolutionary response to global climate change

### Additional Information

For more information including manuscripts, supplementary data, and presentations please visit: <http://genefish.wikispaces.com/CpGCg>

