EPIGENETIC LANDSCAPES IN A MARINE MOLLUSC:

What DNA methylation patterns tell us about gene regulation in the Pacific oyster (Crassostrea gigas)

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Outline
- Background
  - Epigenetics
  - DNA methylation
- Results
  Characterization of DNA methylation in Pacific oysters
- Discussion & Future Directions

Epigenetics
- Heritable changes in trait or phenotype, caused by a mechanism other than mutation to the DNA sequence
- Most well understood epigenetic mechanism is DNA methylation
  - Regulates gene expression
    - Development
    - Tissue-specific expression
    - Genome stability
    - Environmental response
DNA methylation: invertebrates

- Only a handful of species have been evaluated
- Model invertebrates lack DNA methylation
- Most have 'intermediate' methylation
- Primarily in exons
- Important regulatory functions – e.g. honey bee

Summary of Previous Results

- CpG O/E
  - Predicted degree of DNA methylation

Goals

- EPIGENOME (DNA methylation)
- GENES (DNA)
- TRAITS
  - color
  - growth
  - disease resistance
  - ENVIRONMENT
  - nutrition
  - temperature
  - pathogens
  - nightfall
Goals

EPIGENOME (DNA methylation)

GENES (DNA)

ENVIRONMENT

color
disease resistance
growth
temperature
pathogens
nutrition

TRAITS

Approach

- High-throughput bisulfite sequencing:
  - Gill
  - Gametes (male)
- Other resources:
  - RNA-seq datasets: gill, male gonad (Zhang et al, 2012)

Workflow

- Prepare gDNA library for methylation analysis
- Data Analysis

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- Illumina library
- Bisulfite conversion
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- Prepare gDNA library for methylation analysis
- Data Analysis
  - BSMAP software
  - Map to reference genome

**Results**
- 250,876 CG dinucleotides

**Results**

![Galaxy Trackster](scaffold_86_200000bp.png)
Results

- 250,876 CG dinucleotides
- Distribution in genomic elements

Relationship with expression
Results

- Relationship with expression

![RNASeq data (Zhang et al., 2012)](image)

Differentially methylated regions

- DMR definition:
  - 100bp window
  - ≥25% difference
- 35% of the windows were differentially methylated

DMR: Visualization

- gill
- male gonad
- sperm

DMR: Visualization

- gill
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- sperm
DMR: Visualization

RNA-Seq methylation

Gill
Male gonad
Gill
Sperm

Summary

GENES (DNA)

EPIGENOME (DNA methylation)

ENVIRONMENT

Traits: color, disease resistance, growth

Environment: temperature, nutrition, pathogens, radiation
DNA methylation landscape is complex
- Genes with high transcript abundance, have highest gene body methylation
- Methylation patterns are tissue specific
- Tissue-specific methylation is frequently found in 'expressed' portions of the genome.
- Fine scale differences in methylation within a gene

Generate DNA methylation and gene expression profiles from the same sample.
- Explore possibility that methylation is associated with alternative splicing
Summary

- GENES (DNA)
- EPIGENOME (DNA methylation)
- ENVIRONMENT

TRAITS:
- color
- growth
- disease resistance
- temperature
- pathogens
- nutrition

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