

Response of DNA methylation to environmental change in the reef coral *Porites astreoides*

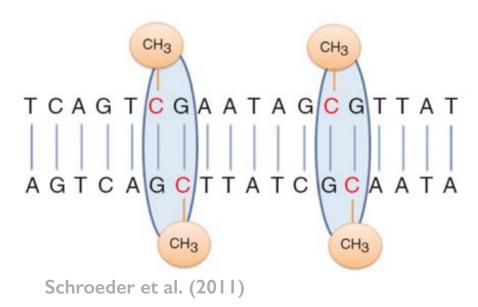
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Histone Modification DNA Methylation Micro-RNA based mechanism (Nucleus) (Cytoplasm) mRNA degradation pre - miRNA mature miRNA mRNA translation repression

Khalil (2014)

CpG methylation

5-methylcytosine (5mC)



Evidence for:

- Environmental induction
- Heritability
- Influence on transcription

Context important

- Evolutionary
- Genomic



Lira-Medeiros et al. (2010), Simpson et al. (2011), Skinner et al. (2014), Morgan et al. (1999)



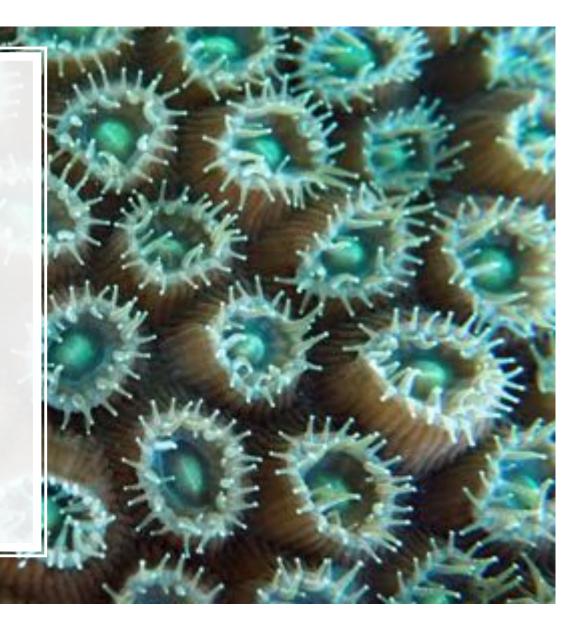
DNA methylation and phenotype



In decline globally

Need to understand mechanisms of adaptation & acclimatization

Sessile and very reliant on phenotypic plasticity

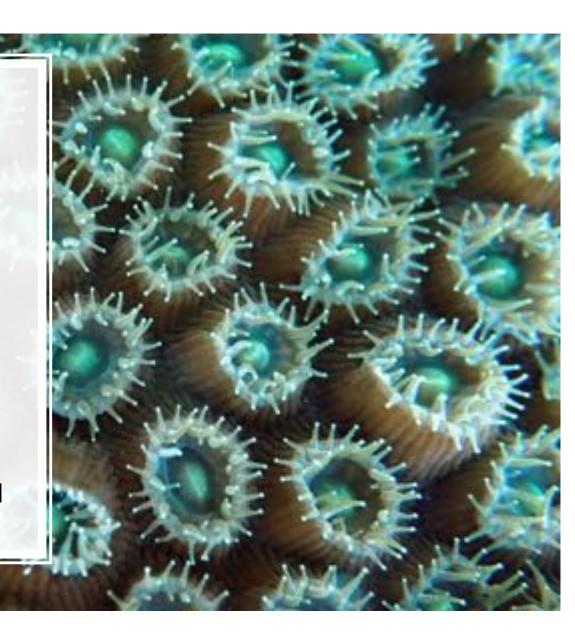




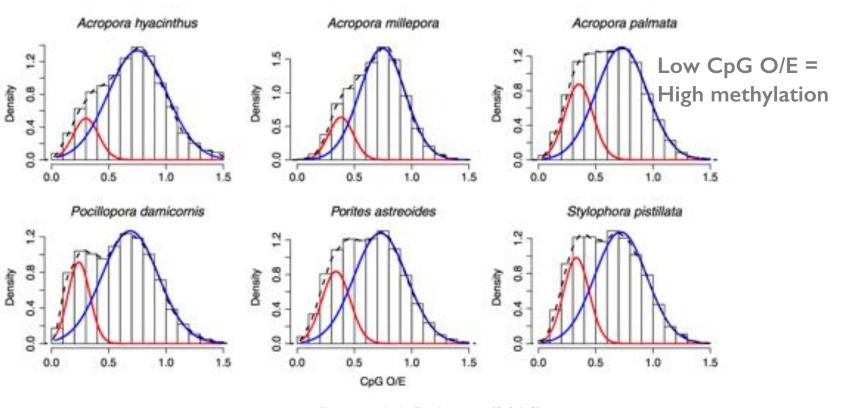
Genomes less methylated than vertebrates

Methylation mostly in gene bodies

Function of gene body methylation not fully understood



Corals, like other invertebrates, have distinct fractions of genes with high and low levels of methylation



Dimond & Roberts (2016)



Hypermethylated genes

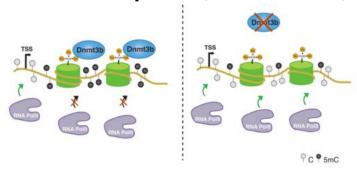
Tend to be housekeeping genes

Essential, conserved functions



5mC promotes optimal codon usage (Dixon et al. 2016)

5mC prevents spurious transcription (Neri et al. 2017)



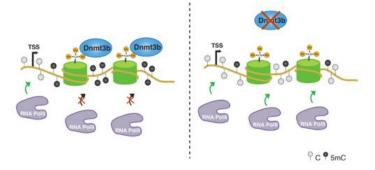
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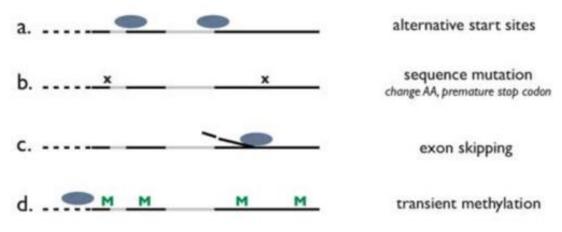
Hypomethylated genes

Tend to be inducible genes

Associated with environmental change & exhibit plasticity



Increased transcriptional opportunities?



Roberts and Gavery (2012)

Hypermethylated genes

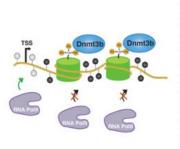
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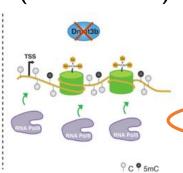
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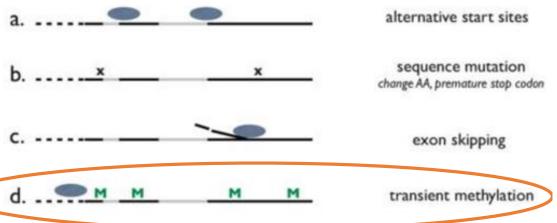
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Methods

One-year common garden transplantation experiment on Belize Barrier Reef

- colonies moved to common garden from 10-20 km away

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One-year common garden transplantation experiment on Belize Barrier Reef

- colonies moved to common garden from 10-20 km away ddRADseq coupled with EpiRADseq (ddRAD variant) to assess methylation
 - EpiRADseq uses methylation-sensitive restriction enzyme
 - Methylation estimated by read counts
 - Reads low/absent in EpiRADseq library = methylated

Methods

One-year common garden transplantation experiment on Belize Barrier Reef

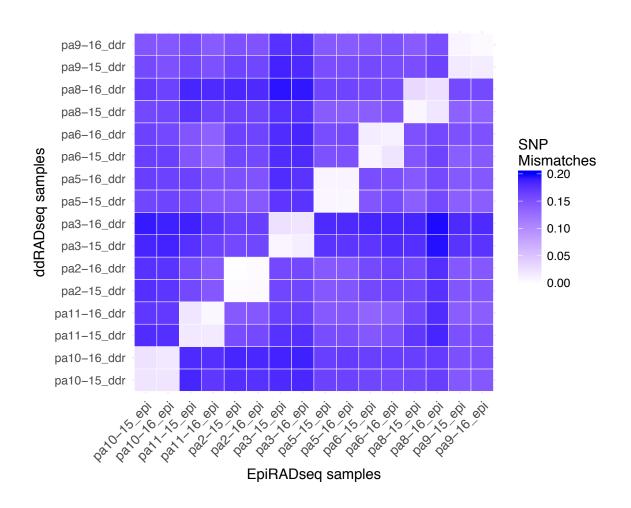
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Genome-independent assembly using iPyrad

- Symbiodinium Clade A genome used to remove symbiont reads

n = 8 colonies x 2 years

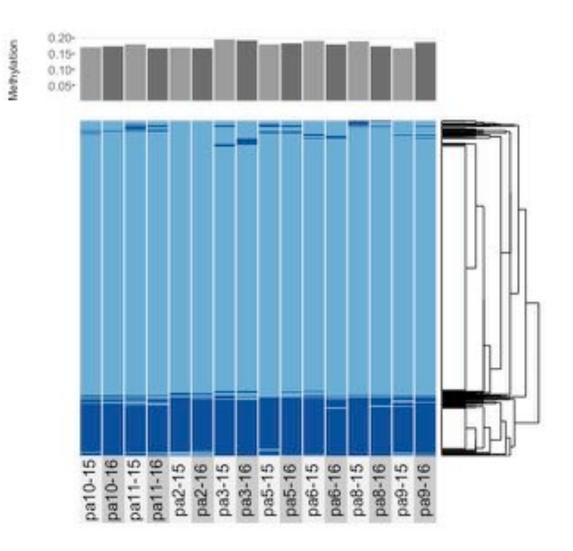
Technical replicates and repeated sampling indicate low error



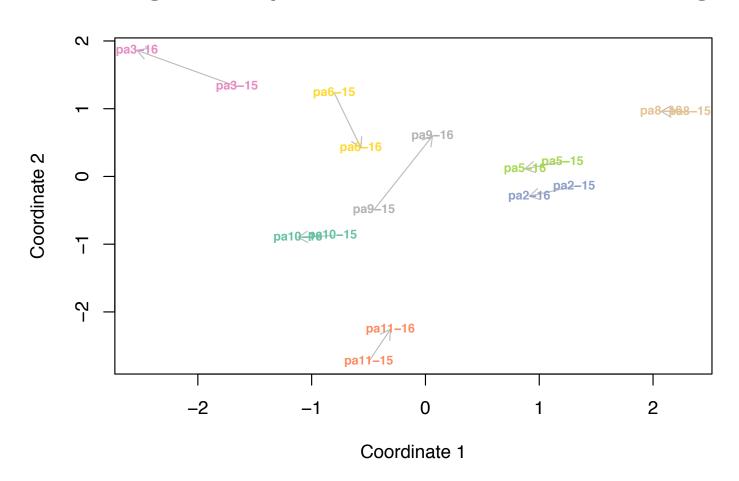
649 shared loci

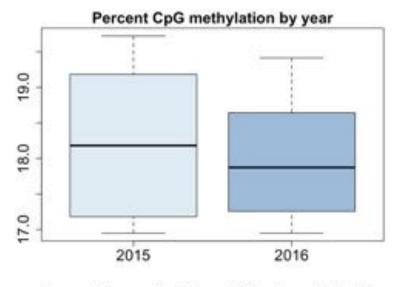
Most loci either constitutively unmethylated or methylated

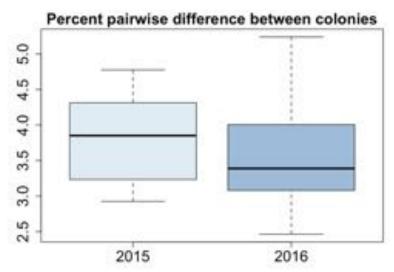
Little change over one year

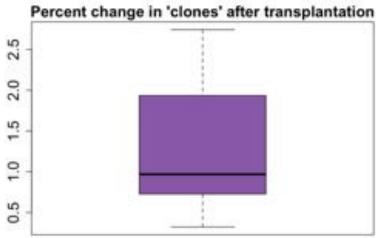


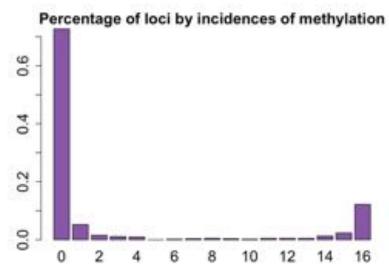
Little change over a year; individuals tend to cluster together













Dimond et al. (2017)

For comparison: Porites porites complex

18% of CpGs methylated

15% differentially methylated among colonies (n = 27)

Conclusions

Methylation shows limited plasticity after one year in a novel environment

- corroborates results of Dixon et al. in GBR Acropora

Robust methods recommended for detecting these small changes

- our method has relatively coarse resolution
- more robust methods generally require a genome

Future directions

Which genes or elements are involved?

- P. astreoides genome coming soon

Is transcription of these genes altered?

- transcript abundance
 - Dixon et al. found little evidence in GBR Acropora
- transcript variants / alternative splicing
 - examples in other taxa

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