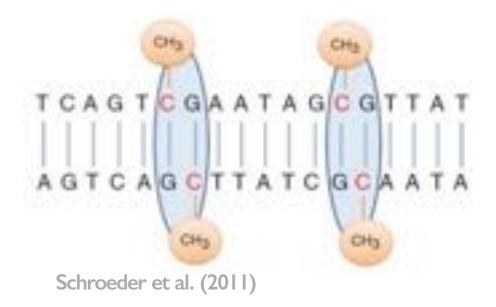


Response of DNA methylation to environmental change in the reef coral *Porites astreoides* and its associated *Symbiodinium*

Jay Dimond & Steven Roberts
University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA USA

CpG methylation

5-methylcytosine (5mC)



Evidence for:

- Environmental induction
- Heritability
- Influence on transcription & phenotype

Context important

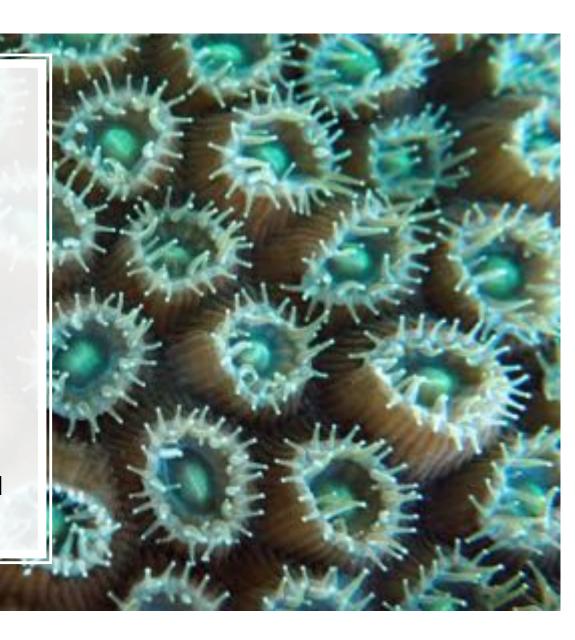
- Evolutionary
- Genomic



Genomes less methylated than vertebrates

Methylation mostly in gene bodies

Function of gene body methylation not fully understood

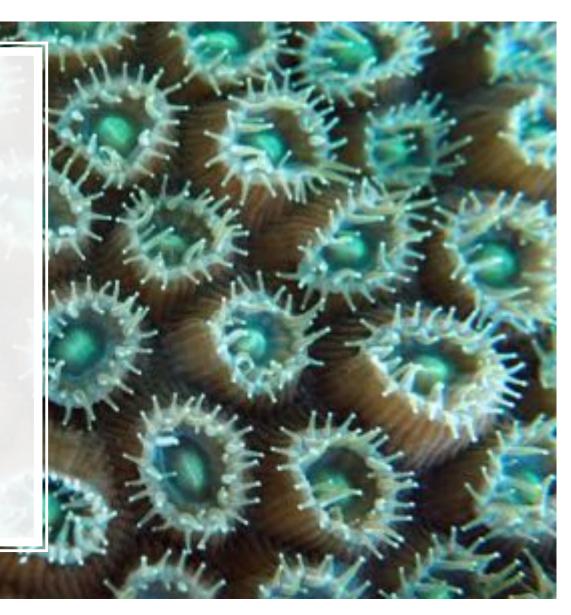




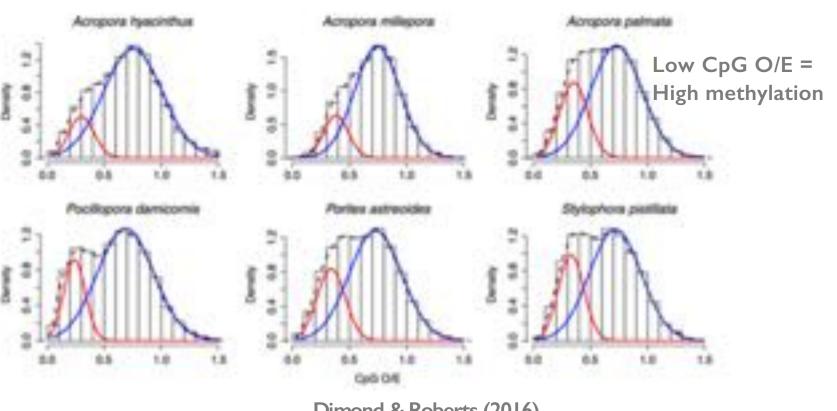
In decline globally

Need to understand mechanisms of adaptation & acclimatization

Sessile and very reliant on phenotypic plasticity



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







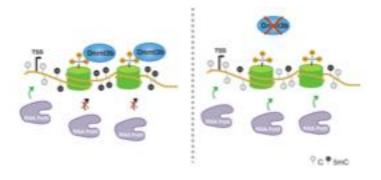
Hypermethylated genes

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)



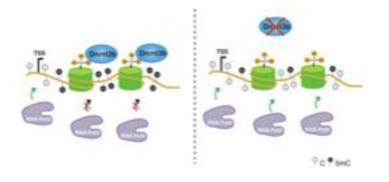
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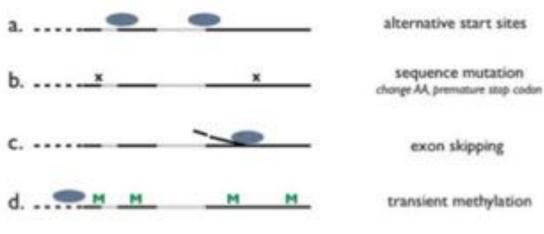


Hypomethylated genes

Tend to be inducible genes
Associated with environmental change & exhibit plasticity



Increased transcriptional opportunities?



Roberts and Gavery (2012)

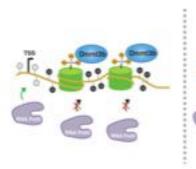
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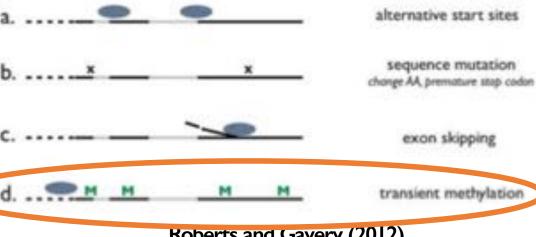


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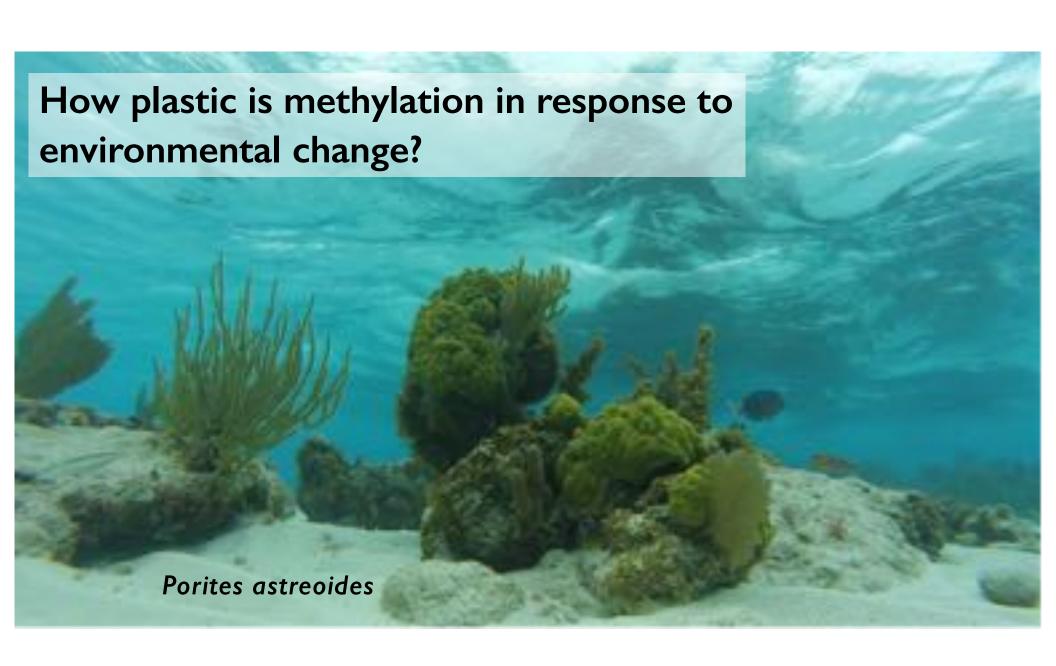
Tend to be inducible genes Associated with environmental change & exhibit plasticity



Increased transcriptional opportunities?



Roberts and Gavery (2012)



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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 - EpiRADseq uses methylation-sensitive restriction enzyme
 - Methylation estimated by read counts
 - Reads low/absent in EpiRADseq library = methylated

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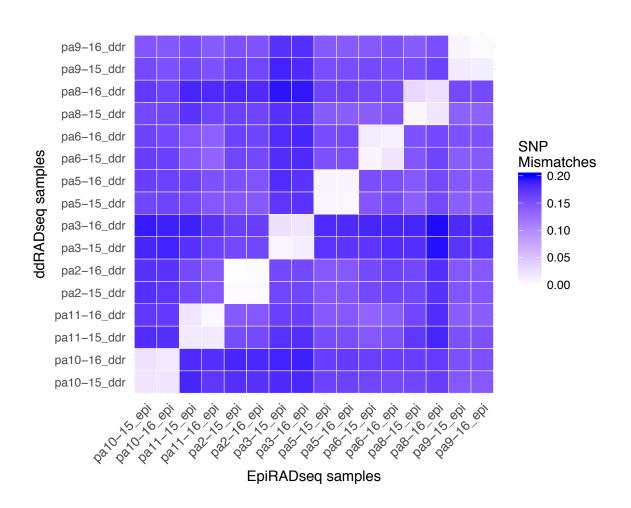
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Genome-independent assembly using iPyrad

- Symbiodinium Clade A genome used to remove symbiont reads

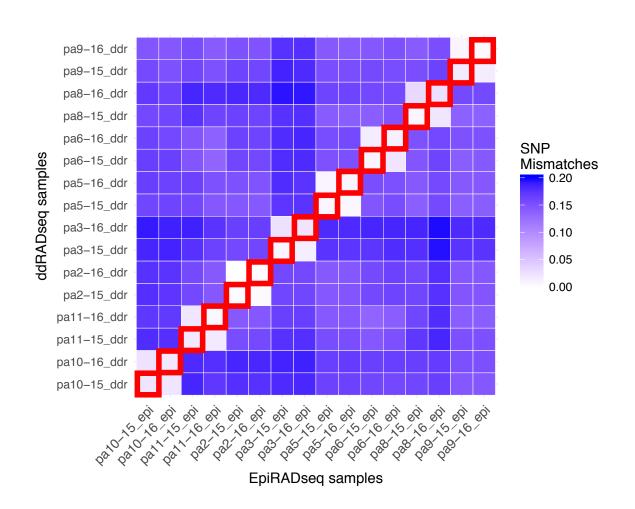
n = 8 colonies x 2 years

Technical replicates and repeated sampling indicate low error



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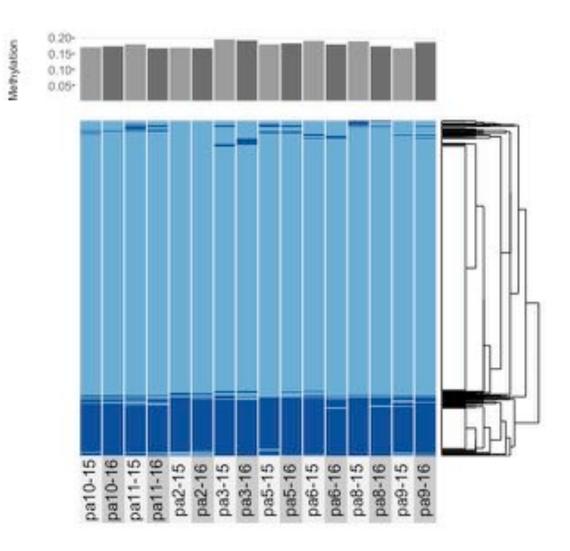
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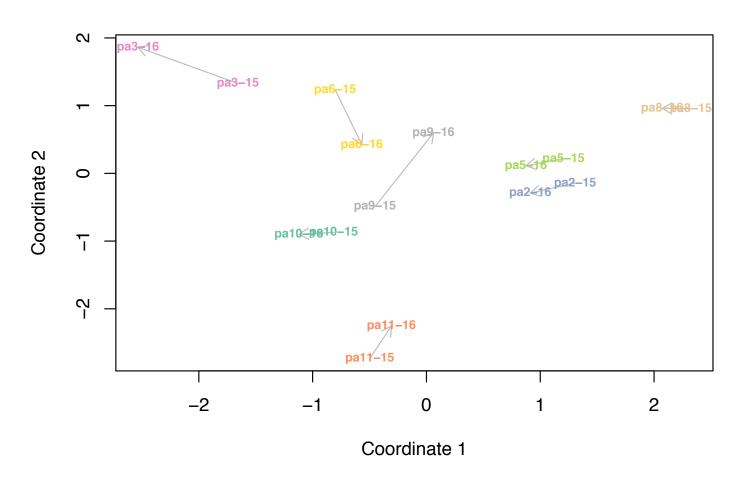
649 shared loci

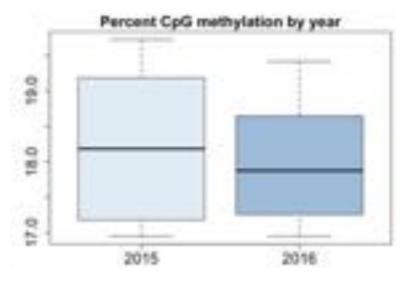
Most loci either constitutively unmethylated or methylated

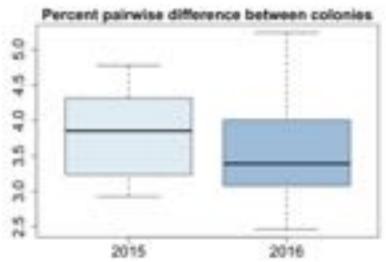
Little change over one year

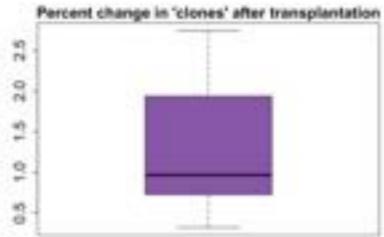


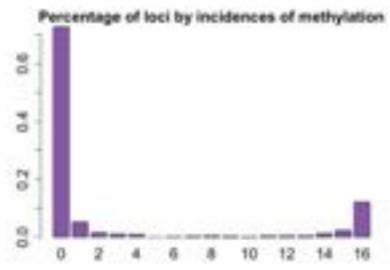
Little change over a year; individuals tend to cluster together

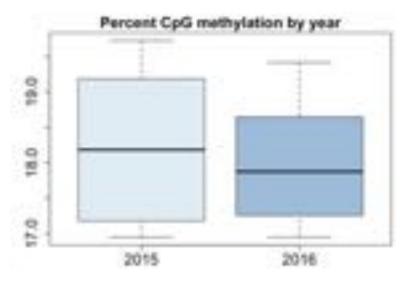


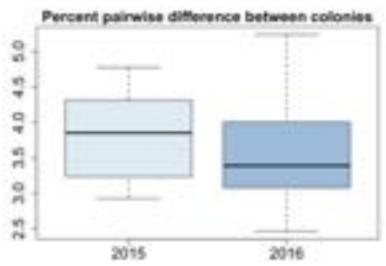


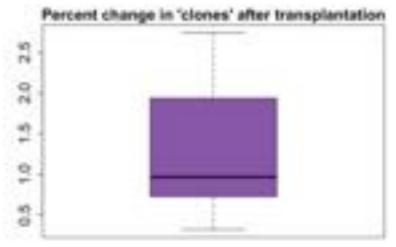


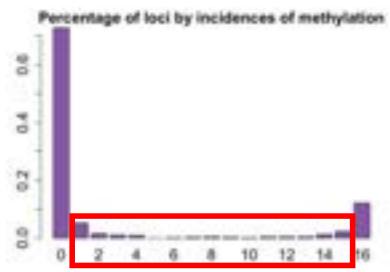












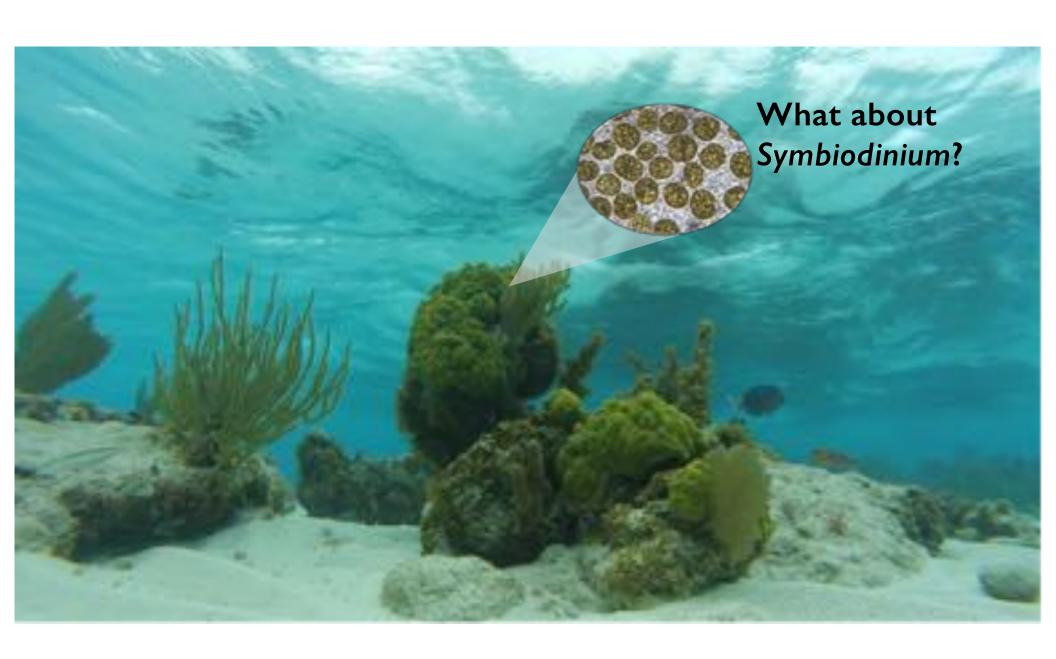


Dimond et al. (2017)

For comparison:
Porites porites complex

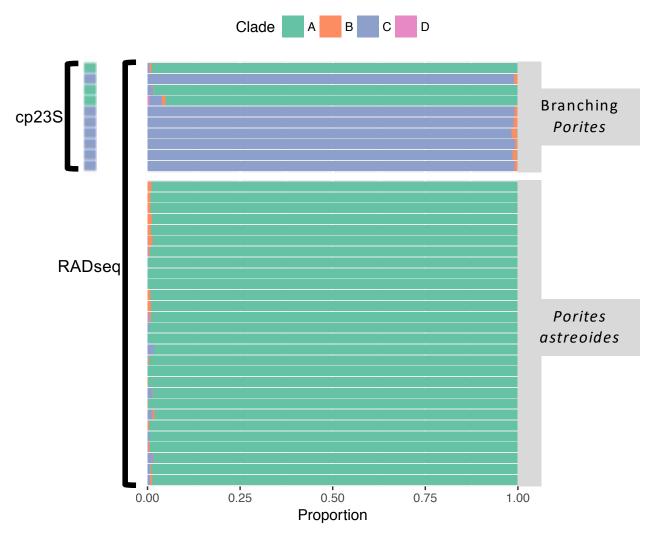
18% of CpGs methylated

15% differentially methylated among colonies (n = 27)



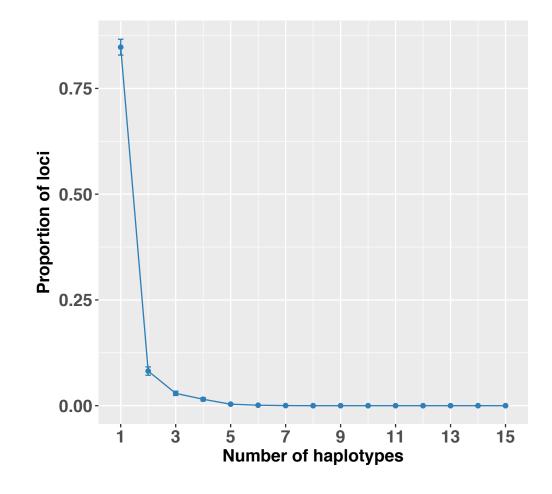
RADseq BLAST searches correctly identified symbionts at clade level

All P. astreoides hosted >98% Clade A

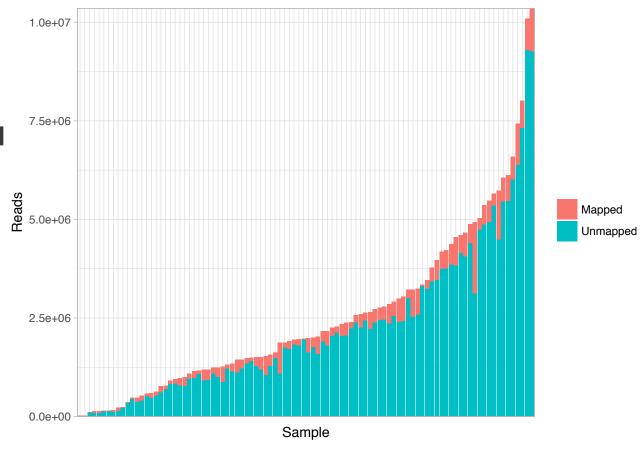


Low haplotype diversity:

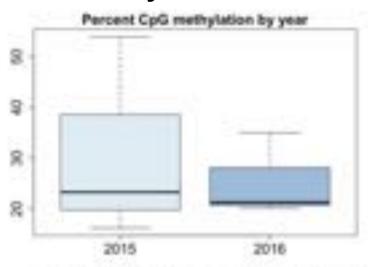
A single haplotype was observed in ~83% of RADseq loci

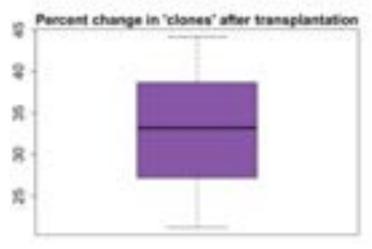


Only ~14% of loci mapped to the S. microadriaticum (Clade A) genome

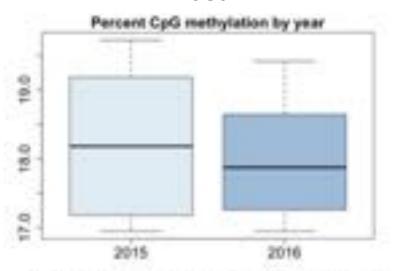


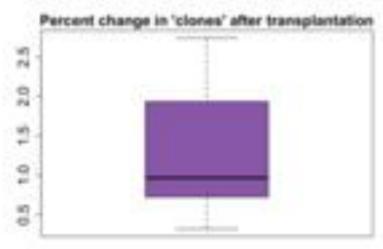
Symbiont



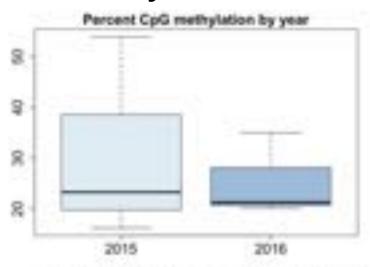


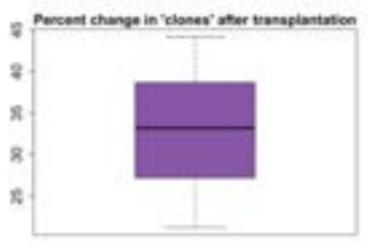
Host





Symbiont





J. Physol. 34, 152-159 (1998)

HYPERMETHYLATION AT CPG-MOTIFS IN THE DINOFLAGELLATES AMPHIDINIUM CARTERAE (DINOPHYCEAE) AND SYMBIODINIUM MICROADRIATICUM (DINOPHYCEAE): EVIDENCE FROM RESTRICTION ANALYSES, 5-AZACYTIDINE AND ETHIONINE TREATMENT¹

Michael R. ten Lohuis² and David J. Miller

Department of Biochemistry and Molecular Biology, James Cook University of North Queensland, Townwille, Queensland 4811, Australia

Plant Physiol. (1996) 117, 189-190.

Light-Regulated Transcription of Genes Encoding Peridinin Chlorophyll a Proteins and the Major Intrinsic Light-Harvesting Complex Proteins in the Dinoflagellate Amphidinium carterae Hulburt (Dinophycae)¹

Changes in Cytosine Methylation Accompany Photoadaptation

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Conclusions

Coral methylation shows limited plasticity after a year in a novel environment

- corroborates results of Dixon et al. (preprint) in GBR Acropora

Symbiont methylation appears to be more abundant and dynamic

- corroborates earlier studies by ten Lohuis & Miller (1998)

Methylation may play a relatively larger role in Symbiodinium biology

Acknowledgements

People

Lorenz Hauser

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