

# Differential transcriptional immune response in the reef building coral, Acropora millepora, to ecologically relevant bacteria

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# Abstract

Background: Disease outbreaks on coral reefs are increasing rapidly. How the coral immune system responds to disease and bacterial challenge is poorly understood. Vibrio coralliilyticus and Alteromonas sp. are two known bacterial pathogen of corals such as Acropora millepora. Here we explored the immunological response of the reef building coral A. millepora to both bacteria. Methods: A. millepora coral fragments were challenged for 48 hours with V. *corallijyticus* or *Alteromonas* sp. at a concentration of 10<sup>6</sup> CFU/ml. Total RNA was extracted from samples collected at 6 and 24h and reverse transcribed to examine gene expression by quantitative real time PCR (qPCR) of 3 putative innate immune genes: complement component 3 (C3), C-type lectin, and heat shock protein 70 (Hsp70). Denaturing gradient gel electrophoresis (DGGE) was run on the 24h samples to study changes in the coral-associated microbial community.

**Results:** After 48h, coral fragments challenged with *V. coralliilyticus* appeared healthy while fragments challenged with Alteromonas sp. showed signs of bleaching and tissue lesions. Correspondence analysis of the microbial community showed that the bacterial community associated with the coral fragments inoculated with Alteromonas sp. were different from controls and V. corallilyticus inoculated colonies. QPCR data showed a significant increase in gene expression of c3-like and hsp70 in Alteromonas sp. inoculated corals at 24h. *Hsp70* showed a significant increase in the *V. corallilyticus* treatment at 24h. *C-type lectin* did not show a response due to treatment.

**Conclusion:** *V. corallilyticus* did not cause visual signs of disease but an increase in *hsp70* expression indicates that the corals were stressed. However, treatment with Alteromonas sp. did cause signs of disease. The increase of expression of c3-like and hsp70 in these infected corals indicates their involvement in the immune response of *A.millepora*. A shift in the bacterial community associated with the diseased corals was detected suggesting that an increase in abundance of one or more opportunistic bacteria could have been the cause of the disease rather than the inoculated bacterium. Further investigation is needed in this regard.



# **Methods**

Figure1: The tank set up for the experiment. A. millepora nubbins from colony A were placed into tanks 1-3 and challenged with 10<sup>6</sup> CFU/ml of *V. coralliilyticus* while the controls were placed into tanks 4-6. Nubbins from colony B were challenged with Altermonas sp. at a concentration of 10<sup>6</sup> CFU/ml in tanks 7-9. The controls from this colony were also placed into tanks 4-6.





c-typ

Figure 2: Sampling times for the experiment as well as the temperature profile. 6 and 24h samples were assesse by QPCR. 24h samples were assessed t DGGE.

#### Results



Alteromonas sp.

Control

Figure 3: Photographs of A. millepora nubbins at the conclusion of the 48 hour experiment. V. coralliilyticus and control nubbins appear healthy while Alteromonas sp. inoculated nubbins show signs of tissue lesions (white color).



QPCR was performed using the Roto Gene SYBR Green PCR master mix (Qiagen, Valencia, CA). Primer concentration of 1µM was used for *c3-like*, hsp70, rpl12, and actin. A 0.5µM primer concentration was used for *c-type lectin*. Primer sequences for the 3 genes of interest are found below.

Sene	Primers (5' to 3')
3-like	For: GTGAAGGTGGAACCAGAGGA
	Rev: GAACCGGAAGTGATTGTCGT
pe lectin	For: CAGGTCTGGATCGGACTCAT
	Rev: CATGTCCAGTGGTTGTACGC
sp70	For: GAGCCCTCAGTAACCAGCAC
	Rev: CATTGTGGAGCGGAAAAGTT



V. coralliilyticus

**Figure 4:** Correspondence analysis (CA) of the bacterial 16s rDNA-DGGE banding pattern of the microbial community associated with the control and challenged coral nubbins 24h post inoculation. CA1 accounts for 26.9% of the variation and CA2 accounts for 20.8% of the variation. CA1 separates Alteromonas sp. inoculated nubbins

from both sets of controls as well as *V. corallilyticus* inoculated nubbins. Numbers indicate gel bands.



**Figure 5:** Relative expression of *c3-like*, *c-type lectin*, and *hsp70* in coral nubbins challenged with V. corallilyticus and Alteromonas sp. at 6 and 24h post inoculation. Lines above bars indicate significance at p<0.01 (green), p<0.05 (orange), (\*) between treatment and control. Error bars indicate standard deviation. *Alteromonas* sp. inoculated nubbins show a significant increase in expression for c3-like and hsp70. V. corallilyticus inoculated nubbins show an increase in expression for *hsp70*.

## Conclusions

- At ambient seawater temperatures and 10<sup>6</sup> CFU/ml, V. corallilyticus does not appear to cause disease wile Alteromonas sp. does.
- Increases in the transcriptional response of *hsp70* and *c3-like* in the Alteromonas sp. inoculated nubbins would indicate that a potential immune response was elicited in *A. millepora*.
- Increase in expression of *hsp70* in *V. corallilyticus* inoculated nubbins would indicate that these nubbins were under stress.
- Correspondence analysis indicates that a shift in the bacterial community occurred in the Alteromonas sp. inoculated nubbins.
- Disease signs in *A. millepora* may have been caused by an opportunistic group of bacteria as a result of the microbial community shift rather than caused directly by Alteromonas sp.

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