Next-generation marine invasion: using transcriptomics to explore adaptation in a global invader



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# ~50,000 invasive species in US

















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# \$120 billion annual cost













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primary threat to 42% of endangered species

# Invasions as natural experiments in evolution





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From R. Shine via CaneToadsinOz.com



# Invasions as natural experiments in evolution





#### From R. Shine via CaneToadsinOz.com





From Huey et al. 2000

## Traditional assumption: many marine systems are open



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From Gaither et al. 2013

# ...but the ocean is complex.



# Recent genomic work suggests local adaptation in many high-gene flow marine species

#### Atlantic herring



Lamichhaney et al. 2012

#### Red abalone



De Wit & Palumbi 2012

Purple sea urchin



Pespeni & Palumbi 2013

Atlantic cod



Nielsen et al. 2009

# What can genomics tell us about adaptation in marine invasive species?

## European green crab *Carcinus maenas*



# Global range of *C. maenas*



Range data from Carlton & Cohen 2003; Hidalgo et al. 2005; Best et al. 2009

# What can genomics tell us about adaptation in *C. maenas*?







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### Are populations locally adapted?



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### Are populations locally adapted?

### How quickly can genetic adaptation arise?



# Study region



# Invasion history



# Invasion history



#### West coast: British Columbia California

East coast: Newfoundland Maine New Jersey Europe: Norway Portugal



#### Long-term SST at study sites (25-year average: 1987 - 2011)



Data from NOAA/NWS National Centers for Environmental Prediction (Revnolds *et al.* 2002).



Are there physiological differences between populations that suggest local adaptation?



From Tepolt & Somero 2014



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From Tepolt & Somero 2014

# Heat tolerance differs between populations, suggesting local adaptation.



# South is more heat-tolerant than north in the native range



South is more heat-tolerant than north in the East Coast invasive range Break between Maine and Newfoundland



# California is idiosyncratic



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# Do the genetic data support local adaptation?

### Transcriptome sequencing (Sequence just messenger RNA)



### 1,430,000,000 raw reads (71,500,000,000 bp of data)

### Transcriptome sequencing (Sequence just messenger RNA)



### Assembled *de novo* transcriptome 116,241 contigs

# Single-Nucleotide Polymorphisms (SNPs)



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# Principal components analysis



#### Genetic structure at 10,809 SNPs in 1,673 contigs



#### All clusters significantly differentiated (p < 0.0001)



# Genetic structure at all loci



#### Genetic diversity shows serial bottlenecking Loss of diversity with each introduction



# Genetic differentiation between sites



# Genetic differentiation between sites corresponding to differences in heat tolerance



Field sites that differ in heat tolerance are also genetically different, supporting local adaptation.

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# Do differences between populations appear driven by selection?

# Outlier analysis to identify selected SNPs



# Distribution of population differentiation at all 10,809 SNPs



# Identification of neutral SNPs



# Genetic structure: all loci vs neutral loci



# Genetic structure: all loci vs neutral loci



# Selection appears strongest in native range



Differences between populations are driven in part by selection, which is strongest in the native range. What can *C. maenas* tell us about adaptation in marine systems?

Are populations locally adapted? Physiology and genetics both suggest local adaptation



What can *C. maenas* tell us about adaptation in marine systems?

Are populations locally adapted? Physiology and genetics both suggest local adaptation

How quickly can genetic adaptation arise? As little as 25 years, but much stronger in native range.



Pre-adaptation in native range

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Capacity for rapid adaptation in invasive range

Pre-adaptation in native range

Capacity for rapid adaptation in invasive range

Adaptation is important, even in high-dispersal marine systems.

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# Mille grazie!



# The Gherardi family

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