

Marine Biotechnology and Bioinformatics

for Teachers

Project Background: The Science



Tracking an invasive species

The Marine Biotechnology and Bioinformatics for Teachers workshop centers around a real-life scientific question:

Is the invasive mussel, *Mytilus galloprovincialis*, displacing the native mussel, *Mytilusrossulus*, in Monterey Bay?

To answer this question, we track the number of native and invasive species at the same location over time.

What are invasive species?

Invasive species are organisms with two key characteristics: They are introduced into an environment in which they did not evolve, and they significantly out-compete native species.



European green crab

European oyster mussel

Asian sea star

Why study invasive species?

Many sectors of society are impacted by invasive species:

Ecological impacts. Invasive species can alter the relationships of native species, and displace previously abundant organisms. As a result, they are the largest threat to biodiversity after habitat loss.

Economic impacts. In the U.S. the cost of damage and control of invasive species accounts for more than \$138 billion each year (Pimentel et al. 2005). This price tag does not include the costs associated with species extinction and loss of ecosystem services.

Human health impacts. Introduced species can act as vectors, spreading diseases that affect human health.

What can we learn by tracking an invasive species?

Tracking an invasive species over space or time yields data that scientists use to address why some organisms are successful invaders. Policymakers can use this data to make informed decisions relevant to natural resource management.

Why use Biotechnology and Bioinformatics?

To answer our question, we need to be able to do one thing: identify different mussel species. This would be an easy task if the mussels were morphologically distinct. However, the two mussels are cryptic species, which means they look so much alike, we need to use genetic tools to tell them apart.

What we did

Three components are necessary to generate our data:



Field Work

We collect mussels using random sampling to ensure that they represent the local population.

Biotechnology

We isolate DNA from cells and copy important genes. We must make millions of copies of each gene in order to determine DNA differences. Differences can be seen as bands on a gel or as actual DNA sequence.



Bioinformatics

We compare our gene sequences to others in an online DNA database. Organisms that are the same species will have more similar sequences.

Redundancy yields solid results

An interesting aspect of mussel identification is that the two species under investigation are capable of interbreeding. The result is a hybrid mussel with genes from both species. This means that multiple genes must be analyzed to correctly identify each mussel as native, invader, or hybrid.

Gel photograph identifying different mussel species

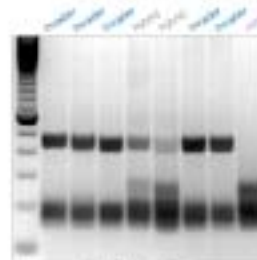


Photo credit: Loren Dittel

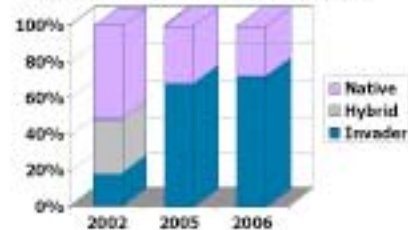
What we've learned so far

Over the past two summers, workshop participants have...

- Identified 50 mussels
- Generated 15 unique DNA sequences

By adding this data to what we already know, we've learned that the invader, *M. galloprovincialis*, is displacing the native, *M.rossulus*, in Monterey Bay.

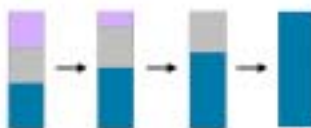
Proportion of mussel types in Monterey Bay, 2002-2006



2002 Data Source: Stealy & Barnes, 2008

Conclusions

Our data indicate that the invasive mussel is displacing the native. If this trend continues, the native mussel species will disappear from Monterey Bay as it has from southern California. The remaining mussels will have very limited genetic diversity due to the small gene pool from which the invasive population originated.

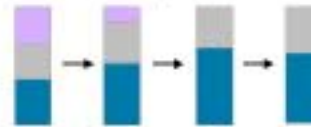


■ Native ■ Hybrid ■ Invader

What about the hybrids?

Although it is clear that invasive mussels are displacing the natives, the stability of hybrid mussels within Monterey Bay populations is not as apparent. If hybrids do maintain their presence in local populations, then the native mussel's genetic information will be retained in the gene pool. This will increase the genetic diversity of local mussel populations, and have a direct effect on the ability of Monterey Bay mussels to adapt to changing environmental conditions, such as those associated with global climate change.

Future workshops will enable us to gather more data, which are necessary to determine which of these outcomes is most likely.



■ Native ■ Hybrid ■ Invader

References

- Waltz & Stealy (2008) Marine Biology, 143: 1208-1202
- Pimentel et al. (2005) *Ecology of Invasions* 12: 274-289
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