

Assessment of Genetic Diversity
and Connectivity in Fish
Replenishment Areas in the
Hawaiian Yellow Tang
(*Zebrasoma flavescens*).



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Why Yellow Tangs?

Roughly 76% of fish collected from island of Hawai`i for aquarium trade are yellow tangs.

Density in 1999 was about 43% lower in collection areas versus protected areas. Concern for sustainability of the fishery.

Ongoing WHAP research indicates recruitment of tangs into FRAs is beginning to increase in the absence of collection pressure.

Z. flavescens represents a convenient indicator species.

Recruitment Processes & Genetics

Z. flavescens exhibits a pelagic larval stage that can potentially interconnect populations by oceanic currents.

Two recruitment ideas

1. Pelagic larvae drifting at sea may mix populations to an extent that all sample groups look genetically very similar.
2. Mezo-currents, seasonal winds, and larval behaviour proposed as possible mechanisms that may restrict extent of mixing between sub-populations of fish.

Recruitment Processes & Genetics

Z. flavescens exhibits a pelagic larval stage that can potentially interconnect populations by oceanic currents.

Two possibilities

1. Possible that just a few major breeding areas (sources) are responsible for eventual recruitment of tangs into many different coastal ecosystems on a random basis.



Little genetic diversity between sub-populations.

Recruitment Processes & Genetics

Z. Flavescens exhibits a pelagic larval stage that can potentially interconnect populations by oceanic currents.

Two possibilities

Greater genetic diversity between sub-populations.

2. Localised currents and larval behaviour proposed as possible mechanisms that may restrict extent of mixing between sub-populations of fish.

Recruitment Processes & Genetics

Z. Flavescens exhibits a pelagic larval stage that can potentially interconnect populations by oceanic currents.

Two possibilities

Greater genetic diversity between sub-populations.

Management/
sustainability

2. Localised currents and larval behaviour proposed as possible mechanisms that may restrict extent of mixing between sub-populations of fish.

Project rationale

To investigate the usefulness of molecular genetic markers as a tool for fisheries management.

To establish and adopt molecular genetic techniques as a leading edge technology.

To provide a tool (and resources) that is adaptable to other species (eg. More ecologically important rather than commercially important). Could also be adapted to conservation management of delicate or endangered species.

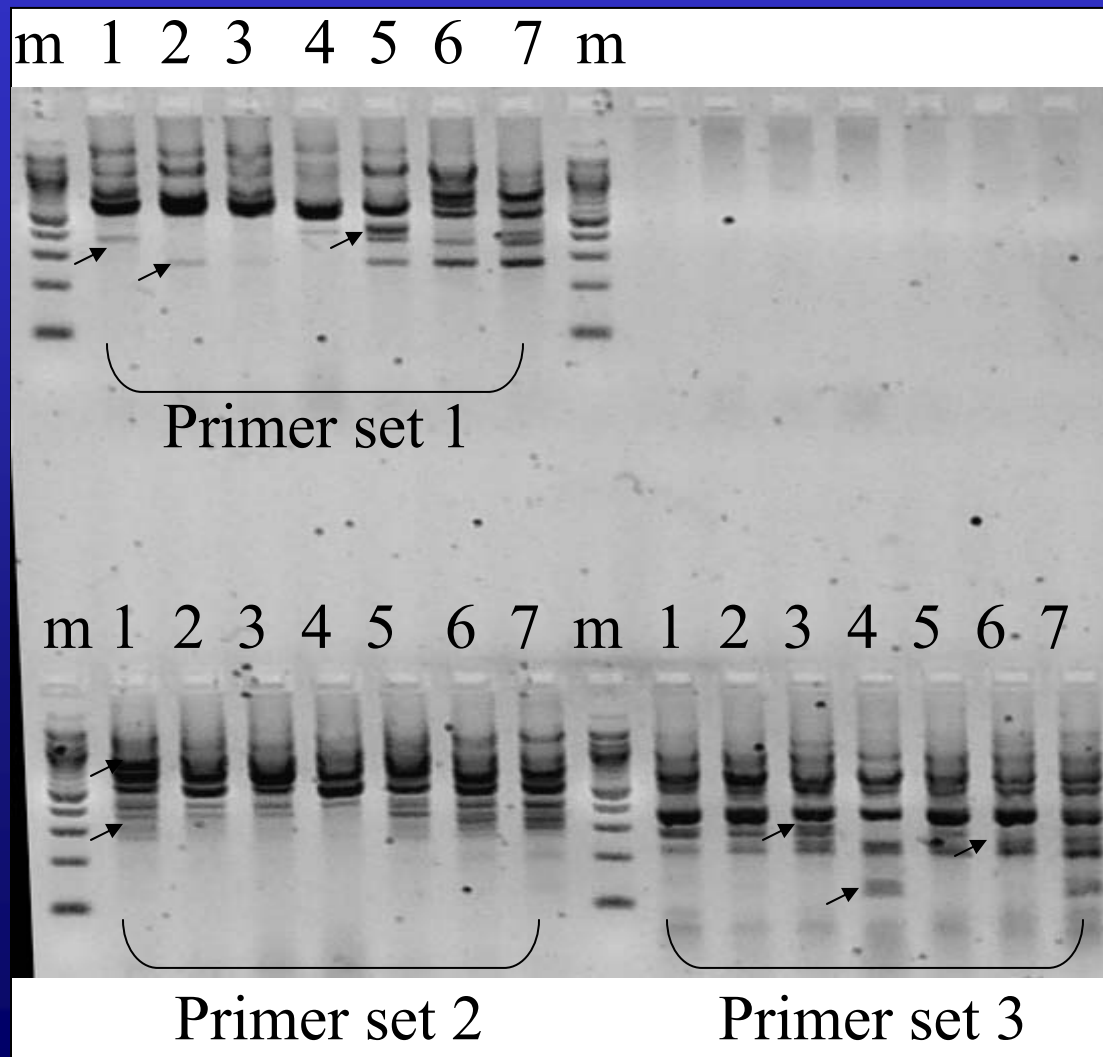
Current genetic knowledge in *Z. flavescens*

Previously published data: a region of mitochondrial DNA known as D-loop was sequenced in a small number of individuals (<30). Little variation found!

Our feasibility trial: Randomly Amplified Polymorphic DNA (RAPD) technique indicated differences between individuals from 7 collection sites along the west coast of Hawai`i.

Microsatellites are a more powerful and useful molecular tool than either mtDNA sequencing or RAPDs (but more expensive to set up) for assessment of genetic diversity. There is presently no microsatellite data for *Z. flavescens*!

Trial RSCA using 3 different primer combinations shows that variation exists between individuals taken from 7 collection sites on west coast of Hawai`i.



- 1 = Ka'u
- 2 = Ke'ei
- 3 = Honokohau
- 4 = Makalawena
- 5 = Puako
- 6 = Keauhou
- 7 = Lepakahi

m = DNA reference marker

Arrows indicate unique bands = genetic variation

Project objectives

To investigate genetic diversity in yellow tangs, along the west coast of Hawai`i, between leeward and windward sides of Hawai`i, and (if possible) between Hawai`i and O`ahu.

To investigate and establish microsatellite markers as a tool for fisheries monitoring and management in Hawai`i.

To provide resources for future research.

Project directions

1. Microsatellite library construction and marker development.
2. Extraction of DNA from (~500) samples previously collected (much larger sample set than any previous study in this species = more meaningful results).
3. Assess samples with markers.
4. Examine genetic variability (statistical analysis and population genetics – computer aided analysis).

Present status of our investigation

DNA already extracted from 50 individuals for pilot RSCA.

DNA sent to Genetic Identification Services (GIS) in California for microsatellite library construction.

(Status – should be completed by Jan 30th, followed by marker development expected by mid-Feb).

Previously collected samples (thanks Jeff Eble & Bill Walsh) are being sent to WSU Vancouver for DNA extraction, ready for genetic marker assessment.

Many thanks to Dr Bill Walsh for presenting
this material.

Glad to answer any outstanding questions
regarding molecular research.

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