Hybridization in the California tiger salamander: Geography, ecology, and management

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Outline

- Current ideas on hybrid distribution
- Ecological impacts
- How to move forward

Genomics:

1) Genomics is a discipline in genetics that applies recombinant DNA, DNA sequencing methods, and bioinformatics to sequence, assemble, and analyze the function and structure of genomes (the complete set of DNA within a single cell of an organism). *Wikipedia*

2) Collecting a lot of sequence data for an organism or study (100's to 10,000,000's of markers).

The TIGER of vernal pools (*Ambystoma californiense*

Two species of tiger salamander in the Western US

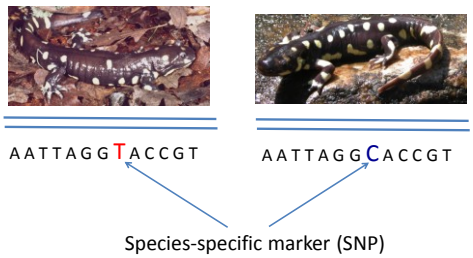
Hybridization

Hybridization with an introduced species.

This is a huge conservation concern for California Tiger Salamander (CTS).

Its an equally huge opportunity for speciation studies.

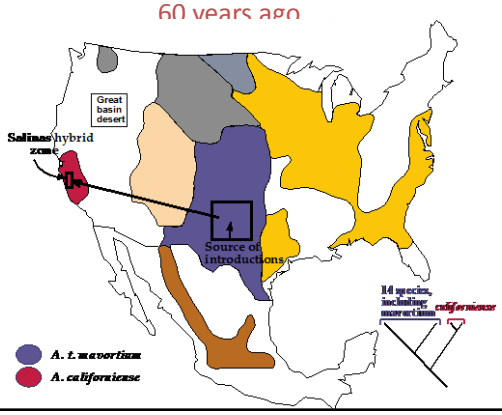
How we study hybrids with DNA



Dynamics of DNA

Potential Haplotypes	Fitness	Outcome
a. Introduced SI — 1 — DI	Good	Allele 1 should increase in frequency until recombination
b. Native DN — 2 — SN	Bad	Allele 2 should decrease in frequency until recombination
c. "Super" Recombinant SI — 2 — SN	Best	Allele 2 should become fixed
d. Deleterious Recombinant DN — 1 — DI	Worst	Allele 1 should go extinct

60 years ago



Waterdogs

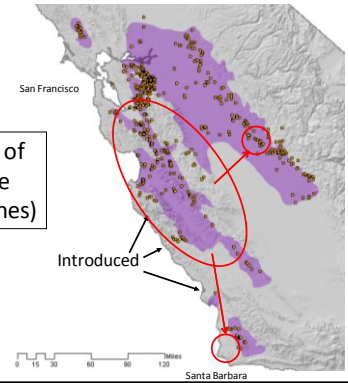
"... 8- to 10-inch long salamanders are preferred by most trophy bass specialists."

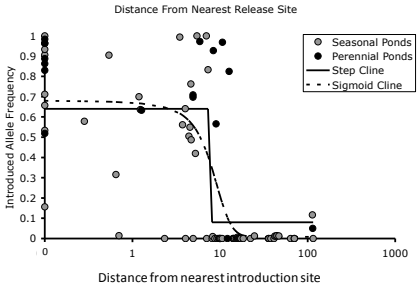
photo by Larry Larsen

Recent ~10-20 salamander generations old

Where are introduced genes?

About 1/3 of the entire range (8 genes)

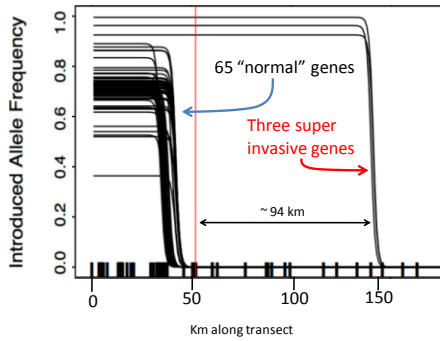




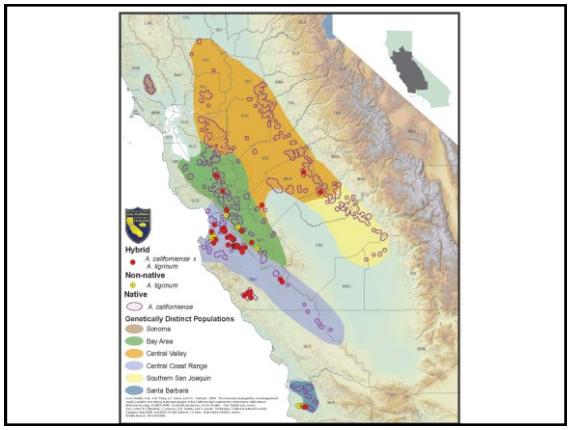
Introduction front moving ~ 1 km/generation (8-10 markers)

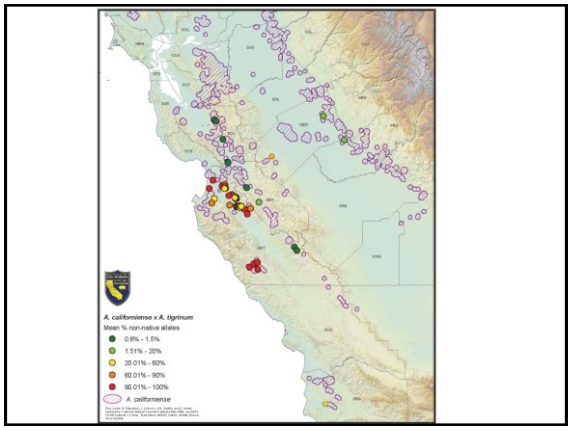
Fitzpatrick & Shaffer 2007 Ecological Applications

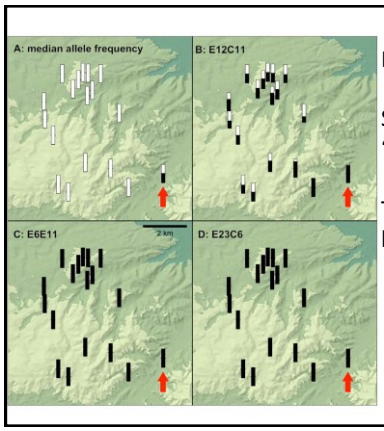
62 ponds, 68 genes



Fitzpatrick et al., 2010 PNAS







Ft. Ord, 2009

Superinvasive vs "normal" genes.

This year, it may have changed.

Now what?

-Go genomic- 8500 markers, scored for ~1000 salamanders from the mid-1980's, early 2000's, and now.

-How much and at what rate have genes moved across the landscape?

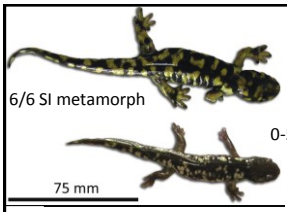
Does it matter?

Two approaches

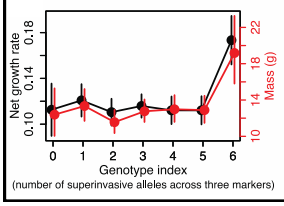
Hybrid swarm, mesocosm

A: largest native B: smallest native C: smallest contemporary hybrid D: largest contemporary hybrid E: *Taricha torosa* larva E: *Pseudacris regilla* larva

Ryan et al. 2009 PNAS



SI genes, laboratory



Data from the lab

Genetic background is 25% - 75% non-native

Huge effect!

Community ecological approach

Replicated mesocosm communities

What are the larval impacts of
- -Superinvasive alleles
- -Hybrid swarm
- -No tiger salamander

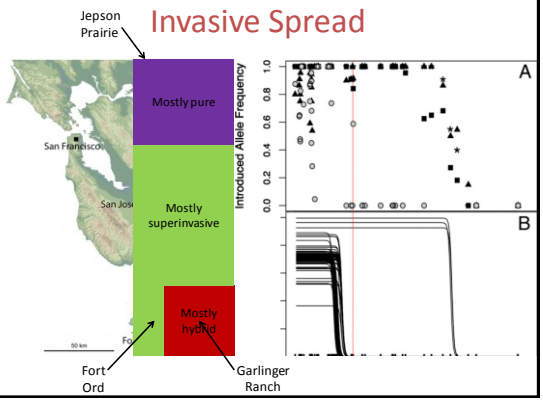
Compared to Pure CTS?

Our Approach: Ecological Equivalency

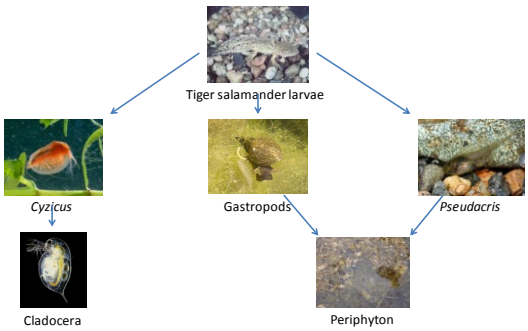
- Mesocosm experiment (4 x 2 factorial)
- Treatments: larval genotype, larval density
- 4 levels of larval genotype:
  - pure CTS
  - superinvasive
  - full hybrid
  - no tiger salamander
- 2 levels of larval density:
  - 4 larvae per tank
  - 8 larvae per tank
- 5 replicates of each – 40 cattle tanks total

Searcy, C. A., H. B. Rollins, and H. B. Shaffer Submitted, Ecological equivalency of endangered and invasive tiger salamanders.

Invasive Spread

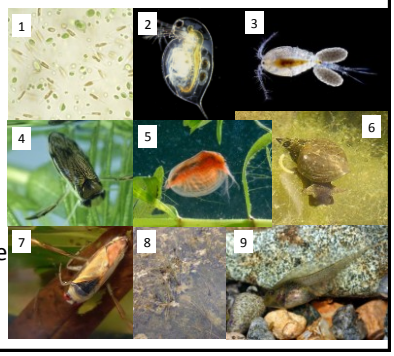


Food Web

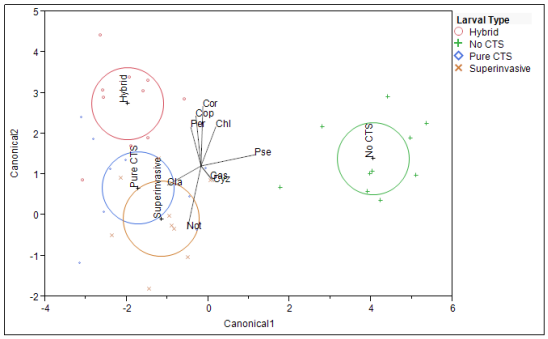


Community Metrics

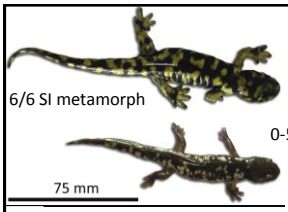
Densities of:
1) Chlorophyll
2) Cladocera
3) Copepoda
4) Corixidae
5) *Cyzicus*
6) Gastropoda
7) Notonectidae
8) Periphyton
9) *Pseudacris*

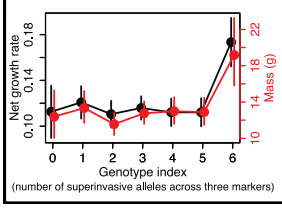


Community Composition



SI genes, laboratory





Data from the lab

Genetic background is 25% - 75% non-native

Huge effect!

Conclusions

1) CTS & SI virtually identical

2) CTS and hybrid swarm definitely different

3) No tiger salamanders the largest effect (by far)

Management thoughts

-All ponds locally the same
-We know CTS move a lot
-So, locally, manage for connectivity
-Throughout, manage hydroperiod

Some key references

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