

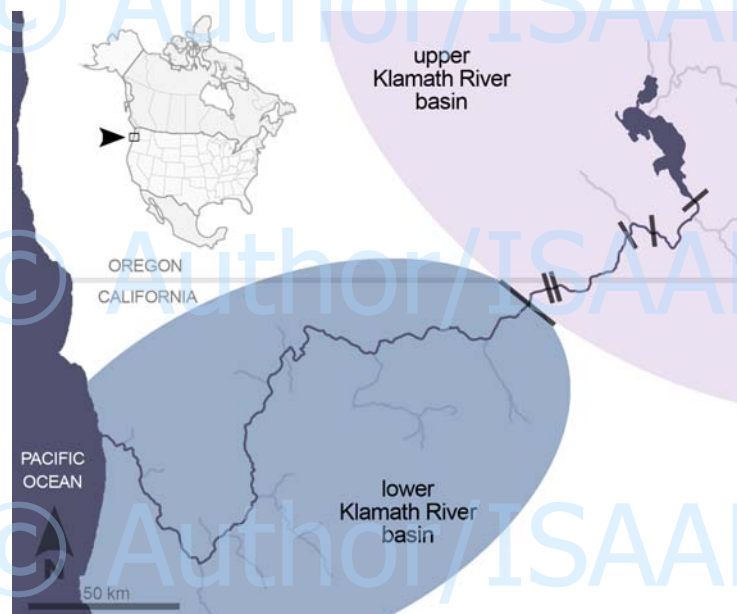
Spatial, temporal and host factors  
structure the *Ceratomyxa shasta* population  
in the Klamath River basin.

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Project funded by the Bureau of Reclamation

Klamath River Basin



## *Ceratomyxa shasta* - 2 monitoring approaches

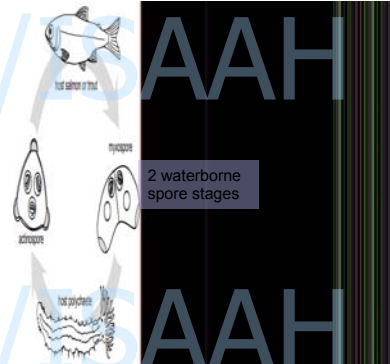
### Water samples

3 x 1L, filtered @5 $\mu$ m, qPCR  
= total abundance

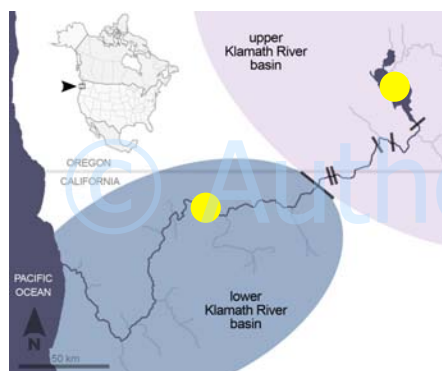
### Sentinel fish

different salmonid species/strains  
4 d in cages in river, monitored 60-90d in lab  
= presence/absence/dose/host factors

Results of 2 studies presented today



## Study 1: 2 sites, 2 fish species

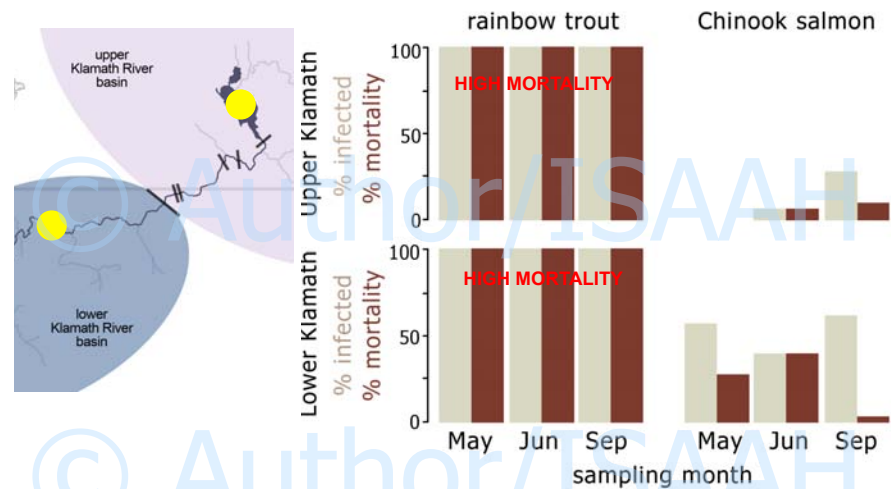


Upper vs Lower basin sites  
similar parasite abundance (water)

non-native rainbow trout  
= presence/absence

native Chinook salmon  
= gauge impact on wild populations

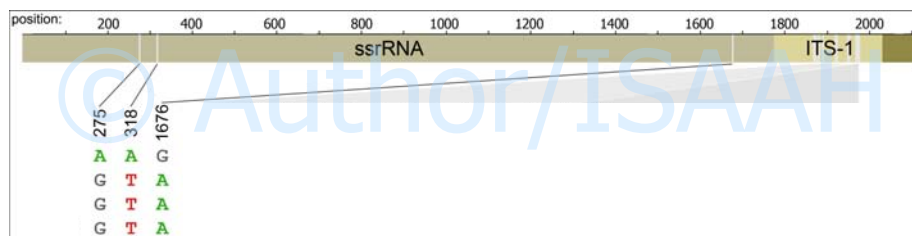
## Result: different infection patterns



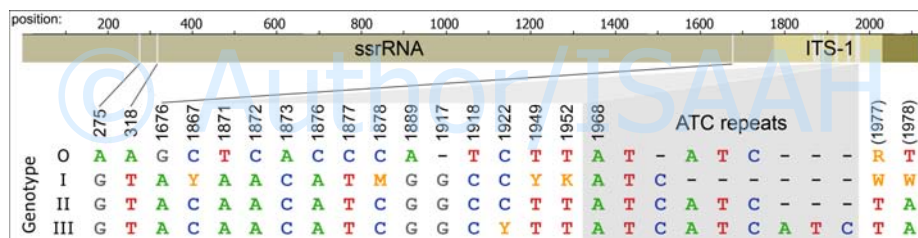
## Different parasite genetics?

examine ssrRNA & ITS-1 loci

determine genetic types ("genotypes")

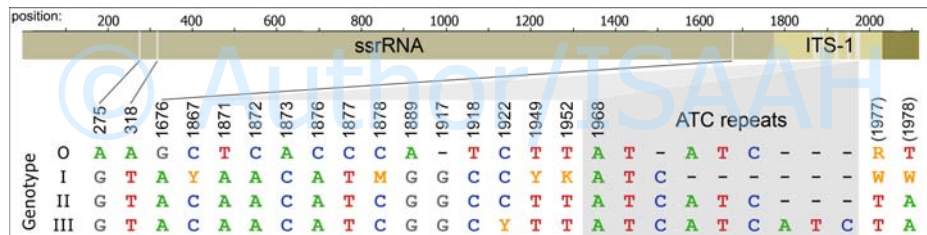


@ ssrRNA only low-level variation = intraspecific



## Different parasite genetics?

@ ITS-1 locus = more variation



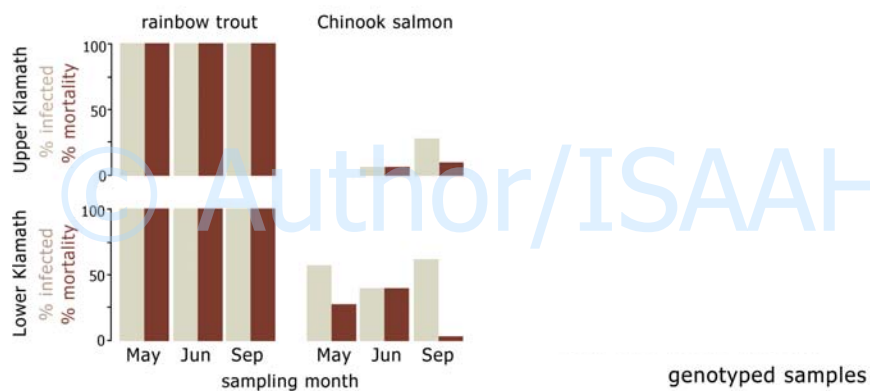
4 primary genotypes

O I II III

## Host infection versus parasite genotype

infection data

genetic data



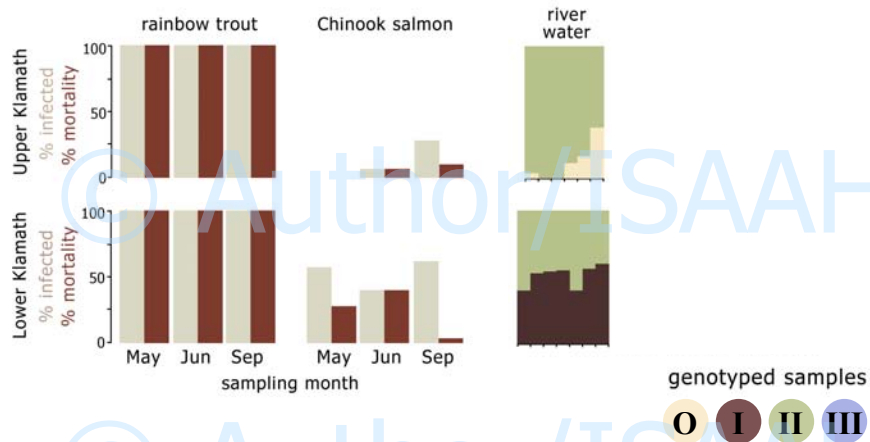
genotyped samples

O I II III

## Host infection versus parasite genotype

infection data

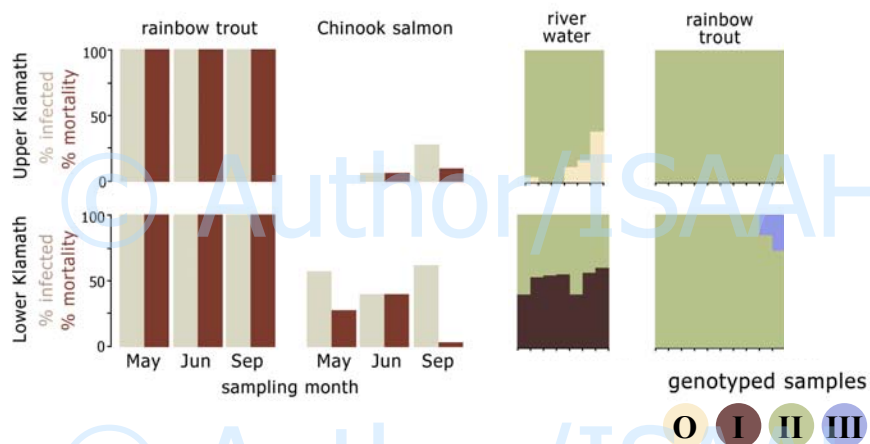
genetic data



## Host infection versus parasite genotype

infection data

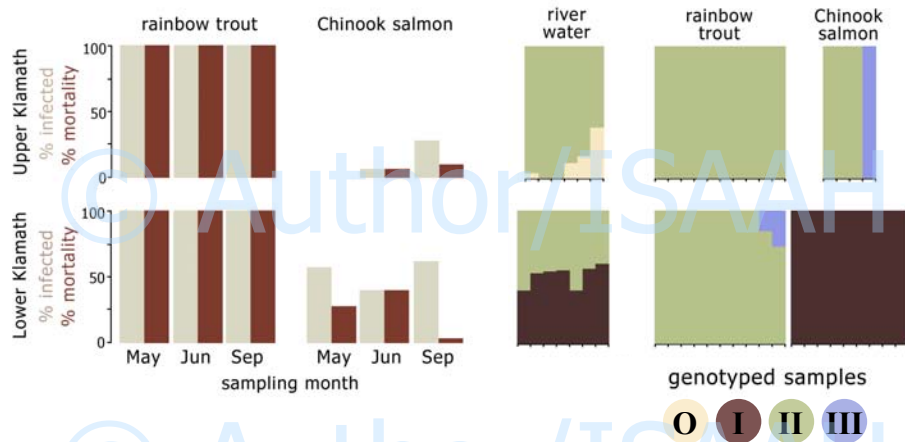
genetic data



## Host infection versus parasite genotype

infection data

genetic data



Atkinson & Bartholomew (2010)  
International Journal for Parasitology

## Study 2: Is there a correlation between parasite genotype and other salmonid hosts?

Compare 3 sites, 3 months

Native anadromous fish

Coho salmon

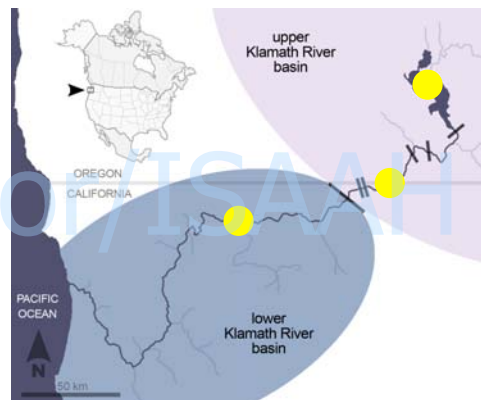
steelhead trout

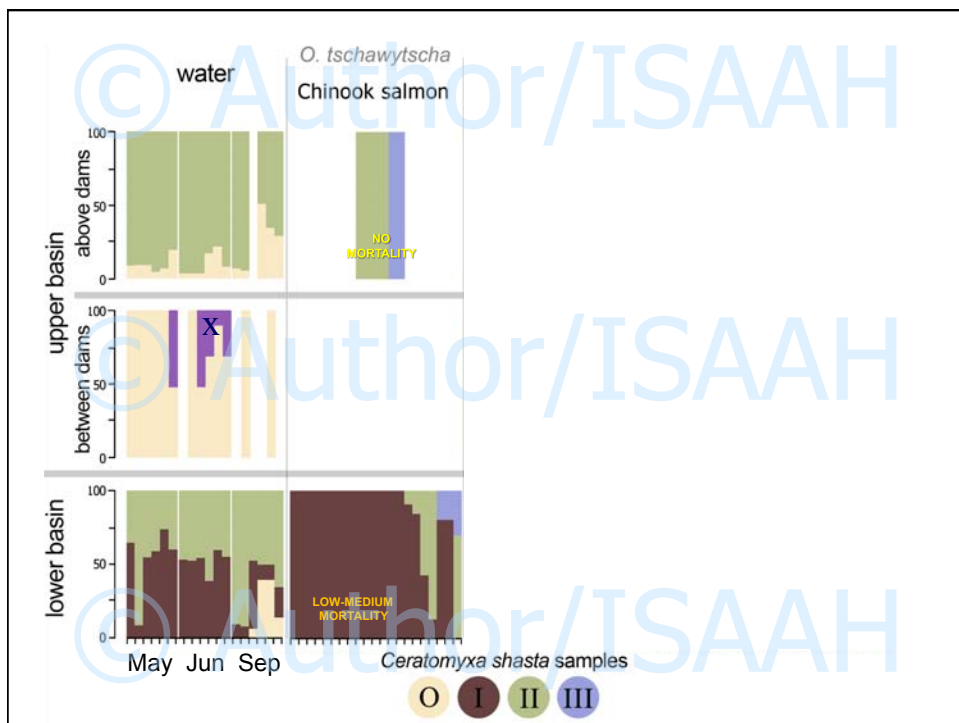
Chinook

Native resident fish

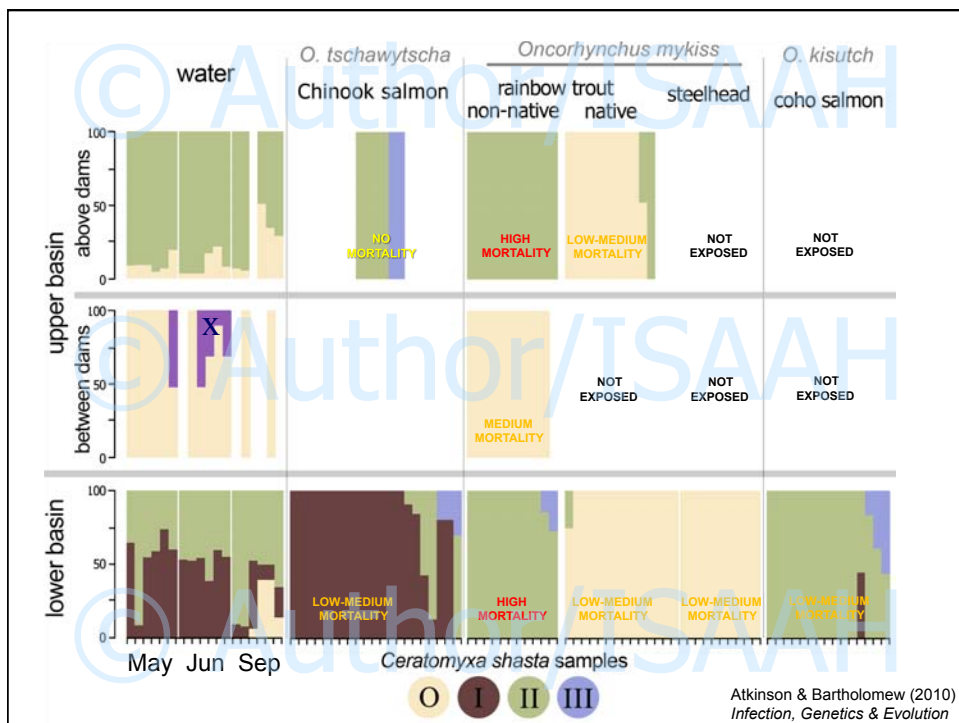
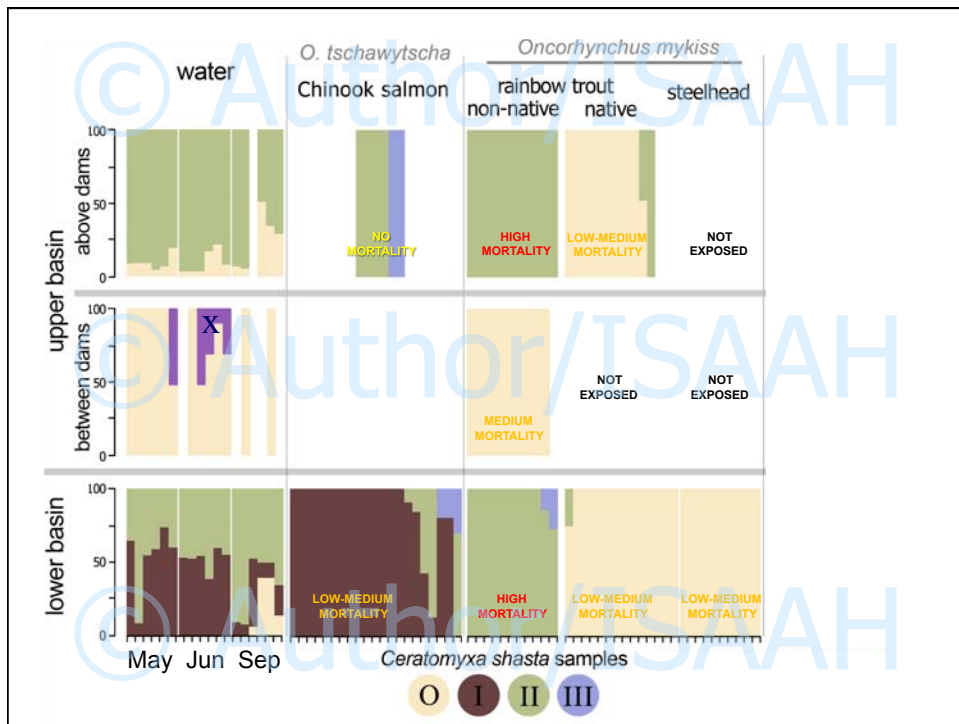
redband rainbow trout

Non-native rainbow trout









Atkinson & Bartholomew (2010)  
Infection, Genetics & Evolution

## Summary - *C. shasta* population has structure

4 primary ITS-1 genotypes

Distinct host preferences & virulence differences

Genotype O - throughout system, host = all *O. mykiss*, low virulence?

Genotype I - lower basin, Chinook, moderate virulence

Genotype II - upper & lower basin, coho (moderate virulence)  
non-native rainbow (high virulence)

Genotype III - throughout system, all species, low/no virulence?

Mid-basin "genotype X" - spore morphology? fish host?

Ongoing research - Matt Stinson, Charlene Hurst