Connecting managed river conditions with salmon disease/pathogens in the **Central Valley**

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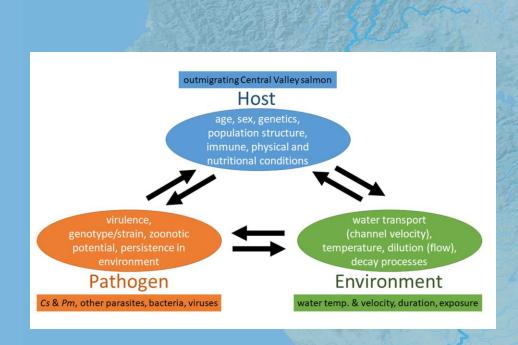


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Big Picture

Our goal is to fill gaps of how exposure to pathogens and interacting stressors affect outmigration survival of Chinook salmon

We are doing this by monitoring salmon pathogens and developing a disease transmission model



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Summary of project objective

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Main Objectives

1) Screen environment for pathogens

1) Screen fish for pathogens

- 1) Build a model to simulate pathogen exposure and health outcome
- Use the above to better understand the connection to management



Screening Environment (water)

Samples collected bi-weekly

• Screen for:

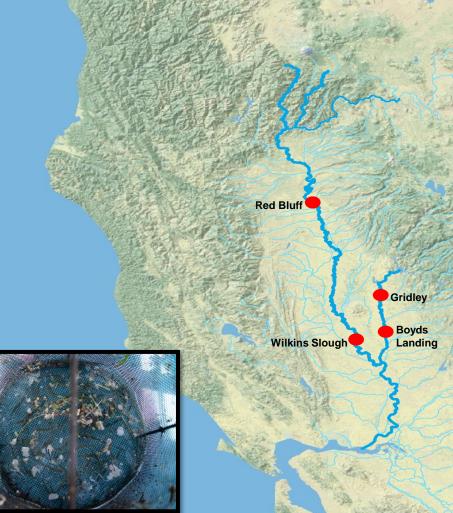
- C. shasta *Known pathogen of concern
- eDNA panel 36 pathogens





Screening Environment (sentinel fish)

- Hatchery fall-run exposed to ambient river conditions
- Tissue sampled
 - gill, kidney, intestine
- Screened for same pathogens as water



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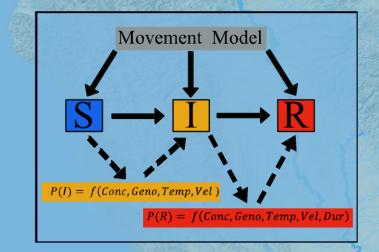
Screening Wild Salmon (rotary-screw trap samples)

- 80 outmigrating winter run sampled
- Gill tissue processed for pathogens
- Additional tissues processed via histology



Disease Transmission Model

Link a movement and exposure model to simulate prevalence and probability of mortality associated with C. shasta exposure



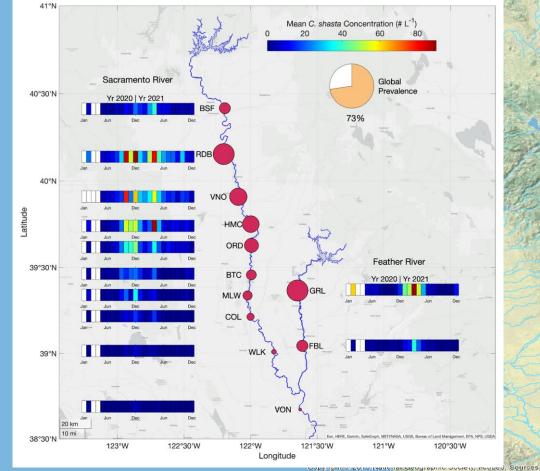
*Note methods can be applied to other pathogens of concern.

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Results



Screening Environment (C. shasta water)



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Screening Environment (additional pathogens)

Ichthyophthirius multifiliis	_
Ceratonova shasta	
Dermocystidium salmonis	
Parvicapsula minibicornis	
Yersinia ruckeri	
Rickettsia-like organism	
Aeromonas hydrophila	
Piscirickettsia salmonis	
Gill chlamydia	
Sphaerothecum destructuens	
Tetracapsuloides bryosalmonae	
Kudoa thyrsites	
Parvicapsula pseudobranchicola	-
Candidatus Branchiomonas cisticola	
Renibacterium salmoninarum	
Loma salmonae -	
Spironucleus salmonicida	
Parvicapsula kabatai	
Paranucleospora theridion	
Nucleospora salmonis	
Neoparamoeba perurans	
Myxobolus insidiosus	
Myxobolus cerebralis	
Myxobolus arcticus	
Ichthyophonus hoferi	
Gyrodactylus salaris	
Facilispora margolisi	
Cryptobia salmositica	
Nanophyetus salmincola	
Vibrio salmonicida	
Vibrio anguillarum	
Tenacibaculum maritimum	
Piscichlamydia salmonis	
Moritella viscosa	
Flavobacterium psychrophilum	
Aeromonas salmonicida	
	0 0.2 0.4 0.6 0.8
	Scaled Relative Abundacne (%)

*Note: relative abundance does not account for differecnes between single and multi-cellular organisms (i.e., bacteria vs protozoa) and molecular amplification

Esri, USGS, NOAA

Screening Environment (sentinel fish)

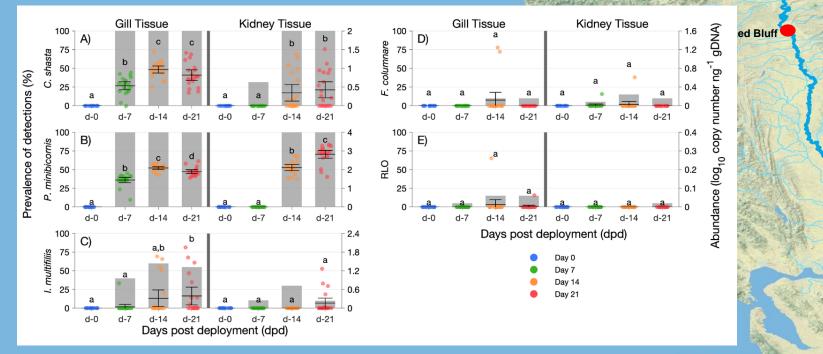


10.1093/conphys/coad066



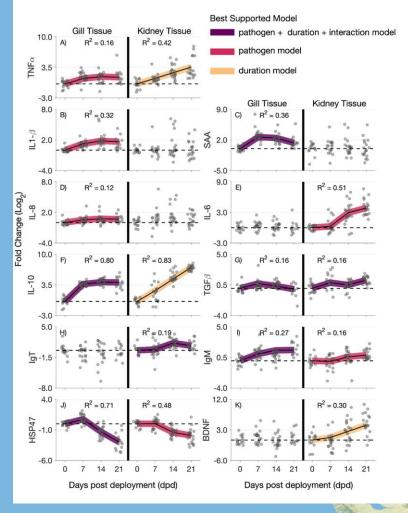
Research article

Responses to pathogen exposure in sentinel juvenile fall-run Chinook salmon in the Sacramento River, CA



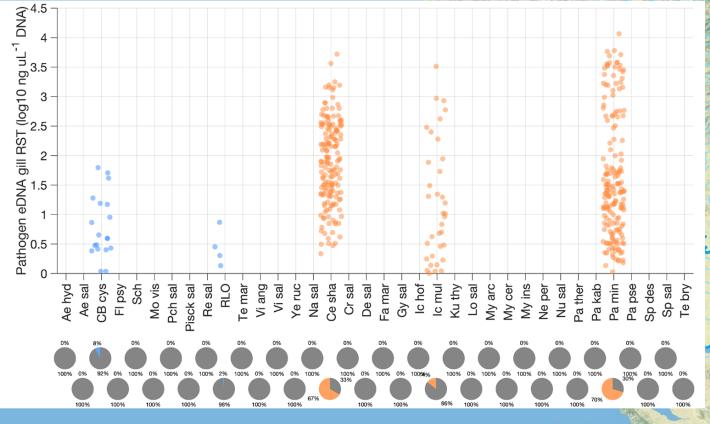
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Screening Environment (sentinel fish)



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Screening Wild Salmon (rotary-screw trap samples)

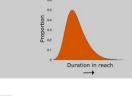


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Integrating data and disease transmission model

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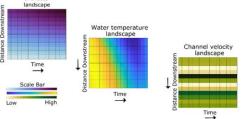
Outline of models to estimate C. shasta infection and mortality



C. shasta

C

in wat



Viability

Genotypes infectious to Chinook Spore Stage (%)

> C* = exposure concentration Du = exposure duration Te = exposure temperature Ve = exposure velocity

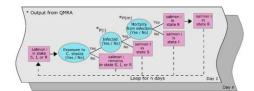
(A) Movement Model: Based on empirical tagging studies to estimate outmigrating timing

(B) Exposure Model:

Based on empirical water samples and hydraulic and water temperature models to estimate spatially and temporally explicit exposure

(C) QMRA Model:

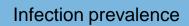
Based on A and B models and used to estimate probability of infection and mortality for individuals

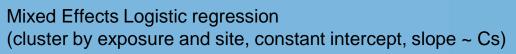


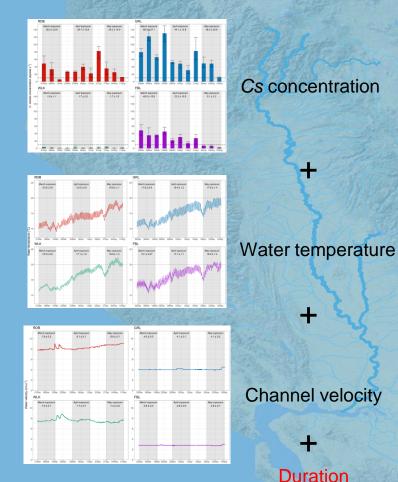
(D) SIR Model:

Based on A, B, and C models and used to estimate probability of infection and mortality for population

Dose-Response Model







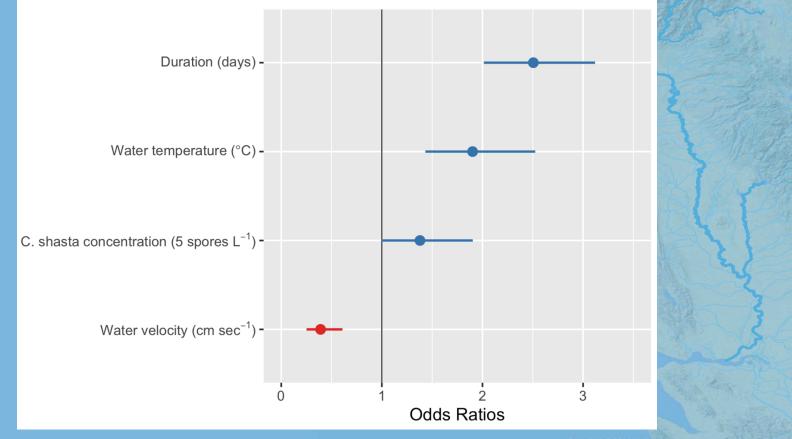
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Infection model skill

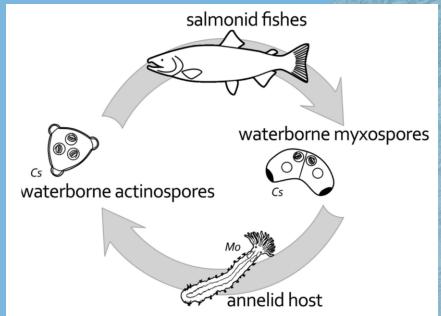
RDB GRL 100 99 100 100 100 100 100 100 100 100 100 100 100 100 100 93 92 87 87 80 80 60 60 40 Prevelence of C. shasta in intestine tissues (%) 40 20 20 13 12 1 1 0 0 0 0 0 0 0 0 0 0 March March March April April Day 7 May May May Day 0 Day 7 Day 14 Hatchery March March March April Day 0 Hatchery April Day 7 April May May May Day7 Day14 April Day 7 Day 14 Day 0 Hatchery Day 14 Day 0 Hatchery Day 7 Day 14 Day 14 Day 0 Hatchery Day 0 Hatchery FBL WLK 100 98 100 100 100 100 100 97 100 100 99 100 100 95 93 93 84 80 80 80 60 60 44 40 40 40 20 20 20. a 0 0 0 0 0 Ω 0 March March Day 14 April Day 0 Hatchery May May Day 7 Day 14 March March March Day 7 Day 14 April Day 0 Hatchery April May Day 14 Day 0 May Day 7 March April Day 7 April Day 14 May April Day 7 May Day 14 Day 0 Day 7 Day 0 Hatchery Day 0 Hatchery Hatchery Hatchery

Prediction

Infection model inference

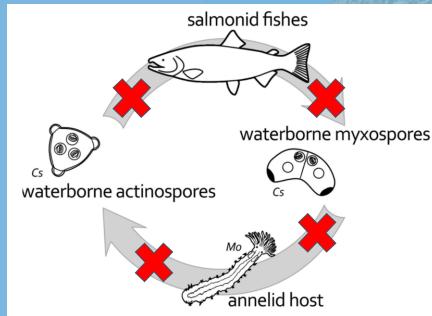


Ongoing Research for Central Valley



Better understand pathogen lifecycle dynamics and relation to water management

Ongoing Research for Central Valley



Better understand pathogen lifecycle dynamics and relation to water management

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Conclusions

- Multiple lines of evidence (water, sentinel, RSTs) point to consistent detection of some pathogens
- Gene expression and histology indicates host response
- Understating ultimate fate of infection and side effect is critical in relation to management knobs

Investigators & Collaborators:

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and others...

Thanks for listening!

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