



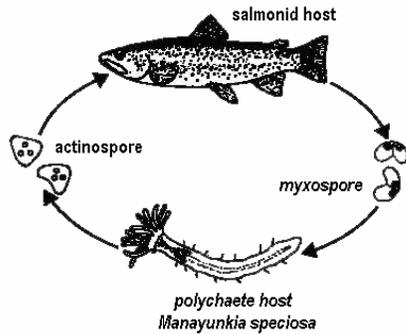
## Cross Channel and Vertical Distribution of *Ceratomyxa shasta* Spores in Klamath River Drift

**The Issue:** Recent studies have documented significant mortality in juvenile salmon and steelhead populations in the Klamath River due to infectious disease, primarily caused by the endemic parasites *Ceratomyxa shasta* and *Parvicapsula minibicornis*. In 2004, infection rates in juvenile Chinook salmon ranged from about 20 to 70% for *C. shasta* and from 40% to 96% for *P. minibicornis*. In 2005, dual infection rates at or near 100% were observed for consecutive weeks in April, a critical period for outmigration of juvenile anadromous fishes.

The life cycles of *C. shasta* and *P. minibicornis* are complex, requiring both a vertebrate and invertebrate host to complete their development. The invertebrate host for *C. shasta* is a freshwater polychaete worm *Manayunkia speciosa*. Fish are infected with *C. shasta* by contacting actinospores produced within *Manayunkia*. The form of contact is unclear, but is thought to be by random encounter with spores in the drift. Following mortality of infected fish, myxospores are released into the water where they enter the drift. Drifting spores are available to polychaetes, which as filter feeding organisms, may collect and ingest the myxospores, thereby completing the life cycle. New information also suggests that the invertebrate host for *P. minibicornis* may also be *Manayunkia*.



**Klamath River Chinook salmon exhibiting a swollen abdomen**



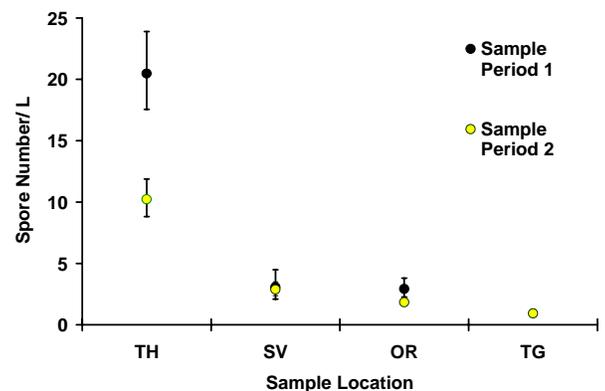
**Recent Advances in Technology:** Quantitative polymerase chain reaction (QPCR) assays now allow researchers to quantify volumetric densities of *C. shasta* and *P. minibicornis* spores from water samples collected in the field. This technique is being used to index spatial and temporal trends of *C. shasta* and *P. minibicornis* abundance in the Klamath River. Monitoring spore densities may be useful in assessing the effectiveness of flow prescriptions or other management actions directed at decreasing infection rates in juvenile fishes. Before a large-scale spore monitoring program is implemented, a thorough understanding of the variability of spore densities in the drift is needed. These data are critical in designing an effective sampling protocol as it is currently unknown if a single sample is representative of the overall drift.

### Objectives

- Test the hypothesis - Ho: Densities of *C. shasta* spores in the mid-water column drift do not differ across the channel of riffle or riffle/run transitional habitats in the Klamath River.
- Test the hypothesis – Ho: Densities of *C. shasta* spores in the near-shore drift do not differ at varying depths within riffle or riffle/run transitional habitats in the Klamath River.

### Study Design

- Two sample events were conducted in summer 2005 at four locations between Iron Gate Dam and the Klamath River estuary
- A cross-channel transect was established in riffle/run habitat type at each location. Transects were further divided into six cells corresponding to proximity to right or left shore and shoreline, near-shore, and mid-channel strata.
- One liter water samples were collected about 15 cm below the water surface in each of the six cells, and 0.5\*depth and 10 cm off the bottom at one near-shore strata. Each station was sampled 3 times.
- Water samples were filtered for *C. shasta* spore DNA and submitted to Oregon State University's Microbiology Dept. for QPCR analysis.
- Cycle threshold values, a measure of spore disease and *C. shasta* spore densities, were compared using an analysis of variance statistical test.



### Results

- *C. shasta* spore DNA was present during each sample event at all sample locations. No significant differences were observed between sample depths or lateral strata within sample locations. Significant differences were identified, however, between sample events and locations. Three or more 1-L samples should be collected at each site for quantitative studies.