

A Rickettsia-like organism is associated with Strawberry Disease lesions in rainbow trout

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Strawberry disease (SD) is a skin disorder of rainbow trout (*Oncorhynchus mykiss*) that causes red inflammatory lesions in market sized fish; these lesions can result in economic losses due to product downgrading or rejection. SD was first described in Washington State in the 1950's but its etiology remains unknown. Recovery time can be reduced with oxytetracycline treatment thereby suggesting a role for a bacterial agent. Many agents have been suggested including *Flavobacterium psychrophilum*, the etiologic agent of coldwater disease and rainbow trout fry syndrome. In a 2006 study, small subunit rRNA (16S) sequences matching *F. psychrophilum* were recovered from paraffin-embedded SD lesions from 2 of 4 affected fish and none from 3 healthy fish.

We employed non-culture-based, 16S rRNA sequence libraries to characterize the microbial community associated with SD lesions from trout collected in southern Idaho. Libraries were made from 7 SD-affected fish and 2 healthy skin samples. *F. psychrophilum* 16S rRNA sequences were present in one of the lesion libraries (2 of 139 recovered sequences). Sequences belonging to a Rickettsiales-like organism (RLO) were recovered from 3 of the lesion libraries at 54% (75/139), 32% (22/69), and 1% (1/88) prevalence. No RLO sequences were found in healthy tissue libraries. The full-length RLO 16S rRNA sequence was recovered, sequenced, and found to be most closely related to members of a divergent lineage within Rickettsiales that have been isolated from ixodid ticks. Lesions and healthy skin from 8 fish were tested using a nested PCR assay developed to detect the novel RLO 16S rRNA. Five of the lesion samples were positive, while none of the paired, healthy tissues were positive resulting in a significant association between SD lesions and the presence of RLO ($P = 0.01$). A similar nested PCR assay to test for the *F. psychrophilum* 16S rRNA sequence was performed on the same samples and *F. psychrophilum* 16S rRNA sequences were found in both healthy and SD samples; no significant association was demonstrated ($P = 0.28$). While these observations provide support for a close association between RLO and SD, additional experimental, molecular, and epidemiological evidence is needed to demonstrate a causal association.