# MICROSATELLITE ANALYSIS ON PACIFIC LAMPREY FROM THE WILLAMETTE BASIN PROPOSAL FOR FUNDING

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***Background:***

The migratory strategies and resulting population structure of Pacific lampreys are unknown. Reports of size differences among different river systems (e.g., Beamish 1980; Kostow 2002) and differences in allozyme allele frequencies between different drainages (Beamish and Withler 1986) indicate that there may be some local adaptation and reproductive isolation among Pacific lampreys from different locations. Likewise, a study using amplified fragment length polymorphism (AFLP) analysis of DNA found significant differences in AFLP variation in Pacific lampreys from the Pacific Northwest, Alaska, and Japan (Lin *et al.* 2008). In contrast, using mitochondrial DNA analysis, Goodman *et al.* (2008) found few genetic differences among Pacific lampreys from different locations, suggesting a lack of reproductive isolation between locations. However, allozymes, AFLPs, and mitochondrial DNA may not provide the resolution required to sufficiently study population structure in Pacific lampreys. Microsatellites are them marker of choice for detecting population structure in closely related populations (Chistiakov *et al.* 2006). Up until now, Pacific lamprey microsatellite markers were not available for use but have recently been developed in the Docker laboratory through a collaboration with Dr. Timothy Whitesel (USFWS–Columbia River Fisheries Program Office).

***Objectives:***

We are proposing to use these microsatellite markers to conduct genetic analysis on the fish tagged during 2009 and 2010 as part of the study by Benjamin Clemens and colleagues to determine the migration characteristics and habitat use of the imperiled adult Pacific lamprey in the Willamette Basin. Our goal is to determine whether any genetic variation in microsatellites coincides with distinct migration behaviors and especially location of spawning. Microsatellite analysis will help to clarify the population structure of Pacific lampreys and inform any future management decisions.

***Deliverables:***

Genetic analysis would be performed by December 31, 2011, and analysis would be complete by February 28, 2012.

***References:***


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