Conservation and Genetic Stock Identification: A Study Investigating the Stock-Specific Distribution and Performance of Juvenile Chinook Salmon in the Columbia River Estuary

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Research, management and conservation of salmon populations have primarily targeted the freshwater phase of the salmon lifecycle, however recent attention has focused on the importance of the estuarine and ocean phases in the abundance and distribution of Pacific salmon (Brodeur et al. 2000). One potentially critical and interesting life-history phase of Pacific salmon is early entry into salt water (Casillas 1999). Coded wire and PIT tag recoveries, scale analysis and length at age data have all provided insight into the use of estuarine and nearshore habitats by juvenile salmonids. Nevertheless, there are significant gaps in our understanding of how and when juveniles use these environments. The research presented here is the genetic component of a multidisciplinary, multiagency collaboration investigating the stock-specific temporal and spatial distribution of juvenile chinook salmon (*Oncorhyncus tshawytscha*) in the Columbia River estuary.

The first goal of our study was to establish a Columbia River microsatellite genetic baseline to evaluate genetic structure and differentiation among populations and evolutionarily significant units (ESUs) of chinook salmon in the Columbia River basin. The second goal of the study was to use the genetic baseline and individual assignment tests to identify putative source populations and ESUs of juvenile chinook salmon mixtures sampled at different spatial and temporal scales in the Columbia River estuary. We collected genotypes at eight microsatellite loci for 3,040 individuals from 65 chinook salmon populations representing all eight ESUs and nearly all major production areas in the Columbia River basin for the genetic baseline. Two hundred and sixty-six juvenile chinook salmon of unknown origin were collected from marsh, forested and shrub habitats in the Columbia River estuary and genotyped at the same eight loci. Fish were assigned to their most likely population, ESU, or larger reporting group (i.e., pooled genetically similar ESUs) of origin using individual assignment tests (implemented in WHICHRUN; Banks and Eichert 2000).

Preliminary genetic analyses indicate that there is significant geographic structuring in the Columbia River basin. The observed genetic relationships between populations were broadly concordant with previous genetic studies (Waples et al. in press and references therein). There was a compelling separation of populations representing "stream-type" and "ocean-type" lineages (Healy 1991; Myers et al. 1998) based on the F_{ST} neighbor joining dendogram (Fig. 1). Consistent with expectation, the multilocus individual assignments suggest that most juveniles collected from the estuary originated from populations in the lower Columbia River ESU (Fig. 2). Juveniles from many of these populations are fry or fingerling migrants and are thought to spend significant time rearing in the estuary. We also observed fish in our juvenile mixtures from the Upper Willamette River, Mid-Columbia River, and Upper-Columbia River spring run ESUs. Juveniles originating from these areas were formerly thought to migrate quickly through the estuary

Fig. 1. Condensed representation of a mid-point rooted neighbor joining dendogram depicting genetic relationships (F_{ST}) among chinook salmon ESUs, genetic reporting groups (I-IV), and lineages . Genetic reporting groups are identified as follows: I = Lower Columbia River (LCR), II = Upper Willamette River (UWR), III = Deschutes and Snake River fall (DR/SR fa), IV = Upper Columbia River summer/fall (UCR su/fa), and V = Interior spring (Int. sp).
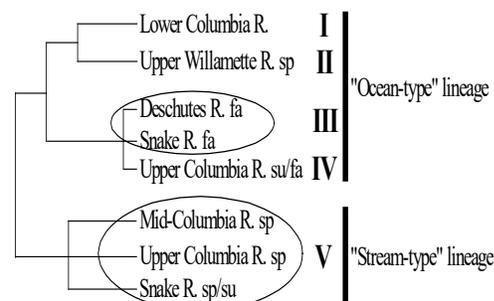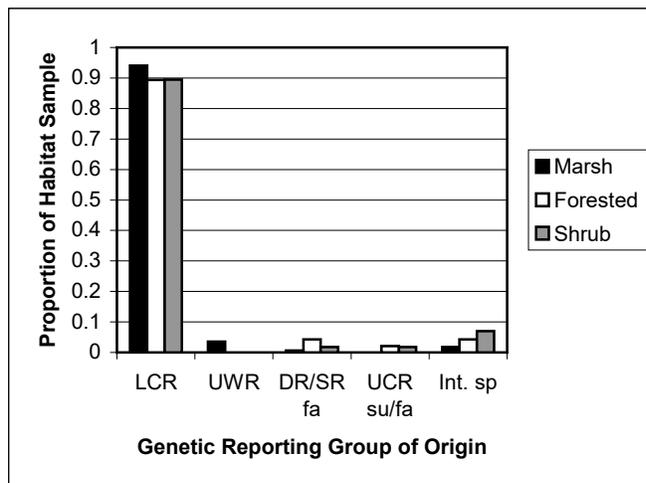
Fig. 2. Summary of reporting group assignments for chinook salmon juveniles sampled in different habitats in the Columbia River Estuary.

to the ocean (Healy 1991). However, our data suggest that off-channel wetland habitat may also provide rearing habitat for juveniles from at least some spring run populations.

Quantitative evaluation of assignment error is in progress, but preliminary evidence suggests that ESU assignment is relatively certain, whereas assignment to specific population is more tenuous. We are conducting a comprehensive evaluation of statistical power and accuracy of our genetic baseline that includes simulations and analysis of coded-wire-tagged fish. Given our preliminary results, we are expanding our sample coverage in the lower Columbia River and assaying nine more microsatellite markers for the genetic baseline and mixture analysis. We are also analyzing additional juvenile mixtures from the Columbia River estuary to test for stock-specific habitat associations, condition factors and contaminant loads. Our data represent an integral part of a much larger study to characterize and quantify a broad range of ecological parameters in estuarine and nearshore marine environments. The goal is to develop empirical (and theoretical) associations between habitat attributes (e.g., salinity, depth, channel morphology, vegetation type, prey resources, etc.) and the distribution and performance of juveniles (e.g., abundance, residence time, condition, and growth). This improved understanding will help evaluate specific mitigation and restoration actions and will help predict juvenile salmon response to environmental change.

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