Parentage analysis for Chum salmon fry captured below experimental adult outplanting site in Graham Creek, Oregon

Maureen P. Small^{1*}, Kristen M. Homel², and Vanessa Smilansky¹

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¹ Washington Department of Fish and Wildlife, Molecular Genetics Lab, 1111 Washington St. SE, Olympia, WA, 98501, <u>*smallmps@dfw.wa.gov</u>, 360-902-2682

² Oregon Department of Fish and Wildlife, 57420 Old Portland Road, Suite 3, Warren, Oregon 97053, 503-910-3091

Introduction:

In 2013, the first experimental outplanting of adult Chum salmon *Oncorhynchus keta* was completed in two Oregon streams as part of efforts to reintroduce Chum salmon in the Oregon portion of the lower Columbia River. Graham Creek and Stewart Creek, within the Clatskanie River Population, were selected as the experimental sites based on similarities in land use, stream size, and gravel availability (Figure 1). Chum salmon returns to Big Creek Hatchery (age-3 progeny of the Big Creek broodstock) were used as the source for the outplanting. Before outplanting, a fin clip was removed from each adult for future genetic analysis, the individual was tagged with a unique combination of external Floy tags, and bio data was recorded (length, condition, sex, and scales removed for aging).

In both streams, adult traps were installed below spawning habitat in order to keep Chum salmon in the stream once they were outplanted. During high water events, the traps were not a complete barrier and some adults left the outplant sites. Furthermore, some adults disappeared so quickly from the stream it appeared they were removed by predators (possibly human) before they could spawn. Only a portion of the carcasses could be found and examined to determine that they had spawned.

Following spawning, adult traps were removed and juvenile traps were installed to estimate Chum salmon fry production. In Stewart Creek, a single fry trap was used, but in Graham Creek, two traps were used (Figures 2 and 3). The upstream trap was designed to trap efficiently during low flows (Figures 2). The downstream trap was an inclined-plane trap (Figure 3) and was positioned in tidewater in a location to capture fry during moderate flows.

Chum salmon fry were captured in both Stewart and Graham creeks, and fin clips were removed for future parentage analysis. At Stewart Creek, > 700 Chum salmon fry were captured and with a trap efficiency of 19%, an estimated 4,336 Chum salmon fry outmigrated. In Graham Creek, only 15 fry were captured, 14 of which were captured in the inclined-plane trap in tidewater. Because the upstream fry trap fished well for other species in Graham Creek, and the same trap design was very effective in Stewart Creek, it appeared that there was little Chum salmon fry production from the adults outplanted in Graham Creek. Further, because the trap where 14 of these fry were captured was tidally influenced, it is possible that the captured Chum salmon fry could have originated from spawners outside of Graham Creek: the fry could have entered the stream at high tide and been captured in the inclined-plane trap. This report documents the parentage for the Graham Creek will be examined in a later report.

Methods:

Tissue samples (fin clips) were collected from all adult Chum salmon planted in Graham Creek (N = 22, Table 1) in fall 2013 and from all Chum salmon juveniles caught in the Graham Creek fry traps outmigrating in winter 2014 (N =15, Table 2). Genotypes for each individuals were assessed at 16 microsatellite loci [Oke-3 (Buchholz et al. 2001), Oki-1 (Smith et al. 1998), Omy-1011 (Rexroad III et al. 2002), One-101, One-102, One-106, One-108, One-111, One-114 (Olsen et al. 2000), One-18 (Scribner et al. 1996), Ots-1, Ots-2M, Ots-3M (Banks et al. 1999), Ots-103 (Small et al. 1998), Ots-G311 (Williamson et al. 2002), Ssa-419 (Cairney et al. 2000)]. DNA was extracted with a silica membrane protocol following manufacturer's instructions (Macherey-Nagel). Microsatellite loci were amplified via the polymerase chain reaction and scored and binned as detailed in Small et al. (2009).

We assigned juveniles to potential parents in pedigree analyses using the programs COLONY (Wang 2004, 2007, Wang and Santure 2009). COLONY uses maximum likelihood to construct full- and halfsibling family groups among juveniles and assigns parents to the full-sibling families. If parents are unsampled, COLONY constructs the hypothetical parents for sibling families. COLONY has four options

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for run length (short, medium, long and very long), three options for analysis (full likelihood, pair likelihood and full-pair likelihood), and three options for precision (low, medium and high). Because the data set was small (and thus ran relatively quickly), we ran medium runs with full-pair likelihood and high precision. The program requires the input of a file with estimated percentage of allele scoring errors to direct the stringency on acceptable mismatches within possible families. We tested three levels of allele scoring errors (1%, 0.1% and 0.01%) to observe how possible scoring errors influenced the outcome. Scoring errors arise when there are non-amplifying (null) alleles such that a heterozygote is scored as a homozygotes, large-allele drop-out (larger-sized alleles are missed because they do not amplify as well as smaller-sized alleles), or the scoring program scores a PCR artifact rather than the true allele. These types of errors are generally minimal but can be a source of error when trying to match offspring to parents genetically. We ran the COLONY analyses three times with the three scoring error levels and compared results.

Results:

Two families were represented in the out-migrating juveniles. Fourteen juveniles were from family 1: male 14LG0015 mated with female 14LG0003; and one juvenile was from family 2: male 14LG0018 mated with female 14LG0006 (Table 3). Parents in family 1 were planted into Graham Creek within a day of each other and parents in family 2 were planted into Graham Creek within 2 days of each other. The results were the same regardless of error rate level. Outplanting adult Chum salmon in Graham Creek was thus successful in that two experimental families were represented in the outmigrating juveniles.

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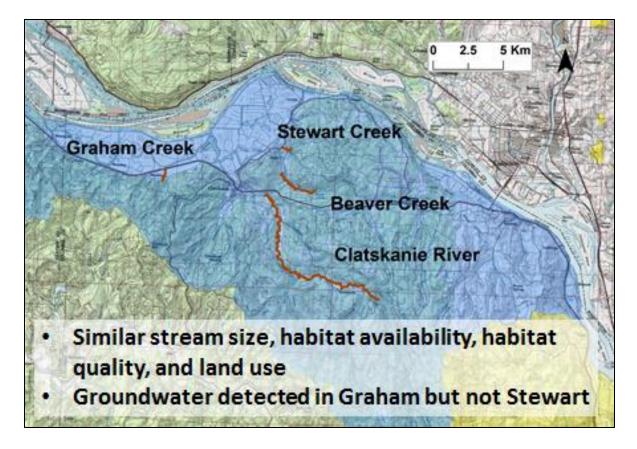


Figure 1. Experimental Chum salmon *Oncorhynchus keta* outplanting sites on Graham Creek and Stewart Creek in the Clatskanie River Population, Oregon.



Figure 2. Stationary fry trap in Graham Creek in the Clatskanie River Population, Oregon.



Figure 3. Inclined-plane fry trap in Graham Creek in the Clatskanie River Population, Oregon

Table 1. Outplant location, outplant date, fork length, sex, and genetic sample number for adult Chum
salmon Oncorhynchus keta experimentally outplanted in Graham Creek OR, 2013.

OUTPLANT SITE	STAGE	OUTPLANT DATE	FORK LENGTH (mm)	SEX	WDFW code	TAG #
Graham	ADULT	15-Nov-13	610	F	14LG 001	105
Graham	ADULT	18-Nov-13	635	F	14LG 002	416
Graham	ADULT	18-Nov-13	635	F	14LG 003	421
Graham	ADULT	18-Nov-13	635	F	14LG 004	419
Graham	ADULT	19-Nov-13	690	F	14LG 005	406
Graham	ADULT	21-Nov-13	600	F	14LG 006	455
Graham	ADULT	04-Dec-13	652	F	14LG 008	5
Graham	ADULT	04-Dec-13	661	F	14LG 009	7
Graham	ADULT	04-Dec-13	687	F	14LG 010	9
Graham	ADULT	04-Dec-13	680	F	14LG 011	11
Graham	ADULT	08-Nov-13	687	М	14LG 012	351
Graham	ADULT	15-Nov-13	675	М	14LG 013	103
Graham	ADULT	18-Nov-13	700	М	14LG 014	415
Graham	ADULT	18-Nov-13	705	М	14LG 016	423
Graham	ADULT	18-Nov-13	685	М	14LG 017	425
Graham	ADULT	19-Nov-13	685	М	14LG 018	404
Graham	ADULT	19-Nov-13	650	М	14LG 019	411
Graham	ADULT	19-Nov-13	720	М	14LG 020	409
Graham	ADULT	21-Nov-13	670	М	14LG 021	451
Graham	ADULT	04-Dec-13	710	М	14LG 022	1

Table 2. Capture date, fork length, and genetic sample for Chum salmon Oncorhynchus keta fry
captured at the Graham Creek reintroduction site.

TRAP SITE	STAGE	DATE	FORK LENGTH	WDFW
			(mm)	code
Graham Creek	FRY	25-Apr-14	39	14LF 001
Graham Creek	FRY	25-Apr-14	38	14LF 002
Graham Creek	FRY	25-Apr-14	39	14LF 003
Graham Creek	FRY	25-Apr-14	39	14LF 004
Graham Creek	FRY	25-Apr-14	39	14LF 005
Graham Creek	FRY	25-Apr-14	39	14LF 006
Graham Creek	FRY	25-Apr-14	40	14LF 007
Graham Creek	FRY	25-Apr-14	40	14LF 008
Graham Creek	FRY	25-Apr-14	39	14LF 009
Graham Creek	FRY	25-Apr-14	40	14LF 010
Graham Creek	FRY	25-Apr-14	40	14LF 011
Graham Creek	FRY	25-Apr-14	39	14LF 012
Graham Creek	FRY	25-Apr-14	40	14LF 013
Graham Creek	FRY	25-Apr-14	40	14LF 014
Graham Creek	FRY	4-May-14	41	14LF 015

Table 3. Parent assignments from COLONY.

	OffspringID	FatherID	MotherID
family 1	14LF0001	14LG0015	14LG0003
family 1	14LF0002	14LG0015	14LG0003
family 1	14LF0003	14LG0015	14LG0003
family 1	14LF0004	14LG0015	14LG0003
family 1	14LF0005	14LG0015	14LG0003
family 1	14LF0006	14LG0015	14LG0003
family 1	14LF0007	14LG0015	14LG0003
family 1	14LF0008	14LG0015	14LG0003
family 1	14LF0009	14LG0015	14LG0003
family 1	14LF0010	14LG0015	14LG0003
family 1	14LF0011	14LG0015	14LG0003
family 1	14LF0012	14LG0015	14LG0003
family 1	14LF0013	14LG0015	14LG0003
family 1	14LF0014	14LG0015	14LG0003
family 2	14LF0015	14LG0018	14LG0006