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Supplementary information

Threatened salmon rely on a rare life history strategy in a warming landscape

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Supplementary Information

Threatened salmon rely on a rare life history strategy in a warming landscape

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1. Otoliths sampling and clustering analysis

1.1. Adult otoliths sampling

Adult spring-run otoliths were collected during annual snorkel (Deer Creek) and redd (Mill Creek) surveys by the California Department of Fish and Wildlife[1]. Otoliths were retrieved from all salmon carcasses encountered during surveys occurring in the Fall of 2007, 2008, 2012, 2013, 2014 and 2018 (Supplementary Tables 1, 2). A fairly small number of carcasses were recovered each year, due to difficult watershed accessibility and low adult returns, including some years where carcasses were only recovered in one of the watersheds (Supplementary Table 1). A total of 123 otoliths were used for isotope analysis. We grouped the samples from the two populations together for analysis due to the low sample size and unequal representation across watersheds within a year. Because the two watersheds are close geographically and similar isotopically[2] and hydrologically[3] and the salmon populations are similar genetically[4], we assume common processes at-play within the watersheds generate the life-history diversity observed.

Supplementary Table 1. Mill and Deer Creek otoliths life history type classification. N = number of otoliths used for isotope analysis. Escapement values represent the number of adult spawners estimated to have returned to Mill and Deer Creek watersheds in a given year. Escapement data comes from GrandTab (https://www.calfish.org/ProgramsData/Species/CDFWAnadromousResourceAssessment.aspx).

Year	Population	N	Escapement	Percent adult analyzed (N/Escapement* 100)	Early migrant (n)	Intermediate migrant (n)	Late migrant (n)

2007	Deer Creek	13	644	2%	2	7	4
2008	Deer Creek	12	140	9%	4	5	3
2014	Deer Creek	3	830	0.5%	0	1	2
2018	Deer Creek	34	159	22%	1	0	33
2007	Mill Creek	18	920	2%	8	3	7
2012	Mill Creek	11	768	1%	0	0	11
2013	Mill Creek	22	644	3%	9	7	6
2014	Mill Creek	10	679	1%	2	0	8

Supplementary Table 2. Mill and Deer Creek juvenile emigration and adult return years summary. AN = Above Normal, BN = Below Normal, W = Wet, D = Dry, C = critical. Orange cells show years of record warm period for the California Current System[5,6]. Yellow cells show cohort-averaged Sacramento Water Index < 6.5, defining dry freshwater hydrological conditions.

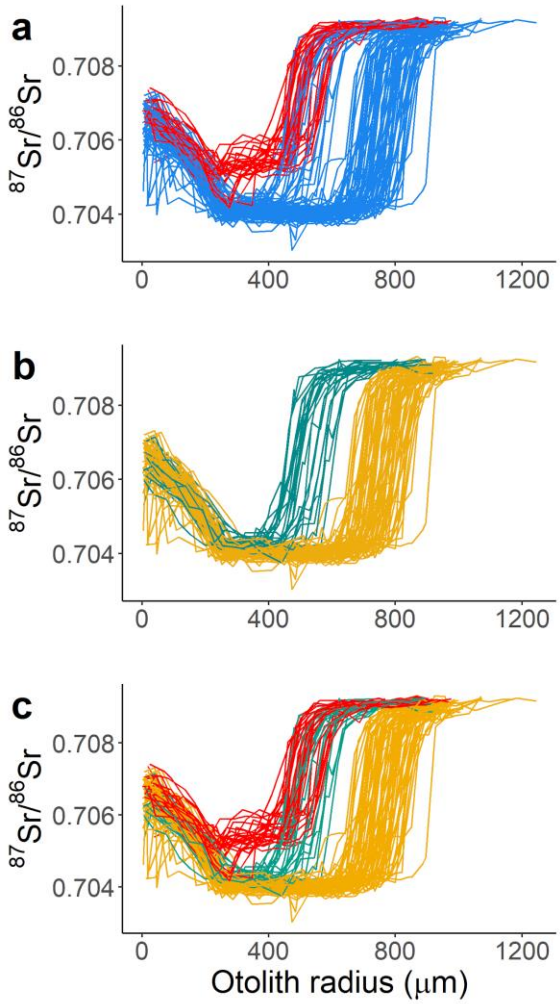
Return years in study	**Age at return***	**Brood year**	**Emigration year / Water year ****	**Water Year Type**	**Sacramento Water Index**	**Mean Sacramento Water Index**
2007	3	2004	2005	AN	8.5	8.0
2007	4	2003	2004	BN	7.5	
2008	3	2005	2006	W	13.2	10.8
2008	4	2004	2005	AN	8.5	
2012	3	2009	2010	BN	7.1	6.4
2012	4	2008	2009	D	5.8	
2013	3	2010	2011	W	10.5	8.8
2013	4	2009	2010	BN	7.1	
2014	3	2011	2012	BN	6.9	8.7
2014	4	2010	2011	W	10.5	
2018	3	2015	2016	BN	6.7	5.4
2018	4	2014	2015	C	4.0	

* Most spring run adults return to spawn at ages 3 and 4[7].

** Most spring run adults spawn around September[7], and the California Water Year (and Sacramento Water Index) is calculated based on runoff from Oct 1 to Sept 30 (https://cdec.water.ca.gov). Thus, the water year for brood year + 1 incorporates river flows experienced by spring-run juveniles from egg incubation through to emigration.

1.2 Clustering analysis

We conducted a clustering analysis on the 123 strontium profiles obtained from the otolith isotope analysis (see Methods for details on the clustering analysis steps). Because two main changes could be observed among the strontium profiles, one occurring in the 200 – 400 µm region and one in the region after 600 µm, we developed a two-step clustering analysis approach. The first clustering analysis focused on the 0 – 400 µm region of the 123 profiles, and the second one was applied on the entire region (i.e., 0- 1000 µm) for a subset of profiles. We first performed the FPCA on the truncated profiles. The first three harmonics of the FPCA were selected for this first cluster analysis, since they were found to explain the majority of the data variance (99%). The best BIC model was the VEE (ellipsoidal, equal shape and orientation) model which identified two main groups (Supplementary Fig. 1a): a homogeneous group of observations (red profiles in Supplementary Fig. 1a) and a heterogeneous one (blue profiles in Supplementary Fig. 1a) that exhibited differences in the 600 µm region. A second FPCA was then performed on the second (heterogeneous) group identified during the first cluster analysis (blue profiles in Supplementary Fig. 1a). We used the first harmonic of the FPCA (which explained 80% of the data variance) for the clustering analysis. The best BIC model was the E (univariate, equal variance) model and identified two main groups (Supplementary Fig. 1b). Therefore, three groups emerged from the combined cluster analyses (Supplementary Fig. 1c), and were used further to characterize the life history diversity of Mill and Deer Creek spring-run Chinook salmon populations.



Supplementary Figure 1. (a) Strontium profile groups as identified by the first cluster analysis performed on the 0 – 400 µm region of the 123 profiles. (b) Strontium profile groups as identified by the second cluster analysis performed on the entire region (i.e., 0- 1000 µm) of the blue profiles. (c) Strontium profile groups as identified by the combined cluster analyses results of (a) and (b). Red, green and yellow profiles are associated with early, intermediate and late migrants respectively.

2. Reconstruction of fish size and age at natal and freshwater exit and comparison with juvenile trapping data

2.1 Rotary screw trap's juvenile size groups

Raw data of juveniles caught in Mill and Deer creeks' rotary screw traps between 1995 and 2010 were provided by the California Department of Fish and Wildlife (CDFW). Based on personal communication with M. Johnson (CDFW) and on the general shape of the trap data we defined three juvenile size groups; the early migrant group was composed of fish < 45mm, the late migrant group was defined using the following step function:

- for the months of October, November and December, late migrant = fish > 50mm
- for the months of January and February, late migrant = fish > 60mm
- for the month of March, late migrant = fish > 76mm
- between the 1st and 14th of April, late migrant = fish > 85mm
- between the 15th and 30th of April, late migrant = fish > 95mm
- for the months of May and June, late migrant = fish > 100mm,

and the intermediate migrant group included the rest of the juveniles (i.e., fish longer than 45mm and shorter than late migrants; Fig. 2a).

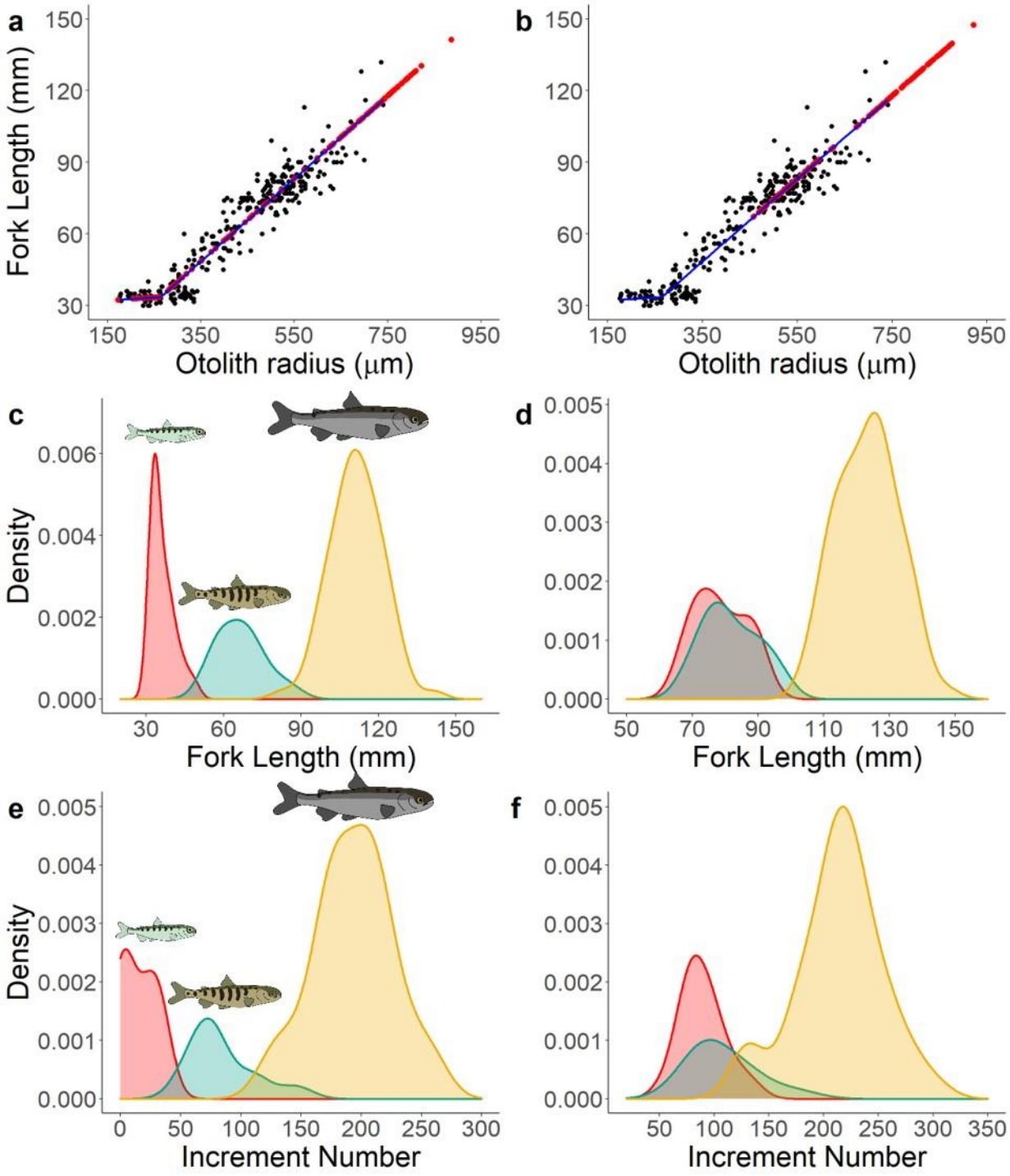
2.2 Reconstructed fish size and age

We applied an otolith radius – fork length relationship for Central Valley fall-run Chinook salmon[8] to reconstruct fish sizes at natal and freshwater exit. While applying otolith-fish size calibration curves across different ESUs can produce spurious size reconstructions[9], Central Valley fall and spring run Chinook salmon spawn and emigrate at similar sizes and exhibit overlapping geographic distributions. The reconstructed natal exit sizes ranged from 32 to 141mm (Supplementary Fig. 2a), and the reconstructed size distributions are very similar to those observed in Mill and Deer creeks' rotary screw traps (Fig. 2a. vs. Supplementary Fig. 2c, respectively), suggesting congruence among datasets.

Otolith increment numbers measured for growth rate estimation give the number of days since emergence and provide a good proxy for fish age. Using the measured otolith radius and increment numbers we tested whether the sizes and ages at natal and freshwater exit were significantly different among life history types. First, homogeneity of variances in fish sizes and ages at natal and freshwater (FW) exit among individuals with the same life history type were confirmed using *leveneTest* function in R[10] ($F_{size,natal}(14,108) = 0.91$, p-value = 0.54,

$F_{age,natal}(14,71) = 1.08$, p-value = 0.39 & $F_{size,FW}(14,108) = 0.77$, p-value = 0.70, $F_{age,FW}(14,71) =$ 0.82, p-value = 0.64). We found that fish size and age at natal exit were significantly smaller for early migrants (mean otolith radius = 262µm ± 43µm SD, or a reconstructed fork length of 36mm ± 4mm SD, and 15 days ± 14 days SD) than intermediate (mean otolith radius = 454µm ± 52µm SD, or a reconstructed fork length of 67mm ± 9mm SD, and 84 days ± 27 days SD) and late migrants (mean otolith radius = 714µm ± 58µm SD, or a reconstructed fork length 111mm ± 10mm SD, and 194 days ± 33 days SD; one-way ANOVA $F_{size}(2,120) = 724.9$ and $F_{age}(2,83) =$ 275.8, p-values < 2e-16 and Tukey test with significance level $\alpha = 0.05$ p-values = 0 and 1e-07 for both size and age comparison; Supplementary Fig. 2c, 2e).

Reconstructed freshwater exit sizes ranged from 67 to 147mm (Supplementary Fig. 2b). Early migrants spent, on average, 89 days (± 19 days SD) in freshwater and had a mean otolith radius at freshwater exit of 524µm (± 45µm SD) or a reconstructed fish size of 79mm (± 8mm SD), while intermediate migrants spent, on average, 108 days (± 29 days SD) in freshwater and had a mean otolith radius at freshwater exit of 542µm (± 48µm SD; equivalent to 82mm ± 8mm SD; Supplementary Fig. 2d, 2f). Conversely, late migrant juveniles were still larger than the two other groups, with a mean otolith radius at freshwater exit of 783µm (± 53µm SD; equivalent to 123mm ± 9mm SD), and they spent, on average, 214 days (± 39 days SD) in freshwater. Size and age at freshwater exit were significantly different between late and early or intermediate migrants (one-way ANOVA $F_{size}(2,120) = 357.7$ and $F_{age}(2,83) = 107$, p-values < 2e-16, and Tukey test with significance level $\alpha = 0.05$ p-values = 0 for both size and age comparison), but not significantly different between early and intermediate migrants (Tukey test p-values = 0.40 and 0.34 for size and age comparison respectively).



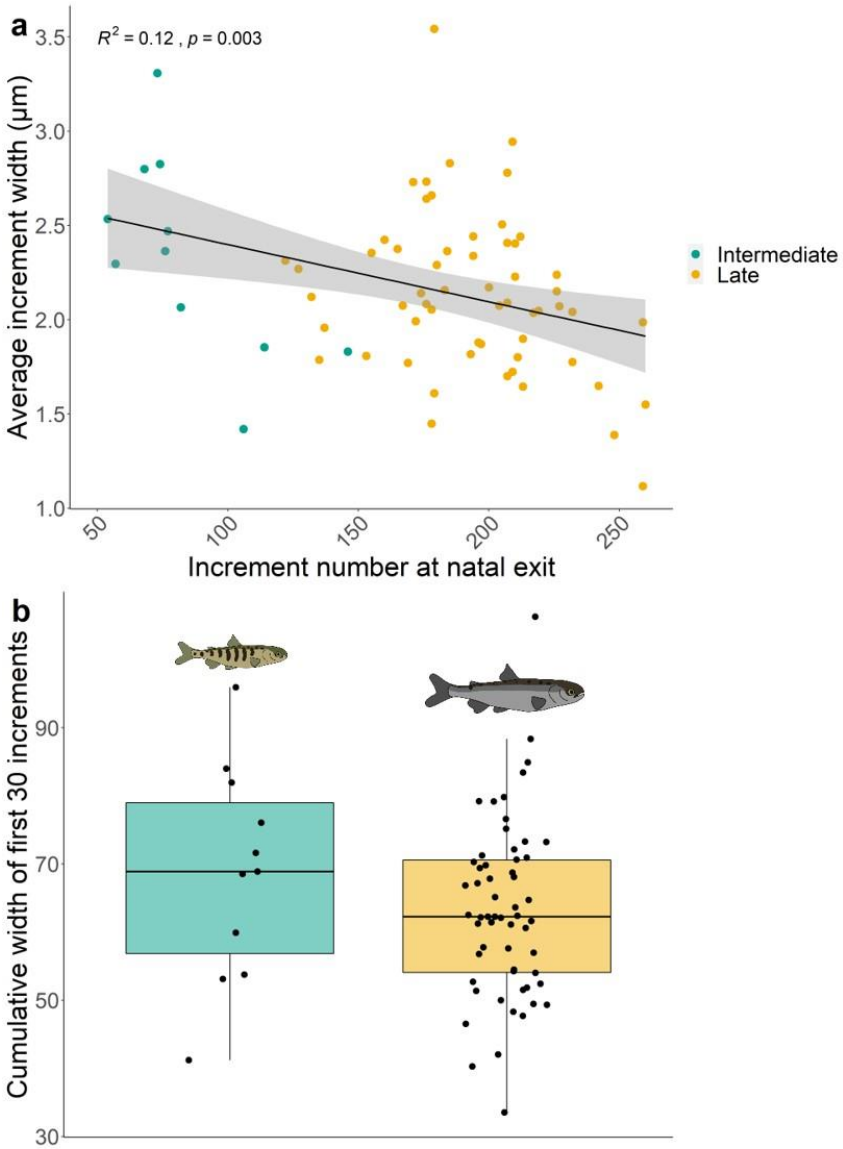
Supplementary Figure 2. Reconstructed juvenile spring-run fork length (red dots) at (a) natal exit, and (b) freshwater exit, based on the otolith radius – fork length model (blue line) developed in Sturrock et al.[8] from fall-run fish data (black dots). Reconstructed fish size distribution at (c) natal exit, and (d) freshwater exit, for each life history type and all years combined. Measured otolith increment number (a proxy for fish age) distribution at (e) natal exit, and (f) freshwater exit, for each life history type and all

years combined. Note that sample sizes were not identical among years (Supplementary Table 1), and fork length and otolith increment number distributions were not standardized by sample size.

3. Early-life growth rate and life history relationship

We looked at the relationship between early-life growth and life history type for fish rearing in natal tributaries at least 30 days after emergence. Because the majority of early migrants have migrated downstream by day 30, we only compared intermediate (N = 11) and late migrant (N = 58) growth rates. Homogeneity of variances in 15- and 30-day average growths among individuals with the same life history type was confirmed using *leveneTest* R function ($F_{avg,15/30}(14,71) = 1.03$, p-value = 0.43). Similar to what we observed for the first 15 days after emergence, there was a negative association between average daily growth and the number of days spent in the natal tributary (Supplementary Fig. 3a).

We also found equal variances in 15-day cumulative growths among individuals with the same life history type ($F_{cum,15}(13,64) = 0.66$, p-value = 0.79), and a Tukey test was used to compare 15-day growths across life history types (Fig. 4). However, homogeneity of variances in cumulative growths over the first 30 days among life history types was not confirmed ($F_{cum,30}(11,61) = 2.27$, p-value = 0.02), and we used a non-parametric Wilcoxon test (using *wilcox.test* function in R) for intermediate and late migrant's growth comparison. Growth over the first 30 days was faster on average for intermediate (mean cumulative width of first 30 increments = 69 µm ± 16 µm SD) than late migrants (63 µm ± 13 µm SD; Supplementary Fig. 3b), however the growth difference was not statistically significant (two-samples Wilcoxon test W = 404, p-value = 0.17).



Supplementary Figure 3. (a) Intermediate and late migrant's daily otolith increment width (a proxy for fish growth rate) averaged over the first 30 days after emergence and plotted against the otolith increment number (a proxy for age) at natal exit. A linear regression (using *lm* R function) is represented by the black line, with the grey shade showing the 95% confidence interval. (b) Boxplot of intermediate and late migrant's cumulative increment width at day 30 (a proxy for somatic growth achieved in the first 30 days). The horizontal line in each box represents the median value, lower and upper hinges of the boxes correspond to the 25th and 75th percentiles. The upper whiskers extend from the hinge to the largest value no further than 1.5*interquartile range (IQR) from the hinge. The lower whisker extends from the hinge to the smallest value, 1.5*IQR of the hinge, at most. The black dots are the actual measurements, jittered for visual aid.

4. Central Valley habitat suitability forecast

The amount of suitable habitat (in km) for accessible and inaccessible Central Valley stream reaches across the three periods (i.e., 2005-2015, 2040, and 2080) was estimated for comparison (Supplementary Table 3).

Supplementary Table 3. Amount of suitable rearing habitat (km) in accessible only and accessible & inaccessible reaches for Central Valley spring-run Chinook salmon juveniles under 2005-2015 stream temperature conditions and two climate change scenarios (2040 and 2080). Rearing temperature suitability may be bottlenecked for early and intermediate migrants in May and for late migrants in August.

	May_2005-2015	**May_2040**	**May_2080**	**Aug_2005-2015**	**Aug_2040**	**Aug_2080**
Accessible	763 km	489 km	418 km	171 km	111 km	76 km
Accessible & Inaccessible	1950 km	1637 km	1500 km	366 km	265 km	201 km

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