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UNITED STATES DISTRICT COURT
DISTRICT OF OREGON
PORTLAND DIVISION

NATIONAL WILDLIFE FEDERATION, et al.,

Plaintiffs,

v.

**NATIONAL MARINE FISHERIES SERVICE, et
al.,**

Defendants.

Case No.: 3:01-CV-00640-SI

**FEDERAL DEFENDANTS'
UNOPPOSED MOTION FOR
LEAVE TO FILE A REPLY
RE: JUNE 23, 2015
SUMMARY JUDGMENT
HEARING QUESTIONS AND
OREGON'S RESPONSE [ECF
2045-2046]**

MOTION

Federal Defendants move for leave to file the attached, limited reply concerning the Court's June 23, 2015 hearing questions and Oregon's supplemental brief and extra-record declaration (ECF 2045-2046). The proposed reply is warranted because Oregon's supplemental filing and new declaration introduce new arguments and technical analysis for the first time, including analysis and argument that is simply inaccurate. It further shows that Oregon is taking positions that contradict its own statements made outside of litigation and is advancing theories that do not address the factors relevant to the issues before the Court. These points are explained briefly below and in more detail in the proposed reply (Attachment A).

Pursuant to Local Rule 7-1, undersigned counsel conferred telephonically with counsel for the State of Oregon, the NWF et al. Plaintiffs, and amicus Nez Perce Tribe, and these parties have no objection to the motion for leave. No other party consulted has indicated that they object to this motion for leave.

MEMORANDUM IN SUPPORT

At oral argument, the Court requested further clarification regarding two tables in the 2014 BiOp. Federal Defendants provided that clarification. ECF 2040. Oregon filed two responses to Federal Defendants' supplemental filing (ECF 2043, 2045), the latter without receiving leave of Court. Without leave, Oregon also submitted another post-hoc declaration raising new rationalizations second-guessing NMFS's analysis contained in the 2008 and 2014 biological opinions (BiOps). *See* ECF 2045-2046.

Oregon's latest filing is improper and prejudicial for a host of reasons. Among others, Oregon's response raises new arguments and new evidence that are scientifically flawed, inaccurate, and contradict Oregon's own positions taken outside of litigation. For example, as explained in Federal Defendants' proposed reply, Oregon claims that NMFS inflated mean recruits to spawner ("R/S") estimates by excluding years where the abundance of spawners is estimated to be five or fewer fish. ECF 2045 at 4. As we explain, Oregon misunderstands why those years were excluded. Very low spawner estimates create unrealistically *high* R/S for their

brood year. Thus, the agency *conservatively* excluded low return years from its calculations so as not to bias *upwards* its mean R/S calculations. Oregon itself has acknowledged this relationship between low spawner years and mean R/S in non-litigation settings. Thus, Oregon's response is not only inaccurate, but contradicts its own positions taken in the scientific forums. Federal Defendants' proposed reply addresses these and other, similar issues, and it shows why the Court should ultimately disregard Oregon's post-hoc challenges to the 2008 and 2014 BiOp.

The Court should also permit a response because it is well settled that when a party presents new evidence after the close of briefing, a court must permit an opposing party to file a supplemental pleading to counter the new evidence or arguments. *See, e.g., Provenz v. Miller*, 102 F.3d 1478, 1483 (9th Cir. 1996) ("Where new evidence is presented in a reply to a motion for summary judgment, the district court should not consider the new evidence without giving the [non]movant an opportunity to respond.") (citation omitted); *see also Or. Natural Desert Ass'n v. Cain*, 17 F. Supp. 3d 1037, 1048 (D. Or. 2014) ("When a party has raised new arguments or presented new evidence in a reply to an opposition, the court may permit the other party to counter the new arguments or evidence.") (citations omitted). Here, Oregon has prepared a new declaration with its response, and Federal Defendants request an opportunity to address this new information.

Finally, Federal Defendants' proposed reply is limited to addressing the new arguments and evidence proffered by Oregon. Because the reply is firmly grounded in the Administrative Record and does not present new evidence, there is no prejudice to any party. The proposed reply also does not introduce new issues that would delay resolution of this case by justifying additional post-hearing briefing by the parties. For these reasons, Federal Defendants respectfully request leave to file the attached, short reply.

Dated July 15, 2015

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CERTIFICATE OF SERVICE

I certify that the foregoing was electronically filed today through the Court's electronic filing system, which will generate automatic service upon on all Parties enrolled to receive such notice. I also certify that the following will be manually served via overnight mail:

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INTRODUCTION

Nearly a decade after this consultation process began, and despite using NMFS's data in its own declarations, Oregon has now decided, apparently for the first time, to actually examine the data and how NMFS calculates abundance, spawner, and recruit-to-spawner (R/S) estimates. Based on this examination, Oregon now asserts that there are errors in how NMFS calculated or reported numbers and performed its analysis.

Oregon's post-argument filings are remarkable on many levels. First, despite being an active participant in the administrative process and having the opportunity on many occasions to review this very data and present contrary views to the agencies before issuance of the biological opinion, Oregon has waited until a post-summary judgment filing to present its specific critiques in the form of an extra-record declaration. Of course, this is inconsistent with fundamental principles of administrative law because it deprives the agencies (and regional sovereigns) of the opportunity to review and respond to those issues during the consultation process. This reason, standing alone, would justify disregarding the filing entirely.

Second, procedural improprieties aside, the filing provides yet another example of the problem with much of Oregon's case: a lack of understanding of the BiOp's analysis. Indeed, for the majority of "errors" Oregon identifies, Oregon either misunderstands or misconstrues NMFS's analysis. For the actual errors identified, Oregon is noticeably silent on whether the errors affected NMFS's analysis. For good reason—the few transcription errors Oregon identifies underestimate natural-origin abundance and R/S therefore result in a *more conservative* analysis. And Oregon presents several "new" issues that allegedly undermine NMFS's analysis; for instance, that NMFS inflated R/S estimates by excluding years with low or zero estimated spawners. OR Supp. Br. at 4 (ECF 2045); Supp. Kostow Decl. ¶ 7 & Table 2 (ECF 2046). But Oregon neglects to consider basic aspects of salmonid biology, its own statements on the issue, and NMFS's explanation for why its approach actually results in lower, *more conservative* estimates of mean R/S productivity.

Finally, while this might be Oregon's most recent filing, it may as well be Exhibit 1

illustrating Oregon’s improper attempt to create a battle of the experts. Once again, Oregon has put before the Court its declarant’s alternative scientific theories. However, even if those theories had any merit—which they do not—the theories do not undermine NMFS’s rigorous scientific analysis and expertise underpinning the 2014 BiOp. Under these circumstances, the Court should uphold NMFS’s 2014 BiOp.

DISCUSSION

Oregon presents new argument and another *post-hoc* declaration¹ regarding NMFS’s technical analysis. It attempts to bolster its challenge to the 2014 BiOp “by listing various questions that it claims were left unanswered,” *Kern County Farm Bureau v. Allen*, 450 F.3d 1072, 1081 (9th Cir. 2006), and it otherwise faults NMFS for failing to explain and justify every technical detail of its analysis, *see, e.g.*, OR Supp. Br. at 7. In its zeal to create a fault with the 2014 BiOp, Oregon first overlooks the law, which imposes no such obligations on NMFS.

The ESA does not require the agency to exhaustively summarize the data or exhaustively show the relationship of the data to the rule. *Kern Cnty.*, 450 F.3d 1081-82; *see also* 16 U.S.C. § 1536(b)(3)(A) (requiring “a *summary* of the information on which the opinion is based”) (emphasis added). Nor does the ESA demand that “every detail of the agency’s decision be stated expressly in the [biological opinion].” *Defenders of Wildlife v. U.S. Dep’t of Navy*, 733 F.3d 1106, 1120 n.6 (11th Cir. 2013) (quoting *In re Operation of Mo. River Sys. Litig.*, 421 F.3d 618, 634 (8th Cir. 2005)). Indeed, “the fact that the [agency’s] explanation for its choices does not fully address every possible issue that flows from that choice does not render the [agency’s]

¹ Oregon’s third *post hoc* declaration strays even farther from the standards governing judicial review in this case. With the new declaration, Oregon presents its own views on a “proper” technical analysis and invites the Court to improperly substitute Oregon’s views for those of NMFS and its experts. *See, e.g.*, Supp. Kostow Decl. ¶¶ 3, 7, 11-13 (arguing that a better way to evaluate abundance is to consider only adult fish on the spawning grounds, “dummy” values should be inserted in place of actual data, evaluating point estimates is meaningless, and its preferred smolt-to-adult return (SAR) analysis is “better”). This is materially the same type of *post hoc* evidence that must be excluded in these record review cases. *San Luis & Delta-Mendota Water Auth. v. Jewell*, 747 F.3d 581, 604 (9th Cir. 2014) (rejecting similar declarations that required the court to resolve “contrary positions as a matter of scientific fact”). Federal Defendants therefore object to the Supplemental Kostow Declaration and preserve their prior objections to the Court’s consideration of the extra-record declarations filed in this case.

determination unreasonable or unsupported. We do not require agencies to analyze every potential consequence of every choice they make; to do so would put an impossible burden on agencies.” *Jewell*, 747 F.3d at 621; *Lands Council v. McNair*, 537 F.3d 981, 988 (9th Cir. 2008) (*en banc*) (the court is not to “act as a panel of scientists that instructs the [agency] ..., chooses among scientific studies ..., and orders the agency to explain every possible scientific uncertainty”).

Against these standards, Oregon’s complaints fall short. Oregon does not dispute that NMFS fully considered the underlying data, methods, and issues. Thus, there is no “entire[] fail[ure] to consider” any relevant issue. *Motor Vehicle Mfrs. Ass’n v. State Farm Mut. Auto. Ins. Co.*, 463 U.S. 29, 43 (1983). Moreover, as discussed below, NMFS adequately explained both the methods used and the analysis performed, such that the agency’s path is “reasonably discernable.” *Jewell*, 747 F.3d at 625-26 & n.39 (deferring to the agency’s choice of data sets and rejecting argument that the agency “must explain why it decided to include” certain years in abundance calculations). That leaves Oregon with nothing more than “quibble[s] with the science employed in the issuance of the” 2014 BiOp, and this “disagreement cannot, in light of the agency’s care, raise an issue as to the agency’s procedure in evaluating and reviewing the data before it.” *Friends of Endangered Species v. Jantzen*, 589 F. Supp. 113, 119 (N.D. Cal. 1984), *aff’d*, 760 F.2d 976 (9th Cir. 1985). Thus, Oregon’s newest criticisms of NMFS’s analysis should be rejected.²

² This result is particularly warranted because Oregon has waived any objections to NMFS’s technical analysis. At any point during the consultation process, Oregon could have evaluated the data and methods and raised concerns or questions with NMFS. *See, e.g.*, 2008 BiOp at 8.3-47 (presenting estimates derived from the same methods used in the 2014 BiOp); 2014 NOAA C30417:256522, 256527, 256537 (circulating to the sovereigns for review the summary estimates and offering to make underlying data available). Had Oregon done so, NMFS would have responded. *See, e.g.*, 2008 NOAA C1155, 2014 NOAA C33559, C34293 (responding to Oregon’s comments actually received). As it stands, Oregon chose not to pay attention to these details, either with the 2008 and 2014 BiOps or with the exact same data and analysis presented in the *U.S. v. Oregon* BiOp (a biological opinion Oregon represents fully complies with the law). *See* 2008 NOAA B377:8.3-43-8.3-48 (*U.S. v. Oregon* extinction risk and metrics analysis, replicating the analysis performed in the 2008 and 2014 BiOps); *see also* ECF 2001 at 27 n.24 (discussing Oregon’s position on the *U.S. v. Oregon* BiOp). Having failed to raise its confusion or concerns with NMFS and request an explanation, Oregon should not be heard to complain

I. OREGON FAILS TO IDENTIFY ANY ERROR IN TABLE 2.1-5 THAT UNDERMINES NMFS'S ANALYSIS.

Oregon alleges a series of technical and mathematical errors in NMFS's development of Tables 2.1-5. What Oregon does not show, however, is that NMFS ignored a relevant issue, that its methods and analysis are not fairly discernable, or that NMFS made a "clear error" of judgment in performing its analysis. *Lands Council*, 537 F.3d at 994 (agency decision is arbitrary and capricious only where "the record plainly demonstrates that [the agency] made a clear error in judgment").

Oregon begins by arguing that NMFS erred in calculating the 10-year geomean abundance in Table 2.1-5 because 90% of the broodstock (that Oregon and others collect for the safety-net hatchery) are added back into estimates. OR Supp. Br. at 3. Principally, Oregon claims that this metric should examine only fish present on the spawning grounds, and incorporating broodstock into the estimates is therefore improper. Supp. Kostow Decl. ¶ 3. This is not an error, but rather Oregon's mere disagreement with NMFS's methods.

The 10-year geomean abundance estimate represents one (of many)³ measures of fish abundance examined in the 2008 and 2014 BiOps. NMFS used this abundance estimate to evaluate changes in abundance over time, as well as the relationships of current abundance to the Interior Columbia Technical Recovery Team's (ICTRT) recovery abundance thresholds. *See* 2014 BiOp at 80 (table identified as a "comparison" of abundance estimates); 2014 NOAA C34293:288224 ("Both the 2010 Supplement and the 2014 Supplemental Opinion update those

now. *Vt. Yankee Nuclear Power Corp. v. NRDC*, 435 U.S. 519, 553-54 (1978) ("[A]dministrative proceedings should not be a game or a forum to engage in unjustified obstructionism by making cryptic and obscure references to matters that 'ought to be' considered and then, after failing to do more to bring the matter to the agency's attention, seeking to have that agency determination vacated on the ground that the agency failed to consider matters 'forcefully presented.'").

³ NMFS analyzed numerous measures of abundance to inform its comprehensive inquiry into the status of the listed salmonid populations. *See, e.g.*, 2014 BiOp at 70 (considering that most populations had increased abundance from the 5-year status review); *id.* at 73 (considering 10-year abundance trends from the 2013 GPRA Report); *id.* at 105 (Table 2.1-15) (evaluating the BRT abundance trend); *id.* at 110 (annual abundance expressed as percentage of ICTRT abundance thresholds); *id.* at 120 (considering recent aggregate population estimates derived from dam counts); *id.* at 421-23. All of this analysis supported NMFS's conclusions that recent natural-origin abundance has increased but is still below ICTRT recovery abundance thresholds.

mean abundance estimates and *compare them to the ICTRT recovery abundance thresholds and to the previous estimates in the 2008 BiOp.*” (emphasis added)). In view of this comparative purpose, NMFS used methods that allow for an apples-to-apples comparison—it adopted the ICTRT’s estimates in the 2008 BiOp, *see, e.g.*, 2008 BiOp at 8.3-47 & n.1; 2014 NOAA B282:27646, and it updated those estimates using the ICTRT’s methods in 2014, *see* 2014 BiOp at 79 (explaining adoption and updating of the ICTRT’s methods); 2014 NOAA C34293:288224-25 (Response A7). Given the purpose of this metric, NMFS’s methods are entirely rational. *See* Fed. Supp. Br. at 10 (ECF 2040) (explaining importance of comparing estimates in the same units).

In arguing that the 10-year geomean abundance estimate must be calculated differently, Oregon simply ignores the purpose and function of the metric. It also wrongly assumes that no other metric examines fish presence on the spawning grounds. The 10-year geomean total adult spawners estimates consider only fish on the spawning grounds, and that data (including natural-origin fish on the spawning grounds) is used to derive the “S” term in the R/S calculations. *See* Fed. Supp. Br. at 7 & n.12 (explaining this metric’s intent to analyze actual spawners on the spawning grounds, and that the annual data used in the calculations supplies the input for the R/S productivity calculation).⁴ Oregon fails to explain why each metric must examine the same thing, much less why NMFS’s 10-year geomean abundance estimate rendered its 2014 analysis arbitrary and capricious.

Oregon next identifies a few instances where minor, technical errors were made in developing Table 2.1-5. Oregon is correct that NMFS inadvertently excluded age-6 fish from the mean natural-origin abundance calculations. OR Supp. Br. at 4. Age-6 fish are rare, and the effect of including age-6 fish in the abundance calculations would *increase* abundance and

⁴ NMFS added the 90% of broodstock removals to the “R” term in R/S calculations, as is done in ICTRT R/S estimates and as is undisputed by Oregon. *See* Supp. Kostow Decl. ¶ 3 (“[I]t may be appropriate to include [broodstock removals] in a measure of recruits...”).

associated 10-year geomean abundance estimates. *See* Attachment A.⁵ In isolated instances, Table 2.1-5 also carried forward values reported in the 2013 sovereign review draft BiOp (2014 NOAA C30417:256527) and NMFS inadvertently did not update these values based on the final spreadsheets (2014 BiOp C34270). These errors are identified in Attachment B, which demonstrates that these errors did not affect NMFS’s evaluation or the relationships examined in the 2014 BiOp.⁶ Oregon does not assert otherwise.

In short, Oregon does not identify any “clear error” in NMFS’s addition of broodstock into the 10-year geomean abundance estimates. Moreover, while Oregon identifies “minor technical mistakes” that resulted in a more conservative analysis, it “develops no argument suggesting that the alleged errors resulted in prejudicial treatment or that the agency’s ultimate decision would have been any different but for these inaccuracies.” *Hill Dermaceuticals v. FDA*, 709 F.3d 44, 47-48 (D.C. Cir. 2013).

II. OREGON’S ALLEGATIONS THAT NMFS INFLATED MEAN R/S ESTIMATES MISCONSTRUE THE DATA AND ARE INCONSISTENT WITH OREGON’S OWN ACTIONS TAKEN OUTSIDE OF LITIGATION.

Oregon develops a new argument regarding Table 2.1-9 that NMFS systematically overestimated R/S by excluding from the mean R/S calculations years where zero or less than five spawners were estimated. OR Supp. Br. at 4; Supp. Kostow Decl. ¶ 7 & Table 2. Oregon’s theory is that where no spawners are estimated (the “S” in “R/S”), there must be no returns (the “R” in “R/S”) and the R/S therefore must equal zero (or a “dummy” value of “0.000001”). *Id.*

⁵ Column Q of the spreadsheets (*e.g.*, 2014 NOAA C34270, “Up Gr Ronde_11” tab) is where the error occurred, and that column is only used to calculate 10-year geomean natural-origin abundance. Thus, the error does not affect any remaining metrics or calculations in the BiOp, and Oregon does not contend otherwise.

⁶ For the Marsh Creek populations, the effect of the transcription error was to *underestimate* the most recent 10-year geomean abundance and most recent 10-year geomean total adult spawner estimates. *See* Attachment B. For the Innaha population, a cell reference error resulted in an incorrect total adult spawners estimate, but this error did not affect the mean R/S estimate reported in Table 2.1-9 of the 2014 BiOp for this population. *Id.* For the Yankee Fork population, Oregon is incorrect that there was an error “across all values.” Supp. Kostow Decl. ¶ 5. The error is limited to the 10-year geomean percent natural-origin spawners. *See* Attachment B. And Federal Defendants were unable to find an error in the “wild abundance value” for the Methow population, as Oregon asserts. Supp. Kostow Decl. ¶ 5; *see also* Attachment B.

This argument is new, and the reason it has not been raised previously—either by the experts during the consultation or by Oregon in litigation—is because the theory lacks scientific merit.

First, an estimate of zero spawners does not necessarily mean there were actually no spawners (or returns). The data underlying the R/S estimates are not 100 percent coverage surveys that census every fish present on the spawning grounds. Abundance numbers are based on surveys of redds⁷ and other methods that produce an *estimate*. *See, e.g.*, 2014 NOAA B128:9866; *see also* Exhibit 1 at 12 (ICTRT).⁸ In most, if not all, cases where zero spawners were estimated, there were returning adults identified as progeny from these brood years, indicating spawning did occur. For example, with Oregon’s example of the Sulphur Creek population, OR Supp. Br. at 4, zero spawners were estimated in 1984, but that brood year had 55 returns. *See* 2014 NOAA C34270 (“Sulphur Creek_12” tab, cell U:38, where Column U equation copied into cell U:38). Thus, although the “S” in “R/S” is estimated as zero spawners, the data belie Oregon’s theory that this situation means there were no returns, much less that R/S equals zero (or a “dummy” value of near zero). *See* Exhibit 2 at 5 (Table 76 note “a”) (Oregon acknowledging outside of litigation that returns occur in years where “no parents [were] observed”).

Second, Oregon’s arguments ignore basic principles of salmonid biology—that productivity is at its highest in years where spawner numbers approach zero. *See* 2014 BiOp at 114 (Figure 2.1-25) (showing highest R/S at lowest spawner densities); 2014 Corps 4:910-945 (2014 BiOp, Appendix C). For example, the Upper Grande Ronde spring/summer Chinook population had an estimated 8.2 returns and 2.82 spawners for the 1989 brood year, for an R/S ($8.2/2.82$) of 2.91. *See* 2014 NOAA C34270 (“Up Gr Ronde_11” tab, Cell U:43; O:43). Similarly, the 1999 brood year had an estimated 7.44 returns and 4 spawners, for an R/S of 1.86. *Id.* (Cell U:53; O:53). These R/S values, which NMFS did not include in its mean R/S estimates,

⁷ A “redd” is “[a] nest constructed by female salmonids in streambed gravels where eggs are deposited and fertilization occurs.” 2014 BiOp at 26.

⁸ The referenced page numbers for the Exhibits are those located in the footer of the document.

are much *higher* than those estimated in the surrounding years, and certainly did not equal zero. *But see* Supp. Kostow Decl. at 5, Table 2 (equating these years as having an R/S of “0.000001”). By pretending that R/S actually equals zero in the years with very low or no estimates of spawners, Oregon inverts the actual biological relationships occurring with salmonid populations, relationships that Oregon readily acknowledges in non-litigation forums. *See* Exhibit 2 at 4 (Oregon Native Fish Status Report) (“Therefore, the highest recruit-per-spawner values will occur at those spawner densities nearest to zero.”); *id.* at 5 (Table 76 & note “a”) (finding that R/S is merely undefined, not that it equals zero or a “dummy” value of near zero).⁹

Contrary to Oregon’s claims, NMFS conservatively responded to this situation. As Dr. Toole explained in 2008:

[T]he ICTRT did not include years with very low spawner numbers (less than 5 spawners) in their R/S calculations because inclusion of these low values tends to bias R/S averages upward (ICTRT 2007a, [2008 NOAA B194]). NMFS also adopted this conservative approach—removing these years from the average R/S estimates, and *thereby lowering the average R/S estimates for some populations.*

2008 Declaration of Dr. Toole at ¶ 30 (ECF 1566) (emphasis added); Exhibit 1 at 13 (ICTRT, similarly explaining that “the bias induced in estimates of productivity at low abundance can substantially inflate productivity estimates”); *see also* 2014 BiOp, Appendix C at C-31–C-36 (2014 Corps 4:940-945) (exploring R/S at low spawner levels using different assumptions, such as deleting years with zero spawners, deleting years with 5 or less spawners, and adding 1 to spawners and recruits using all data available). Oregon’s post-hoc litigation arguments—that NMFS’s methods inflate (rather than lower) mean R/S estimates—are simply wrong.

Oregon’s only remaining complaint with Table 2.1-9 is the allegation that NMFS departed from its “described methods” by not calculating R/S for each salmonid population based on the exact same set of brood years. Supp. Kostow Decl. ¶ 6. But Oregon makes no effort

⁹ Indeed, in 2008, Oregon’s own declarant acknowledged that there were years with zero spawners, but notably did not propose to insert a “dummy” value of zero for those years. *See* Declaration of Ed Bowles ¶ 48 (ECF 1510). Oregon also purportedly “replicate[d] the R/S results in the 2008 FCRPS Biological Opinion” and identified no error of systematically overestimating the R/S values, as Oregon now contends. *Id.* ¶ 47.

to identify NMFS’s “described methods,” which are explicitly stated in the 2014 BiOp (and many other places in the record). As NMFS explained: “The exact years for each population [used to calculate the metrics] correspond to the time periods applied in the ICTRT (2007a) gap analysis report, with the initial year generally ranging from 1979 to 1981. These time periods have been applied consistently to key metrics such as R/S productivity.” 2014 BiOp at 49 n.5; *see also* 2014 NOAA B282:27816 (noting that actual years used vary by population); 2008 BiOp at 8.3-47 (same); 2008 NOAA C1155:6 (Response 2-E); 2008 Declaration of Dr. Toole ¶¶ 26-30 (ECF 1566); 2008 Reply Declaration of Dr. Toole ¶¶ 3-4, 6 (ECF 1649). Thus, contrary to Oregon’s allegations, there is no inconsistency with NMFS’s methods or its application of those methods in Table 2.1-9.¹⁰

III. OREGON’S DISCUSSION OF EXTINCTION RISK PROBABILITIES AND THE ANALYSIS THAT “SHOULD” BE REQUIRED IGNORES A MYRIAD OF RELEVANT FACTORS.

Federal Defendants have already thoroughly addressed the remainder of Oregon’s criticisms regarding the extinction risk, efficiency of the Reasonable and Prudent Alternative (RPA) habitat restoration program, and the problems with Oregon’s preferred smolt-to-adult return (SARs) analysis. Nevertheless, a few additional points raised by Oregon’s supplemental filing merit a brief response.

First, Oregon contends that the Upper Grande Ronde spring/summer Chinook population “is in danger of imminent extinction” and that recent actions have not actually resulted in any reduced extinction risk probabilities for this population. OR Supp. Br. at 5; Supp. Kostow Decl. ¶ 8. Oregon, however, ignores the factors relevant to the inquiry. Most notably, Oregon (in partnership with the Nez Perce Tribe and others) operate the safety-net hatchery program for the Upper Grande Ronde population, as well as many other hatchery programs throughout the

¹⁰ Oregon also ignores its own positions taken in this case, namely, that Oregon was able to “replicate the R/S results” and that “starting and ending dates do not particularly influence the results [for the R/S metric].” Declaration of Ed Bowles ¶¶ 34, 47, 49 (ECF 1510).

State.¹¹ Even though these programs are undeniably important in any extinction risk inquiry, Oregon ignores them entirely.¹² Nor does Oregon address the other factors relevant to that inquiry, such as the ongoing actions that have already improved survival and reduced risk and the full suite of RPA actions that will further affect extinction risk probabilities. *See* Fed. Supp. Br. at 10-19. Oregon also fails to address or acknowledge the ESA construct—that the Section 7(a)(2) inquiry occurs at the species, not population, level, and any extinction risk analysis must consider the effects of multiple populations on the “species” risks of extinction. *Id.* at 17-19. Oregon cannot impugn NMFS’s analysis by failing to address the factors relevant to the extinction risk inquiry.

In any event, Oregon is wrong in arguing that reduced extinction risk estimates reported in the 2014 BiOp (from 70% risk in the 2008 BiOp to a 48% risk in the 2014 BiOp) do not indicate a change in extinction risk probabilities. OR. Supp. Br. at 5-6; Supp. Kostow Decl. ¶¶ 9-10. As we explained, these are conservative estimates that assume the cessation of hatchery supplementation, and they do not account for ongoing and projected changes that influence extinction risks. Fed. Supp. Br. at 14. The estimates do, however, inform evaluation of

¹¹ *See* www.dfw.state.or.us/fish/hatchery/ (last visited July 14, 2015); *see also* www.dfw.state.or.us/fish/HOP/Lookingglass%20HOP.pdf (last visited July 14, 2015) (Oregon’s “Lookingglass Hatchery participates in both harvest and conservation programs. The Grande Ronde Spring Chinook program is a conservation program using supplementation to restore spring Chinook salmon populations in the Grande Ronde Basin.”).

¹² Oregon’s only reference to hatchery programs is a sweeping assertion that hatchery programs are ineffective in increasing abundance of naturally produced fish. Supp. Kostow Decl. ¶ 13. This assertion begs the question why Oregon supports and operates hatcheries throughout the State, including the hatchery program for the Upper Grande Ronde population. It also contradicts its own statements on the issue. *See* 2014 USBR 45747:45766 (Oregon Department of Fish and Wildlife (ODFW), noting the “hatchery program is providing a demographic boost that appears to be critical in preventing the population from going extinct.”). And Oregon overstates its case in relying on Scheuerell et al. (2015). Supp. Kostow Decl. ¶ 13. That study found a mean 2.5% effect of the hatchery program on increasing natural-origin densities for the Upper Grande Ronde population, with a 63% probability that the effect was positive. Exhibit 3 at 7. Another analysis indicated that “the supplemented populations increased by 1-13% relative to nonsupplemented years.” *Id.* at 8. These findings do not equate with proof that there is no benefit as Oregon argues here. Nor does the study show the safety-net programs are ineffectual for their intended purpose. *Id.* at 8 (“[A]rtificial propagation (including supplementation) may be a potentially useful intervention for preventing imminent extinction of specific populations.”).

probabilities of short-term extinction. *Id.* In 2008, there was a 50% likelihood that the short-term extinction risk estimate for the Upper Grande Ronde population was 70% or less; in 2014, the data and analysis show that there is a 50% likelihood that the short-term extinction risk estimate for this population was 48% or less. *See* 2014 BiOp at 85; *see also id.* at 50 (“If a point estimate is greater than the goal, there is greater than 50% likelihood that the goal has been met (for retrospective estimates) or is likely to be met (for prospective estimates).”); *id.* at 50-54, 66-69. This change plainly signals reduced probabilities of short-term extinction.¹³

Second, while admitting that the tributary spawning and rearing habitat for the Upper Grande Ronde population is severely degraded and that improvements in the habitat will increase survival and productivity, Supp. Kostow Decl. ¶¶ 11-12, Oregon asserts that “the immediate problem in the Upper Grande Ronde is poor survival through the FCRPS,” *id.* ¶ 13. Here, again, it is notable what Oregon chooses not to address. Oregon, its experts, and others have identified the immediate threats to the population as severely degraded tributary spawning and rearing habitat. Fed. Supp. Br. at 16 (citing 2014 NOAA C2020, Oregon’s recovery plan). Moreover, juvenile mortality is often substantially higher for Upper Grande Ronde smolts in their journey to the first FCRPS dam than through the FCRPS system itself. *Id.* at 16. For example, only 41.1% and 31.9% of juvenile salmon from this population tagged at the Upper Grande Ronde smolt trap survived from the tributary habitats to the first FCRPS dam (Lower Granite Dam) in 2012 and 2013, respectively. 2014 NOAA B114:9316 (Table B7); 2014 USBR 73583:73685 (Table B7). By way of comparison, juvenile survival from the tributary habitats to McNary Dam (thus passing the four Snake River dams) was estimated at 40.9% and 28.6%, respectively, indicating that very few additional fish were lost between Lower Granite and McNary Dams. *Id.*; *see also* 2014 BiOp at 364 (Figure 3.3-2) (estimating that 55.3% to 71% of wild yearling Chinook salmon survived from Lower Granite to Bonneville dams in 2011 to 2013); 2014 USBR 73583:73638

¹³ Indeed, contrary to its current position, Oregon uses point estimates and asserts that differences in those estimates represent changes in a population’s status. *See, e.g.,* 2014 NOAA C31747:265583 (Oregon arguing that decreased point estimates means the status of a species “declined”).

(Table 28).

Outside of this litigation, Oregon recognizes that factors upstream from the FCRPS dams are an immediate and critical threat to the fish. *See, e.g.*, 2014 USBR 45747:45767 (finding that “high smolt mortality between the release location and Lower Granite Dam” is a significant challenge facing these populations); 2010 NOAA BB251:1093, 1107 (ODFW recognizing that “substantial smolt mortality occurs in the free-flowing portion of the migration corridor before reaching Lower Granite Dam” and the importance of addressing these “factors that currently limit smolt survival and hinder recovery efforts”). Yet, here, in this litigation, Oregon disregards these upstream factors. Notwithstanding Oregon’s litigation position, factors outside of the FCRPS are impacting these fish populations. That Oregon now chooses not to acknowledge this in its analysis does not alter this fact or undermine NMFS’s analysis in the 2014 BiOp.

Third, Oregon continues with its complaints about the RPA tributary habitat restoration program, generically asserting that the program is behind schedule and that the agencies are merely relying on “unspecified ‘supplemental’ habitat actions.” Supp. Kostow Decl. ¶ 11. The assertion that supplemental projects are “unspecified” is false. *See* 2014 NOAA B48:4435-39; 2014 NOAA C32516-17, C32777; Tehan Declaration ¶¶ 53-61 (ECF 2006); *see also, e.g.*, USBR 107159, 107143, 107132, 107127, 107121, 107119 (agencies working with the Umatilla Tribe to develop supplemental projects). Even Oregon admits (outside of litigation) that “[h]abitat restoration projects funded by [Bonneville Power Administration] and Bureau of Reclamation in the Upper Grande Ronde River watershed are addressing habitat capacity which should, in turn, result in an increase in productivity, such as smolts/spawner.” Exhibit 4 at 10, 34. And the legal premise underlying Oregon’s argument—that there must be certainty in implementation schedules and success in order for mitigation to be considered in a BiOp—is not the law. *Ariz. Cattle Growers’ Ass’n v. Salazar*, 606 F.3d 1160, 1164 (9th Cir. 2010) (“[T]he ESA accepts agency decisions in the face of uncertainty” and “does not require that the [agency] act only when it can justify its decision with absolute confidence.”); *NWF v. NMFS*, 839 F. Supp.

2d 1117, 1130 (D. Or. 2011).¹⁴ NMFS appropriately and rationally considered the implementation and effects of the tributary habitat program, and Oregon provides no grounds to second-guess that analysis. *See* 2014 BiOp at 227-318; Tehan Declarations (ECF 2006, 2030).

Finally, Oregon continues to espouse its own preferred way of performing a jeopardy analysis, *see* Supp. Kostow Decl. ¶¶ 11-13, but it also continues to avoid addressing the well-founded criticisms of that analysis. For example, in response to allegations that Oregon's SARs approach is centered on achieving recovery (not avoiding jeopardy), Oregon disavowed that a population must achieve recovery. OR SJ Reply at 19 (ECF 2020). Without explanation, Oregon reverts to arguing that NMFS's analysis is flawed because recovery targets are not reached. Supp. Kostow Decl. ¶¶ 12-13 (arguing that more improvements are needed to reach ICTRT recovery abundance thresholds). Similarly, Dr. Zabel explained that Oregon's analysis is predicated on identifying SAR improvements needed to "instantly achieve recovery *in a single generation.*" Reply Declaration of Dr. Zabel ¶ 14 (ECF 2029). Oregon has never addressed this problem: It has never explained why an analysis focused on achieving recovery in a single generation is biologically meaningful or otherwise renders NMFS's jeopardy analysis arbitrary and capricious. And Oregon continues to advance an analysis predicated on the assumption that nothing is being done to improve survival in the mainstem migration corridor or the estuary. Supp. Kostow Decl. ¶ 13 (asserting that improvements in the tributaries "alone" are not enough, and improvements "after the smolts leave the tributaries is also required" to recover the species in one generation). While Oregon may disagree with the degree of benefits expected from the numerous RPA actions being implemented to improve conditions in the mainstem and estuary habitats, it cannot deny those actions are occurring, and it cannot justify the complete failure to

¹⁴ Indeed, even Oregon has argued against such a standard, contending that an implementation history, combined with Oregon's mere "promise" to improve its hatcheries, is enough to allow NMFS to consider those improvements in an ESA biological opinion. *See* Oregon's Response to Motion for Partial Summary Judgment, *Native Fish Society v. NMFS*, 2013 WL 5279131, 12-cv-431-HA (D. Or.) (ECF 175 at 1) ("NMFS also appropriately considered the history of improvements that ODFW made, as well as those it promised to make, to the Sandy Hatchery programs in approving the [Hatchery Genetic Management Plans]").

address those actions in its analysis. *See* 2014 BiOp at 319-388, 407-415 (discussing actions and associated improvements in the estuary and mainstem habitats). Oregon's arguments are built on unjustifiable assumptions, and this analysis does not undermine NMFS's 2008 and 2014 BiOps.

CONCLUSION

NMFS and the Action Agencies set a high standard in this consultation. The agencies performed a rigorous analysis using the best data and methods available. They shared that analysis, including the underlying data and calculations, with the sovereigns and experts at each step during this multi-year consultation process. The agencies invited the most searching level of scientific scrutiny on all aspects of the 2008 and 2014 BiOps, and they did so specifically to ensure that the resultant analysis considered the relevant factors and was biologically sound. While Oregon's supplemental filings show that there is disagreement with the product of this collaboration, they overlook the consensus among many of the sovereigns and experts in the region that this biological analysis is sound. This fact alone readily shows that, even considering occasional technical imperfections in spreadsheets and tables in the voluminous record, NMFS's analysis is not "so implausible that it could not be ascribed to a difference in view or the product of agency expertise." *Motor Vehicle Mfrs. Ass'n*, 463 U.S. at 43. Oregon's criticisms of NMFS's analysis should be rejected.

Dated July 15, 2015

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CERTIFICATE OF SERVICE

I certify that on July 15, 2015, the foregoing was electronically filed through the Court's electronic filing system, which will generate automatic service upon on all Parties enrolled to receive such notice. I also certify that the following will be manually served via overnight mail:

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APPENDIX A

“Most Recent 10-Year Geomean Abundance” as reported in Table 2.1-5 of the 2014 BiOp, updated to reflect age-6 spawners. Updated calculations developed by modifying the formula in Column Q to add in age-6 fish reported in Column L. To illustrate, the corrected formula for the Upper Grande Ronde population in 2011 (row 65 of 2014 NOAA C34270, “Up Gr Ronde_11” tab) would be “=(P65*J65)+(P65*K65)+(T65*0.9)+(P65*L65),” where the bolded text indicates the equation that incorporates any age-6 fish. Corrections identified in bold, underline text.

ESU	MPG	Population	Most Recent 10-yr Geomean Abundance	
			From Table 2.1-5	Corrected for Age-6 Spawners
Snake River Spring/Summer Chinook	Lower Snake Grande Ronde / Imnaha	Tucannon	375	375
		Catherine Creek	137	137
		Upper Grande Ronde	65	65
		Minam River	489	489
		Wenaha River	436	436
		Lostine/Wallowa Rivers	370	370
		Imnaha River	460	460
	South Fork Salmon	South Fork Salmon Mainstem	813	<u>821</u>
		Secesh River	605	<u>607</u>
		East Fork S. Fork Salmon (Incl. Johnson)	282	<u>283</u>
	Middle Fork Salmon	Big Creek	181	<u>184</u>
		Bear Valley/Elk Creek	471	<u>479</u>
		Marsh Creek	229*	<u>231</u>
		Sulphur Creek	58	<u>59</u>
		Camas Creek	47	47
		Loon Creek	77	<u>78</u>
		Chamberlain Creek	648	<u>658</u>
	Upper Salmon	Lemhi River	81	81
		Valley Creek	101	<u>102</u>
		Yankee Fork	16	16
		Upper Salmon River (above Redfish L.)	360	<u>366</u>
		Lower Salmon River (below Redfish L.)	125	<u>127</u>
		East Fork Salmon River	320	<u>324</u>
Pahsimeroi River		223	<u>225</u>	
Upper Columbia Spring Chinook Salmon	Eastern Cascades	Wenatchee R.	568	568
		Methow R.	398	398
		Entiat R.	148	148
Snake River Fall Chinook Salmon	Main Stem and Lower Tributaries	Lower Mainstem Fall Chinook 1977-Most Recent BY	4576	4576
		Lower Mainstem Fall Chinook 1990-Most Recent BY	4576	4576

* See Appendix B, Marsh Creek population.

APPENDIX B

Comparison of Table 2.1-5 estimates from the 2013 Sovereign Review Draft Biological Opinion (2014 NOAA C30417), the 2014 Biological Opinion (2014 NOAA A1), and the final spreadsheets (2014 NOAA C34270). Corrections identified in bold, underline text.

Marsh Creek Snake River Spring/Summer Chinook ESU	ICTRT	Most Recent 10-year Geomean Abundance (2008)	Corrected 2008 BiOp Estimate	Most Recent 10-year Geomean Abundance (2014)	Most Recent 10-year Geomean Total Adult Spanwers	Most Recent 10-year Geomean Percent Natural-Origin Spawners
Draft BiOp, 2014 NOAA C30417:256527.	500	42	53	221	225	1.00
2014 BiOp, Table 2.1-5.	500	42	53	221	225	1.00
Updated Spreadsheet, 2014 NOAA C34270 (Marsh Creek_12)		42 Cell AC:84	53 Cell AC:85	<u>229</u> Cell AC:86	<u>231</u> Cell AH:89	

Yankee Fork Snake River Spring/Summer Chinook ESU	ICTRT	Most Recent 10-year Geomean Abundance (2008)	Corrected 2008 BiOp Estimate	Most Recent 10-year Geomean Abundance (2014)	Most Recent 10-year Geomean Total Adult Spanwers	Most Recent 10-year Geomean Percent Natural-Origin Spawners
Draft BiOp, 2014 NOAA C30417:256527.	500	13	12	16	32	1.00
2014 BiOp, Table 2.1-5.	500	13	12	16	32	1.00
Updated Spreadsheet, 2014 NOAA C34270 (Yankee Fork 11)		13 Cell AC:84	12 Cell AC:85	16 Cell AC:86	32 Cell AH:89	<u>0.51</u> Cell AL:87

Imnaha Snake River Spring/Summer Chinook ESU	ICTRT	Most Recent 10- year Geomean Abundance (2008)	Corrected 2008 BiOp Estimate	Most Recent 10-year Geomean Abundance (2014)	Most Recent 10-year Geomean Total Adult Spanwers	Most Recent 10-year Geomean Percent Natural- Origin Spawners
Draft BiOp, 2014 NOAA C30417:256527.	750	380	486	460	1288	0.30
2014 BiOp, Table 2.1-5.	750	380	486	460	1288	0.30
Updated Spreadsheet, 2014 NOAA C34270 (Imnaha_11)		380 Cell AC:85	486 Cell AC:86	460 Cell AC:86	1260 Cell Reference Error*	0.30 Cell AL:88

*For the Imnaha spring/summer Chinook population, 2014 NOAA C34270, “Imnaha_11” tab, the formula for each cell of Column O included a term for Column R (jack fraction of hatchery spawners) that referenced the wrong row (year) of Column R. When corrected to reference the same row (year) as the other terms in the formula (*i.e.*, for row 5, “=D5-((D5*(1-E5))*R5)-(P5*I5)”), the “Most recent 10-year geomean total adult spawners” is 1260 (corrected Cell AC:90). That correction did not affect the estimate of natural-origin abundance, so had no effect on the general relationship of natural-origin abundance to the 2008 or ICTRT recovery thresholds for this population. Nor did the correction alter the mean R/S value reported in the 2014 BiOp, Table 2.1-9 (corrected Cell AC:80).

Methow Upper Columbia Spring Chinook ESU	ICTRT	Most Recent 10- year Geomean Abundance (2008)	Corrected 2008 BiOp Estimate	Most Recent 10-year Geomean Abundance (2014)	Most Recent 10-year Geomean Total Adult Spanwers	Most Recent 10-year Geomean Percent Natural- Origin Spawners
Draft BiOp, 2014 NOAA C30417:256527.	2000	180	170	398	1587	0.21
2014 BiOp, Table 2.1-5.	2000	180	170	398	1587	0.21
Updated Spreadsheet, 2014 NOAA C34270 (UCR Methow CH 11)		180 Cell AC:84	170 Cell AC:85	398 Cell AC:86	1587 Cell AC:89	0.21 Cell AL:87

EXHIBIT 1

March 14, 2007 Email from Tom Cooney to Chris Toole, Re: "Appendix A (viability curve methods) and some adds to main document language"

Located in NMFS's 2008 NOAA Administrative Record at C.2.3 (Portfolio of emails from PDF File "2006-10-17_to_2007-03-28")

From: [Tom Cooney](#)
To: [Chris Toole](#);
Subject: Appendix A (viability curve methods) and some adds to main document language.
Date: Wednesday, March 14, 2007 6:09:09 PM
Attachments: [Appendix A March 14 2007.doc](#)
[Additional language March 14.doc](#)

I don't know if I sent you the Appendix A draft when I circulated it to the TRT and Mike F. If not, here it is. I have also attached a couple of additions to paragraphs in the main document that relate to our favorite topics. The plan is to get this in the mail to the ISAB Friday, then work on posting on the web early next week.

Appendix AA

**Population Viability Curves for
Interior Columbia ESUs**
Interior Columbia Basin Technical Recovery Team

March 14, 2007

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Background

The Interior Columbia Technical Recovery Team (ICTRT) adapted a modeling approach for generating viability curves (McElhany et al. 2003) as a means of expressing the productivity and abundance component of population level viability criteria. A viability curve is defined by a set of paired combinations of productivity and abundance values corresponding to a particular extinction or quasi-extinction risk level. The ICTRT viability criterion for abundance and productivity requires a combination that addresses considerations for demographic persistence, the maintenance of genetic integrity and resilience to localized catastrophic risks.

We incorporate a minimum abundance threshold corresponding to the relative size category of the target population to address this range of objectives (Figure A-1). The standard time frame for assessing risk of extinction used in our analyses was 100 years. Each combination of productivity and abundance on a particular viability curve projects to the same modeled risk of extinction over a 100 year period.

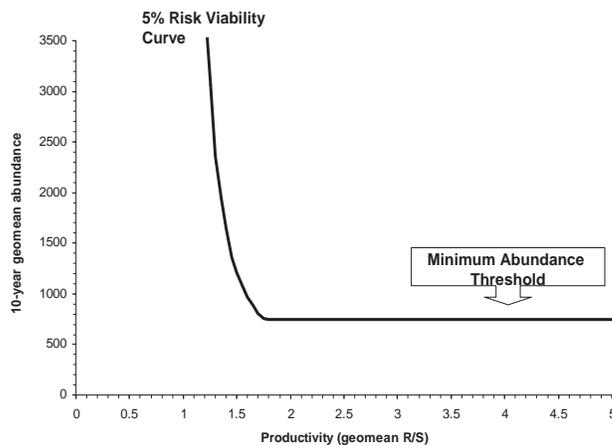


Figure A-1: Viability curve example. Curve represents combinations of abundance and productivity values associated with a 5% risk of extinction in 100 years, truncated to incorporate a minimum abundance threshold of 750.

The viability curve concept is adaptable, as the curves can be generated specific to a form of stock-recruit relationship and type of time series data available for a particular population or set of populations. In this example curve, abundance is expressed in terms of equilibrium spawning level and productivity as the expected geometric mean return per spawner at low to moderate abundance (the slope of the upward ascending limb of a Hockey-Stick function). In assessing the current status of a population against a viability

curve, we recommend using a recent 10 year geomean of natural spawners as a measure of current abundance. Current intrinsic productivity should be estimated using spawner to spawner return pairs from low to moderate escapements over a recent 20 year period.

We developed two sets of ESU specific viability curves, each using a different measure of population growth rate. One set of curves expresses productivity in terms of return per spawner (to the spawning grounds). The alternative set of curves uses short term population growth rate (λ) as a measure of recent geomean productivity. The simple population growth rate based approach allows for assessments in circumstances in which the available data for assessing a population trend or abundance is limited and subject to high measurement error (Holmes, 2001). Fairly detailed annual spawner recruit data sets have been generated for most Interior Basin listed chinook populations and many steelhead populations. Return per spawner based viability assessments can be directly adapted to accommodate large variation in annual abundance relative to potential capacity limitations as well as to autocorrelation in marine survival rates. We provide a detailed description of the derivation of the return per spawner based curves in the following sections, followed by a brief summary of adaptations of these basic steps to generate the population growth rate (λ) based viability curves.

In the following sections, we provide descriptions of the model we used to generate viability curves, descriptions of general and ESU specific input parameters, and a set of viability curves for each ESU. Representative estimates of year to year variability in return per spawner or population growth rates are key input parameters into the model used to generate population viability curves. We discuss key assumptions and uncertainties associated with curve generation and applications. We followed the basic approach for estimating variance and autocorrelation in production rates outlined in Morris & Doak (2002), adapting the approach to apply to time series of spawner to spawner return data sets.

We provide a brief summary of the use of viability curves in assessing current status. We used viability curves corresponding to a 25%, 5% and 1% risk of extinction in 100 years to define population level risks. Combinations of abundance and productivity falling below the 25% risk curve depicted in the chart (Fig. A-2) would be classified as at High risk. Combinations exceeding the 1% risk curve would be rated as at Very Low Risk. Abundance/productivity combinations falling between the 5% and 1% viability curves would be rated at Low Risk.

Under historical conditions, it is likely that most populations would have demonstrated combinations of intrinsic production potential and abundance well above the 5% Viability Curve. At the population level, recovery strategies should be targeted on achieving combinations of abundance and productivity above the threshold represented by the 5% viability curve. Estimates of current status will be based on sampling information and will therefore be influenced to some extent by sampling induced error and bias. We have provided some examples of approaches to directly incorporate provisions to minimize the potential for erroneously assigning a population to a relatively low risk status when the underlying risk may be high.

The last section of this attachment describes a sensitivity analysis of the effects on a curve of variations in each of the input parameters (variance and autocorrelation in productivity, age structure, and quasi-extinction threshold QET).

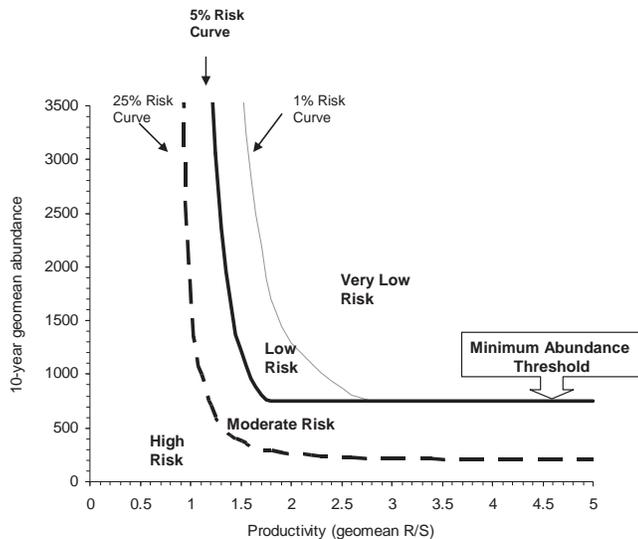


Figure A-2. Viability curve example. Curves represent combinations of abundance and productivity values associated with a 25%, 5% and 1% risk of extinction in 100 years, respectively. 5% and 1% curves truncated to incorporate a minimum abundance threshold of 750.

Viability Curve: Model Structure and Function

We used a stochastic cohort model to generate viability curves. The model generates a projected extinction risk given certain ESU-specific parameter estimates along with combinations of abundance and productivity. Additionally, the model includes an automated grid-search feature allowing the user to generate a viability curve corresponding to a selected risk level (e.g., 5% risk of extinction over a 100-year timeframe). We provide a detailed description of the mechanics of the model in this report.

The model operates on an annual time step. A model analysis consists of a minimum of 1000 iterations, each iteration being projected over at least 100 years. The cumulative results across the iterations are used to generate a probability of extinction corresponding to the input parameters for that analysis.

Stock-Recruit Function

The curves described in this report were generated using a hockey stick stock production function. We chose this function because it accommodates current status assessments based on simple measures of productivity at low abundance and production at capacity. It is also possible to express productivity and abundance/capacity in a viability curve in parameters in terms of the specific metrics in a particular stock-recruitment functions—e.g., Beverton Holt or Ricker curve a and b parameters. In most cases, data used to evaluate current status will be based on a relatively limited number of years. Uncertainty levels and bias in parameter estimates can be very large. Stock recruit function parameter estimates for relatively short data series that are based on fitting a standard function (e.g., Beverton Holt, Ricker or Hockey Stick) using a maximum likelihood or Bayesian fitting routine can contain substantial bias and/or uncertainty. These potential shortcomings are of less consequence if the available data series for a population is of sufficient length and/or if additional information is available to augment the trend data (e.g., environmental correlations, corresponding measures of juvenile production or smolt to adult survivals). Status assessments that use fitted stock recruit curve parameters as an index of current productivity should directly incorporate considerations for sampling induced errors and bias in their assessments.

Model Input Parameters

Two categories of input values are used in generating viability curves for application to Interior Columbia ESU populations. The first set included inputs that were common across all populations, regardless of ESU. Included in these generic inputs were the risk levels chosen for viability curves (e.g., 1%, 5%, and 25%) and the time period for assessing risk (100 years). This set also included values for extinction and reproductive

failure thresholds as described below. The second set of parameters reflects characteristics of the specific populations within each ESU. Each population was assigned a minimum abundance threshold based on its estimated amount of historical spawning rearing habitat (see Attachment B). Population specific inputs included representative age at return proportions and a pair of parameters describing the expected variance and autocorrelation in annual return rates. The data sets used in generating population specific estimates of these parameters are included in population level current status assessments. Draft assessments are available at the ICTRT website. The ICTRT is developing an atlas of the current status assessments. That document will include a brief summary of regional methods for generating population specific estimates of annual abundance, age structure, etc.

Age at Return Distributions

We calculated average age distributions across available trend data sets for populations within each of the Interior Columbia listed salmonid ESUs. In some cases, population specific data sets were not available. If age composition estimates were available for aggregate returns including a population lacking a specific set of estimates, we assumed the aggregate estimate applied to that population.

Productivity: Variance and autocorrelation

One of our major objectives in this analysis was to identify variance and autocorrelation parameters representative of population productivity during rebuilding—a range that would include levels moderately above QET (50 spawners) to levels that would exceed the required equilibrium abundance thresholds specific to each population size category. We develop representative estimates of the variance and autocorrelation in annual return rate estimates for each of the listed Interior Columbia ESUs in this section. The estimates of annual variation in return rates were generated using population specific data sets and were averaged over a set of alternative stock-recruit functions (figure A-3).

Estimates for individual populations were based on relatively short data series subject to high levels of year to year variation. Therefore for those Interior Columbia ESUs represented by multiple populations (i.e., two stream type chinook and three steelhead ESUs), we averaged population level estimates of variance and autocorrelation across populations within ESUs to get representative sets of input parameters for generating viability curves. Population specific annual abundance data sets are described in Attachment B. We compiled brood year return estimates for the 20 most recent complete brood years for each data set.

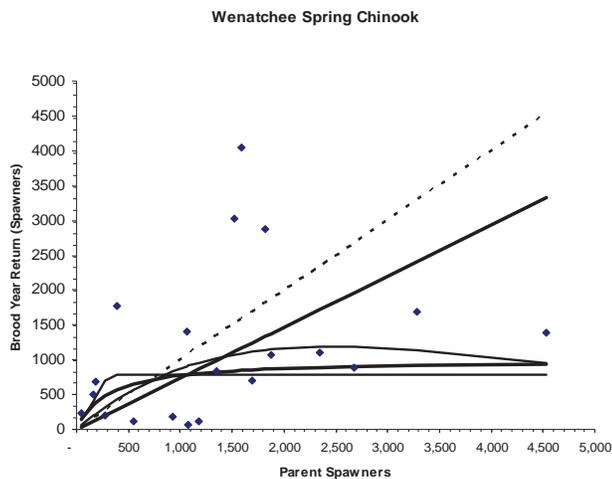


Figure A-3. Wenatchee River Spring chinook salmon population. Example of alternative stock-recruit functions (Random Walk, Hockey-Stick, Beverton/Holt and Ricker functions). Points are annual estimates of natural returns vs. total spawners in natural areas for brood years 1978 to 1999.

Differences in estimates between populations reflect the impacts of measurement error, departures from standard assumptions associated with fitting routines, etc. We considered a finer scale averaging (at the major population group level), but examination of the population level averages indicated more consistency at the ESU level.

We incorporated an autocorrelation parameter into the model used to generate viability curves based on results from our initial evaluation of representative trend data sets for Interior Columbia Basin Chinook and steelhead populations. We evaluated the time series of residuals from fitting a range potential stock recruit functions to the population specific data sets (Figure A-4). The annual residuals consistently demonstrated positive autocorrelation – that is, if the survival rate in a particular year was higher than average, there was a strong tendency for the survival in the following year to also be above average. Years that had relatively low survival rates tended to be followed by years with relatively low survival. The presence of autocorrelation in population growth rates can substantially influence projected extinction risks in population viability assessment models (Morris & Doak, 2002, Wichmann et al. 2005).

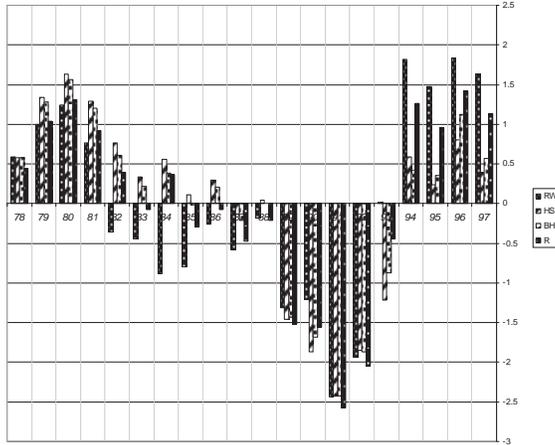


Figure A-4. Wenatchee River Spring Chinook salmon population. Deviations in annual return rates from predicted values using alternative stock/recruit functions.

We estimated simple one year lag correlation coefficients for the sequential series of residuals from fitting the basic stock-recruit functions to the individual trend data sets (Figure A-5). We limited our analysis to lag 1 correlations for several reasons: initial tests indicated lag 1 correlations were substantial and statistically significant; the data series we were evaluating were relatively short compared to the length required to estimate multiple year lag effects; and, incorporating lag 1 autocorrelation can effectively represent longer term cycles/patterns (e.g., Morris & Doaks, 2002).

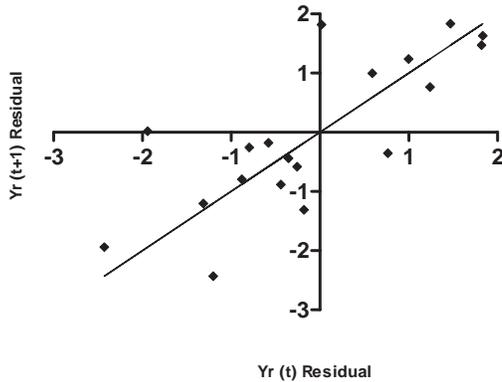


Figure A-5. Autocorrelation in annual variation in return rates. Wenatchee River Spring Chinook salmon population. Deviations in annual return rates from predicted values (Random Walk model). Points: year (t+1) vs. in year (t) residual deviations from predicted. Line represents 1:1 correspondance.

Quasi-Extinction Threshold

We evaluated model projections against a quasi-extinction threshold (QET) of 50 adult spawners per year over four consecutive years (generally corresponding to a brood cycle). A quasi-extinction threshold is defined as “..the minimum number of individuals (often females) below which the population is likely to be critically and immediately imperiled.” (Morris & Doaks, 2002; Ginsburg et al. 1982). We selected 50 as a QET based on four considerations; consistency with theoretical analyses of increasing demographic risks at low abundance, uncertainty regarding low abundance productivity of Interior Columbia ESU populations due to the paucity of escapements less than 50 spawners in the historical record, sensitivity analyses indicating that the probability of multiple very low escapements increases substantially as the QET approaches 1 spawner per year, and consistency with applications by the Puget Sound and the Lower Columbia/Willamette TRTs (McElhany et al. 2003, 2006; Puget Sound TRT, 200). We further discuss each of the rationale in the Population Abundance and Productivity section of our report on viability criteria (ICTRT, 2007).

Reproductive Failure Threshold

The QET is specifically expressed in terms of abundance over a four-year brood cycle. We also applied a Reproductive Failure Threshold (RFT) at the annual escapement time step in our model. In a given spawning year, production from an extremely low number of spawners are subject to decreases in reproductive success due to factors such as inability to find mates, random demographic effects, etc. In our viability modeling, we set production from a particular spawning year to zero if the adult escapement for that year was below the RFT. Initially, we set the RFT at the same value (on a per year basis) used in establishing a Quasi-extinction threshold (QET)—50 spawners. However, we have revised our estimate of the RFT appropriate for application to yearling type chinook and steelhead population model runs to 10 spawners after reviewing updated run reconstruction data sets for Interior Basins Spring/Summer Chinook populations and considering the potential for increases in sampling bias and heightened demographic risks as a function of extremely low abundance levels. We developed two simple analyses to inform setting the RFT at a number appropriate for Interior Basin chinook and steelhead populations. One analysis focused on the relative impact of sampling bias at low escapement levels, the other on a simplified model of demographic risk as a function of low escapements and multiple spawning sites.

Commented [TC1]: New analysis

Low Abundance Sampling Bias

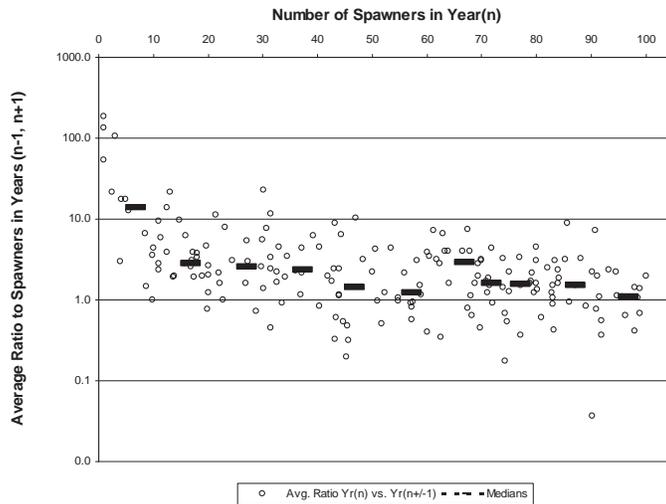
Sampling related errors can substantially increase bias and variability in estimates of productivity derived for low spawning escapement levels. Our estimates of current intrinsic productivities for Interior Columbia Basin populations are based on annual population abundance data series. Natural returns are broken down into age components by applying a sampling based year specific age composition or an average age composition representative of the population. Year specific productivity estimates are then calculated by summing the returns by age corresponding to a particular brood year and dividing by the total parent escapement. Productivity estimates for extremely low spawning escapements in the data series can be biased upwards by sampling induced

errors.

Annual spawner estimates for Interior Columbia Basin yearling type chinook populations are based on redd counts. At very low spawning levels, a single redd represents a substantial proportion of the total return. Annual return per spawner estimates are generated by total estimated returns at age for a given brood year by the parent spawning escapement in that brood year. Missing one or more additional redds at estimated total return levels of 2 to 10 spawners can result in substantial overestimates of spawner return rates.

Year to year variations in estimated spawning abundance is high. We developed a simple example of the potential impact on estimated productivity of year to year variability in abundance and the use of an average age composition to estimate brood year returns. The objective of the exercise was to evaluate the potential for bias in estimating productivity levels associated with extremely low spawning escapements (less than 100 spawners). We incorporated data from Interior Columbia Basin population abundance series into the assessment.

We averaged the relative ratios of low escapement year returns to returns in adjacent years across time series for Interior Columbia Basin population data sets. As an example, the estimated number of spawners in the Bear Valley population of spring/summer Chinook was 16 in 1995. The numbers of spawners estimated for 1994 and 1996 were 56 and 32, respectively. The ratios of the number of spawners in 1994 and 1996 to the estimate for 1995 were 3.5:1 and 2:1, averaging 2.8:1. We ordered spawning escapements and their relative ratios against adjoining return years and calculated median ratios across increments of 10 spawners (Figure A-6).



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A-10

Figure A-6. Average ratios of spawner numbers in year(n) to spawner numbers in years (n+/-1) from Interior Columbia Basin population specific data sets. Ordered by the number of spawners in year n.

Most of the low return levels in the data series were from relatively small populations in the Snake River Spring/summer ESU. For those series, the age information used to allocate natural returns to brood years with low parent escapement levels was an average for the population. For this exercise, we assumed an average age composition of 0.50 age 4 and 0.50 age 5 fish. A simple example will illustrate the level of bias in estimating productivity at low escapements that can arise from the combination of high variability in annual return rates and using average age composition data. Assume that a population data series includes a sequence of 100, 8 and 100 spawners in years 0, 1, and 2 and that the productivity for each of these years is 1.0. Equal proportions of the production from each brood year return at ages 4 and 5. In this scenario, 54 spawners would return in years 4 and 5. Applying the average age structure to year 4, an equal number of spawners (27) would be allocated to brood year 0 and to brood year 1. In this example, the same number of spawners (27) would be estimated as 5 year old spawners in year 6 and allocated to brood year 1. The total estimated returns from brood year 1 would be 55. The productivity from the escapement of 8 spawners in brood year 1 would be calculated as 55 divided by 8, or 6.9 returns per spawner—a substantial overestimate. In this example, estimates of annual productivities for escapements adjacent to the low escapement years would be systematically underestimated as a result of the misallocation of returns.

We evaluated the potential bias as a function of spawner level for escapements falling below 100 across spawning estimates from Interior Columbia population abundance data sets. We calculated median values across estimates grouped in increments of 10 and 25. We estimated the potential bias associated with the median ratios for each group under two different productivity assumptions: a) productivity in the adjacent brood years was equal; and b) productivity in the low escapement year was one 50% of the average productivity for the adjacent years in the series. The results of this simplified exercise indicate that the bias induced in estimates of productivity at low abundance can substantially inflate productivity estimates (Table A-1). The estimated impacts dropped rapidly as the number of spawners increased from 10 towards 50.

Misallocation of spawners to a particular brood year also affects productivity estimates at higher escapement levels. Median ratios of relative escapements in adjacent brood years approach one at higher escapement levels, indicating that the impact of misallocation by age would not result in a directional bias, but would largely translate into increased variance in estimated productivities.

Table A-1. Impact of bias in allocating returns on estimates of brood year specific productivities. Impact illustrated for two relative productivity scenarios: 1) actual productivity for low spawner escapement year equal to productivity for adjacent spawning years; and 2) actual productivity of low spawner brood year 50% of value for adjacent spawning years.

Number of Parent Spawners in Year _n	Median Ratio: Spawners(yr _n) to Spawners (yr _{n+1} , yr _{n-1} .)	Relative Bias: Estimated Productivity (Year _n)	
		Year _n Productivity EQUAL TO Year _{n-1,+1} Productivity	Year _n Productivity 50% OF Year _{n-1,+1} Productivity
2 to 10	15.8 : 1	8.40 X	16.3 X
11 to 20	3.1 : 1	2.05 X	3.6 X
21 to 30	2.7 : 1	1.85 X	3.2 X
31 to 40	2.3 : 1	1.65 X	2.80 X
41 to 50	1.5 : 1	1.25 X	1.75 X
50 to 75	1.7 : 1	1.35 X	2.20 X
76 to 100	1.5 : 1	1.25 X	2.00 X

Demographic Risk at Very Low Spawner Abundance

Given the production observed at low escapements, we also developed a simple stochastic simulation of demographics at very low population sizes to inform a revision of the RFT estimate. Spawning ground survey results indicate that spawning redds are often dispersed across several spawning sites within a population even at very low spawning densities. Under those circumstances the probability that one or more females may return to a site without male spawners. We set up a hypothetical population model assuming three spawning areas. We assumed that the average ratio of males to females was 1:1, with annual returns following a binomial distribution and that returning males and females would randomly distribute among the three spawning areas. We generated 1,000 iterations of the model for total spawning returns ranging from 2 to 16. We calculated the effective number of female spawners for each model iteration, defining an effective female spawner as a female return to a spawning area occupied by at least one male spawner. We averaged the proportion of effective female spawners across 1,000 iterations at each spawning level tested (Figure A-7). The expected proportion of effective female spawners decreased from greater than 0.90 to less than 0.80 as spawner numbers declined to below 10. Below this range, the proportion of effective spawners in this simple model decreased substantially as a function of decreasing return levels.

The results of these simple simulations supported setting an RFT of 10 spawners in the model for generating viability curves for yearling chinook populations. Upper Columbia steelhead populations also utilize tributary habitats for spawning and extended rearing. We applied the same RFT in developing viability curves for these populations. The primary spawning and rearing habitat for Snake River fall chinook is in the mainstem of the Snake River and the lower reaches of major tributaries. Spawning areas within the remaining population of Snake River fall chinook are distributed in relatively small patches across over 100 km of the mainstem Snake River. As a result, we retained a higher RFT of 50 spawners in generating a set of viability curves for application to the Snake River fall chinook population.

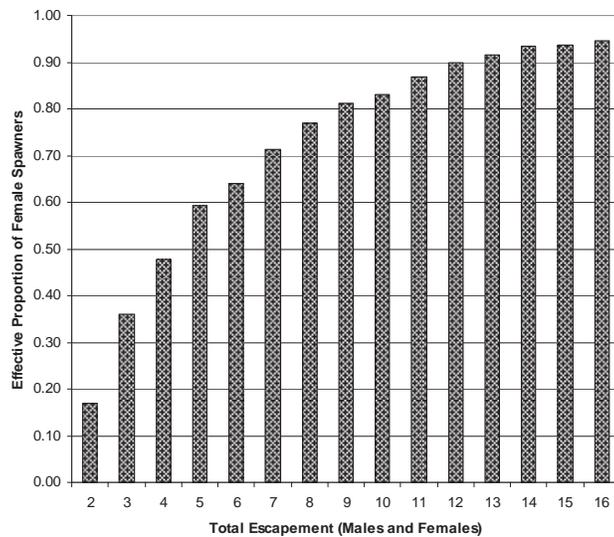


Figure A-7: Hypothetical three spawning area model. Proportion of returning females returning to a sub area with at least one male spawner present. Assumptions: 1:1 male to female ratio (binomial distribution), equal probabilities of migrating to any of the three areas. Effective proportion female spawners = effective female spawners/total female returns.

Model Mechanics

We used a cohort-based extinction risk model (described below) to calculate a standard set of viability curves for application to each ESU. The initial step in deriving a viability curve was the selection of a target risk level/time period, we generated curves corresponding to 1%, 5% and 25% risks of quasi-extinction over a 100 year timeframe.

Automated Grid Search Routine

Viability curves were generated by iteratively running the cohort model through a range of productivity and abundance combinations using an automated grid search routine. We used ESU-specific geometric mean return rate variance and autocorrelation estimates along with averaged age at return proportions as inputs into the model runs. We used the extinction risk model in conjunction with a binary search algorithm to estimate the equilibrium abundance associated with each individual productivity value in the series that yielded the target risk. The model can either be run in batch mode to search for the specific abundance levels associated with each productivity in an input series of values or to find the abundance corresponding to a particular productivity value.

For a given productivity, the model was run with the user-specified upper and lower abundance bounds, and extinction risk was evaluated for both runs. If the target extinction fell between the risks associated with both bounds, the algorithm would seed the model with the abundance halfway between the two previous values. The algorithm continued seeding the model using this “halfway” method until the resulting risk was within 7% of the target risk. At this point, 4000 iterations per run were used to minimize the risk of missing the appropriate abundance. Using 4000 iterations instead of the customary 1000 enabled a more stable and fine-scale risk analysis. Once an extinction risk within 0.5% of the target risk was found, the corresponding abundance value was recorded and the model moved on to the next productivity value in the series. After completing the entire series, the results were used to plot a rough viability curve. The derived values were used to seed the model for a final series of fine-scale iterations to improve accuracy and to smooth the curve.

Cohort Model Structure

User defined values were used to set average productivity and capacity terms specific to the stock recruit function used in the analysis. We used a form of the ‘Hockey Stick’ function in generating the ESU-specific population viability curves presented in this report. A simple modification to the model allows for running the analyses with a Beverton- Holt or a Ricker function (note that the productivity and capacity input values would need to be expressed in the corresponding metrics). The productivity and abundance parameters in the extinction risk model were expressed in terms that can be directly related to estimates that can be derived from abundance data series available for many Interior Columbia populations (equation A-1).

$$R(t) = A * \text{MIN} (S(t), SB) * E(t) \quad \text{eq. A-1}$$

Where:

R(t) = Expected number of adult returns to the spawning area in future years resulting from brood year escapement S(t).

S(t) = Parent year adult escapement.

SB = Spawner Breakpoint: number of spawners corresponding to breakpoint of hockey stick function.

A = Productivity: Estimated as geometric return/spawner at spawning abundance below SB.

ε(i) = process error: random variable, lognormal distribution with a mean of 0, standard deviation of σ.

Running the Model

Each modeled population projection is seeded with a series of five consecutive escapement values (years -4 to 0). For viability curve generation, the model was seeded with the spawner number being evaluated for the particular iteration of the grid search routine. The cohort model can also be used to generate an estimate of risk using population specific current abundance and productivity estimates. For a risk assessment of an individual stock, we used the five most recent spawning escapements as initial values.

Step 1—generating a population projection

The model steps through the escapement series, sequentially generating an estimate of production for each parent escapement. If the parent escapement value is below the user-defined reproductive failure threshold (RFT), the production from that brood year is set to zero. If the adult escapement exceeds the RFT, the model generates an initial production estimate using the embedded stock-recruit function with productivity and capacity terms based on the input values for the particular model run. The model applies an annual deviation to projected returns from each parent year based on a random draw from a normal distribution defined by estimates of ESU specific averages of variance and

autocorrelation. The resulting production from spawning in year (t) is allocated to future returns by applying the user-defined average age distribution. Although age structure was kept static while generating the viability curves, the model was designed so that the user can add stochasticity to the annual brood year age distribution if desired.

The model incorporates autocorrelation into the annual stochastic error term adapting the approach described in Morris & Doak (2002). We used average variance and autocorrelation estimates corresponding to each ESU (see the Population Statistics section below). The model works in annual time steps. A run is initiated by calculating the expected production from the spawning escapement in year 1 and multiplying the result by a factor drawn from a lognormal distribution with mean of 0 and a standard deviation of σ , where σ is the average ESU value. The stochastic error term for year 2 and all subsequent production years is modified to incorporate autocorrelation:

$$\varepsilon(t) = \rho * \varepsilon(t-1) + \sigma' \quad \text{eq. A-2}$$

where ρ is the simple correlation coefficient between sequential annual deviations from expected productivity calculated from the data series for the corresponding ESU and the term $E(0, \sigma')$ represents the portion of the variance in the data series not accounted for by autocorrelation. The adjusted standard deviation in that term, σ' , is calculated as:

$$\sigma' \cong \sqrt{\sigma^2} * \sqrt{1 - \rho^2} \quad \text{eq. A-3}$$

Model year 1 is the first year in each projection that is totally generated by the model (not an initial seed escapement). The model generates an estimate of adult escapement in year 1 by adding together the projected number of 5 year olds produced from the initial seed escapement in year (-4) and the projected number of 4 year old adults produced from initial seed escapement year (-3). The model repeats steps 1 and 2, generating a time series of at least 100 years.

Step 2—projection iteration

At the end of a 100+ year population projection, the model stores the series of annual abundance estimates in a temporary results file or virtual array. Under the basic set-up, 1000 projections (replicates) of 100+ years for each set of input parameters are generated during a model run. Each projection is based on the same input parameters (capacity and starting escapement values, variance, autocorrelation, and age structure), but reflects a unique combination of random draws from the distribution defined by the variance and autocorrelation input values. In other words, each projection for a particular set of model inputs represents an alternative potential future pattern in returns over a 100+ year time period that is consistent with that particular set of model inputs.

Step 3—Compiling a Risk Estimate

After 1,000 projections are accumulated, the model summarizes the results according to the specific risk target metrics input into the model. If the parent escapement from any four consecutive years leading up to (and including) the user-specified timeframe are all less than the QET, then the projection is counted as an extinction. We evaluated the projected risk of extinction over a 100-year period. Finally, the extinction risk for the entire run is calculated as the proportion of projections that were counted as extinct.

Minimum Abundance Thresholds

Populations of listed chinook and steelhead within Interior Columbia ESUs vary considerably in terms of the total area available to support spawning and rearing.

We add a minimum abundance threshold to our ESU specific viability curves corresponding estimates of the historical amount and complexity of tributary spawning habitat for a population. The minimum abundance thresholds were incorporated into the ESU specific viability curves to ensure that the full range of objectives defined for productivity and abundance are achieved, including the desire to maintain genetic characteristics and to maintain sufficient spawner densities in larger tributary habitats. A more detailed discussion of the rationale for the specific minimum abundance thresholds is included in the population viability criteria section of the ICTRT document and in Attachment B.

ESU-Specific Viability Curves

We generated sets of viability curves for application to populations within each of the Interior Columbia ESUs. We used ESU average estimates of variance and autocorrelation derived from representative trend data sets combined with minimum abundance thresholds specific to the general population size categories to generate curves. In addition to depicting the 5% risk of extinction threshold for evaluating population viability, the figures also include risk thresholds corresponding to a relatively high risk of extinction (10% and 25% in 100 years) and a lower risk level (1% in 100 years). We adapted the approach to accommodate the relatively limited amount of data available for Snake River Fall Chinook and Sockeye populations.

We analyzed the incremental and combined effects of filtering the data sets for factors that could inflate population level estimates of variability in return rates: multiple years with very low parent spawning levels, chronic high hatchery origin spawners, and incorporating a specific form of the spawner recruit relationship with relatively poor statistical fit across the data sets. The specific criteria used to screen populations for these factors are summarized in Table A-2.

Table A-2. Screening criteria used to develop representative estimates of variance and autocorrelation in productivity for input into ESU specific viability curve projections.

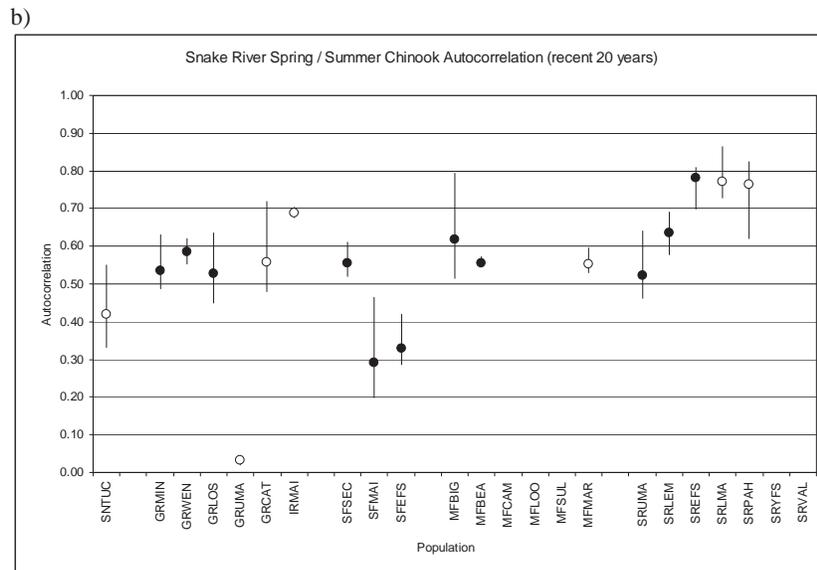
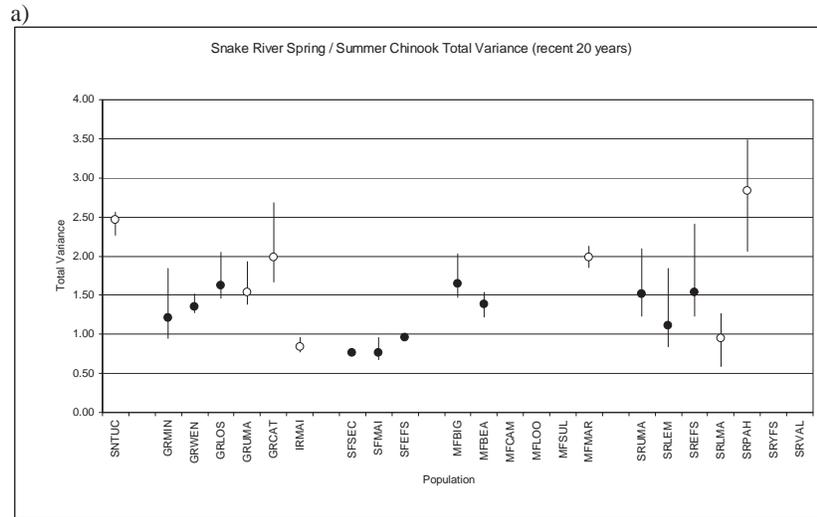
Factor	Criteria
1. Multiple spawnings at extreme low numbers	Most recent 20 year geomean of adult spawners less than 50 per year
2. Multiple years with high hatchery origin spawner proportions	Most recent 20 year average proportion hatchery (to spawning grounds) of greater than 30%.
3. High proportion and annual variability in hatchery proportion	High proportion screen plus standard deviation of hatchery proportion exceeds 30%
4. Worst fit statistical model (across populations)	Based on comparative AICc analyses within ESU populations. Drop model that most often scores lowest (by at least 2 AICc points) across populations within the ESU
5. Combination (1&2) multiple low and high potential hatchery influence	Apply criteria for factors 1 & 2
6. Combination (1&2) plus eliminate worst fit model (4)	Apply criteria for factors 1, 2 and 4

Snake River Spring/Summer Chinook ESU

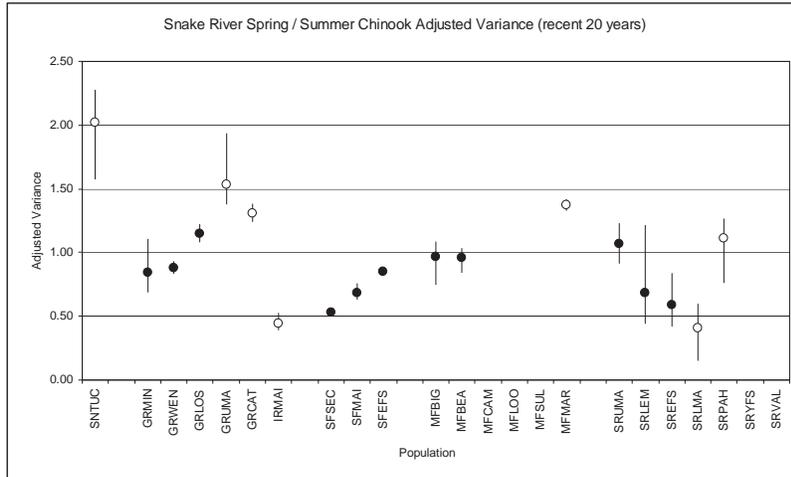
We have developed 23 population specific data series for this ESU. Population level estimates of the variance and autocorrelation are depicted in Figure A-8. The average total variance and autocorrelation estimates based on all 23 population data series increased relative to the averages for the 12 data series available for the first draft of this analysis (ICTRT 2005a). Updates to the individual data series included in the original set accounted for a small component of the increase in both parameters (Table A-3). Most of the increase was due to the addition of the 11 new data series. The geomean in parent spawning levels were below 50 for five of the data series for this ESU, indicating multiple years with very low spawning numbers. The variance in return rates at very low spawning levels is likely significantly increased. Dropping those five data series from calculating the average resulted in reduced total variance and a moderate increase in average autocorrelation. Six of the twenty-three populations had relatively high inputs of hatchery origin fish into natural spawning across the 20 year time frame. Dropping those six populations from the analysis resulted in increased average total variance and autocorrelation. Excluding the s/r function with the worst fit across populations (Random Walk) resulted in reduced total variance and elevated average autocorrelations. Applying all three of the criteria drops ten population data sets from the analysis. The resulting average total variance is 1.24, approximately 10% higher than the estimate based on the original set of 12 population data series.

The viability curves generated for application to populations of Snake River spring/summer chinook within each of the four historical population size categories are depicted in Figure A-12a-d.

Figure A-8a-c. Population estimates of productivity (geomean brood year spawner to spawner return rates) statistics for the Snake River spring summer chinook ESU: a) total variance; b) autocorrelation; c) adjusted variance (after accounting for autocorrelation). Bars represent +/- 1 standard error. Filled symbols indicate population data series that met filters described in text.



c)



Upper Columbia Spring Chinook ESU

The original analysis included data sets for all three of the extant populations in the Upper Columbia spring chinook ESU. Updates to the data sets resulted in a small increase (roughly 3%) in total variance (Table A-3). Estimated average autocorrelation remained at the same value (0.68). None of the data sets were eliminated by the geomean population size and hatchery contribution tests. Eliminating the worst fit s/r model across the data series reduced the total variance to 0.95, approximately 3% below the original values.

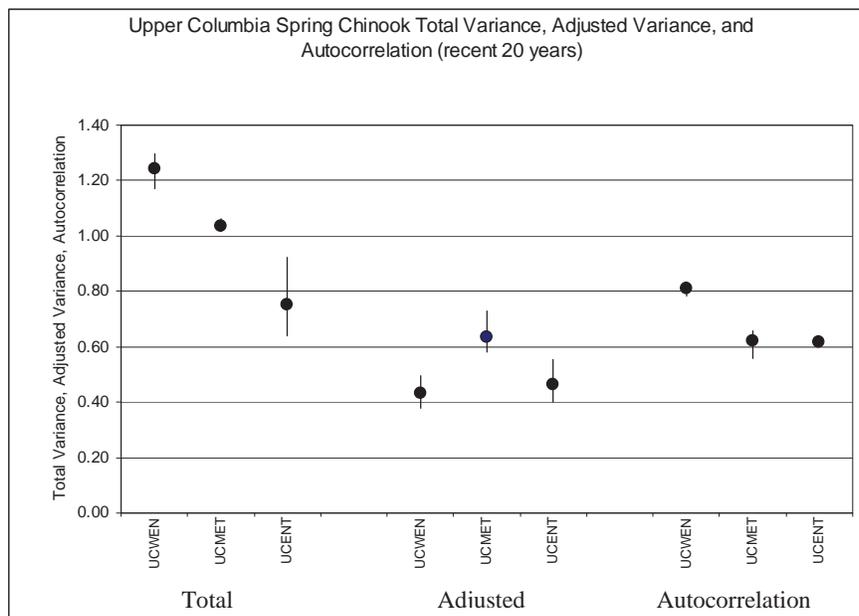


Figure A-9. Population estimates of productivity (geomean brood year spawner to spawner return rates) statistics for the Upper Columbia Spring Chinook ESU. Total variance, autocorrelation, and adjusted variance (after accounting for autocorrelation) are shown. Bars represent +/- 1 standard error. Filled symbols indicate population data series that met filters described in text.

Upper Columbia Steelhead ESU

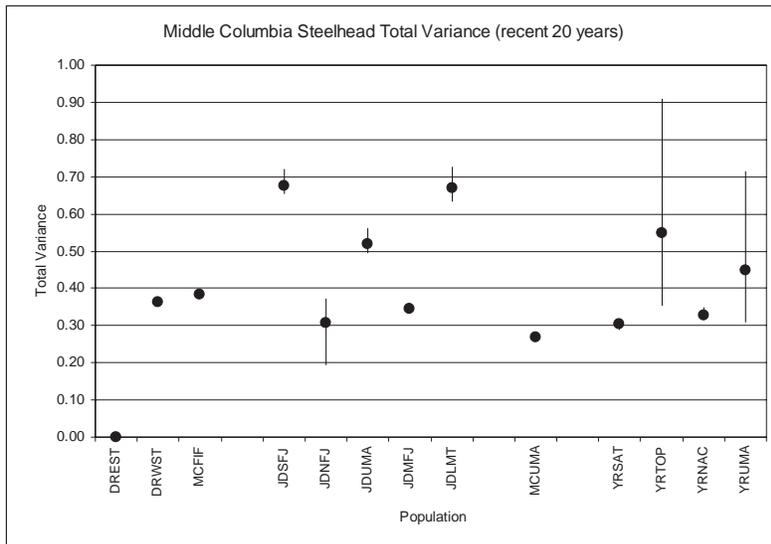
Since the ICTRT has little confidence in estimates of variance and autocorrelation for Upper Columbia Steelhead populations, combined estimates from the Mid-Columbia and Snake River steelhead ESUs were used in generating viability curves for the Upper Columbia ESU (Figures A-10 and A-11).

Mid-Columbia Steelhead ESU

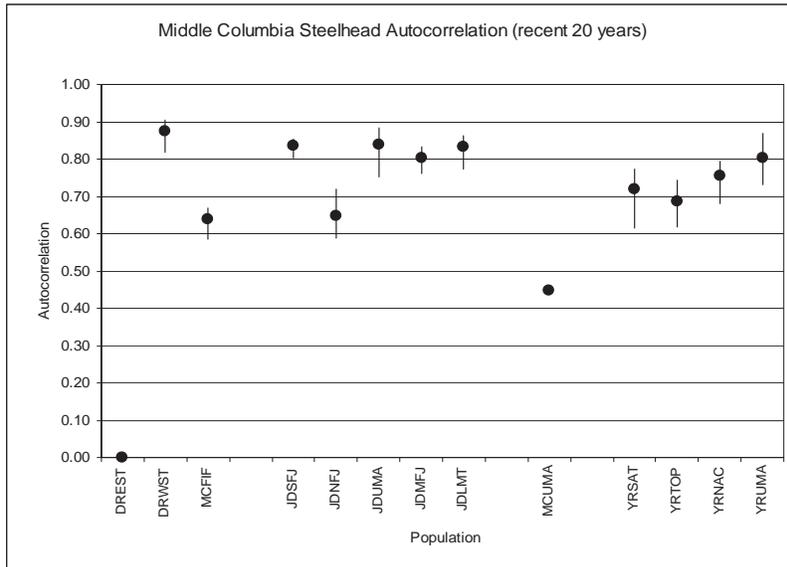
We generated variance and autocorrelation estimates using data sets representative of 13 Mid-Columbia steelhead populations (Figures A-10a-c). We calculated a set of average values across 12 of the data sets for use in generating a representative viability curve for application to populations within the ESU. We dropped the Deschutes River (Eastside) data set due to chronically high estimated proportions of hatchery origin fish on the spawning grounds.

Figure A-10a-c. Population estimates of productivity (geomean brood year spawner to spawner return rates) statistics for the Mid-Columbia Steelhead ESU. a) total variance; b) autocorrelation; c) adjusted variance (after accounting for autocorrelation). Bars represent +/- 1 standard error. Filled symbols indicate population data series that met filters described in text.

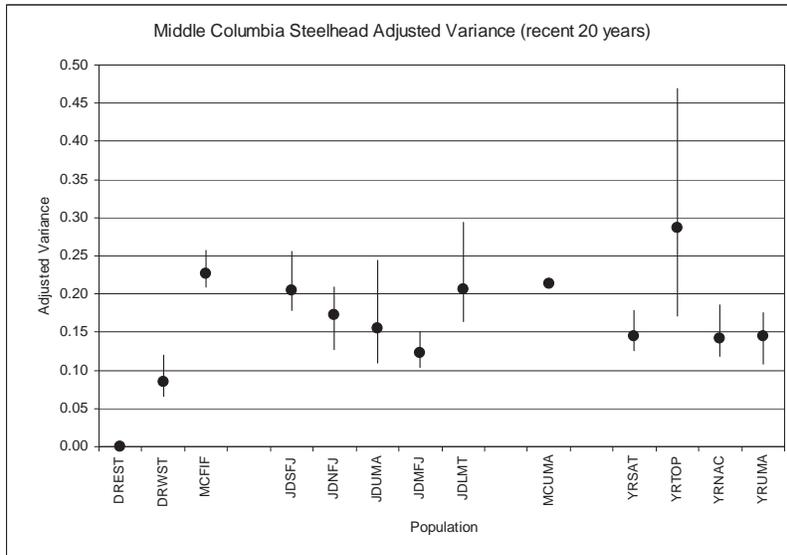
a)



b)



c)



Snake River Steelhead ESU

Population specific trend data sets are available for a relatively small proportion of populations in the Snake River Steelhead ESU. Three new population specific series have been developed in addition to the two original data sets used in previously reported ICTRT analyses. Four out of the five population specific trend series are in the Grande Ronde MPG and the adjacent Imnaha River. The only set specifically corresponding to returns to a particular location in the Idaho portion of the ESU was based on weir counts of fish returning to a section within the Little Salmon River population. Annual counts of wild and hatchery steelhead passing over Lower Granite Dam are available. These aggregate counts represent the combined returns to all populations and hatchery facilities above Lower Granite Dam and include the returns accounted for by the estimates described above. The Lower Granite counts can be broken down into A and B type steelhead runs (TAC ref). The populations with available trend series are all classified as Type A stocks. To complement the population specific trend data sets, we calculated return rate statistics (variance and autocorrelations) for average A and B run populations assuming that the returns not accounted for in the available population sets were distributed among the remaining populations proportional to intrinsic potential habitat.

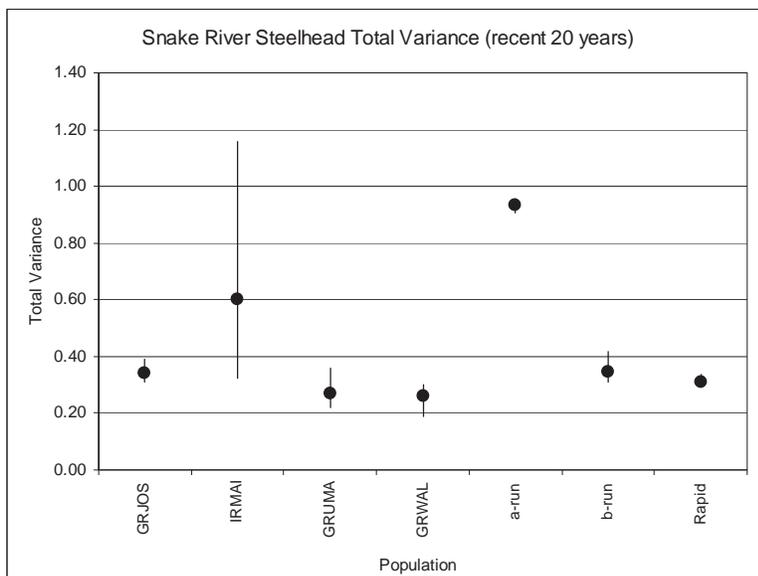
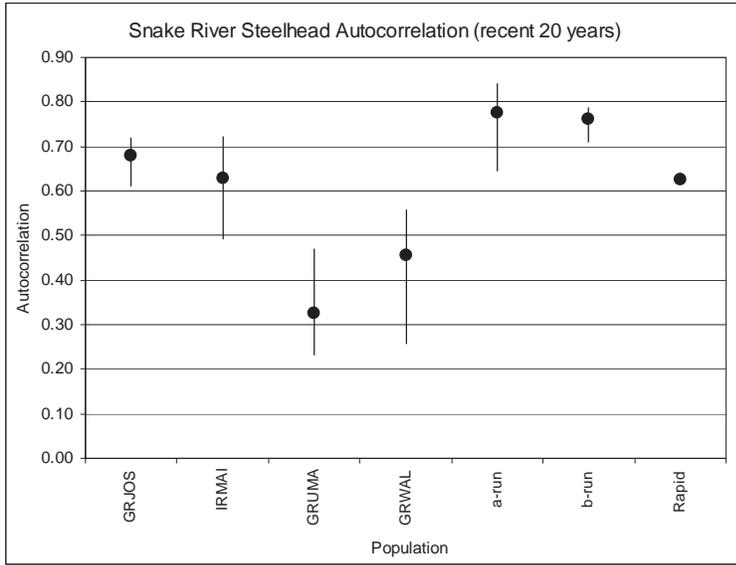
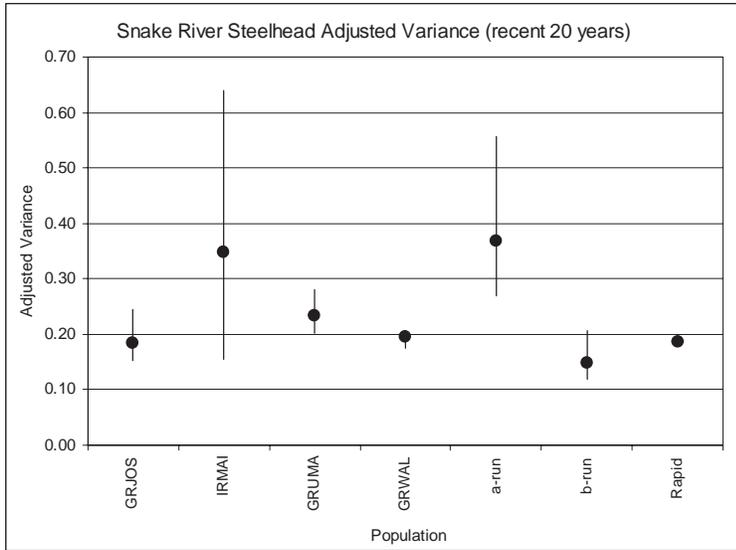


Figure A-11a-c. Population estimates of productivity (geomean brood year spawner to spawner return rates) statistics for the Snake River Steelhead ESU. a) total variance; b) autocorrelation; c) adjusted variance (after accounting for autocorrelation). Bars represent +/- 1 standard error. Filled symbols indicate population data series that met filters described in text.

b)



c)



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Table A-3. Summary statistics by ESU. Average variance and autocorrelation of residuals from stock/recruit function fits.

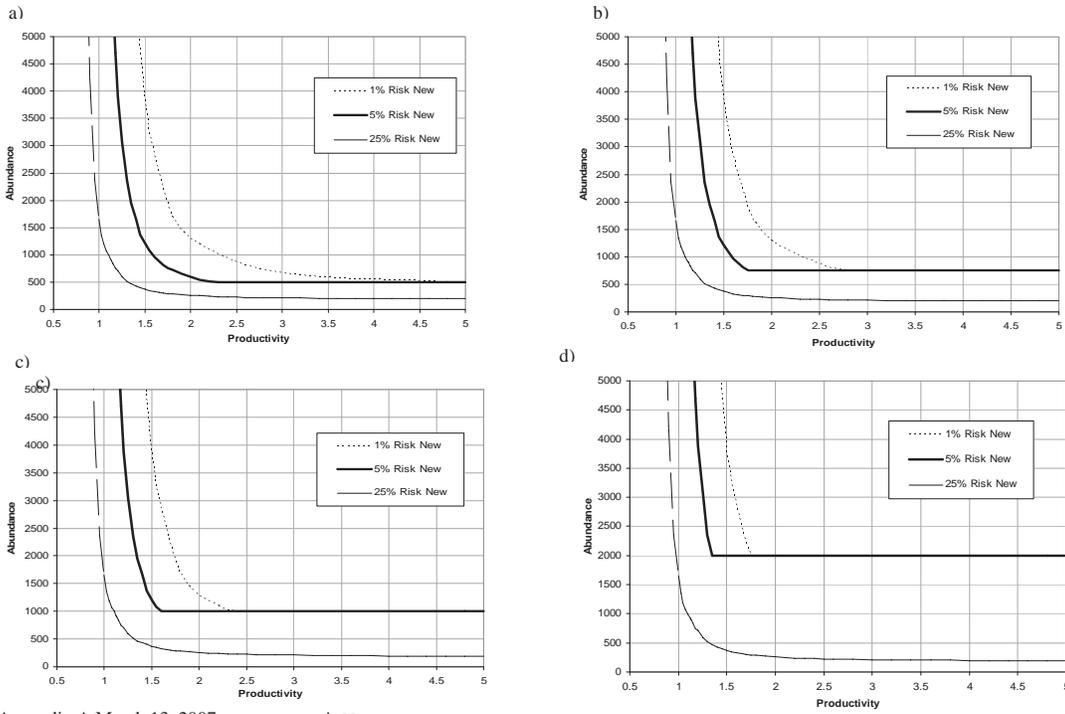
Method	Snake River Spring / Summer Chinook				Upper Columbia Spring Chinook			
	# of Pops	Total Var.	Auto	Adj. Var.	# of Pops	Total Var.	Auto	Adj. Var.
1 Original Values	12	1.18	0.44	0.95	3	0.99	0.68	0.53
2 Updated Values w original populations	12	1.29	0.49	0.94	3	1.02	0.68	0.55
3 Updated Values w all populations	23	1.52	0.54	1.08	3	1.02	0.68	0.55
4 no pops w parent esc geomean<50	18	1.37	0.54	0.97	3	1.02	0.68	0.55
5 no pops w hatchery > 30%	18	1.54	0.54	1.09	3	1.02	0.68	0.55
6 no pops w hatchery OR Stdev > 30%	17	1.55	0.54	1.10	3	1.02	0.68	0.55
7 exclude worst fit model	23	1.43	0.53	1.03	3	0.95	0.68	0.51
8 4 & 5	13	1.33	0.55	0.93	3	1.02	0.68	0.55
9 4, 5 & 7	13	1.24	0.53	0.89	3	0.95	0.68	0.51

Number	Method	Snake River Steelhead			Middle Columbia Steelhead				
		# of Pops	Total Var.	Auto	Adj. Var.	# of Pops	Total Var.	Auto	Adj. Var.
1	Original Values	2	0.49	0.54	0.35	4	0.44	0.69	0.23
2	Updated Values w original populations	2	0.63	0.67	0.34	7	0.54	0.74	0.20
3	Updated Values w all populations	6	0.54	0.61	0.34	13	0.51	0.74	0.23
4	no pops w parent esc geomean<50	6	0.54	0.61	0.34	13	0.51	0.74	0.23
5	no pops w hatchery > 30%	6	0.54	0.61	0.34	12	0.51	0.73	0.24
6	no pops w hatchery OR Stdev > 30%	6	0.54	0.61	0.34	12	0.51	0.73	0.24
7	exclude worst fit model	6	0.39	0.60	0.25	13	0.39	0.75	0.17
8	4 & 5	6	0.54	0.61	0.34	12	0.51	0.73	0.24
9	4, 5 & 7	6	0.39	0.60	0.25	12	0.40	0.74	0.18

Number	Method	Upper Columbia Steelhead			
		# of Pops	Total Var.	Auto	Adj. Var.
1	Original Values	6	0.46	0.64	0.27
2	Updated Values w original populations	9	0.56	0.73	0.23
3	Updated Values w all populations	19	0.53	0.70	0.27
4	no pops w parent esc geomean<50	19	0.53	0.70	0.27
5	no pops w hatchery > 30%	18	0.53	0.69	0.28
6	no pops w hatchery OR Stdev > 30%	18	0.53	0.69	0.28
7	exclude worst fit model	19	0.40	0.71	0.2
8	4 & 5	18	0.53	0.69	0.28
9	4, 5 & 7	18	0.38	0.69	0.2

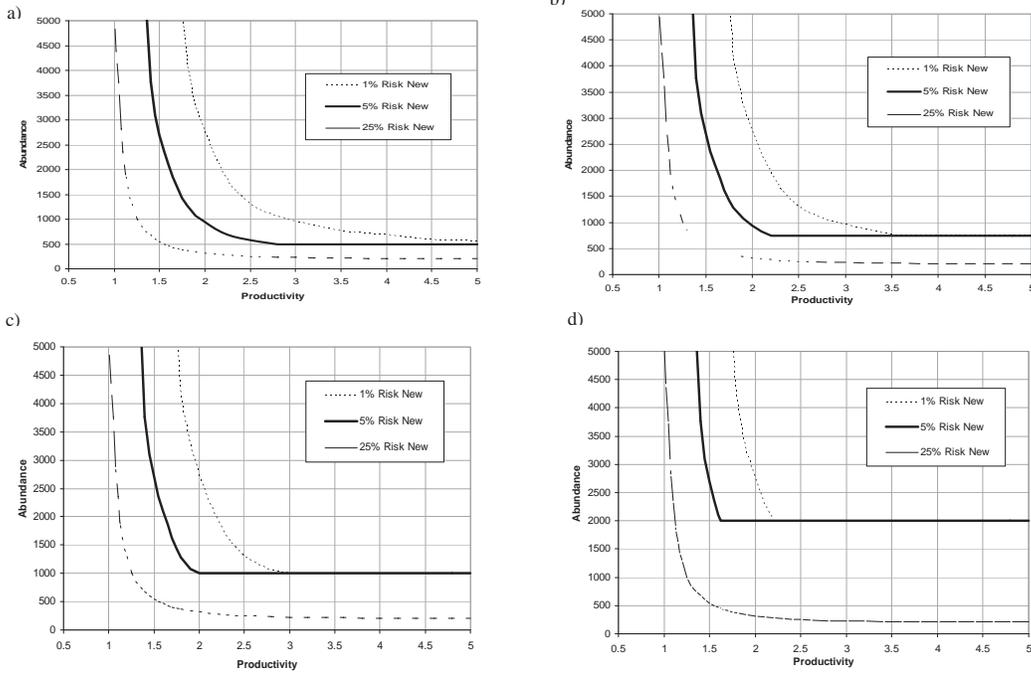
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Figure A-12a-d. Snake River Spring/Summer Chinook ESU viability curves. Variance and autocorrelation parameters used in the generation of the curves were 0.89 and 0.53, respectively. Age distribution was 0.57 age 4, 0.43 age 5.



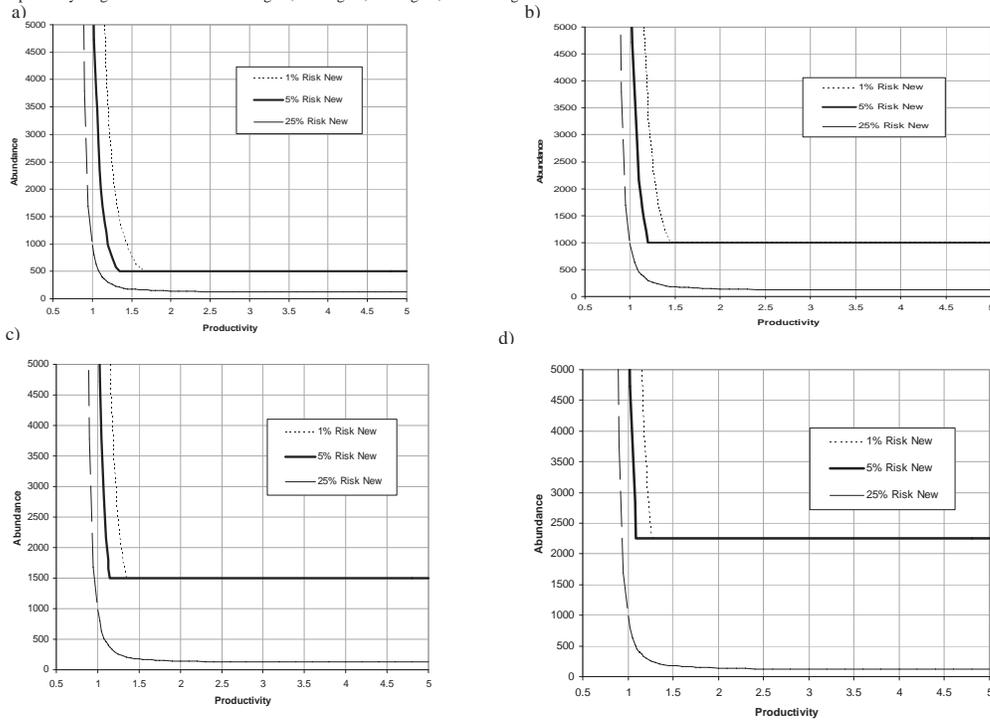
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Figure A-13a-d. Upper Columbia Chinook ESU viability curves. Variance and autocorrelation parameters used in the generation of the curves were 0.51 and 0.68, respectively. Age distribution was 0.60 age 4, 0.40 age 5.



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Figure A-14a-d. Upper Columbia Steelhead ESU viability curves. Variance and autocorrelation parameters used in the generation of the curves were 0.20 and 0.69, respectively. Age distribution was 0.02 age 3, 0.38 age 4, 0.45 age 5, and 0.15 age 6.

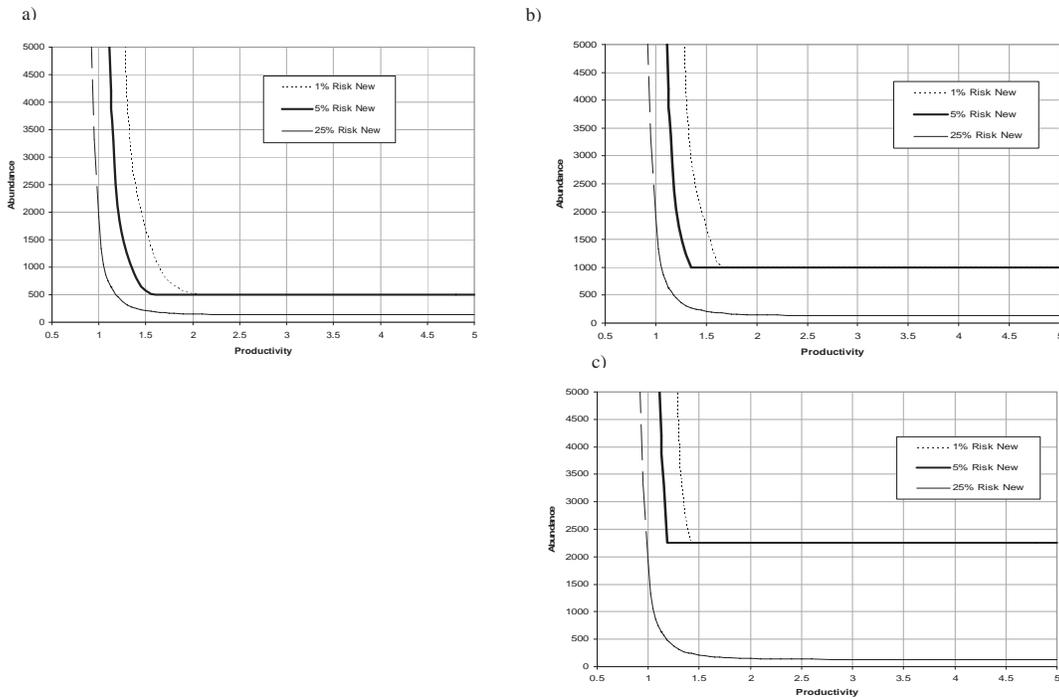


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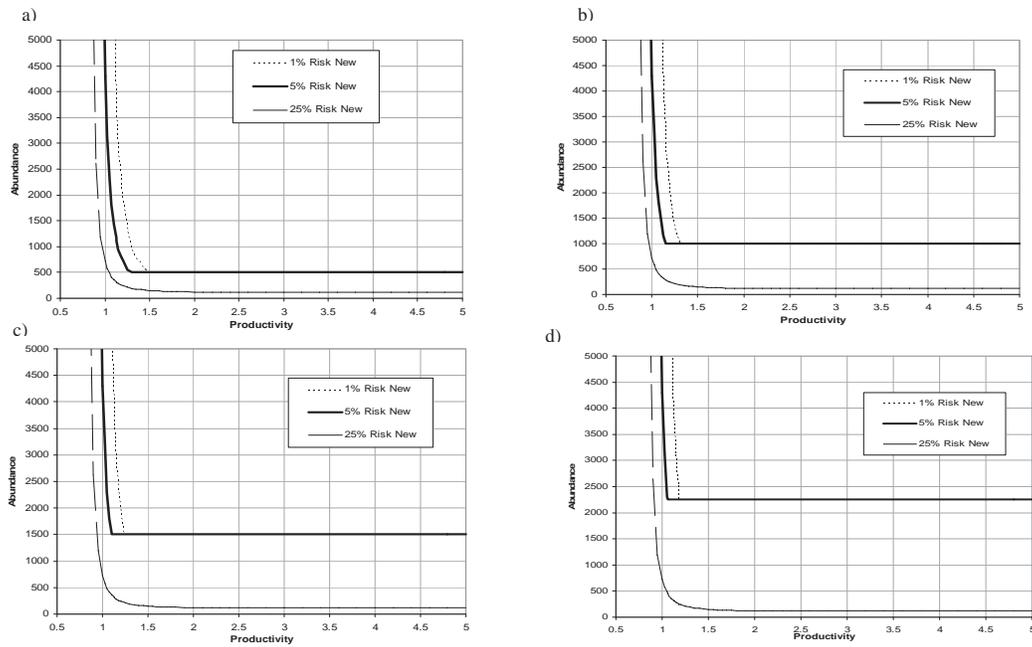
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Figure A-15a-d. Middle Columbia Steelhead ESU viability curves. Variance and autocorrelation parameters used in the generation of the curves were 0.18 and 0.74, respectively. Age distribution was 0.03 age 3, 0.46 age 4, 0.43 age 5, and 0.08 age 6.



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Figure A-16a-d. Snake River Steelhead ESU viability curves. Variance and autocorrelation parameters used in the generation of the curves were 0.25 and 0.60, respectively. Age distribution was 0.03 age 3, 0.60 age 4, 0.35 age 5, and 0.02 age 6.



DRAFT**Fall Chinook ESU**

We calculated a viability curve for Snake River fall chinook following the same analytical steps we applied to yearling chinook and steelhead ESUs. We calculated variance and one year lag autocorrelation statistics for reconstructed brood year spawners and natural returns for 1978-2003. We used a grid-search algorithm to develop a set of viability curves for Snake River fall chinook corresponding to projected risk levels of 25%, 5% and 1% at 100 years (Figure A-17).

We established a minimum abundance threshold for fall chinook consistent with the general abundance/productivity objectives summarized in the July 2003 ICTRT Viability draft report. We are recommending a minimum abundance threshold of 3,000 natural origin spawners for the extant Snake River fall chinook population. No fewer than 2,500 of those natural origin spawners should be distributed in mainstem Snake River habitat.

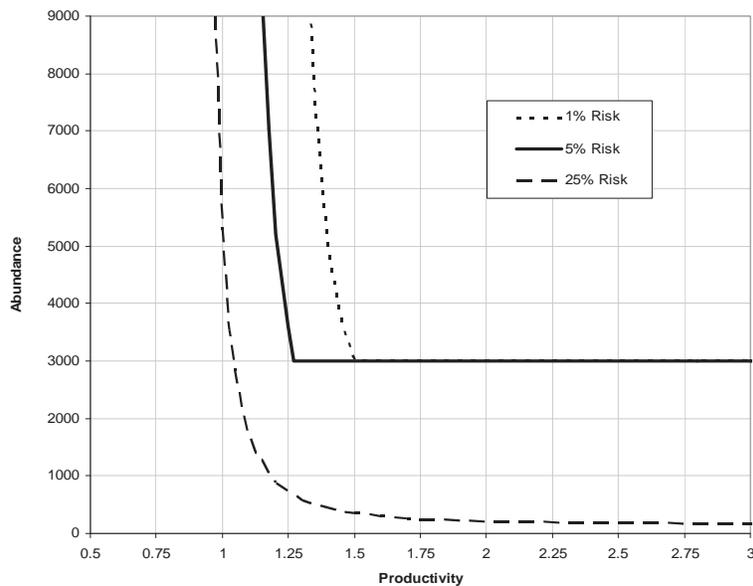


Figure A-17. Viability curves for Snake River Fall chinook. Age structure used was 53% age 3, 43% age 4, and 4% age 5. Adjusted variance (variance unexplained by autocorrelation) and autocorrelation parameters were 0.25 and 0.67, respectively.

The abundance threshold for Snake River fall chinook is based on the Bevan Team recommendation for "...an eight year (approximately 2 generation) geometric mean of at least 2,500 natural origin spawners in the mainstem Snake River annually" (NMFS, 1995). The Bevan Team specifically did not address spawning/rearing areas in the lower mainstems of major tributaries in setting that objective - stating that "...a lack of information precludes

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setting escapement objectives at this time.” It is likely that lower reaches in the Clearwater, Grande Ronde and Tucannon Rivers had the potential to support 500 or more spawners based on physical habitat availability. Fall chinook spawners have been observed in all three areas in recent years (Milks et al. 2005). Preliminary information from scale sampling and pit tag experiments indicates that natural production of fall chinook in the lower Clearwater may exhibit a complex life history pattern including overwintering in mainstem habitat before outmigrating to the sea the following spring.

Sockeye ESU

Historical sockeye production occurred in at least five Stanley Basin lakes as well as in lake systems associated with Snake River tributaries currently cut off to anadromous access (e.g., Wallowa and Payette Lakes). Current returns of Snake River sockeye are extremely low and are limited to Redfish Lake. In previous ICTRT analyses (McClure et al. 2003, McClure et al. 2005) we have concluded that at least three lakes in the Stanley Lakes Basin historically supported independent sockeye populations (Redfish Lake, Alturas Lake and Stanley Lake).

We do not have a sufficient trend data set specifically for Redfish Lake sockeye to use in generating a viability curve. As a surrogate, we used a data set for Lake Wenatchee sockeye to generate estimates of variance and autocorrelation in return rates (adjusted variance = 0.42, autocorrelation=0.41).

The approach we used to generate a viability curve requires input of a representative adult age structure. Bjornn et al. (1968) identified similarities between Redfish Lake and Wenatchee Lake sockeye runs in age at length and the predominance of 2 year ocean residency in returning adults. We generated an estimate of average age structure for Redfish Lake sockeye using smolt age sampling data summarized in Bjornn et al. (1968) as a starting point. Redfish Lake sockeye smolts outmigrated after one or two years residency in freshwater. The proportions varied considerably across brood years. The median proportion age 1 migrants for the 1954 to 1963 year classes was 0.60. Information cited in Bjornn et al. (1968) indicates that almost all returning adults had spent 2 years at sea. Based on these estimates, we assumed that the average age composition of returning adult Redfish Lake sockeye was 60% 4 year olds and 40% 5 year olds.

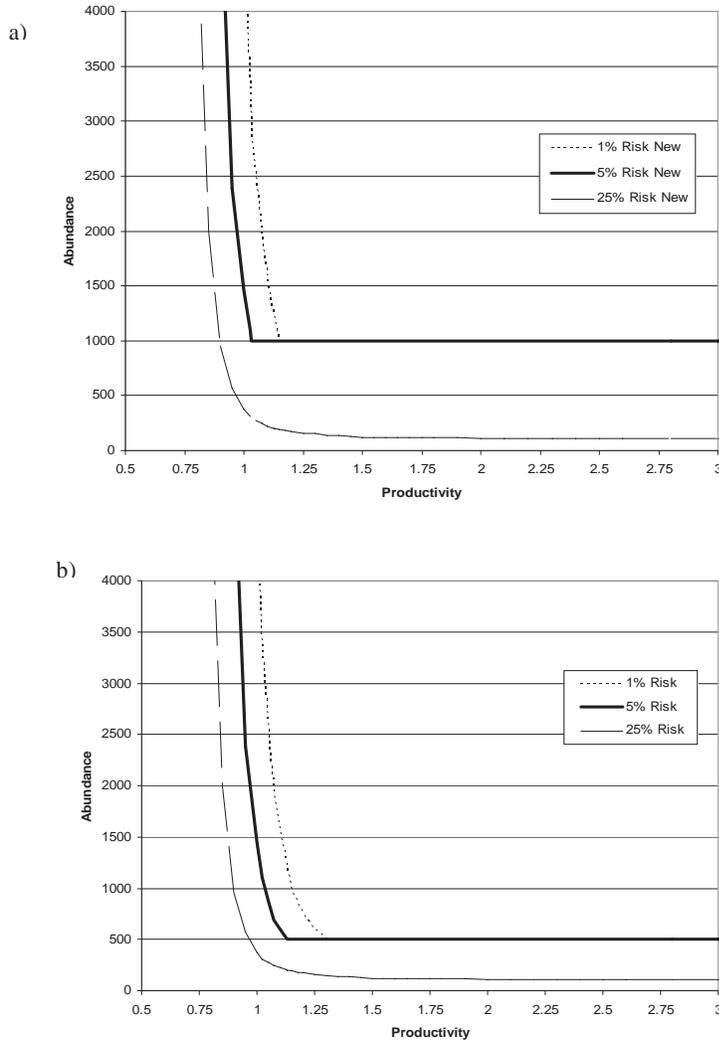
We generated two sets of curves for application to potential Stanley Lake Basin sockeye populations (Figure A-18). We developed relative population size category designations for Columbia Basin lake systems based on relative surface areas (Appendix B). The Stanley Basin Lakes are relatively small compared to other lake systems that historically supported sockeye production in the Columbia Basin. Stanley Lake is assigned to the smallest size category along with Pettit and Yellowbelly Lakes. Redfish Lake and Alturas Lake fall into the next size category – Intermediate. We adapted the recovery abundance levels recommended by the Snake River Recovery Team (Bevan, et al. 1994) as minimum abundance thresholds. We set the minimum spawning abundance threshold at 1,000 for the Redfish and Alturas Lake populations (intermediate category), and at 500 for populations in the smallest historical size category (e.g., Stanley Lake).

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These estimates should be viewed as interim long-term abundance/productivity objectives for Stanley Basin sockeye populations. Returns of Snake River sockeye have been at extremely low levels for a considerable period of time. Initial efforts aimed at recovery will likely put a high priority on increasing survival of juvenile outmigrants and adult returns to levels that will allow for rebuilding. Information on juvenile productivity and on specific year to year variations in Redfish Lake brood year return rates gathered during the initial phase of recovery efforts should allow for future refinements of the interim ICTRT Snake River sockeye abundance and productivity criteria.

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Figure A-18a-b. Viability curves for application to Snake River sockeye lake populations. A) Redfish Lake and Alturas Lake (Intermediate); B) small lake populations (Stanley Lake). Age structure used was 60% age 4 and 40% age 5 adult returns. Adjusted variance (variance unexplained by autocorrelation) and autocorrelation parameters (derived from Lake Wenatchee data) were 0.42 and 0.41, respectively.



DRAFT**Updating Viability Curves**

The ICTRT developed a set of viability curves based analyses of trend data sets available (or applicable) for each ESU as of December, 2005. We recommend that these curves be periodically reviewed and updated as appropriate. At a minimum, additional return year data will become available for each series. Techniques for estimating escapements for populations may be improved, leading to revisions in the estimates used in generating the viability curves. Additional data series may become available. The ICTRT recommends that viability curves should be comprehensively reviewed and updated every 5 years, in phase with periodic population status updates. The choice of a five year interval reflects a balance between ensuring that recovery targets are based on updated information and avoiding frequent, minor changes to criteria resulting from yearly updates. We recommend using a test to ensure that updates leading to relatively substantial changes in viability curves are incorporated, while minimizing the need to update all analyses dependent upon viability curves in response to relatively minor shifts.

The viability curves for Interior Columbia ESUs reflect specific estimates of variance and autocorrelation in return rates. Estimates of these two parameters can be updated as escapement estimates become available for each additional year, or as a result of revisions to run reconstruction methods. We developed the following test to highlight when changes in those estimates are sufficiently large to warrant updating viability curves used in recovery planning.

- 1) Generate an updated version of the 5% viability curve for the Basic size population grouping of the ESU under consideration.
- 2) Compare the resulting curve to the current (without data updates) versions of the 1%, 5% and 25% risk curves for the ESU at abundance levels between 500 and 1000.
 - a. To facilitate the comparison, calculate intermediate risk curves for intermediate levels (3%, 15%) using for the current (without data updates) data.
- 3) Adopt the updated viability curve parameters IF:
 - a. The updated version of the 5% curve exceeds the curve associated with a 3% risk of extinction (previous data set), or
 - b. The 5% curve falls below the curve associated with a 15% risk (previous data set)

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Sensitivity Analyses

Viability Curve Input Parameters

The input parameters driving the form of ESU specific viability curves are each subject to substantial process and measurement uncertainties. We evaluated the sensitivity of viability curves to variations in the input values for variance and autocorrelation in intrinsic productivity and in average age structure. We used the average values calculated from Snake River spring/summer chinook population data sets as a baseline for the sensitivity assessment. We structured the sensitivity analysis to allow for comparisons of the impact of proportional variations across the three input parameters. We generated a range of values for each input parameter using a common set of proportional multipliers (Table A-4).

We evaluated the effects of sequentially varying each of the three input parameters on the viability curves. We generated a set of viability curve parameters corresponding to each of the three inputs. In any given set, the remaining two input parameters were maintained at the baseline level.

Table A-4. Range of input parameters used in viability curve sensitivity analyses.

Proportion of Input Value	Viability Curve Parameter		
	Total Variance (geomean productivity)	Autocorrelation (geomean productivity)	Age Structure (4 yr old proportion)
2.00 x	2.48	--	--
1.50 x	1.86	0.80	.85
1.25 x	1.55	0.65	.71
1.00 x	1.24	0.53	.57
0.75 x	0.93	0.40	.42
0.50 x	0.62	0.27	.28
0.25 x	0.31	0.14	.14

The QET and RFT were held at baseline levels for the variance, autocorrelation and age structure sensitivity runs. In a separate analysis, we evaluated the impact on viability curves of incorporating different values for QET and for RFT.

We used consistent metrics for contrasting the results of the sensitivity runs to facilitate comparisons. We expressed the results of the individual parameter analyses in terms of the minimum productivity associated with threshold abundance levels for the four size categories of spring/summer chinook populations (i.e., 500, 750, 1000 and 2000).

DRAFT**Variance and Autocorrelation**

Projected viability curves are particularly sensitive to input parameters for variance and autocorrelation in productivity (spawner to spawner return rate).

The effect of total variance on the minimum productivity at threshold abundance levels is most pronounced for the basic population category (Table A-5a). Holding all other input parameters at their average values and setting the total variance at 0.75 and 1.25 times the average level used in generating spring/summer chinook viability curves changes the minimum productivity at threshold abundance by -24% and +47%, respectively. The relative change at higher abundance levels is dampened, but follows the same pattern.

Proportionally varying the level of autocorrelation input (holding other input variables constant) also had a substantial effect on the projected viability curve (Table A-5b). The average autocorrelation for the Snake River Spring/Summer Chinook ESU populations was 0.53. Increasing the input value for autocorrelation by 25% or more resulted in substantial increases in the required productivity at threshold abundance levels.

Table A-5a. Estimated productivities as a function of **total variance in productivity** (spawner to spawner return rates). Results at Snake River Spring/Summer Chinook ESU average total variance are in bold type. Results are presented as productivities corresponding to minimum equilibrium escapement levels (5% risk) by population size category (basic, intermediate, large and extra large). All other viability curve input parameters are held at recent geomeans for Snake River spring summer ESU populations.

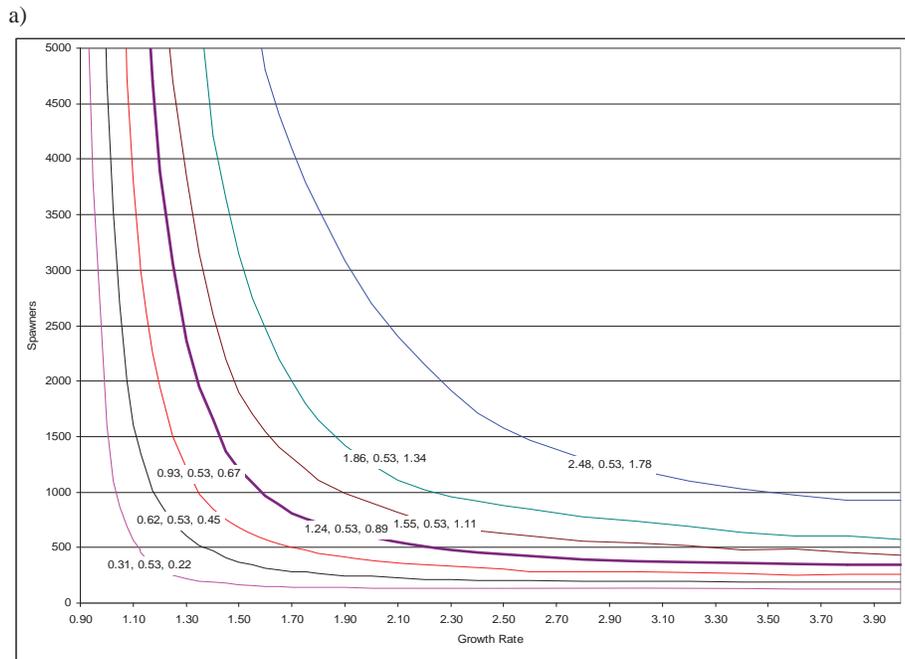
Total Variance (spawner to spawner return rate)	Minimum Population Size			
	500	750	1000	2000
0.31	1.11	1.08	1.04	0.98
0.62	1.34	1.25	1.17	1.08
0.93	1.69	1.44	1.38	1.19
1.24	2.21	1.76	1.56	1.34
1.55	3.25	2.22	1.82	1.48
1.86	5.60	2.88	2.22	1.70
2.48	6.00+	5.00+	3.42	2.22

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Table A-5b. Estimated productivities as a function of **autocorrelation in productivity** (spawner to spawner return rates). Results at Snake River Spring/Summer Chinook ESU average total variance are in bold type.

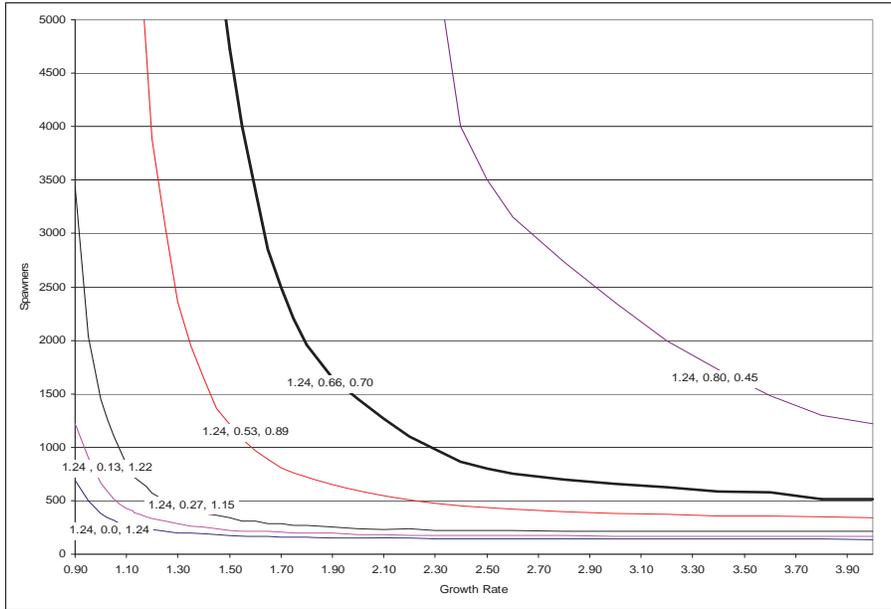
Autocorrelation (Spawner to spawner return rate)	Minimum Population Size			
	500	750	1000	2000
<i>0</i>	0.95	0.88	0.85	n/a
<i>0.13</i>	1.06	0.98	0.93	0.85
<i>0.27</i>	1.25	1.13	1.07	0.96
0.53	2.21	1.76	1.56	1.34
<i>0.66</i>	4.10	2.60	2.25	1.78
<i>0.80</i>	5.00+	5.00+	4.30	3.20

Figure A-19a-b. Sensitivity of Snake River Spring/Summer Chinook viability curve to a) a range of total variance input values above and below the ESU average (1.24 total variance, 0.89 after adjustment for autocorrelation, autocorrelation fixed at ESU average level of 0.53); and b) autocorrelation input values.



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b)



DRAFT**Age structure**

Adult spawning returns for Interior Columbia stream type chinook populations are predominated by 4 and 5 year old fish. In many years a relatively small component of 3 year old returns are present, virtually all of these fish are males. A small percentage of mature adults return at age 6. For the purposes of this analysis we included those fish as age 5 returns. The viability curves derived for Snake River Spring/Summer Chinook population categories incorporate an average age composition for the ESU (0.57 age 4, 0.43 age 5 returns). We systematically varied age composition (Table A-4) and evaluated the sensitivity of projected viability curves, holding other input parameters at the recent average values used in constructing the viability curves for this ESU presented in the ICTRT viability report.

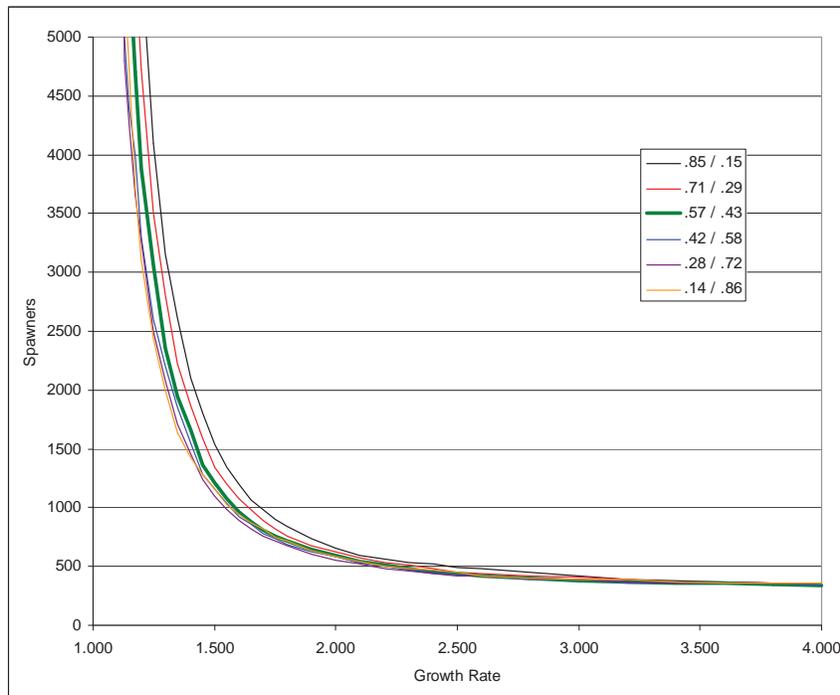


Figure A-20. Sensitivity of a Snake River Spring/Summer Chinook 5% risk viability curve to a range of age structures above and below the ESU average (0.57 age 4; 0.43 age 5). Total variance and autocorrelation were maintained at ESU average levels of 1.24 and 0.53, respectively. A QET of 50 adult spawners per year for four years was used.

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Variations on the average age composition resulted in relatively small changes to projected viability curves (Figure A-20, Table A-6). The relative change in the productivity associated with minimum abundance was greatest for the basic population size category. Reducing the proportion 4 year olds by half decreased the required productivity by approximately 10%, while increasing the proportion by 1.5 resulted in a relative increase of approximately 10%. Changes for other size categories were generally lower (+9% to -4% at the limits of the range in input values).

Table A-6. Estimated productivities as a function of **average age structure** (results at ESU average age structure in bold type). Results are presented as productivities corresponding to minimum equilibrium escapement levels by population size category (basic, intermediate, large and extra large). All other viability curve input parameters are held at recent geomeans for Snake River Spring/Summer Chinook ESU populations.

Age Structure (Prop. 4/Prop. 5 year old spawners)	Minimum Population Size			
	500	750	1000	2000
0.85 / 0.15	2.45	1.78	1.72	1.43
0.71 / 0.29	2.29	1.77	1.68	1.39
0.57 / 0.43	2.21	1.76	1.56	1.34
0.42 / 0.58	2.20	1.73	1.54	1.34
0.28 / 0.72	2.16	1.71	1.53	1.31
0.14 / 0.86	2.13	1.70	1.51	1.30

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Quasi-Extinction Threshold (QET)

The ICTRT viability curves were generated using a QET value of 50 spawners per year for a four year period. We evaluated the sensitivity of the projected viability curves to a range of QET input values. The range of QET values tested included an alternative corresponding to explicit extinction (less than 2 spawners per year), multiples of the 50 spawners per year value used by the ICTRT, and three larger values (150, 200 and 250 spawners per year) corresponding to thresholds applied to populations classified as Medium and Large in LC-WTRT analyses for application to Lower Columbia ESUs (LCWTRT, 2006 viability draft ref).

We generated viability curves (5% risk over 100 years) for each QET value (Figure A-21). To facilitate comparisons, we expressed the results as minimum productivities associated with meeting threshold population size values for Interior Columbia basin Snake River Spring/Summer Chinook populations (Table A-7).

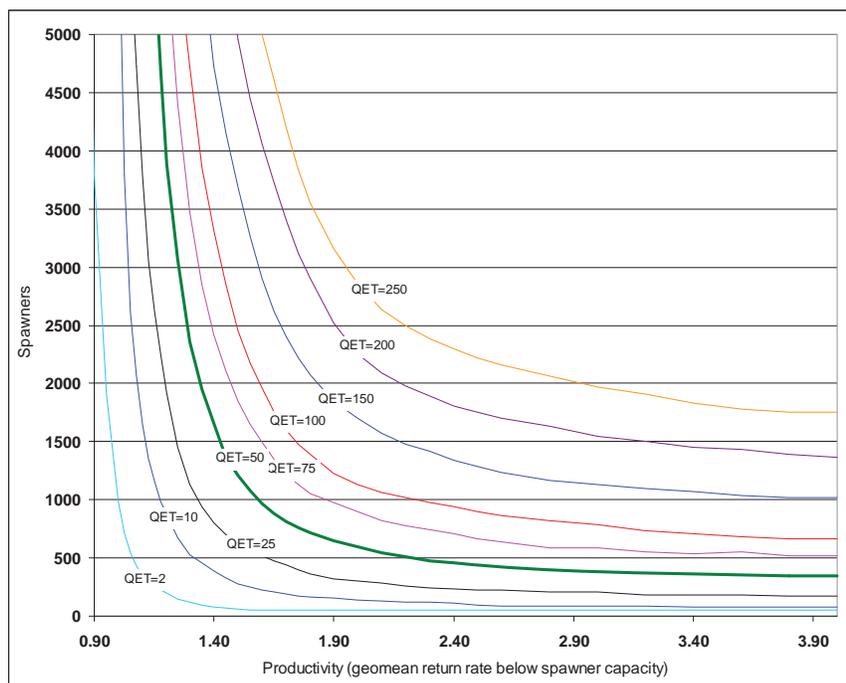


Figure A-21. Sensitivity of Snake River Spring/Summer Chinook viability curve to a range of QET values above and below the level of 50 spawners/year adopted by the ICTRT (1.24 total variance, 0.89 after adjustment for autocorrelation). The RFT was set at 10 in the model runs for QET values of 10 or greater. The RFT was set at 2 for runs in which the QET was 2.

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Table A-7. Sensitivity analysis of **QET input values**. Estimated productivities at minimum equilibrium escapement levels corresponding to alternative population size classes. QET values greater than 100 were included to facilitate comparison to LC-WTRT analyses for larger population categories. In this analysis, the reproductive failure threshold (RFT) was set to 10 spawners except for the QET of 2 (RFT was also set to 2 in this case).

QET Threshold Escapement	Minimum Population Size			
	500	750	1000	2000
2	1.05	1.03	1.00	0.95
10	1.36	1.22	1.18	1.08
25	1.60	1.42	1.34	1.19
50	2.21	1.76	1.56	1.34
100	10.00+	3.50	2.27	1.58
150	10.00+	10.00+	4.20	1.87
200	10.00+	10.00+	10.00+	2.20
250	10.00+	10.00+	10.00+	2.90

The productivities required to meet or exceed the viability curves at minimum average population abundance levels were substantially affected by the choice of a QET value. Increasing the QET value from 50 to 100 roughly doubled the required productivity at threshold abundance levels for the two smallest population size categories. The productivities at threshold abundance levels were increased by approximately 45% for the large category and by 18% for the extra large population size category.

Setting the QET at 25 spawners per year reduced productivities associated with population size category minimum abundance levels by 28% (basic) to 11% (very large).

Setting the QET at 2 fish reduced the projected average productivities at population size category abundance thresholds by 29% to 52% relative to requirements associated with the QET of 50 spawners per year. The relative reductions in required productivity are greatest for populations within the basic size grouping.

We conducted two additional analyses of the sensitivity of model risk projections to the choice of a QET value. One set of tests evaluated the impact of the choice of a QET input on the proportion of relatively low escapements in projected model runs. The second test evaluated the relative impact of incorporating 'the wrong' QET value.

A major rationale in setting the QET at 50 spawners per year in establishing viability curves for Interior Columbia ESU populations was the uncertainty associated with productivities at escapements that were below levels in the historical record. Model runs incorporating lower QETs would be expected to project higher proportions of annual escapements below 50 spawners, even when the productivity and abundance levels incorporated into the runs reflect projected extinction risk of 5% or less. We compared model runs incorporating the range of

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QET values summarized in Table A-6 to evaluate the impact of QET on the expected proportion of relatively low escapements. The RFT was set at 10 fish for all of the QET values except the lowest value (QET = 2). In that case, the RFT was also set at 2 spawners. Each of the model runs incorporated input parameters corresponding to a 5% risk of extinction in 100 years for the particular QET being tested in the run. We calculated the expected proportion of annual spawning escapements at relatively low escapement levels as a function of QET (Table A-8). The number of 100 year simulation runs out of 1000 with a relatively high proportion of escapements below 50 spawners increased as QET was decreased. The proportion of relatively low escapements increased substantially when the QET was lowered from 10 to 2 spawners.

Table A-8. Comparison of the incidence of projected annual spawning escapements below 50 spawners per year as a function of QET. Equilibrium abundance was set at 500 spawners. Productivity was set at the level corresponding to a projected risk of 5% over 100 years. RFT used in model runs in parentheses.

Assigned QET (RFT)	Number of annual spawning escapements less than 50 (in 100 year model runs)		
	10 or more	20 or more	30 or more
2 (2)	46.6%	27.7%	19.4%
10 (10)	20.6	8.4	5.3
25 (10)	12.1%	3.8%	2.2%
50 (10)	1.7%	0.1%	0.0%

We evaluated the potential effects of setting the QET value at a particular level when the 'true' QET is at a different value. We ran these model runs with an equilibrium population abundance of 500 spawners. We ran a set of model projections for each combination of assumed and underlying actual QET values. For each combination, the productivity associated with a 5% risk for the assumed QET was used as input. We ran the model with the actual QET to determine the projected risk associated with the input productivity. The results are summarized in Table A-9. For example, the projected risk of extinction in 100 years if the actual QET value is 50 but the assumed value is 2 would be 47%. Conversely, if the actual QET value is 2 and the assumed QET is 10, the projected 100 year risk is 0.2% (Table A-9).

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Table A-9. Comparison of projected risks across productivities associated with 5% risk at for a basic population with an equilibrium population size of 500. Rows: assigned QET (productivity in parentheses). Columns correspond to actual QET incorporated into model runs. Entries are the projected extinction risk for the combination of assigned and modeled QET. Reproductive failure threshold (RFT) was set to 10 spawners except when QET = 2 (RFT was set to 2 in these cases).

Assigned QET (prod @ threshold)	Effective (Actual) QET			
	2	10	25	50
2 (1.05)	5%	19%	30%	47%
10 (1.36)	0.2%	5%	11%	22%
25 (1.60)	0.1%	2%	5%	14%
50 (2.21)	0.0%	0.2%	1%	5%

Reproductive Failure Threshold (RFT)

The stochastic population viability model used to generate viability curves incorporates a reproductive failure threshold (RFT). For each particular set of input parameters being tested, the model generates a minimum of 1,000 simulations of population performance projected over 100 or more years. Each of the 100 year simulation runs is structured as a series of annual time steps, using the age structure input values to distribute production from a particular brood year across future return years. If spawning escapement in any particular year falls below the RFT value, production from that brood year is set to zero. As a result, there would be no contributions from that particular brood year to future return years. We evaluated four alternative RFT values ranging from 2 to 50 spawners, holding other input values at the levels used in generating the viability curves (table A-10).

Table A-10. Sensitivity analysis of **RFT input values**. Estimated productivities needed to achieve 5% risk at minimum equilibrium escapement levels corresponding to alternative population size classes. The QET was held at 50 spawners for four consecutive years in all runs.

RFT Escapement	Minimum Population Size			
	500	750	1000	2000
2	2.10	1.73	1.54	1.32
10	2.21	1.76	1.56	1.34
25	2.28	1.79	1.60	1.36
50	2.43	1.93	1.69	1.41

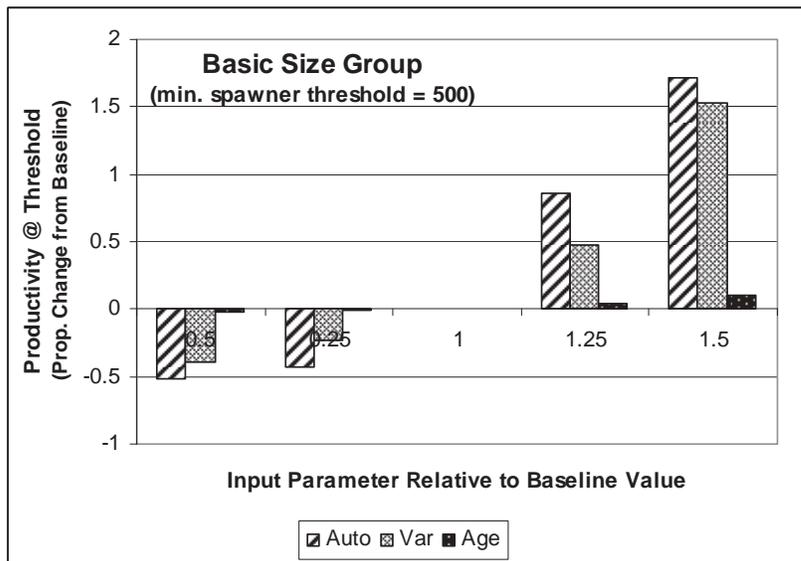
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Relative Sensitivity

We compared the relative sensitivity of projected viability curves to proportional changes in the three population specific input factors. We used the estimated productivities at equilibrium spawning level (500 and 1,000) corresponding to a projected risk level of 5% extinction in 100 years as a standard index of the viability curves. The projected curves were most sensitive to alternative values of autocorrelation in annual productivities (Figure 22). Variations in the input value for total productivity also generated substantial changes in the relative position of the viability curve. Variations in average age structure did not substantially impact the position of the curve in these examples. Viability curves with a minimum abundance threshold for application to relatively small populations (i.e., the Basic size category) were more sensitive to modest variations in the input parameters for autocorrelation and total variance than curves with a Large population size threshold (1,000). Increasing the autocorrelation input value above 0.80 resulted in a substantial increase in the projected productivities for the large size category as well.

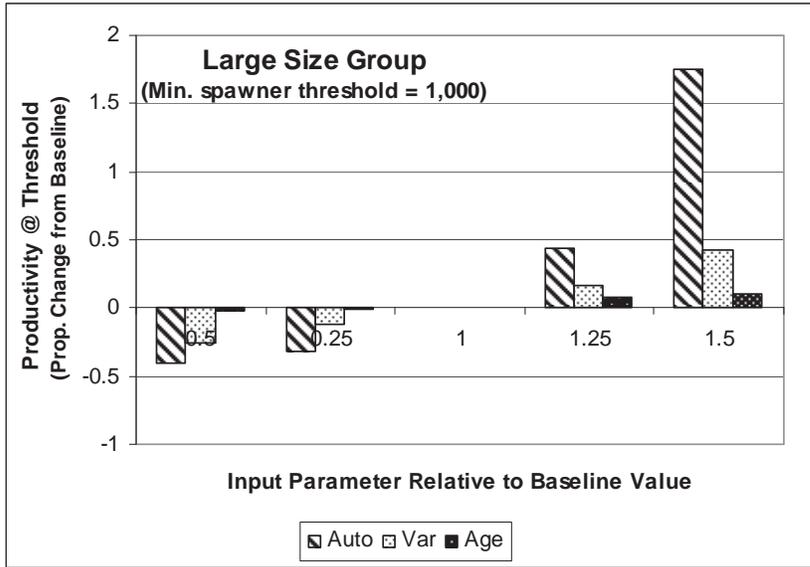
Figure A-22a-b. Relative effects of proportional variations in population input parameters on estimated productivity associated with a projected 5% risk of extinction at equilibrium population size of 500 spawners. Initial input values were geomean estimates for Snake River spring/summer chinook populations. Each parameter was varied from by a standard set of proportions (see Table A-4).

a)



DRAFT

b)



DRAFT**Literature Cited**

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EXHIBIT 2

Excerpts of 2005 Oregon Native Fish Status Report, Volume II, available at <http://www.dfw.state.or.us/fish/ONFSR/report.asp> (last visited July 14, 2015).

2005 Oregon Native Fish Status Report

Volume II Assessment Methods & Population Results



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Average spawner-recruit rates of 1.2 or less during low run years flag very low population productivities for salmon. The average 30-year abundance from the abundance criterion was used as a reference point to identify years where spawner numbers were less than existing habitat capacity. Average salmon escapements are typically less than the hypothetical equilibrium based solely on freshwater habitat capacity because of out-of-subbasin effects, particularly during periods of low ocean survival. A criterion threshold of 1.2 recruits per spawner at low spawner density was developed from an ad hoc inspection of data from a variety of wild populations that were thought to be otherwise viable. This viable condition was verified on basis of meeting the other interim criteria, plus various population viability simulations that indicated the chance of population extinction was very low. For these viable populations it was found that the average values for recruits per spawner associated with spawner levels less than the average abundance level was 1.2 or greater.

Initially, in the development of the productivity interim criterion, the estimation method proposed was based upon spawner-recruit analyses. However, such estimates, technically referred as intrinsic productivity, were often difficult to obtain and susceptible to a number measurement errors. Therefore, as an alternative the present metric was devised (1.2 recruits per spawner for data points from spawner levels less than the 30-year average abundance of wild fish). Essentially, this metric was meant to be a substitute index for intrinsic productivity as estimated via spawner-recruit analyses.

It should be noted, the values obtained for the productivity metric used in this report, average (geometric) recruits per spawner for moderate to low spawner densities, are not directly comparable to estimates of intrinsic productivity as determined from recruitment analysis. For example, the moderate to low spawner data points from a typical population that were found to have an average recruits-per-spawner value of 1.2 would yield a intrinsic productivity estimate via the spawner-recruit analysis in the range of 2.0. This is the case because the two primary spawner-recruit models fit to observed data create a curve where the ratio of recruits-per-spawner increases in relation to decreasing spawner density. Therefore, the highest recruit-per-spawner values will occur at those spawner densities nearest to zero. Typically, intrinsic productivity is reported as the predicted recruits-per-spawner at this near zero spawner abundance. In contrast, the productivity metric used in this evaluation is essentially an average of recruits-per-spawner values for all spawner levels from near zero to the average spawner abundance. Therefore, it is inevitable that from the same raw data, the average productivity metric used here will always be a lower value than the intrinsic productivity estimated via spawner-recruit analysis.

Spawners often include adults of natural and hatchery origin. First generation hatchery fish are not a product of the freshwater habitat and hence are not counted as recruits. Recruits do include offspring of first generation hatchery fish that spawn in natural habitats. The productivity criterion is based on years when total (hatchery plus naturally-produced) spawner abundance is less than the 30-year average abundance of naturally-produced spawners. Large influxes of hatchery fish may consistently increase escapement to levels exceeding the natural habitat capacity. Hence, the natural escapement average provides a more accurate benchmark for identifying intrinsic productivity of a population. Productivity estimates cannot be derived for some populations with consistent high levels of hatchery escapement where total numbers rarely fall below a natural spawner average benchmark.

For some salmon populations, quantifying recruits-per-spawner was not possible because of a lack of data or the inability to separate hatchery fish from naturally-produced fish. Productivity

represented by the 75th percentile of escapements for the period beginning the first year estimates were available (1949-1964) through 1974 (R. Carmichael, personal communication 2004). This period encompasses return estimates prior to declines associated with completion of the lower Snake River dams.

Hatchery to wild ratios from 1986 to 2004 were provided by ODFW (pers. comm., Pat Keniry, 1/5/05). Those data were based on finclip observations on the spawning grounds, scale analysis, and findings from CWT recoveries. For most of the years where data was available, the data to look at percentages of hatchery adults was from carcass recoveries during spawning surveys. Estimates based on carcass recoveries are considered conservative. These recoveries may overestimate the percentages of hatchery fish due to the timing of the surveys – later in the season when later spawning hatchery fish are predominant. Annual hatchery fractions prior to 1986 were derived from provisional estimates compiled by ODFW (pers. comm., Jeff Rodgers, 1/13/04, data compiled by E. Tinus and C. Petrosky for NOAA Fisheries).

Table 75. Abundance data (redds/mile) used in evaluating interim criteria for the Lower Snake Spring Chinook SMU.

Population	Full Seeding Level	25% of Full Seeding	Abundance by Return Year					# Years >25% Full Seeding
			2000	2001	2002	2003	2004	
Wenaha	36.2	9.1	8.8	13.1	10.4	11.5	12.5	4
Wallowa	15.5	3.9	2.6	2.3	2.8	1.1	1.1	0
Minam	10.8	2.7	6.3	9.7	14.3	9.9	10.2	5
Catherine	20.9	5.2	0.3	2.6	3.0	0.7	0.6	0
Lookingglass			<i>Extinct population</i>					
Upper Grande Ronde	14.5	3.6	1.3	0.7	2.0	0.9	1.3	0
Imnaha	35.9	9.0	2.9	8.5	8.7	8.7	2.7	0
Big Sheep ^a	8.8	2.2	0.0	0.7	2.8	1.4	1.0	1

a. Redd densities were not adjusted by the proportion of naturally spawning hatchery fish.

Productivity

Productivity was estimated using spawner abundance estimates, hatchery composition, and annual age composition. Abundance and hatchery composition data were obtained from sources described above. Age composition data through the 2002 return year were provided by ODFW (pers. comm., Jeff Rodgers, 1/13/04, data compiled by E. Tinus and C. Petrosky for NOAA Fisheries). Data from 2003 were from non-finclipped fish sampled during spawner surveys and were obtained from Pat Keniry, ODFW (pers. comm., 3/15/04). The 2004 age composition data were not yet available so the run reconstruction used the average age composition for the previous five years.

Table 76. Productivity estimates used in evaluating interim criteria for the Lower Snake Spring Chinook SMU.

Population	Recent Complete Brood Years of Below Full Seeding	Productivity (R/S)					Years > 1.2
		Year 1	Year 2	Year 3	Year 4	Year 5	
Wenaha	1995-1999	1.0	2.4	2.9	4.4	8.8	4
Wallowa	1995-1999	4.7	2.8	1.3	5.0	0.2	4
Minam	1995-1999	1.4	1.4	2.6	5.1	1.8	5
Catherine	1995-1999	1.8	1.2	1.5	3.8	0.2	4
Lookingglass		<i>Extinct population</i>					
Upper Grande Ronde	1995-1999	0.1	0.9	0.3	0.6	-- ^a	1
Imnaha	1995-1999	0.6	0.9	1.0	2.9	0.5	1
Big Sheep		<i>Insufficient data – high hatchery fraction</i>					<i>Fail</i>

a. There were no parents observed in index reaches for the 1999 brood year, though recruits returned four and five years later. Could not divide by “0”.

EXHIBIT 3

Analyzing large-scale conservation interventions with Bayesian hierarchical models: a case study of supplementing threatened Pacific salmon

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Keywords

Before–after control–impact, captive breeding, hatchery, multivariate, salmon, supplementation, time series.

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Abstract

Myriad human activities increasingly threaten the existence of many species. A variety of conservation interventions such as habitat restoration, protected areas, and captive breeding have been used to prevent extinctions. Evaluating the effectiveness of these interventions requires appropriate statistical methods, given the quantity and quality of available data. Historically, analysis of variance has been used with some form of predetermined before–after control–impact design to estimate the effects of large-scale experiments or conservation interventions. However, ad hoc retrospective study designs or the presence of random effects at multiple scales may preclude the use of these tools. We evaluated the effects of a large-scale supplementation program on the density of adult Chinook salmon *Oncorhynchus tshawytscha* from the Snake River basin in the northwestern United States currently listed under the U.S. Endangered Species Act. We analyzed 43 years of data from 22 populations, accounting for random effects across time and space using a form of Bayesian hierarchical time-series model common in analyses of financial markets. We found that varying degrees of supplementation over a period of 25 years increased the density of natural-origin adults, on average, by 0–8% relative to nonsupplementation years. Thirty-nine of the 43 year effects were at least two times larger in magnitude than the mean supplementation effect, suggesting common environmental variables play a more important role in driving interannual variability in adult density. Additional residual variation in density varied considerably across the region, but there was no systematic difference between supplemented and reference populations. Our results demonstrate the power of hierarchical Bayesian models to detect the diffuse effects of management interventions and to quantitatively describe the variability of intervention success. Nevertheless, our study could not address whether ecological factors (e.g., competition) were more important than genetic considerations (e.g., inbreeding depression) in determining the response to supplementation.

Introduction

Human activities such as habitat modification, alteration of biogeochemical cycles, overharvest, and spread of

non-native species affect all of the earth's ecosystems (Vitousek et al. 1997), increasing extinctions of both terrestrial (Hoekstra et al. 2005) and marine species (Dulvy et al. 2003). In response, a variety of conservation actions

have been employed to recover or prevent the extinction of at-risk species. Habitat restoration efforts in both terrestrial and aquatic ecosystems are now widespread (van Andel and Aronson 2012), but their effects can be limited. For example, reforested plantations (Chazdon 2008) and organic farms (Gabriel et al. 2010) have enhanced local biodiversity, but they have not matched the composition and structure of the original landscapes they replaced. Protected reserves are used increasingly in marine (Mora et al. 2006) and terrestrial ecosystems (Jenkins and Joppa 2009), but measures of their effectiveness vary broadly due to mobility of animals, poaching, data quality, and interpretation of effects (Kaplan et al. 2013). Captive breeding programs have offered hope for animals facing imminent extinction, but high costs and negative genetic impacts can limit their application (Williams and Hoffman 2009).

In most rivers along the west coast of the continental United States, populations of *Oncorhynchus* spp. (Pacific salmon) have been reduced to small fractions of their historical abundances and are the focus of widespread conservation efforts. For these purposes, Pacific salmon species are grouped into evolutionarily significant units (ESUs), defined as a group of salmon that (1) is reproductively isolated from other conspecific populations, and (2) represents an important component in the evolutionary legacy of the species (Waples 1991). Currently, 28 of the 49 extant Pacific salmon ESUs are listed as “threatened” or “endangered” under the US Endangered Species Act (ESA). A wide variety of anthropogenic causes (e.g., habitat loss, hydropower development, overharvest) and natural drivers (e.g., climate variability) have contributed to these declines (Ford 2011).

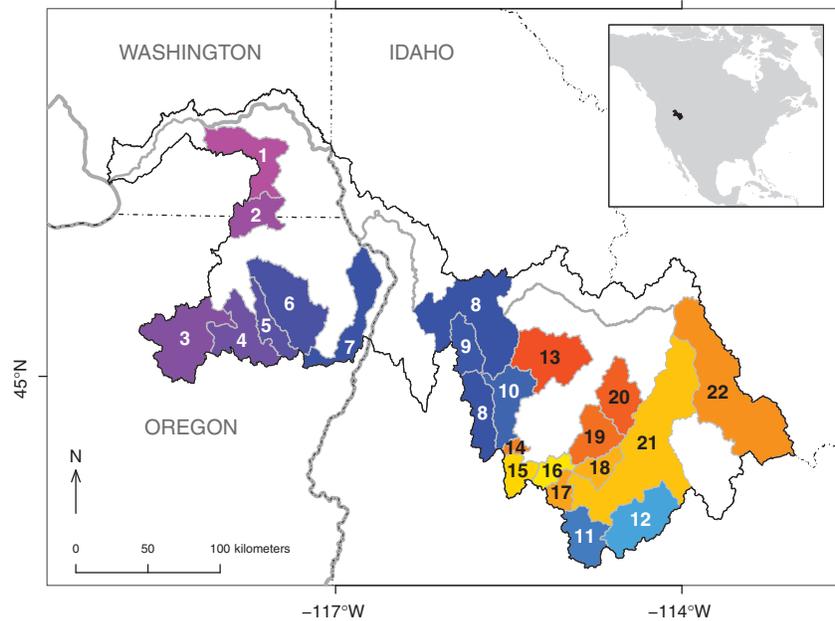
Efforts to rebuild depressed populations are extensive and expensive. For example, in the Columbia River Basin, which contains 13 listed ESUs of Pacific salmon, more than 15,000 habitat restoration projects have been undertaken at an annual cost of over \$150 million USD (Barnas and Katz 2010). In addition, artificial propagation of salmon has been used widely as a mitigation measure for more than a century. In the US Pacific Northwest, salmon hatcheries release about 400 million juveniles per year at a cost of roughly \$40 million USD (Naish et al. 2008). Many of these fish are produced to meet tribal, commercial, or recreational harvest demands, or to mitigate for habitat loss. However, since the mid-1980s, hatcheries have been used increasingly to rebuild wild populations through supplementation programs, in which hatchery fish are encouraged to return to spawn in natural streams (Waples et al. 2007). Despite their widespread use, however, the effectiveness of these programs in achieving conservation goals remains poorly understood (Waples et al. 2007; Neff et al. 2011).

When designed appropriately a priori, large-scale interventions can be treated as large-scale experiments, with effect sizes estimated through carefully constructed analysis of variance (ANOVA) applied to data from before–after control–impact (BACI) studies (e.g., Keough and Quinn 2000). However, we often seek to estimate effect sizes following a natural disturbance or “unplanned experiment” (e.g., Buhle et al. 2009), when it is impractical or simply too late to assign experimental units randomly; in such cases, no true “control” exists (Stewart-Oaten and Bence 2001). Additional problems can arise when model assumptions are violated with respect to homogeneity of variance and uncorrelated errors (Carpenter et al. 1989; Underwood 1994).

Time-series models overcome these limitations by addressing explicitly the sequential nature of monitoring data. In particular, hierarchical or “state-space” models have two components that make them amenable to observational ecological studies (Royle and Dorazio 2008) that lack an explicit experimental design: (1) a process component, which describes the underlying dynamics of a true but unobserved state, and (2) an observation component, which relates the state(s) to an associated series of observations (the data). In addition, hierarchical models can accommodate missing data, different error distributions, and data from varying sources (e.g., visual surveys and net samples). Hierarchical models have a long history in fields such as engineering and economics (West and Harrison 1997), and reports of their application are now increasingly common in the ecological literature, especially in meta-analyses that examine effects across multiple spatial or temporal scales (e.g., Bennett and Adams 2004; Kulmatiski et al. 2008; Gabriel et al. 2010).

Here, we used a form of hierarchical time-series model that is used commonly for analyzing intervention effects in financial markets (e.g., effect of a promotional campaign on consumer spending; West and Harrison 1997) to examine the effects of large-scale hatchery supplementation on spring- and summer-run *O. tshawytscha* (Chinook salmon) from the Snake River basin, which encompasses regions of Washington, Oregon, and Idaho in the northwestern United States (Fig. 1). The Snake River spring- and summer-run (SRSS) ESU is one of 16 *O. tshawytscha* ESUs and was listed under the ESA in 1992. Using 43 years of monitoring data, we asked whether 11–23 years of supplementation have increased the density of naturally produced adults (i.e., fish that were born in the wild, not reared in a hatchery) in 12 supplemented populations, and if so, by how much. We found that, on average, supplementation has increased adult density among the 12 supplemented populations by only 3.3%.

Figure 1. Map of the Snake River spring/summer Chinook salmon ESU (black outline) showing the supplemented populations (numbers 1–12 in purple/blue colors) and reference populations (numbers 13–22 in yellow/orange colors) used in the analysis (1: Tucannon R.; 2: Wenaha R.; 3: Grand Ronde R. – Upper Mainstem; 4: Catherine Cr.; 5: Minam R.; 6: Lostine R.; 7: Imnaha R.; 8: South Fork Salmon R. – Mainstem; 9: Secesh R.; 10: South Fork Salmon R. – East Fork; 11: Salmon R. – Upper Mainstem; 12: Salmon R. – East Fork; 13: Big Cr.; 14: Sulfur Cr.; 15: Bear Valley Cr.; 16: Marsh Cr.; 17: Valley Cr.; 18: Salmon R. – Yankee Fork; 19: Loon Cr.; 20: Camas Cr.; 21: Salmon R. – Lower Mainstem; 22: Lemhi R.). Inset map shows the location of the ESU within North America.



Materials and Methods

Study species and data

Adult *O. tshawytscha* spawn in rivers and streams in late summer, and their eggs are buried in a nest (redd), where they incubate over winter before emerging as juveniles in spring. Juveniles from populations within the SRSS ESU then rear in fresh water for approximately 1 year before migrating to sea during the spring of their 2nd year. After spending 1–4 years foraging in the northeast Pacific Ocean, mature adults return from the ocean and migrate upstream to spawn in their natal streams (i.e., returning adults are 3–6 years old; >85% are age 4 or 5).

Our data set included information from 12 supplemented and 10 unsupplemented reference populations (Fig. 1), although some populations were not sampled in every year. In addition, data collection in the Tucannon River (a supplemented population) did not begin until brood year 1979. None of the missing data posed any problems for our analyses, however, because the hierarchical model described below imputes the true density for all populations and years, regardless of whether or not we have a direct estimate for a specific population or year. Furthermore, although populations from the Wenaha and Minam rivers were never intentionally supplemented, they did in fact receive some level of supplementation through straying of hatchery adults. Therefore, we included them as supplemented populations in our primary analysis, but then repeated the analysis after excluding them from the data set.

We used data on the numbers and age structure of spawning adults provided by the Interior Columbia Technical

Recovery Team (Ford 2011). We divided numbers of fish by hectares of available spawning habitat to standardize experimental effects across populations from different sized watersheds. The estimated area of available spawning habitat for each population was based on wetted channel width derived from 200-m reaches within the current spawning distribution, as delineated in a GIS derived from the 1:100,000-scale National Hydrography Dataset (Ford 2011).

Abundance and productivity data for fishes are commonly indexed by “brood year,” or the year during which eggs were spawned. For example, the total number of adult Chinook salmon produced from brood year 2004 would be the sum of all 3-, 4-, 5-, and 6-year-old adults returning in calendar years 2007, 2008, 2009, and 2010, respectively. Thus, although adult survey data were complete through calendar year 2012, we necessarily restricted our analyses to brood years 1964–2006 to allow for a full accounting of the entire life cycle. Referencing the data by brood year also allowed us to easily track any subsequent intervention effects on the density of natural-origin adults in the years following supplementation, as discussed below.

Hatchery supplementation

In general, hatchery supplementation programs try to select natural-origin adults for broodstock (Fig. 2). Juveniles are then reared from the eggs in a relatively safe environment, which reduces the high mortality they would otherwise experience in the wild. Juveniles are then released back into rivers and streams, from which they ultimately migrate to sea, and to which they return to spawn as adults. A primary goal of supplementation programs is

to increase the production of natural-origin adults. Thus, we were not simply interested in whether releasing more juveniles led to more returning adults of the same generation (i.e., whether hatchery-reared juveniles had greater survival from egg to adulthood). Rather, we sought to determine whether augmentation of the adult spawning population by hatchery-produced adults led to greater densities of natural-origin adults in the *following* generation. That is, a given population was considered supplemented in a brood year if fish born and reared in a hatchery were found on natural spawning grounds as adults (see Fig. 2). Because we were interested in the overall effects of naturally spawning hatchery fish on subsequent natural-origin abundance, we considered a population to be supplemented if any adult hatchery-origin fish were present, regardless of whether they were intended to spawn there or had strayed from a neighboring hatchery.

Hatchery supplementation in this region began in the early 1980s, but efforts were not uniform across time or the ESU (Fig. 3A). Some populations (e.g., Tucannon R.) received continued supplementation, whereas others (e.g., Lostine R.) had alternating periods with supplementation turned on or off. Thus, for each population i in brood year t , we treat supplementation as a binary indicator variable $I_{i,t}$ to indicate whether supplementation is “on” ($I_{i,t} = 1$) or “off” ($I_{i,t} = 0$). In our model described below, however, we require the actual shift, if any, in state $S_{i,t} = I_{i,t} - I_{i,t-1}$ when supplementation is turned on (i.e., $S_{i,t} = 1 - 0 = 1$), turned off (i.e., $S_{i,t} = 0 - 1 = -1$), remains on (i.e., $S_{i,t} = 1 - 1 = 0$), or remains off (i.e., $S_{i,t} = 0 - 0 = 0$). For any reference population i , $I_{i,t} = 0$, and hence $S_{i,t} = 0 - 0 = 0$ for all t .

Hierarchical time-series model

Census data on at-risk species are typically incomplete across time and space (i.e., lots of missing values) and

characterized by relatively large sampling and observation errors (e.g., nonexhaustive counts, misidentification), which can confound parameter estimation and subsequent inference regarding population viability (Holmes 2001; Holmes and Fagan 2002). Thus, we used a multivariate, hierarchical time-series model to describe year-to-year changes in population density of natural-origin spawners. This approach offers a parsimonious, phenomenological description of population dynamics that allows us to estimate supplementation effects instead of focusing on the various functional forms of population dynamics.

We used a form of hierarchical time-series model that is common in financial analyses of promotional campaigns (West and Harrison 1997). In general, the model treats consumer demand for a product as a stochastic process that might include a trend, seasonal effects (e.g., sales of ice cream generally decrease in winter), or external influences (e.g., sales of bottled water increase during a heat wave). For example, a manufacturer may initiate a promotional campaign in an effort to increase sales of a product. Following the onset of advertising, the manufacturer uses the hierarchical time-series model to evaluate how much sales increased as a result of the promotion after accounting for other market forces.

In any given year, the spawning adults from any population are a mix of overlapping generations, so we modeled density as a biased random walk, such that

$$X_{i,t} = X_{i,t-1} + a_t + b_i S_{i,t} + w_{i,t} \quad (1)$$

Here, $X_{i,t}$ is the true but unobserved density (log-transformed adults ha^{-1}) of natural-origin spawning adults from population i born in brood year t ; a_t is an annual growth rate common to all populations (i.e., it reflects large-scale drivers of temporal variation); b_i is the effect of supplementation on population i ; and $S_{i,t}$ is the supplementation indicator described above for population i

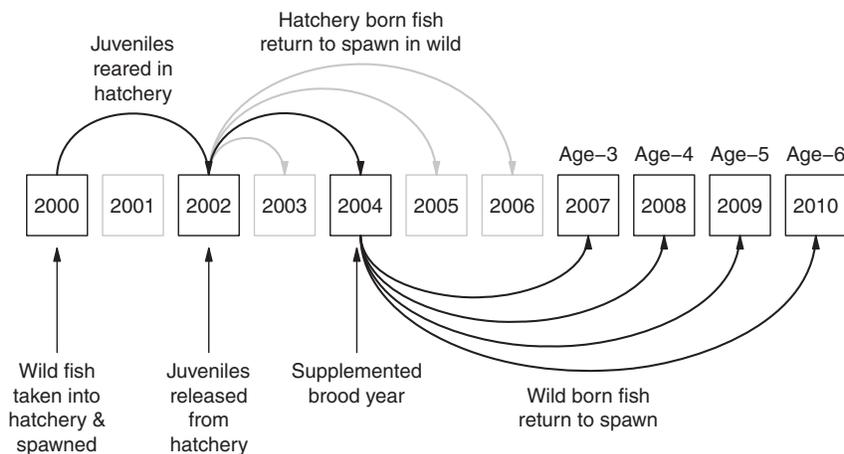


Figure 2. Diagram of the general model for supplementation evaluation. In this example, natural-origin adults are captured on the spawning grounds in 2000, brought into the hatchery, and spawned. Two years later, their offspring are released as smolts, which migrate to sea, and then return as adults over the following 1–4 years, such that brood years 2003–2006 are all then considered supplemented. For the 2004 brood, the total returning adults is then the sum of all 3-, 4-, 5-, and 6-year-old adults returning in 2007, 2008, 2008, and 2010, respectively. Note that sometimes hatcheries release juveniles after 1 year, but the same idea applies.

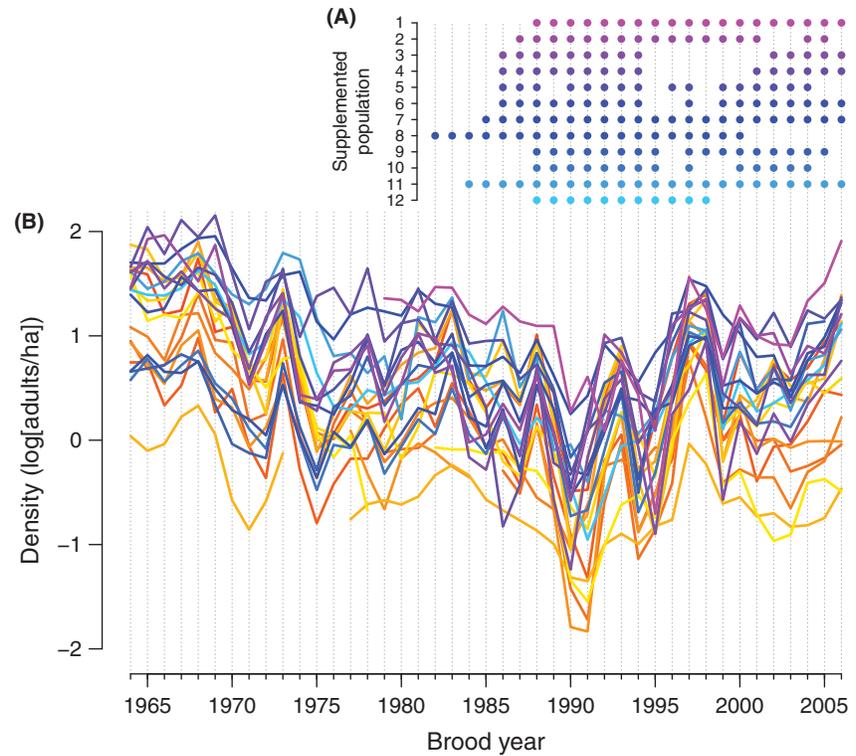


Figure 3. Time series of the supplemented years (A) and densities of adult Chinook salmon (B) indexed by brood year; colors are the same as in Figure 1. Numbers on the y -axis in (A) refer to the 12 supplemented populations shown in Figure 1; dots indicate populations and brood years in which the parents' generations were supplemented (see Methods for details). Breaks in some time series in (B) indicate missing years of data.

in brood year t . Finally, $w_{i,t}$ is a random process error representing environmental stochasticity.

Specifically, we modeled annual population growth rate (a_t) as a first-order Markov process because the large-scale drivers of environmental variability important to salmon survival (e.g., upwelling currents, temperature) tend to be highly autocorrelated from year to year (Zabel et al. 2006; Scheuerell et al. 2009). Thus,

$$a_t \sim N(a_{t-1}, p), \text{ and} \quad (2a)$$

$$a_0 = 0 \quad (2b)$$

We set the initial growth rate (a_0) equal to zero because its estimation is confounded with the initial state ($X_{i,0}$). We assigned the precision (i.e., the inverse of the variance $1/p$) a Gamma(0.001, 0.001) prior.

We treated supplementation effects as random and drawn from a normal distribution with mean m_b and variance c . This allowed us to examine not only site-specific effects of supplementation, but also to evaluate the ESU level mean effect of supplementation. Thus, if population i is within the supplemented set, then

$$b_i \sim N(m_b, c), \quad (3)$$

and $b_i = 0$ if i is within the reference set. Following Gelman (2006), we assigned noninformative Unif(-100, 100) and Unif(0, 100) priors to the mean (m_b) and standard deviation (c), respectively, of the random effects.

We used the estimates of b_i to calculate the percent change in population density owing to supplementation, which follows from equation (1). If the log-density in a nonsupplemented state for population i is x_i , then the log-density in its supplemented state is $x_i + b_i$. Therefore, the percent change in density is $[\exp(x_i + b_i) - \exp(x_i)] / \exp(x_i)$, which reduces to simply $\exp(b_i) - 1$.

The variance of the process errors $w_{i,t}$ differs among populations to reflect any residual heterogeneity in local environmental conditions not captured by the random year or supplementation effects, such that

$$w_{i,t} \sim N(0, q_i) \quad (4)$$

We assigned the process precision (i.e., the inverse of the process variance $1/q_i$) a Gamma(0.001, 0.001) prior. For each population, we assumed the initial state at $t = 0$ ($X_{i,0}$) was also random with an unknown mean (m_{X0}) and a fixed and relatively uninformative variance of 10^4 , such that

$$X_{i,0} \sim N(m_{X0}, 10^4) \quad (5)$$

As mentioned above, the hierarchical framework further accommodates sampling or observation errors that may exist in our density measurements. Specifically, $Y_{i,t}$ is the observed density of spawning adults (log-transformed adults ha^{-1}) from population i born in year t , which is corrupted by a normally distributed observation error $v_{i,t}$, such that

$$Y_{i,t} = X_{i,t} + v_t, \text{ and} \quad (6)$$

$$v_{i,t} \sim N(0, r) \quad (7)$$

In this case, we assumed the observation variance r does not vary among populations because similar methods were used to enumerate spawning adults (see Appendix S1 in Supporting Information for alternative assumptions about variance structures). We assigned the precision of the observation errors (i.e., the inverse of the observation variance $1/r$) a Gamma(0.001, 0.001) prior, which should be minimally informative given the large number of groups and time points in our analysis (Gelman 2006).

We used Bayesian inference to estimate all model parameters and the unobserved true state of annual natural spawner densities in each population. We used the freely available R v3.0.2 software (R Development Core Team 2013) combined with the JAGS v3.4.0 software (Plummer 2003) to perform Gibbs sampling with 10 parallel chains of 4×10^5 iterations. Following a burn-in period of 6×10^5 iterations, we thinned each chain by keeping every 400th sample to eliminate any possible autocorrelation, which resulted in 10^4 samples from the posterior distributions. We assessed convergence and diagnostic statistics via the CODA package in R (Plummer et al. 2006). Specifically, we used visual inspection of trace plots and density plots and verified that Gelman and Rubin (1992) potential scale reduction factor (R_{hat}) was less than 1.1, to ensure adequate chain mixing and parameter convergence (the maximum value of R_{hat} was 1.002 across all parameters and states). See Appendix S1 in Supporting Information for R and JAGS code.

We initially considered additional forms of hierarchical models that differed with respect to random or fixed effects of year and supplementation, as well as different variance-covariance structures (see Appendix S2 in Supporting Information). We used the deviance information criterion (DIC, Spiegelhalter et al. 2002) to evaluate relative support from the data for each of the competing models. Based on this initial model selection exercise, we present the structure and results only from the highest ranked model because the difference in DIC between first- and second-ranked models was extremely large (see Table S2 in Supporting Information).

Results

Dramatic declines in densities of natural-origin adults across all 22 populations of Snake River spring/summer Chinook salmon were evident from the mid-1960s to the early 1990s, when the ESU was listed as threatened (Fig. 3B). Supplemented populations then increased in

natural spawner density into the late 1990s, as did reference populations. Following a peak in density around brood year 1997, both reference populations and treatment populations where supplementation had been stopped appeared to decrease in density more so than those populations that continued to receive hatchery supplementation. Prior to the onset of supplementation, populations that were ultimately chosen for supplementation appeared to have a higher mean density of natural spawners than reference populations.

We found very limited support for a supplementation effect at both the individual population and ESU levels (Table 1). Mean values of the posterior distributions for the population-specific supplementation effects (b_i) ranged from -0.00044 to 0.081 , and the 95% credible intervals included 0 for all populations. Thus, on average supplemented populations increased by 0–8.4% relative to nonsupplemented years. The probability that b_i was positive (i.e., the intended direction) ranged from 0.50 to 0.84 for individual populations (Table 1). Equivalently, then, there was a 16–50% chance that supplementation may have actually caused some decrease in densities of wild adults across the ESU. The hypermean of supplementation effects at the ESU level (m_b) had a mean value of 0.033 and a 95% credible interval of -0.077 to 0.15 ; the probability that m_b was positive was 0.73 (Table 1).

When we repeated our analysis after excluding the Wenaha and Minam populations, which had some

Table 1. Summary statistics for population-specific supplementation effects (b_i) and their hypermean (m_b), including the posterior mean, 95% credible interval (CI), and probability that b_i or m_b is positive.

ID	Population	Mean	95% CI	Pr(+)
1	Tucannon R.	0.032	(−0.21, 0.27)	0.66
2	Wenaha R.	0.046	(−0.13, 0.29)	0.72
3	Grand Ronde R. – Upper Mainstem	0.025	(−0.16, 0.20)	0.63
4	Catherine Cr.	−0.00044	(−0.26, 0.16)	0.50
5	Minam R.	0.042	(−0.086, 0.17)	0.75
6	Lostine R.	0.0063	(−0.15, 0.13)	0.54
7	Imnaha R.	0.022	(−0.14, 0.17)	0.63
8	South Fork Salmon R. – Mainstem	0.081	(−0.070, 0.36)	0.84
9	Secesh R.	0.025	(−0.19, 0.22)	0.63
10	South Fork Salmon R. – East Fork	0.068	(−0.070, 0.26)	0.83
11	Salmon R. – Upper Mainstem	0.0074	(−0.18, 0.15)	0.54
12	Salmon R. – East Fork	0.039	(−0.14, 0.25)	0.69
m_b	Hypermean	0.033	(−0.077, 0.15)	0.73

hatchery-origin adults but were never intentionally supplemented, the supplementation effect increased for all populations, but also tended to be more variable (Table S1). In this case, the supplemented populations increased by 1–13% relative to nonsupplemented years. In particular, the hypermean (m_b) had a mean value of 0.056 and a 95% credible interval of -0.086 to 0.20 ; the probability that m_b was positive increased from 0.73 to 0.80.

Year effects (a_t), which accounted for large-scale temporal variation common to all populations across the ESU, were highly variable and generally much larger in magnitude than supplementation effects (Fig. 4). Larger up-and-down swings in year effects appeared more commonly in the latter portion of the study period, particularly during the 1990s. The mean of the year effects was -0.041 during the first half of the time series when abundance declined across the entire ESU, but then jumped to 0.029 during the second half of the period as populations increased on average. Relative to the hypermean of supplementation effects, the magnitudes (absolute values) of the a_t were more than twice m_b for 39 of 43 years (Fig. 4).

After controlling for supplementation and year effects, we found considerable variability among populations in the standard deviation of the process errors (Fig. 5). In particular, populations from the western and eastern portions of the ESU had much larger variance in process residuals than those populations in the middle of the ESU. There was very little difference, however, in the average standard deviations of reference and supplemented populations (i.e., the mean of $SD_{sup} - SD_{ref}$ was 0.016 with 95% credible limits of 0.0097 and 0.020).

Discussion

We found that over varying timespans since the 1980s, hatchery supplementation of threatened *O. tshawytscha*

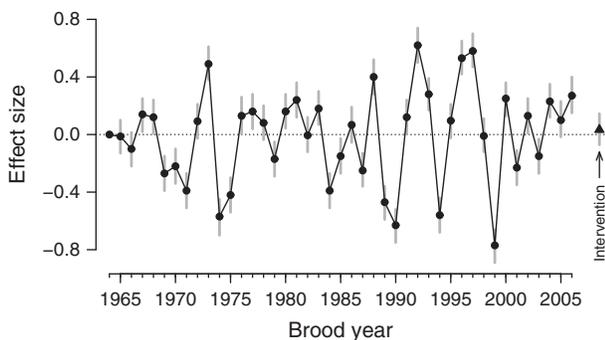


Figure 4. Time series of estimated year effects. Points are medians of the posterior distributions. Vertical bars indicate 95% credible limits for each year effect. For comparison, the median (triangle) and 95% credible limits for the mean of the experimental effects (m_b) are also shown.

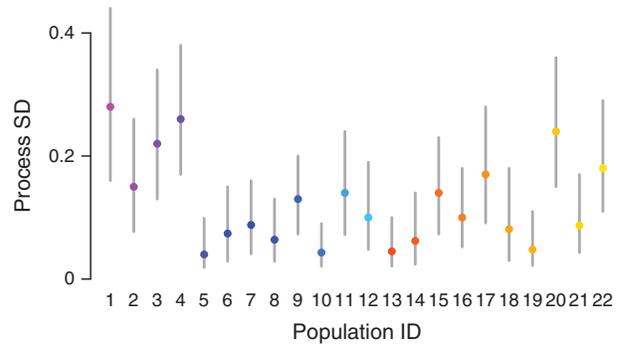


Figure 5. Estimated standard deviation (SD) of the process errors for each of the 22 populations. Colored points are medians of the posterior distributions. Gray vertical bars indicate 95% credible limits on the estimated SD. Colors and IDs are the same as in Figure 1.

has had rather minimal effects on increasing the density of naturally spawning adults. For example, in the East Fork Salmon River, we estimated with 95% probability that 11 consecutive years of supplementation (i.e., the fewest among all populations) ultimately produced somewhere between a 13% decrease and 28% increase in the density of natural-origin adults. Similarly, 23 successive years of supplementation in the Upper Mainstem Salmon River (i.e., the most among all populations) resulted in densities of natural-origin adults that were between 17% less and 16% greater than years prior to supplementation. Notably, the 95% credible interval of the estimated effect of supplementation spanned zero in all cases, indicating some nonzero probability that hatchery supplementation actually had negative impacts on natural-origin adults. Therefore, although that the probability of a positive effect of supplementation on spawning abundance was greater than 50% in all but one population, the effect appears small and uncertain compared to large-scale drivers of temporal variation (i.e., estimated year effects) such as climate, habitat alterations, and hydroelectric dam system operations.

There are a number of possible explanations for our failure to find strong evidence for a positive effect of supplementation. First, our findings are consistent with other studies, which indicate that hatchery-produced salmon often have poor reproductive success in the wild (Araki et al. 2008; Christie et al. 2014) and may even depress the abundance of wild adults (Buhle et al. 2009). Thus, although artificial propagation (including supplementation) may be a potentially useful intervention for preventing imminent extinction of specific populations (Neff et al. 2011), supplementation may be largely ineffective as a recovery tool for increasing the density of natural-origin adults within this ESU over the long term.

Second, the theoretical basis of supplementation assumes that target populations are well below carrying capacity (Cuenco 1994; Naish et al. 2008). However, whether this assumption is fulfilled is questionable in this ESU, and the failure of supplementation to increase abundance in our study may be that populations are closer to current carrying capacity than is generally appreciated. For example, a recent analysis of this same ESU of Chinook salmon found strong density-dependent survival of juveniles, despite reductions in spawning adults to orders of magnitude below historical numbers (Thorson et al. 2013). If habitat capacity has been reduced due to long-term structural alterations, then supplementation without concomitant habitat restoration will be unlikely to provide strong conservation benefits and may simply result in displacement of natural-origin fish by hatchery fish. Alternatively, if capacity reduction is due in part to losses of materials and energy provided by spawning and dead adult salmon (e.g., Scheuerell et al. 2005), then supplementation itself might be expected to help increase carrying capacity.

Finally, our study took a broad view of supplementation and considered the presence of any hatchery-origin fish in a population to be an indicator of supplementation. However, some of these fish were strays from hatchery programs using semidomesticated stocks never intended for supplementation, and it is possible that differences in hatchery practices may obscure a more positive signal from more recent programs using only “best practices” (e.g., Moberg et al. 2005). Excluding the two populations that were never intentionally supplemented resulted in a larger but more variable estimate of the supplementation effect. Also, it is important to note that even if supplementation does result in a modest abundance increase, there are concerns that long-term use of artificial propagation could reduce genetic fitness (Araki et al. 2008), contribute to ecological risks such as competition for resources (Berejikian et al. 2000), and serve as vectors for diseases or parasites (Naish et al. 2008).

Massive efforts are underway worldwide to conserve at-risk species, and societies would like to know what they are getting for their investment. Our understanding of the efficacy of conservation interventions, or large-scale ecological experiments, depends on three important aspects. First, appropriate design considerations (e.g., replication, spacing, contrasts) are necessary to assess dynamic threats to biodiversity patterns and processes (Pressey et al. 2007). In particular, BACI designs, including paired and multiple BACI designs, are effective tools in evaluating both the effects of human development (e.g., Torres et al. 2011) and habitat improvements (e.g., Bro et al. 2004) on species of concern. For post hoc analyses such as the one illustrated here, however, we could not use a standard multiple

BACI design, but we did use an approach that provided the necessary contrast in the model formulation, given the nonsystematic application of hatchery supplementation over very large spatial and temporal extents (i.e., our study spanned 56,764 km² and 45 years), and missing data from some sites and years. Second, there is no substitute for adequate monitoring and data reporting (Downes et al. 2002; Bennett and Adams 2004). We were perhaps fortunate to study an ESA-listed species because widespread interest in recovery and conservation of these species encourages comprehensive reporting of monitoring data (Barnas and Katz 2010). Without such data, there can be no meaningful analysis of conservation efforts, regardless of their cost. Third, any inferences regarding the “significance,” size, and magnitude of experimental effect(s) will follow directly from the choice of statistical analysis (Osenberg et al. 1994; Carpenter et al. 1998; Downes et al. 2002). Here, we were specifically interested in estimating the hierarchical effects of supplementation on populations within a larger ESU, but there would have been no way to do that with an ANOVA model. Standard ANOVA models must also be modified to account for changes in variance as opposed to shifts in mean state (Underwood 1994), but the Bayesian hierarchical model (BHM) framework allowed us to easily examine a variety of assumptions about possible step changes and gradual changes in environmental process variances.

We believe BHMs have several advantages in a general ecological context, specifically in cases that do not fit the standard BACI design. As Clark (2005) notes, BHMs can describe complex relationships because they allow for stochasticity at multiple levels of spatial and temporal organization (e.g., individuals within populations), they can incorporate disparate sources of information (e.g., visual counts and net samples), and they can estimate large numbers of unobserved variables and parameters. In addition, they provide not only an estimate of the central tendency, but also an explicit accounting and propagation of all sources of uncertainty throughout the entire model. Similar hierarchical approaches have become increasingly popular in ecological meta-analyses (e.g., Bennett and Adams 2004; Kulmatiski et al. 2008) and analyses of management effects on habitat occupancy and species diversity (e.g., Zipkin et al. 2010; Giovanini et al. 2013; Iknayan et al. 2014). Bayesian hierarchical models also allow for direct quantification of the probability that a parameter takes a specific value. In our case, we could state explicitly the probability that supplementation had a positive effect at both the population and ESU levels.

Ecologists have worked for decades to understand how natural disturbances and human impacts affect communities and ecosystems. In cases where highly replicated, randomized, and relatively small experimental units have

been used, a simple statistical analysis can demonstrate whether the manipulations caused the observed effect (Carpenter *et al.* 1989; Downes *et al.* 2002). However, scaling experiments up to levels where conservation and management decisions must be made can yield invaluable insights that might otherwise remain obscured (see review by Carpenter *et al.* 1995). Such comprehensive evaluations require additional consideration as to how the data are analyzed. Ad hoc and unbalanced designs, the desire to incorporate random effects across multiple levels of organization, and correlations across time and space can all create problems for traditional approaches. Here, we have shown how Bayesian hierarchical models, which have been used effectively in other disciplines, can address these potential shortcomings and integrate information from a variety of sources to answer questions about ecological responses to a large-scale conservation intervention.

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Conflict of Interest

None declared.

Data Accessibility

The R and JAGS script for running the model is included in supplementary material (Appendix S1). All data used herein have been archived on a US government server and can be accessed at <https://www.webapps.nwfsc.noaa.gov/apex/?p=261:home:0>

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Appendix S1. R and JAGS script for fitting hierarchical intervention-effects model.

Appendix S2. Alternative model formulations for estimating supplementation effects.

Table S1. Summary statistics for population-specific supplementation effects (b_i) and their hyper-mean (m_b), including the posterior mean, 95% credible interval (CI), and probability that b_i or m_b is positive. These results pertain to the data set that excludes the Wenaha and Minam populations, which were never intentionally supplemented, but did receive some hatchery-origin strays from nearby populations.

Table S2. Model selection results for alternative model formulations discussed in Appendix S2. The various model forms focused on changes to the year effect (**a**) and the variance-covariance matrices for the process (**Q**) and observation (**R**) errors.

1 **SUPPORTING INFORMATION for ECE-2014-08-0384.R1**2 **Appendix S1 R and JAGS script for fitting hierarchical intervention-effects model.**

```
3 #-----
4 # user inputs
5 #-----
6
7 # file where to save JAGS model
8 file.JAGS <- "interventionModel.txt"
9
10 # number of reference popns
11 n.ref <- 10
12
13 # number of reference popns
14 n.int <- 12
15
16
17 #-----
18 # inits
19 #-----
20
21 # load necessary pkgs
22 library(runjags)
23 library(R2jags)
24
25
26 #-----
27 # get data
28 #-----
29
30 # data file is matrix with rows=n.yrs & cols=(n.ref+n.int)
31 # Y <- cbind(refData, intData)
32
33 # indicator file is matrix containing -1/0/1; dim(chi)==dim(Y)
34 # chi <- ...
35
36 # number of years of data
37 n.yrs <- nrow(Y)
38
39
40 #-----
41 # JAGS setup
42 #-----
43
44 # begin JAGS model description
45 cat("
46
47 # model specification
48
49 # i = popn
50 # t = brood year
51 # X = unobserved true log[spawner density] (ie, state)
```

```

52 # alpha = random effect of popn growth
53 # beta = random effect of supplementation
54 # chi = indicator function (-1/0/1)
55 # Y = observations (log[spawner density])
56 # Q = process variance
57 # R = observation variance
58
59 # State eqn
60 #  $X_{i,t} = X_{i,t-1} + \alpha_t + \beta_i \chi_{i,t} + v_{i,t}$ 
61 #  $v_{i,t} \sim N(0, Q_i)$ 
62
63 # Obs eqn
64 #  $Y_{i,t} = X_{i,t} + w_{i,t}$ 
65 #  $w_{i,t} \sim N(0, R)$ 
66
67 data {
68   # calc total number of sites
69   n.tot <- n.ref + n.int
70 } # end data specification
71
72 model {
73
74   #-----
75   # PRIORS
76   #-----
77
78   # mean of initial states
79   X0.mu ~ dunif(-100,100);
80   # SD of initial states
81   X0.sig <- 100;
82   # precision of initial states
83   X0.tau <- 1/(X0.sig*X0.sig);
84   # priors for initial states
85   for(i in 1:n.tot) { X0[i] ~ dnorm(X0.mu,X0.tau) }
86
87   # alpha = random effect of year
88   # initial value is zero
89   alpha0 <- 0;
90   # var in RW for alpha
91   tau.Qa ~ dgamma(0.001,0.001);
92   sig.Qa <- 1/sqrt(tau.Qa)
93
94   # beta = random effect of supplementation (ie, beta = 0 for ref popns)
95   # hyper mean across all popns
96   beta.mu ~ dunif(-100,100);
97   # hyper SD across all popns
98   beta.sig ~ dunif(0,100);
99   # precision across all popns
100  beta.tau <- 1/(beta.sig*beta.sig);
101  # set priors for betas
102  for(i in 1:n.int) { beta[i] ~ dnorm(beta.mu,beta.tau) }
103
104  # Q = process variance
105  # assume different among all popns with no cov

```

```

106 # diffuse gamma prior on precision
107 for(i in 1:n.tot) {
108   tau.Q[i] ~ dgamma(0.001,0.001);
109   sigma.Q[i] <- 1/sqrt(tau.Q[i]);
110 }
111
112 # R = obs variance
113 # assume same among all popns with no cov
114 # diffuse gamma prior on precision
115 tau.R ~ dgamma(0.001,0.001);
116 sigma.R <- 1/sqrt(tau.R);
117
118 #-----
119 # LIKELIHOOD
120 #-----
121
122 # first year; no effect of supplementation at start of ts
123 # predicted bias
124 alpha[1] ~ dnorm(alpha0, tau.Qa);
125 for(i in 1:n.tot) {
126   X.mu[1,i] <- X0[i] + alpha[1];
127   # predicted level vector
128   X[1,i] ~ dnorm(X.mu[1,i], tau.Q[i]);
129   # evaluate likelihood for first year
130   Y[1,i] ~ dnorm(X[1,i], tau.R)
131 }
132 # years 2:T
133 for(t in 2:n.yrs) {
134   # predicted bias
135   alpha[t] ~ dnorm(alpha[t-1], tau.Qa);
136   # loop over popns
137   for(i in 1:n.ref) {
138     # mean of the state
139     X.mu[t,i] <- X[t-1,i] + alpha[t];
140     # estimated state
141     X[t,i] ~ dnorm(X.mu[t,i], tau.Q[i]);
142     # evaluate likelihood
143     Y[t,i] ~ dnorm(X[t,i], tau.R);
144   } # end loop over ref popns
145   for(i in (n.ref+1):n.tot) {
146     # mean of the state
147     X.mu[t,i] <- X[t-1,i] + alpha[t] + chi[t,i]*beta[i-n.ref];
148     # estimated state
149     X[t,i] ~ dnorm(X.mu[t,i], tau.Q[i]);
150     # evaluate likelihood
151     Y[t,i] ~ dnorm(X[t,i], tau.R);
152   } # end loop over sup popns
153 } # end t loop over year
154
155 } # end model description
156
157 ", file=file.JAGS)
158 # end JAGS model description
159

```

```

160 # data to pass to JAGS
161 data.JAGS <- c("chi", "Y", "n.ref", "n.int", "n.yrs")
162
163 # params/states for JAGS to return
164 par.JAGS <- c("alpha", "beta", "beta.mu", "X",
165             "sigma.Q", "sig.Qa", "sigma.R")
166
167 # MCMC parameters
168 mcmc.length <- as.integer(1e6)
169 mcmc.burn <- as.integer(6e5)
170 mcmc.thin <- 400
171 mcmc.chains <- 10
172
173 mod.JAGS <- list(data=data.JAGS,
174                inits=NULL,
175                parameters.to.save=par.JAGS,
176                model.file=file.JAGS,
177                n.chains=mcmc.chains,
178                n.burnin=mcmc.burn,
179                n.thin=mcmc.thin,
180                n.iter=mcmc.length,
181                DIC=TRUE)
182
183 # start timer
184 timer.start <- proc.time()
185
186 # fit the model in JAGS & store results
187 mod.fit <- do.call(jags.parallel, mod.JAGS)
188
189 # stop timer
190 (run.time.in.min <- round(((proc.time()-timer.start)/60)["elapsed"], 0))
191
192 # save workspace
193 sav.JAGS <- paste("JAGSinterModel", Sys.Date(),
194                 "iter", mcmc.length,
195                 "burn", mcmc.burn,
196                 "thin", mcmc.thin,
197                 "nc", mcmc.chains,
198                 sep="_")
199 save(list=ls(), file=paste(sav.JAGS, "RData", sep="."))
200
201
202 #-----
203 # JAGS diagnostics
204 #-----
205
206 # summary of JAGS output
207 print(mod.fit)
208
209 # summary plots of JAGS output
210 plot(mod.fit)
211
212 # Gelman diagnostics
213 # need to unpack separate chains

```

```
214 mcmcList <- vector("list",length=dim(mod.fit$BUGSoutput$sims.array)[2])
215 for(i in 1:length(mcmcList)) {
216   mcmcList[[i]] <- as.mcmc(mod.fit$BUGSoutput$sims.array[,i,])
217 }
218 mcmcList <- mcmc.list(mcmcList)
219
220 # table of Rhat (pt est, upper CI)
221 (gmDiag <- gelman.diag(mcmcList))
222
223 # maximum Rhat across all params/states
224 gmDiag$psrf[which(gmDiag$psrf[,1]==max(gmDiag$psrf[,1])),]
225
226 # plots of Rhat over iteration
227 for(i in 1:nvar(mcmcList)) { gelman.plot(mcmcList[,i]) }
```

228 **Appendix S2** Alternative model formulations for estimating supplementation effects.

229 In addition to the hierarchical model presented in the main body of the manuscript, we
 230 also tried several alternative formulations to estimate supplementation effects, which we outline
 231 here. To begin, we write out the general model in matrix notation, such that the process model
 232 becomes

$$233 \quad \mathbf{X}_t = \mathbf{X}_{t-1} + \mathbf{a}_t + \mathbf{B}\mathbf{S}_t + \mathbf{w}_t.$$

234 In this case, \mathbf{X}_t is an $i \times 1$ vector of unknown states (i is the number of populations) at time t , \mathbf{a}_t is
 235 an $i \times 1$ vector of year effects, \mathbf{B} is an $i \times i$ diagonal matrix of supplementation effects, \mathbf{S}_t is an $i \times$
 236 1 vector of 1s and 0s indicating whether or not population i was supplemented in year t , and \mathbf{w}_t is
 237 an $i \times 1$ vector of process errors, such that

$$238 \quad \mathbf{w}_t \sim \text{MVN}(\mathbf{0}, \mathbf{Q}),$$

239 and \mathbf{Q} is a variance-covariance matrix for the process errors. The observation model is simply

$$240 \quad \mathbf{Y}_t = \mathbf{X}_t + \mathbf{v}_t,$$

241 where \mathbf{Y}_t is an $i \times 1$ vector of observed spawner densities, and \mathbf{v}_t is an $i \times 1$ vector of observation
 242 (sampling) errors, such that

$$243 \quad \mathbf{v}_t \sim \text{MVN}(\mathbf{0}, \mathbf{R}),$$

244 and \mathbf{R} is a variance-covariance matrix for the observation errors.

245 One alternative we considered is that the elements of \mathbf{a}_t follow a purely random process,
 246 such that

$$247 \quad \mathbf{a}_t \sim \text{MVN}(\mathbf{m}_a, \mathbf{C}_a).$$

248 Because the year effects are shared among all populations (i.e., all elements of \mathbf{a}_t are the same),
 249 the matrix form reduces to the univariate case. Another possible alternative would be to assume
 250 that the year effects (\mathbf{a}_t) are instead fixed rather than random, but that would mean estimating as

251 many year effects as there are years (i.e., 39 in our case), and may not provide much meaningful
 252 information anyway.

253 Other cases to consider include assumptions about the form of the process and
 254 observation variance-covariance matrices, \mathbf{Q} and \mathbf{R} , respectively. One can decide *a priori*
 255 whether or not any of the variance terms should be shared among populations. Similarly, one can
 256 decide whether or not to estimate any covariance(s), and if so, whether or not any of the
 257 covariance terms should be shared among populations.

258 In our case, we initially allowed for possible site-specific differences in the variance of
 259 the observation errors, but we had good reason to believe it could be shared given similarities in
 260 sampling programs and the manner in which data were collected. Thus, we compared the
 261 following forms for \mathbf{R} (ignoring covariances for moment):

$$262 \quad \mathbf{R} = \begin{bmatrix} r_1 & 0 & 0 & \cdots & 0 \\ 0 & r_2 & 0 & \cdots & 0 \\ 0 & 0 & r_3 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & r_i \end{bmatrix} \text{ or } \mathbf{R} = \begin{bmatrix} r & 0 & 0 & \cdots & 0 \\ 0 & r & 0 & \cdots & 0 \\ 0 & 0 & r & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & r \end{bmatrix}.$$

263 From a model-fitting standpoint, the form on the left has i parameters whereas the more simple
 264 form on the right has only 1, and for which we ultimately found overwhelming support from the
 265 data. In an analogous manner, one could evaluate different hypotheses about the covariance
 266 structure, such that (ignoring possible differences in variances) one might compare

$$267 \quad \mathbf{R} = \begin{bmatrix} r & \eta & \eta & \cdots & \eta \\ \eta & r & \eta & \cdots & \eta \\ \eta & \eta & r & \cdots & \eta \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \eta & \eta & \eta & \cdots & r \end{bmatrix} \text{ to } \mathbf{R} = \begin{bmatrix} r & 0 & 0 & \cdots & 0 \\ 0 & r & 0 & \cdots & 0 \\ 0 & 0 & r & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & r \end{bmatrix}.$$

268 We chose to model all populations as following their own process rather than treat them
 269 as multiple observations of a single process. That is, it seemed most reasonable that each
 270 population should reflect its own unique dynamics. Additionally, our random year effect
 271 accounted for large-scale temporal covariance, and therefore we set all covariance elements in
 272 both \mathbf{Q} and \mathbf{R} to 0. Those cases where we did, in fact, try to estimate covariance parameters had
 273 either very high DIC values compared to other models or they simply failed to converge for
 274 those parameters.

275 Of particular interest to us was whether there was any evidence from the data for a
 276 temporal change in the variance-covariance matrix \mathbf{Q} for the process errors. To do so, we
 277 allowed for changes in \mathbf{Q} under 2 scenarios: a step change and a linear trend. To begin, we
 278 defined \mathbf{Q}_t to be a diagonal matrix with the time-dependent process variance of population i
 279 along the diagonal and zeroes elsewhere, such that

$$280 \quad \mathbf{Q}_t = \begin{bmatrix} q_{1,t} & 0 & 0 & \dots & 0 \\ 0 & q_{2,t} & 0 & \dots & 0 \\ 0 & 0 & q_{3,t} & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & q_{i,t} \end{bmatrix}.$$

281 Next, examine evidence for a step-change h in the variance of those populations receiving
 282 supplementation, we set

$$283 \quad q_{i,t} = q_i + hS_{i,t},$$

284 and $S_{i,t}$ is a binary variable indicating whether ($S = 1$) or not ($S = 0$) supplementation affects
 285 population i in year t ($S = 0$ for all t in reference populations). To look for evidence of a linear
 286 change k in a variance over time, we set

$$287 \quad q_{i,t} = q_i + k(t - d_i + 1)S_{i,t},$$

288 with d_i as the first year of supplementation for population i . However, we found essentially no
289 data support for this model and therefore used the more simple form presented in the main text.

290 **Table S1.** Summary statistics for population-specific supplementation effects (b_i) and their hyper-
 291 mean (m_b), including the posterior mean, 95% credible interval (CI), and probability that b_i or m_b
 292 is positive. These results pertain to the data set that excludes the Wenaha and Minam
 293 populations, which were never intentionally supplemented, but did receive some hatchery-origin
 294 strays from nearby populations.

295	ID	Population	Mean	95% CI	Pr(+)
296	1	Tucannon R.	0.057	(-0.25, 0.37)	0.71
297	2	Wenaha R.	NA	NA	NA
298	3	Grand Ronde R. – Upper Mainstem	0.068	(-0.17, 0.38)	0.76
299	4	Catherine Cr.	0.012	(-0.31, 0.19)	0.55
300	5	Minam R.	NA	NA	NA
301	6	Lostine R.	0.066	(-0.089, 0.24)	0.80
302	7	Imnaha R.	0.042	(-0.14, 0.20)	0.70
303	8	South Fork Salmon R. – Mainstem	0.12	(-0.059, 0.41)	0.90
304	9	Secesh R.	0.040	(-0.23, 0.25)	0.67
305	10	South Fork Salmon R. – East Fork	0.089	(-0.065, 0.29)	0.87
306	11	Salmon R. – Upper Mainstem	0.015	(-0.20, 0.18)	0.57
307	12	Salmon R. – East Fork	0.060	(-0.15, 0.30)	0.74
308	m_b	hyper-mean	0.056	(-0.086, 0.20)	0.80

309 **Table S2.** Model selection results for alternative model formulations discussed in Appendix S2.
 310 The various model forms focused on changes to the year effect (**a**) and the variance-covariance
 311 matrices for the process (**Q**) and observation (**R**) errors. The options for **a** were Markov (as in the
 312 main text) or random (as in Appendix S2). In all cases the process errors were assumed to be
 313 independent (i.e., no covariance in **Q**), with the additional assumption that their variances were
 314 time invariant (as in the main text), followed a step-change with supplementation, or increased
 315 linearly during the period of supplementation. The observation errors were assumed to be
 316 independent and identically distributed (IID; as in the main text), independent but distributed
 317 differently (IDD), or non-independent and identically distributed (NID).

318	<u>Rank</u>	<u>a</u>	<u>Q</u>	<u>R</u>	<u>ΔDIC</u>
319	1	Markov	Invariant	IID	0
320	2	Random	Invariant	IID	154
321	3	Markov	Invariant	IDD	210
322	4	Markov	Invariant	NID	441
323	5	Random	Invariant	NID	451
324	6	Random	Invariant	IDD	551
325	7	Markov	Linear	IID	791
326	8	Markov	Linear	NID	859
327	9	Random	Linear	IDD	963
328	10	Random	Linear	NID	966
329	11	Markov	Linear	IDD	1346
330	12	Random	Step	IID	1441
331	13	Random	Linear	IID	1450

332	14	Markov	Step	IID	1520
333	15	Random	Step	IDD	1695
334	16	Markov	Step	NID	1776
335	17	Markov	Step	IDD	1903
336	18	Random	Step	NID	1946

EXHIBIT 4

Investigations into the Life History of Naturally Produced Spring Chinook Salmon and Summer Steelhead in the Grande Ronde River Subbasin

Annual Report 2014

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ABSTRACT

Juvenile Spring Chinook Salmon and Summer Steelhead Life History Monitoring

We determined migration timing, abundance, and survival of juvenile spring Chinook salmon *Oncorhynchus tshawytscha* and steelhead *Oncorhynchus mykiss* using rotary screw traps at five locations in the Grande Ronde River Subbasin. In Catherine Creek, we estimated 30,791 juvenile spring Chinook salmon and 25,939 steelhead migrated from upper rearing areas, and 58% of the Chinook salmon and 21% of the steelhead migrated in fall. In Lostine River, we estimated 68,046 juvenile spring Chinook salmon and 22,094 steelhead migrated from upper rearing areas, and 74% of the Chinook salmon and 72% of the steelhead migrated in fall. In Minam River, we estimated 70,074 juvenile spring Chinook salmon and 48,605 steelhead migrated from upper rearing areas, and 74% of the Chinook salmon and 46% of the steelhead migrated in fall. In upper Grande Ronde River, we estimated 32,842 juvenile spring Chinook salmon and 19,774 steelhead migrated from upper rearing areas, and 50% of the Chinook salmon and 18% of the steelhead migrated in fall. In middle Grande Ronde River, we estimated 56,469 juvenile spring Chinook salmon and 132,413 juvenile steelhead migrated from the Upper Grande Ronde Watershed.

Combining abundance estimates and survival estimates with estimates of spawners, obtained from Lower Snake River Compensation Plan - Oregon Evaluation Project, we estimate smolts per spawner, which is an indicator for the Viable Salmonid Population (VSP) parameter, productivity. We estimated that in Catherine Creek the number of spring Chinook salmon smolt equivalents leaving Catherine Creek was 20,494 for the 2014 migratory year (2012 brood year), for productivity of 32 smolts per spawner. We estimated that in Lostine River the number of spring Chinook salmon smolt equivalents leaving Lostine River was 61,259 for the 2012 brood year, for productivity of 36 smolts per spawner. We estimated that in Minam River the number of spring Chinook salmon smolt equivalents leaving Minam River was 38,706 for the 2012 brood year, for productivity of 62 smolts per spawner. We estimated that in upper Grande Ronde River the number of spring Chinook salmon smolt equivalents leaving upper Grande Ronde River was 27,278 for the 2012 brood year, for productivity of 71 smolts per spawner.

In 2014, we saw relatively high numbers of juvenile spring Chinook salmon from all of our study streams, resulting from the high number of spawners in 2012, continuing the increasing trend in juvenile migrants. We continue to see smaller juvenile spring Chinook salmon at higher spawner densities, which results in lower survival to Lower Granite Dam. The lower survival of the out-migrants results in low estimates of smolts/spawner, one indicator of the VSP parameter productivity. The higher number of spawners, whether of hatchery or natural origin, produced more total migrants but produced lower numbers of smolts per spawner, due to reduced survival rates of smolts. Habitat restoration projects funded by BPA and Bureau of Reclamation in the Upper Grande Ronde River watershed are addressing habitat capacity which should, in turn, result in an increase in productivity, such as smolts/spawner.

Steelhead emigrant abundance was above the trend line in all four streams we have been monitoring since 2000. In the future, this project will combine the out-migrant estimates, age

structure, and survival rates to quantify the number of smolts by age and relate to the appropriate number of spawners to estimate smolts/spawner, a VSP indicator of productivity.

Steelhead Spawner Surveys

We conducted 119 surveys in the Upper Grande Ronde River (UGRR) basin and 73 surveys in the Joseph Creek basin from 17 March through 11 June 2014 to determine summer steelhead *Oncorhynchus mykiss* redd abundance and adult escapement for these two populations. We sampled 29 random, spatially-balanced sites throughout the UGRR basin encompassing 61.3 km (6.9%) of an estimated 892 km of available steelhead spawning habitat. In Joseph Creek, we surveyed 25 sites encompassing 51.8 km (13.5%) of the 384 km of available spawning habitat. During these surveys we observed 65 steelhead redds and 19 live steelhead in the UGRR basin and 130 redds and 18 live steelhead in the Joseph Creek basin. We observed two carcasses in Joseph Creek basin and no carcasses in the UGRR basin.

On 18.7 km of Deer Creek, 18 redds, five live steelhead, and three carcasses were observed during five survey visits. A total of 48 wild-origin adult steelhead were passed above a permanent weir on Deer Creek, resulting in a 2.67 fish:red ratio for the 2014 spawning season.

Abundance of Steelhead Spawners at the Population Level

Using the fish:red ratio extrapolated from Deer Creek surveys, adult steelhead escapement estimates for the UGRR and Joseph Creek basins were 2,512 (95% C.I.: 1,538–3,487) and 2,522 (95% C.I.: 1,744–3,300) respectively. Escapement estimates in the UGRR sub-basin had been relatively stable from 2008-2012, but showed a substantial decrease in 2013. Estimates from 2014 rebounded from this low, but still were lower than the long term average. The UGRR estimate was roughly half of its running average over that period of time. This was the third GRTS-based steelhead spawning ground survey in Joseph Creek, and estimates were the highest we have observed through this project.

Steelhead and Chinook Salmon Parr Surveys, Parr Density, and Distribution.

Salmonids were observed at all 60 of the surveyed CHaMP sites in 2014. Steelhead were found at all 60 sites, Chinook salmon at 29, and bull trout *Salvelinus confluentus* at only eight sites.

In the UGRR sub-basin, Chinook were usually the dominant salmonid in mainstem snorkel survey, with counts in the hundreds, while counts were in the dozens for tributaries. There were fewer tributary observations of Chinook in 2014 than in previous years. In total, 4,586 juvenile Chinook were observed during snorkel surveys.

Steelhead were more widely distributed than Chinook, with individuals observed at all sites in 2014. Counts were higher than Chinook, with 5,563 individuals observed. Steelhead counts were much higher than in previous years, but this is an artifact of a change in methods. Previously, only steelhead >70mm in length were counted. In 2014, we counted all steelhead that could be positively identified.

Catherine Creek and UGRR had the highest densities of Chinook, similar to previous years. Steelhead densities were highest in lower Fly Creek and Catherine Creek.

Juvenile Chinook salmon and steelhead density estimates, were significantly higher (Kruskal-Wallis with Dunn's Test, $p < 0.05$) in pools than fastwater units or runs (Appendix Table B-26). There was no statistically significant difference between densities in fastwater units compared to runs.

Introduction

The goal of this project is to investigate the critical habitat, abundance, migration patterns, survival, and alternate life history strategies exhibited by spring Chinook salmon and summer steelhead juveniles from distinct populations in the Grande Ronde River and Imnaha River subbasins (Figures 1 and 2). This project will provide information on abundance of spring Chinook salmon and steelhead parr, estimates for egg-to-migrant survival for spring Chinook salmon and migrant survival for steelhead, estimate the Viable Salmonid Population (VSP) Indicator smolts per spawner for four populations of spring Chinook salmon, and assess stream conditions in selected study streams. This study provides a means for long term monitoring of juvenile salmonid production in the Grande Ronde and Imnaha River subbasins that is essential for assessing the success of restoration and enhancement efforts including hatchery supplementation and habitat improvement. As hatchery supplementation of spring Chinook salmon continues in the Grande Ronde Subbasin, we will monitor abundance of migrants, life history characteristics, and survival to various life stages to provide data to the Lower Snake River Compensation Plan - Oregon Evaluation project to determine the effectiveness of this management action.

This project coordinates and collaborates with many projects, including Columbia River Intertribal Fish Commission (CRITFC) and their project 2009-004-00 Monitoring Recovery Trends in Key Spring Chinook Habitat Variables and Validation of Population Viability Indicators, the Columbia Habitat and Monitoring Program (CHaMP) project 2011-006-00, and Lower Snake River Compensation Plan - Oregon Evaluation project. This project provides data for the Interior Columbia Technical Recovery Team (ICTRT) spring Chinook salmon life cycle model.

Objectives for FY14:

1. Document the in-basin migration patterns and estimate abundance of spring Chinook salmon juveniles in Catherine Creek and the upper Grande Ronde, Minam, and Lostine rivers.
2. Determine overwinter mortality and the relative success of fall (early) migrant and spring (late) migrant life history strategies for spring Chinook salmon from tributary populations in Catherine Creek and the upper Grande Ronde, and Lostine rivers, and the relative success of fall (early) migrant and spring (late) migrant life history strategies for spring Chinook salmon from the Minam River.

3. Estimate and compare smolt survival probabilities at main stem Columbia and Snake River dams for migrants from five local, natural populations of spring Chinook salmon in the Grande Ronde River and Imnaha River subbasins.
4. Document the annual migration patterns for spring Chinook salmon juveniles from five local, natural populations in the Grande Ronde River and Imnaha River subbasins: Catherine Creek, Upper Grande Ronde, Lostine, Minam, and Imnaha rivers.
5. Document patterns of movement and estimate abundance of juvenile steelhead from tributary populations in Catherine Creek, the upper Grande Ronde, Lostine and the Minam rivers including migration timing, and duration.
6. Estimate and compare survival probabilities to main stem Columbia and Snake River dams for summer steelhead from four tributary populations: Catherine Creek and the upper Grande Ronde, Lostine, and Minam rivers.
7. Describe aquatic habitat conditions, using water temperature and discharge, in Catherine Creek and the upper Grande Ronde, Lostine, and Minam rivers.
8. Estimate reach survival through the Grande Ronde Valley of Chinook salmon migrants from Catherine Creek.
9. Estimate adult steelhead escapement to the Upper Grande Ronde and Joseph Creek populations.
10. Estimate density and distribution of steelhead parr from the Upper Grande Ronde population and Chinook salmon parr from the Upper Grande Ronde and Catherine Creek populations.

The project addresses the following strategy questions associated with Fish Population Status Monitoring:

- Assess the status and trend of juvenile abundance and productivity of natural origin fish populations.
What are the status and trend of juvenile abundance and productivity of fish populations?
- Assess the status and trend of spatial distribution of fish populations.
What are the status and trend of spatial distribution of fish populations?
- Assess the status and trend of diversity of natural and hatchery origin fish populations.
What are the status and trend of diversity of natural and hatchery origin fish populations?

The focal species are Snake River Spring/Summer Chinook salmon and Snake River steelhead.

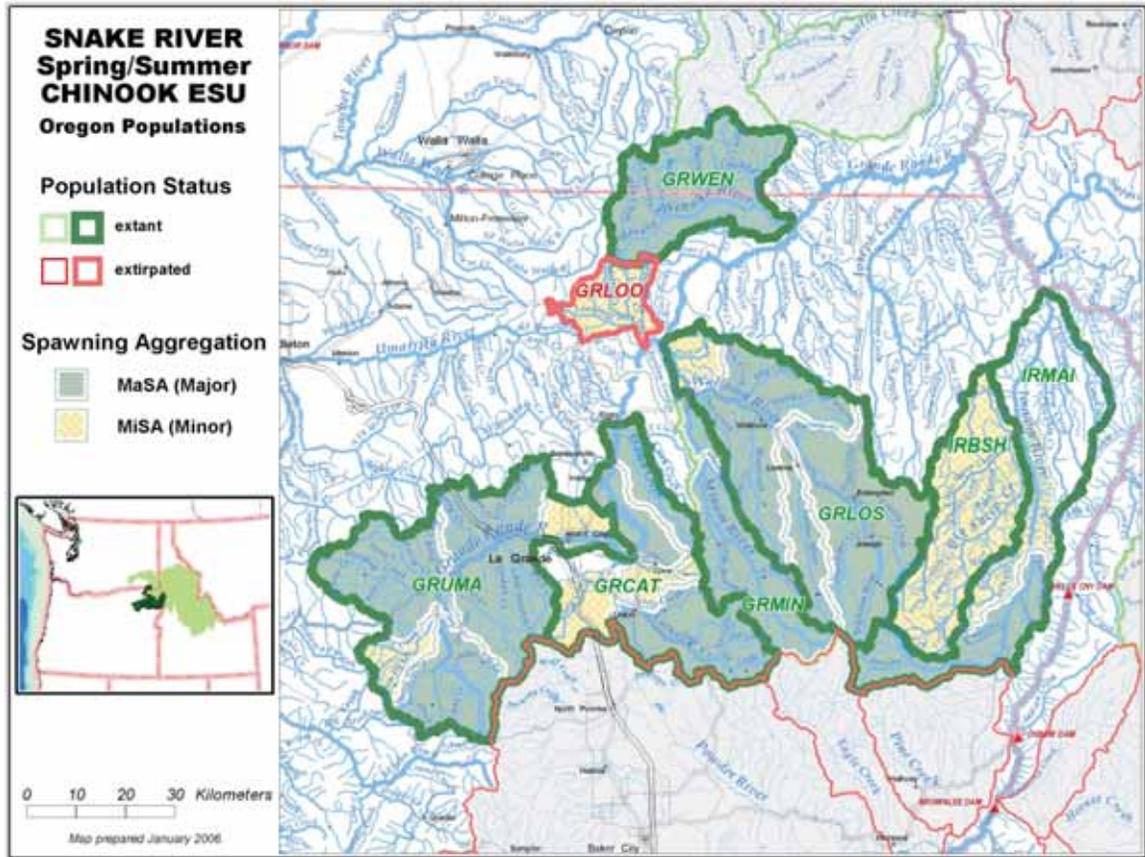


Figure 1. Map of the Grande Ronde-Imnaha spring Chinook salmon MPG with individual Chinook salmon populations identified. This project monitors these populations within this MPG: Upper Grande Ronde River (GRUMA), Catherine Creek (GRCAT), Minam River (GRMIN), Lostine River (GRLOS), and Imnaha River (IRMAI).

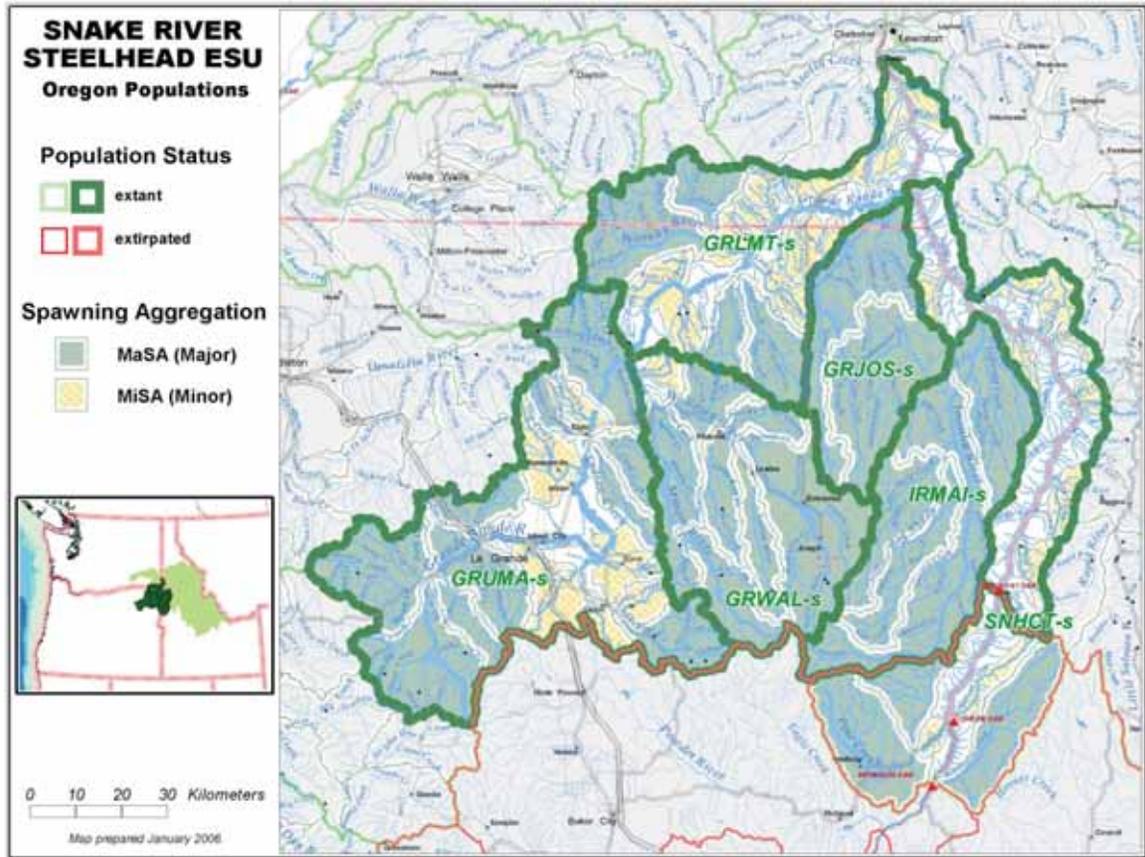


Figure 2. Map of the Grande Ronde-Imnaha steelhead MPG with individual steelhead populations identified. This project monitors these populations within this MPG: Upper Grande Ronde River (GRUMA-s), Wallowa River (GRWAL-s), and Joseph Creek (GRJOS-s).

Juvenile Spring Chinook Salmon and Summer Steelhead Life History Monitoring

Introduction

Numerous enhancement activities, including hatchery supplementation and habitat restoration, have been undertaken to recover spring Chinook salmon populations in Grande Ronde River Subbasin. Supplementation programs have been initiated by Oregon Department of Fish and Wildlife, the Confederated Tribes of the Umatilla Indian Reservation, and the Nez Perce Tribe using endemic broodstock from Catherine Creek and Lostine and upper Grande Ronde rivers. This study provides a means for long term monitoring of juvenile salmonid production in the Grande Ronde and Imnaha River subbasins that is essential for assessing the success of restoration and enhancement efforts including hatchery supplementation and habitat improvement. As hatchery supplementation of spring Chinook salmon continues in the Grande Ronde Subbasin, we will monitor abundance of migrants, life history characteristics, and survival to various life stages to determine the effectiveness of this management action.

Methods

Life history of spring Chinook salmon and summer steelhead (1992-026-04):

<http://www.monitoringmethods.org/Protocol/Details/217>

The locations of the rotary screw traps are shown in Figure 3.

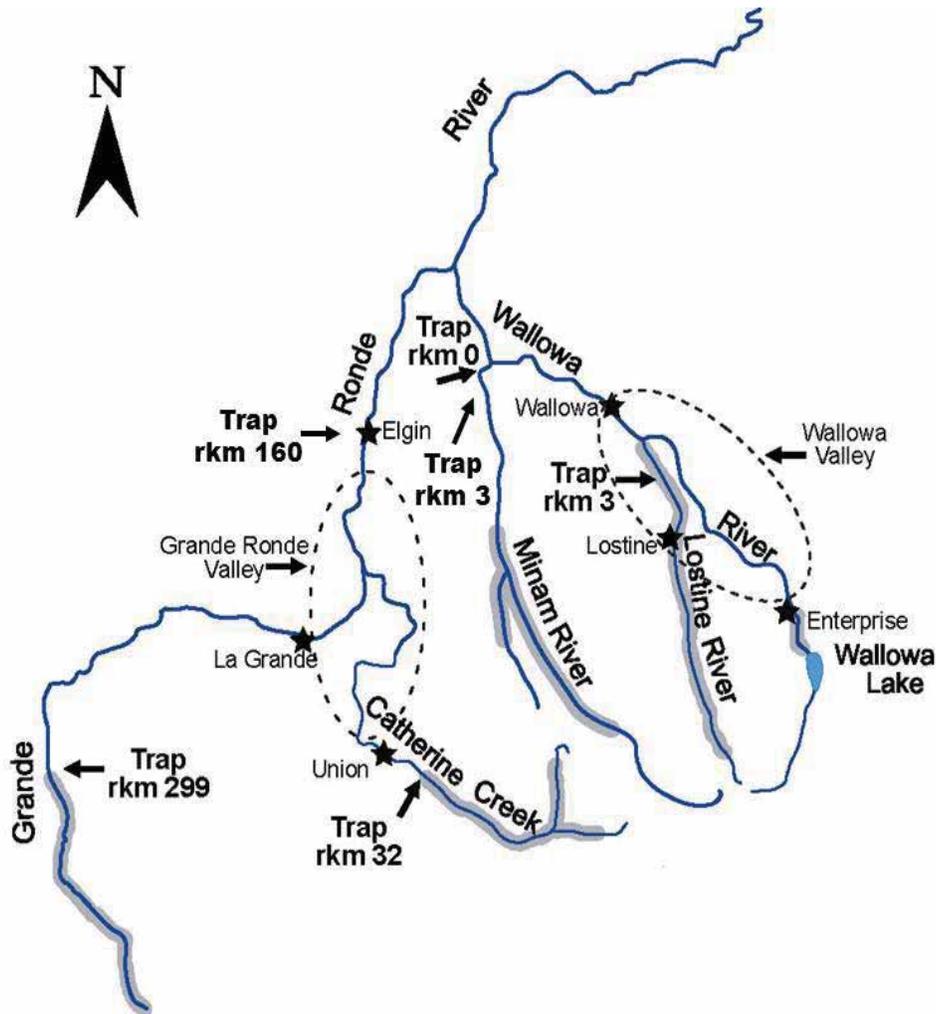


Figure 3. Locations of fish traps in Grande Ronde River Subbasin during the study period. Shaded areas delineate spring Chinook salmon spawning and upper rearing areas. Dashed lines indicate Grande Ronde and Wallowa river valleys.

Results

Spring Chinook Salmon

We estimated a minimum of $30,791 \pm 2,501$ juvenile spring Chinook salmon emigrated from Catherine Creek upper rearing areas during MY 2014 (Figure 4). Based on total minimum estimate, 58% ($18,012 \pm 1,308$) migrated early and 42% ($12,779 \pm 2,132$) migrated late.

We estimated a minimum of $68,046 \pm 5,999$ juvenile spring Chinook salmon emigrated from Lostine River during MY 2014 (Figure 5). Based on the minimum estimate, 74% ($50,518 \pm 5,426$) of juvenile spring Chinook salmon migrated early, while 26% ($17,528 \pm 2,558$) migrated late.

We estimated a minimum of $70,074 \pm 7,036$ juvenile spring Chinook salmon emigrated from Minam River during MY 2014 (Figure 6). Based on the minimum estimate, 74% ($51,948 \pm 6,590$) of juvenile spring Chinook salmon migrated early and 26% ($18,126 \pm 2,465$) migrated late.

We estimated a minimum of $32,842 \pm 4,663$ juvenile spring Chinook salmon emigrated from upper Grande Ronde River during MY 2014 (Figure 7). Based on the minimum estimate, 50% ($16,362 \pm 1,217$) of juvenile spring Chinook salmon migrated early and 50% ($16,480 \pm 4,502$) migrated late.

The middle Grande Ronde River trap at Elgin fished for 100 d between 26 February 2014 and 17 June 2014. We estimated a minimum of $56,469 \pm 23,066$ juvenile spring Chinook salmon emigrated from upper rearing areas.

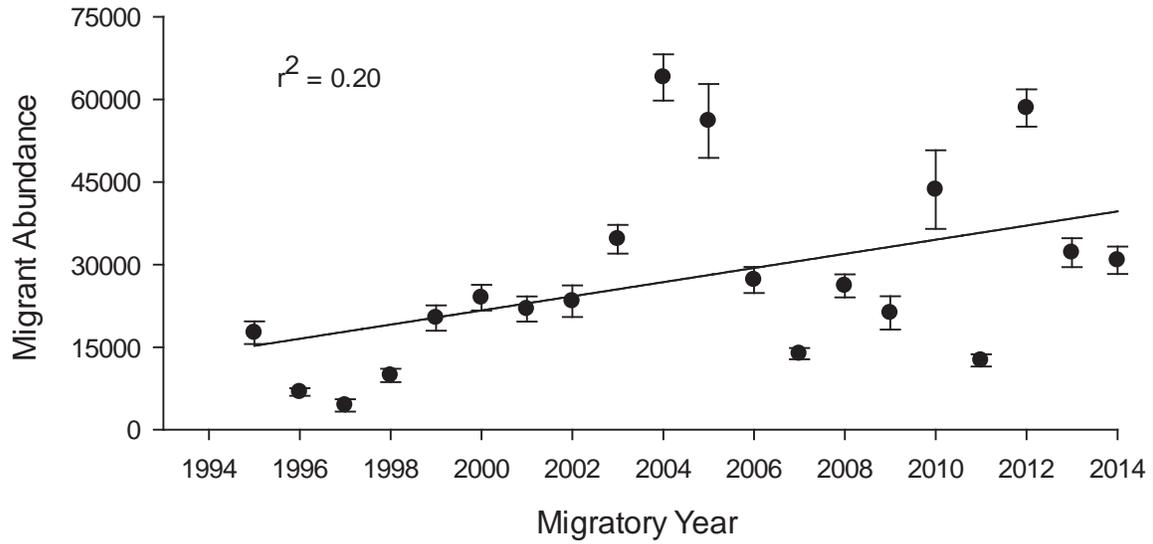


Figure 4. Spring Chinook salmon migrant abundance estimates at the Catherine Creek trap site by migratory year. Error bars are 95% confidence intervals.

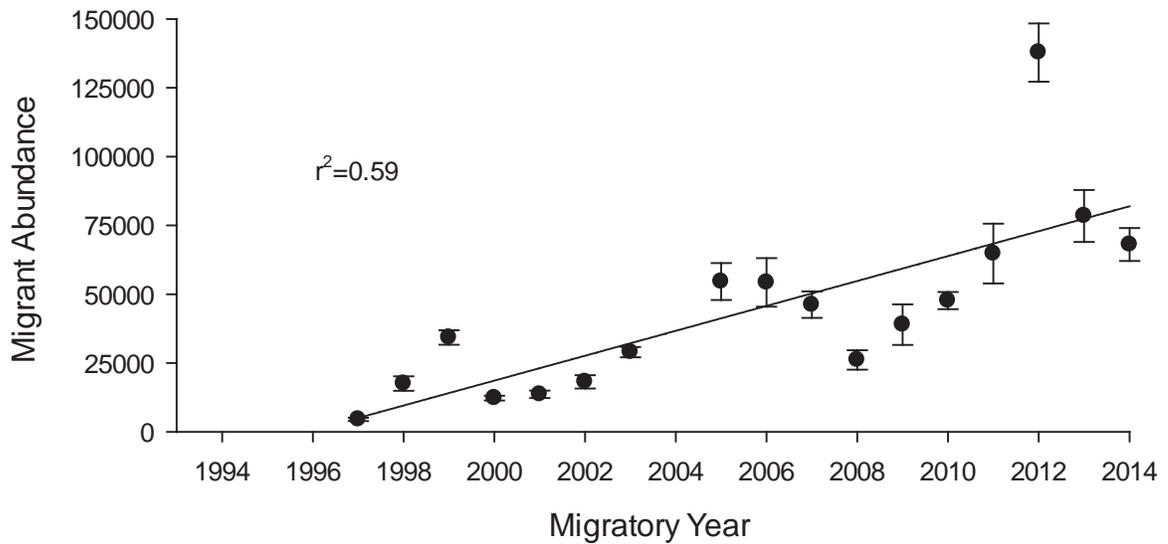


Figure 5. Spring Chinook salmon migrant abundance estimates at the Lostine River trap site by migratory year. Error bars are 95% confidence intervals.

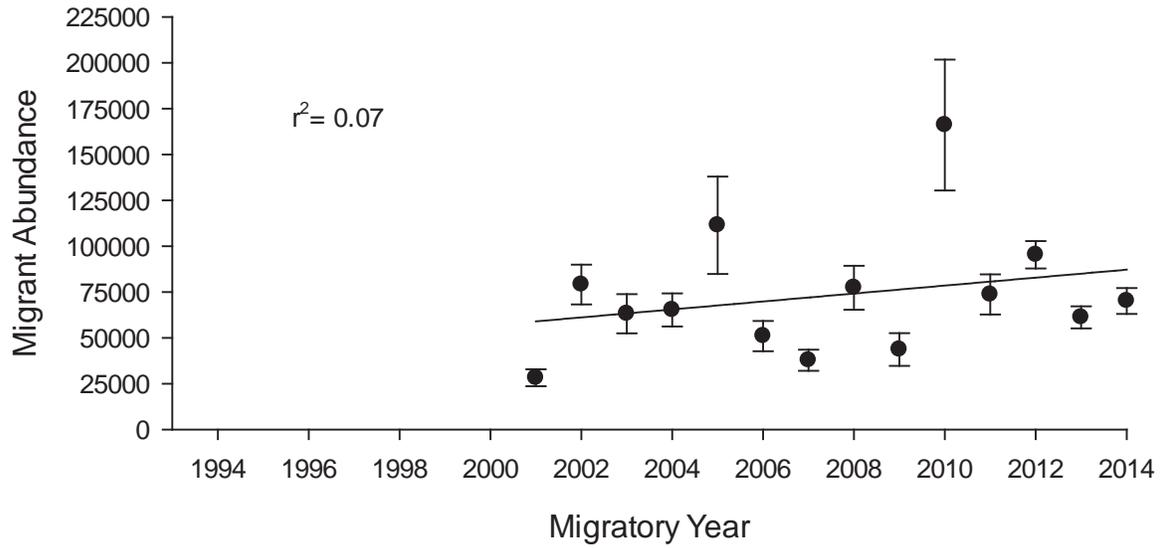


Figure 6. Spring Chinook salmon migrant abundance estimates at the Minam River trap site by migratory year. Error bars are 95% confidence intervals.

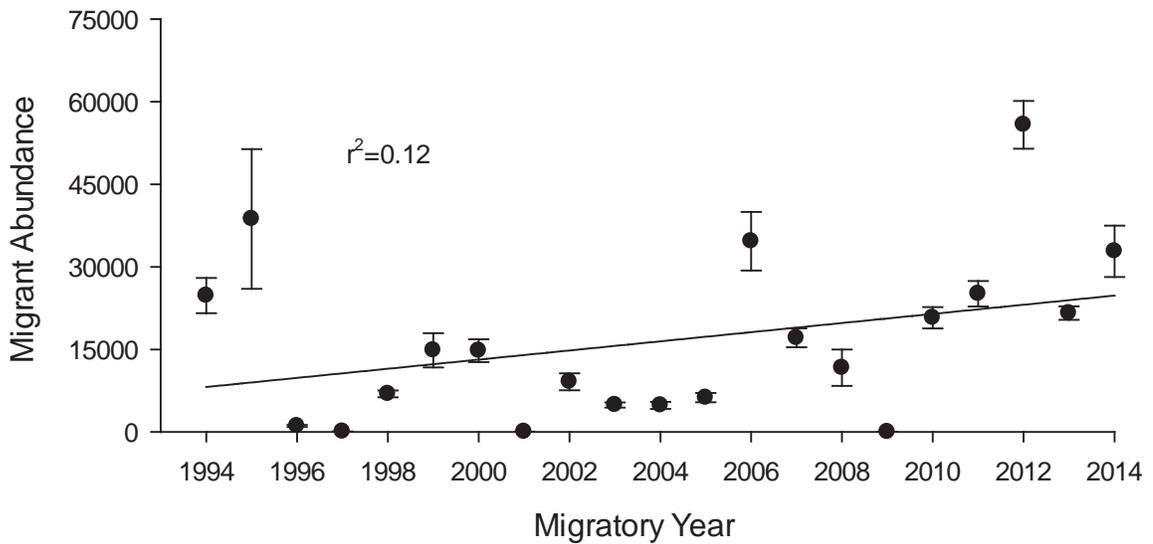


Figure 7. Spring Chinook salmon migrant abundance estimates at the upper Grande Ronde River trap site by migratory year. Error bars are 95% confidence intervals.

Fork lengths of juvenile spring Chinook salmon migrants at each of our rotary screw traps are shown in Figures 8 – 11. Mean fork lengths of migrants at the Catherine Creek, Minam, Lostine, and upper Grande Ronde River traps during the 2014 migratory year were within the range of fork lengths seen at these traps in previous years. We have observed that the length of fall

migrants is negatively correlated with the abundance of parr in late summer (ODFW unpublished data).

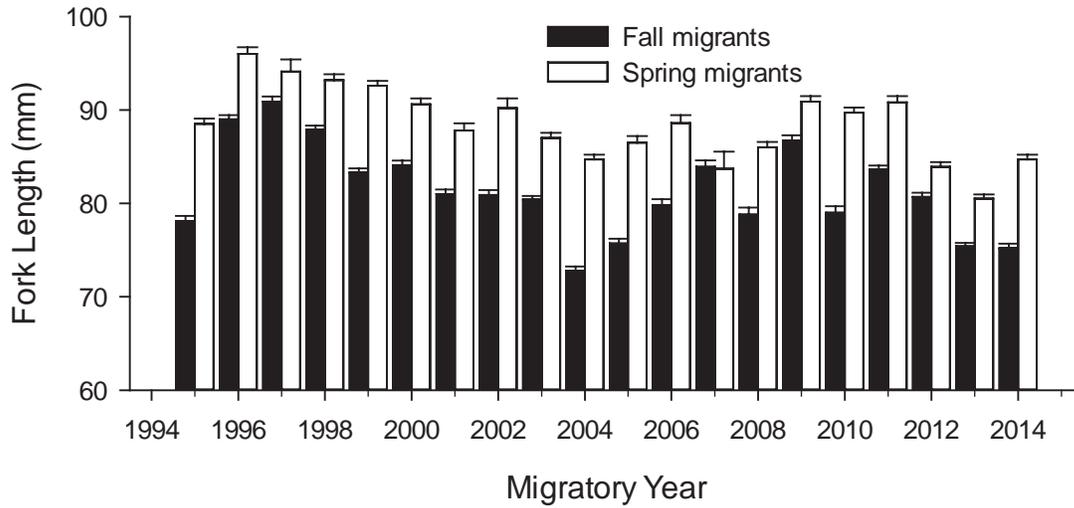


Figure 8. Fork length of spring Chinook salmon migrants captured at the Catherine Creek rotary screw trap by migratory year. Error bars are 95% confidence intervals.

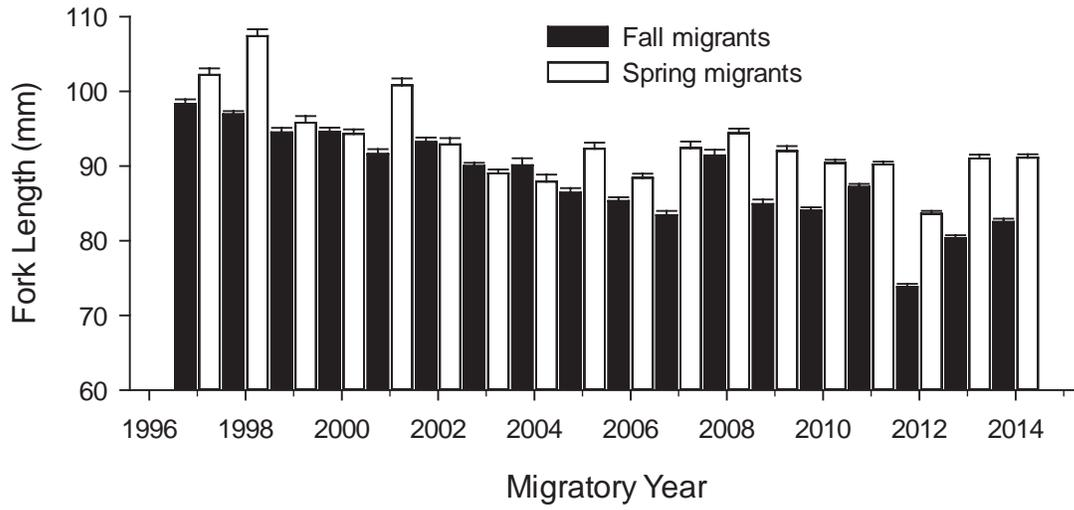


Figure 9. Fork length of spring Chinook salmon migrants captured at the Lostine River rotary screw trap by migratory year. Error bars are 95% confidence intervals.

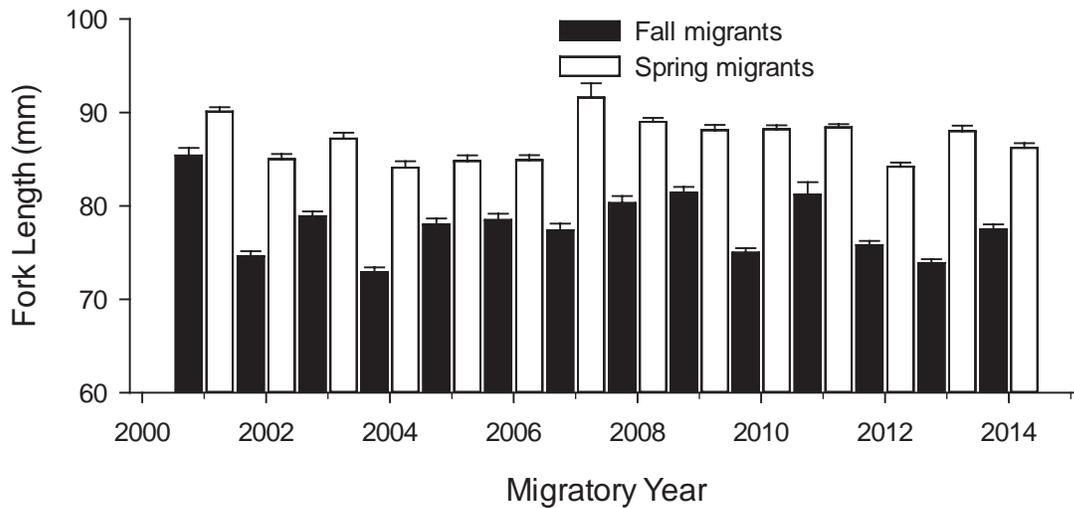


Figure 10. Fork length of spring Chinook salmon migrants captured at the Minam River rotary screw trap by migratory year. Error bars are 95% confidence intervals.

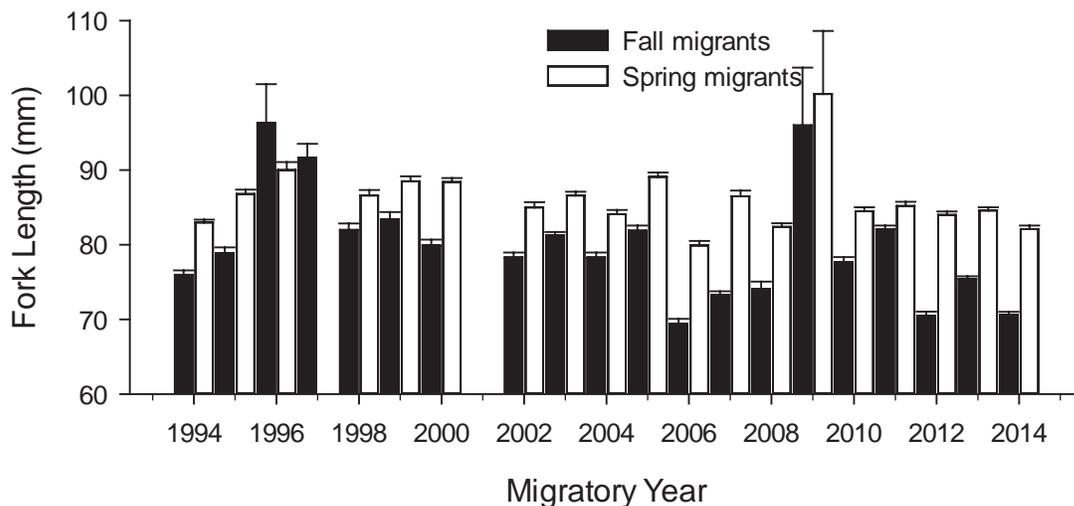


Figure 11. Fork length of spring Chinook salmon migrants captured at the upper Grande Ronde River rotary screw trap by migratory year. Error bars are 95% confidence intervals.

Survival probabilities to Lower Granite Dam for parr tagged during summer 2013 were 0.092 for Upper Catherine Creek, 0.019 for Lower Catherine Creek, 0.128 for Imnaha, 0.127 for Lostine, 0.134 for Minam, and 0.102 for upper Grande Ronde river populations (Figure 12). Generally, survival probabilities during MY 2014 fell within ranges previously reported; however, Lower Catherine Creek survival probability estimate (0.019) is the lower than any survival estimate previously reported.

Catherine Creek fall, winter, and spring tag group survival probabilities to Lower Granite Dam were 0.144, 0.116, and 0.340, respectively. Survival probabilities for Lostine River fall, winter, and spring tag groups were 0.209, 0.206, and 0.520, respectively. Probability of survival for the middle Grande Ronde River spring tag group was 0.677. Survival probabilities for Minam River fall and spring tag groups were 0.227 and 0.573, respectively. Upper Grande Ronde River fall, winter, and spring tag group survival probabilities to Lower Granite Dam were 0.201, 0.072, and 0.340, respectively. Survival probabilities, similar to past years, were generally higher for spring tag groups, likely because these fish were not subject to overwinter mortality that summer, fall, and winter tag groups experienced (Figure 12).

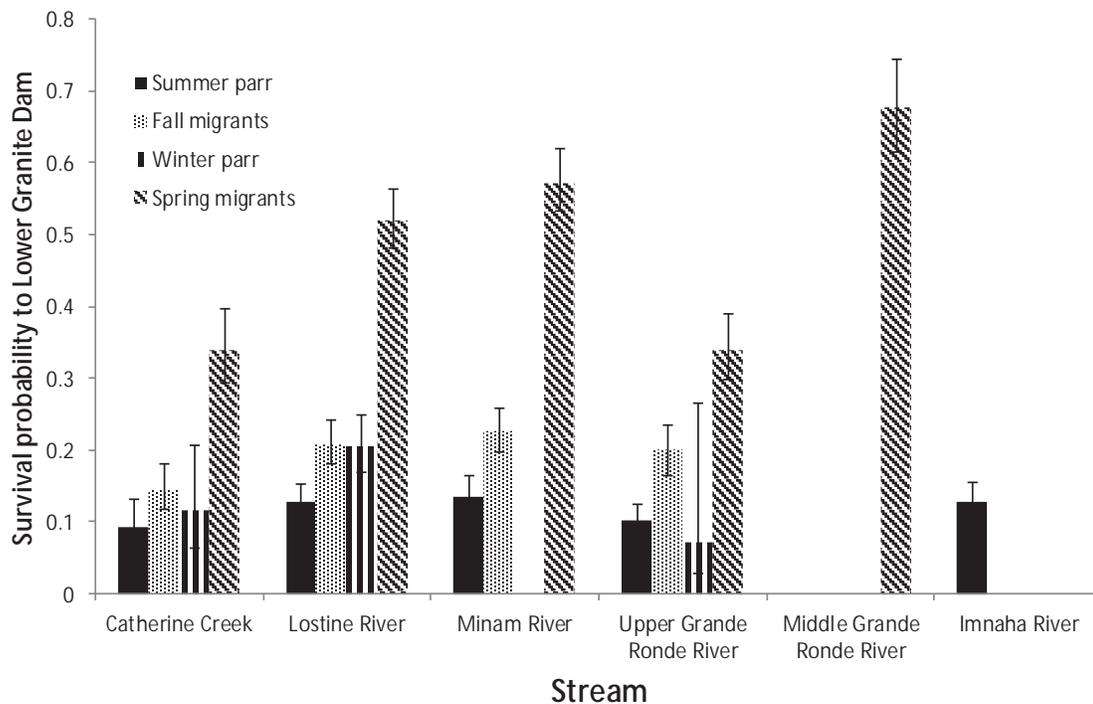


Figure 12. Survival probability to Lower Granite Dam of juvenile spring Chinook salmon PIT tagged at various life stages for the 2014 migratory year. Error bars are 95% confidence intervals.

Smolt equivalents are defined as the estimated number of smolts from a population that successfully emigrate from a specified area (Hesse et al. 2006). Combining the survival probability data with our migrant abundance estimates, we estimated the number of smolt equivalents produced in our study streams upstream of our rotary screw traps. In migratory year 2014 we estimated 20,494 smolt equivalents from Catherine Creek, 61,259 smolt equivalents from Lostine River, 38,706 smolt equivalents from Minam River, and 27,278 smolt equivalents from upper Grande Ronde River (Figure 13).

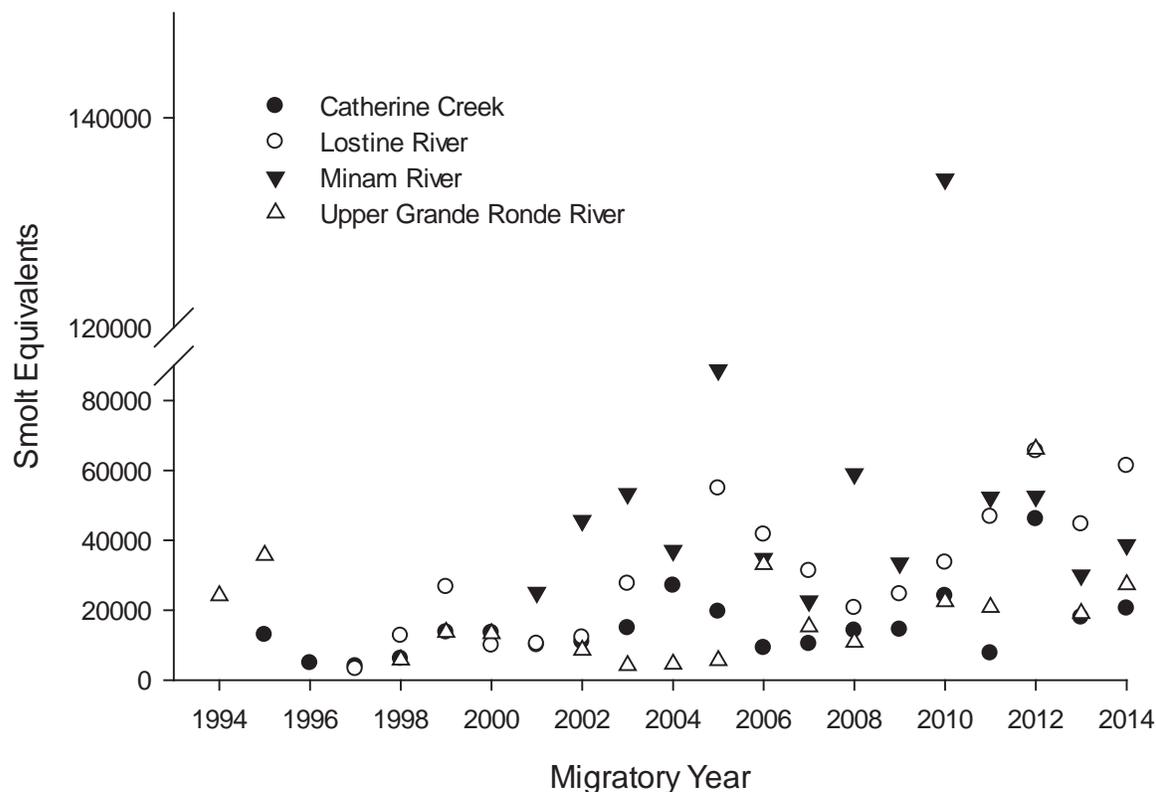


Figure 13. Spring Chinook salmon smolt equivalents produced from redds upstream of rotary screw traps in four study streams by migratory year.

Estimated productivity of spring Chinook salmon in Catherine Creek was 32 smolts per spawner for the 2012 brood year (2014 migratory year, Figure 14). Estimated productivity of spring Chinook salmon in Lostine River was 36 smolts per spawner for the 2012 brood year (2014 migratory year, Figure 15). Estimated productivity of spring Chinook salmon in Minam River was 62 smolts per spawner for the 2012 brood year (2014 migratory year, Figure 16). Estimated productivity of spring Chinook salmon in upper Grande Ronde River was 71 smolts per spawner for the 2012 brood year (2014 migratory year, Figure 17).

Plots of smolts per spawner versus spawners for each of the study streams show that productivity, as measured as smolts per spawner, decreases at higher spawner densities (Figures 18 – 21).

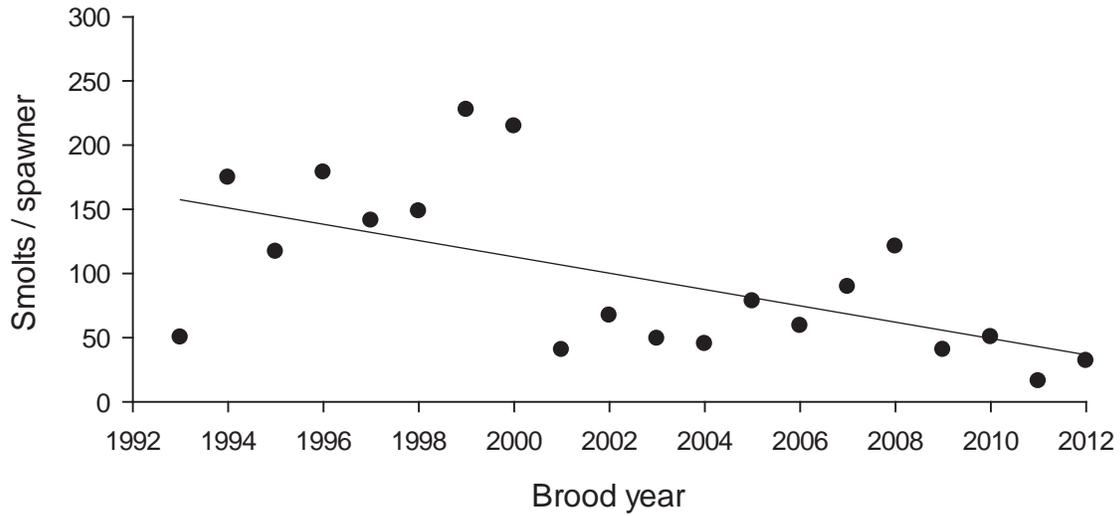


Figure 14. Spring Chinook salmon smolt equivalents produced per spawner in Catherine Creek by brood year.

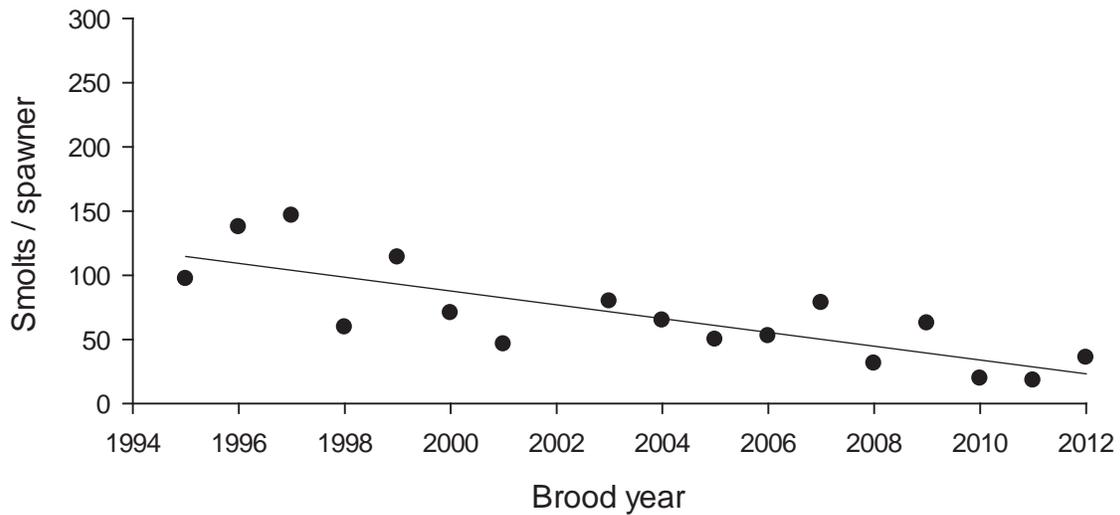


Figure 15. Spring Chinook salmon smolt equivalents produced per spawner in Lostine River by brood year.

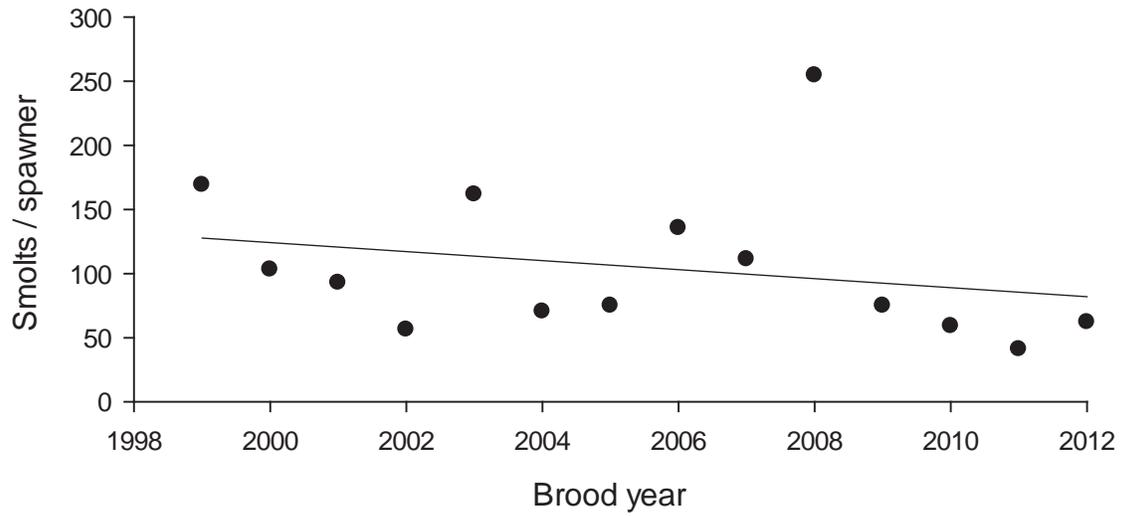


Figure 16. Spring Chinook salmon smolt equivalents produced per spawner in Minam River by brood year.

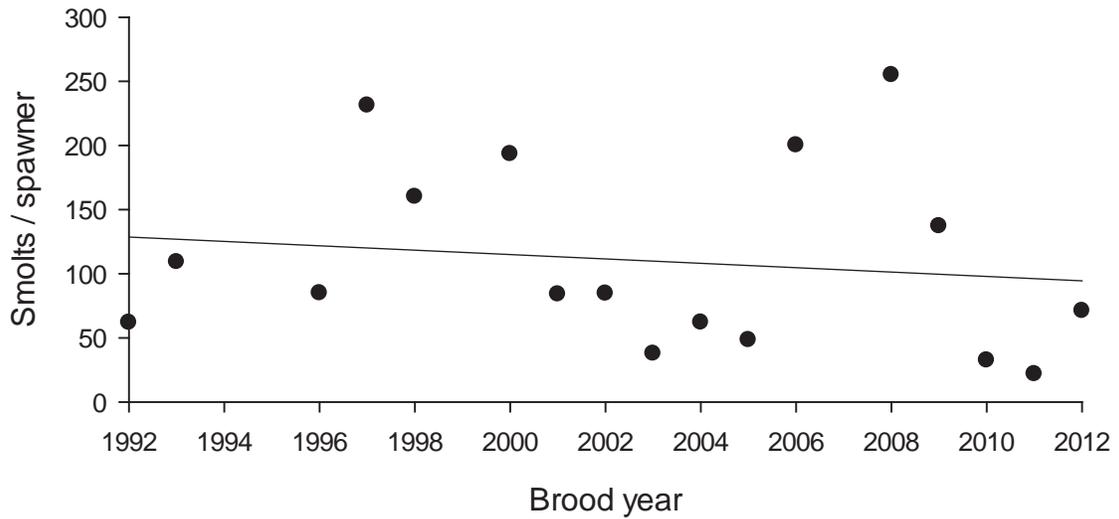


Figure 17. Spring Chinook salmon smolt equivalents produced per spawner in upper Grande Ronde River by brood year.

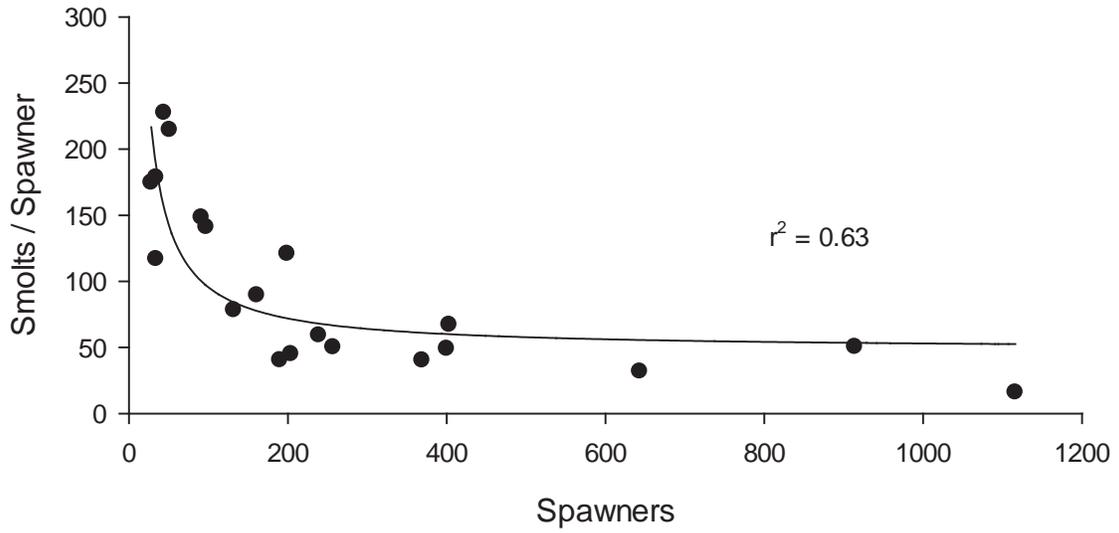


Figure 18. Spring Chinook salmon smolt equivalents produced per spawner in Catherine Creek by number of spawners.

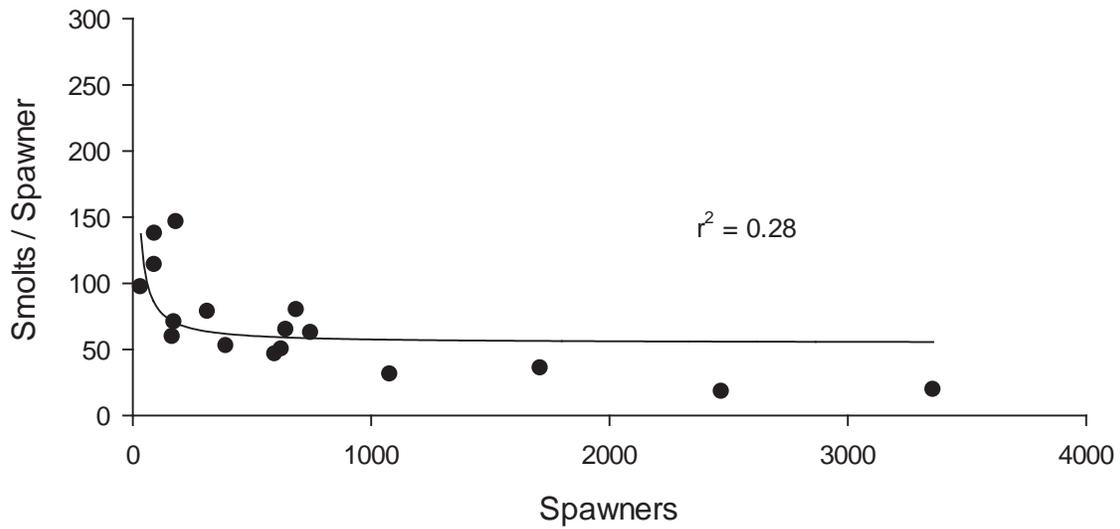


Figure 19. Spring Chinook salmon smolt equivalents produced per spawner in Lostine River by number of spawners.

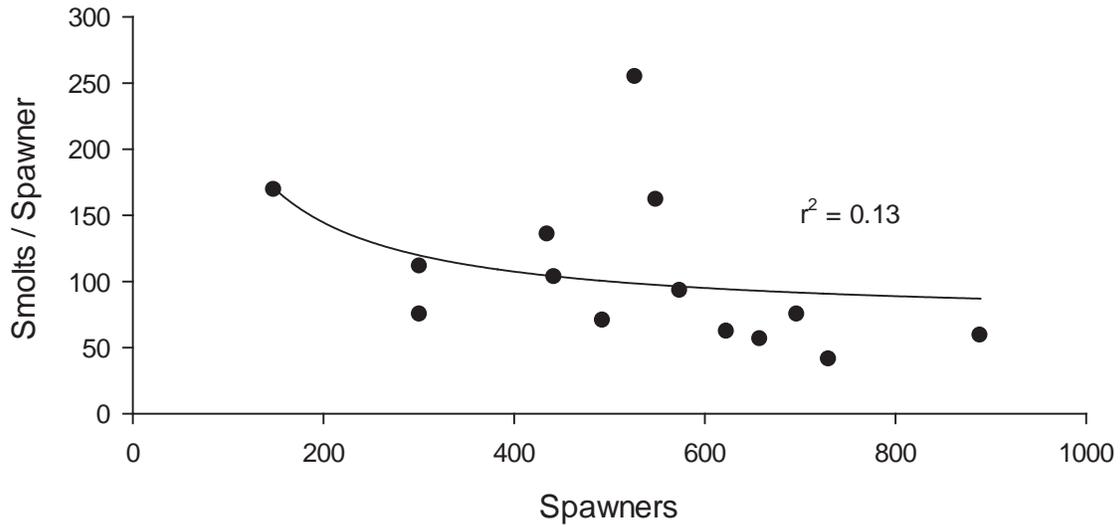


Figure 20. Spring Chinook salmon smolt equivalents produced per spawner in Minam River by number of spawners.

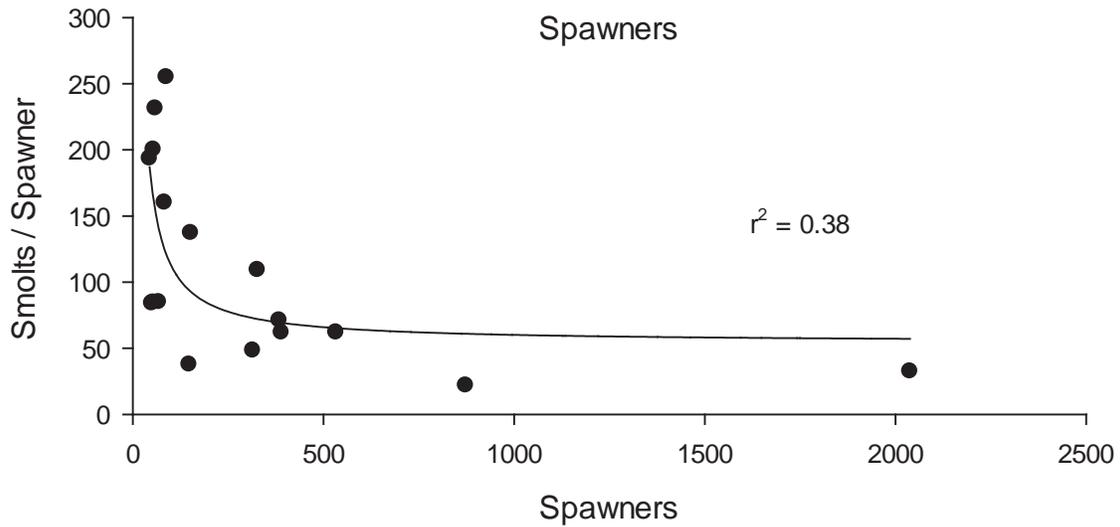


Figure 21. Spring Chinook salmon smolt equivalents produced per spawner in upper Grande Ronde River by number of spawners.

Radio-telemetry studies in 2014 consisted of determination of overwinter habitat use of early migrating juvenile spring Chinook salmon through the Grande Ronde River between our rotary screw trap and Elgin, OR. We found that the majority of juvenile spring Chinook salmon stayed within 10 km of the rotary screw trap through December 2014.

Steelhead

We estimated a minimum of $25,939 \pm (95\% \text{ CI}, 4,463)$ juvenile steelhead migrated from Catherine Creek upper rearing areas during MY 2014 (Figure 22). Based on total minimum abundance estimate, 21% ($5,366 \pm 730$) migrated early and 79% ($20,573 \pm 4,403$) migrated late. MY 2014 proportion of juvenile steelhead emigrating from upper rearing areas as late migrants (79%) is within those proportions previously reported during 1997-2014.

We estimated a minimum of $22,094 \pm 4,646$ steelhead emigrated From Lostine River upper rearing areas during MY 2014 (Figure 23). Based on total minimum abundance estimate, 72% ($15,889 \pm 4,464$) of juvenile steelhead migrated early and 28% ($6,205 \pm 1,286$) migrated late. MY 2014 proportion of juvenile steelhead emigrating from upper rearing areas as late migrants (28%) is within those proportions previously reported during 1997-2014.

We estimated a minimum of $48,605 \pm 7,824$ juvenile steelhead migrated from Minam River rearing areas during MY 2014 (Figure 24). Based on total minimum abundance estimate, 46% ($22,290 \pm 6,288$) migrated early and 54% ($26,315 \pm 4,655$) migrated late. Proportion of juvenile steelhead emigrating as late migrants, during MY 2014, is consistent with proportions from previous migration years.

We estimated a minimum of $19,774 \pm 2,951$ juvenile steelhead emigrated from upper Grande Ronde River rearing areas during MY 2014, which is within estimates from previous migration years (Figure 25). Based on total minimum abundance estimate, 18% ($3,516 \pm 539$) were early migrants and 82% ($16,258 \pm 2,902$) were late migrants. Predominant late migration of juvenile steelhead in upper Grande Ronde River is consistent for all migration years studied to date.

The middle Grande Ronde River trap fished for 100 d between 26 February 2014 and 17 June 2014. We estimated a minimum of $132,413 \pm 54,664$ juvenile steelhead emigrated from upper rearing areas.

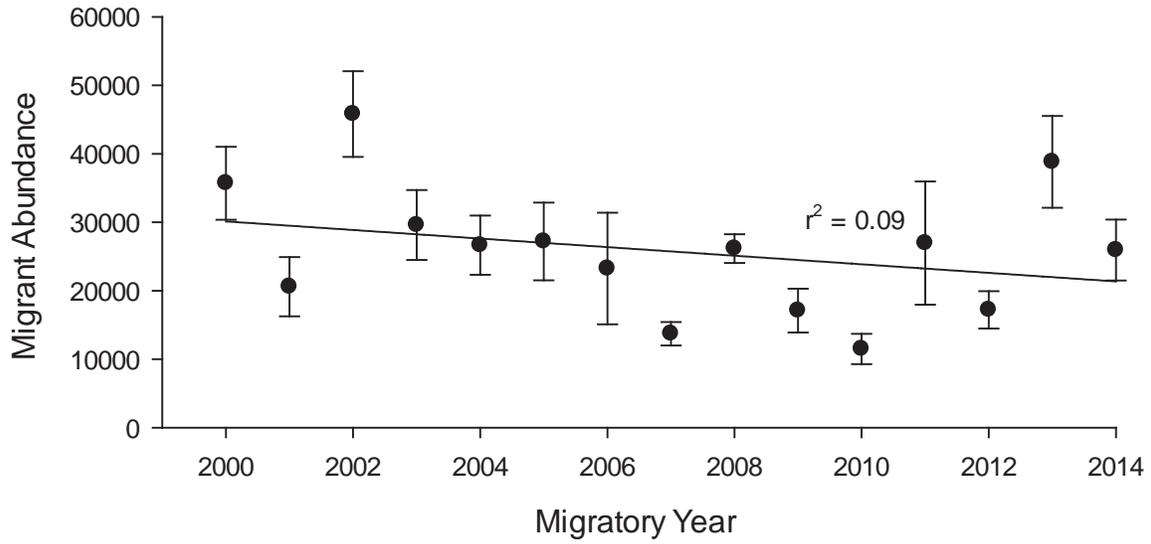


Figure 22. Steelhead migrant abundance estimates at the Catherine Creek trap site by migratory year. Error bars are 95% confidence intervals.

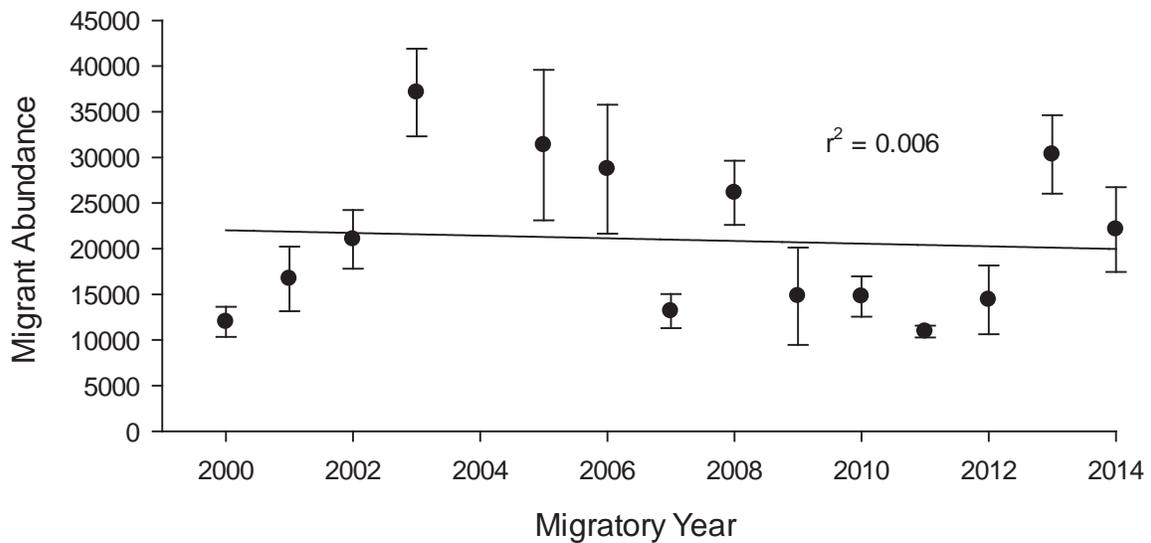


Figure 23. Steelhead migrant abundance estimates at the Lostine River trap site by migratory year. Error bars are 95% confidence intervals.

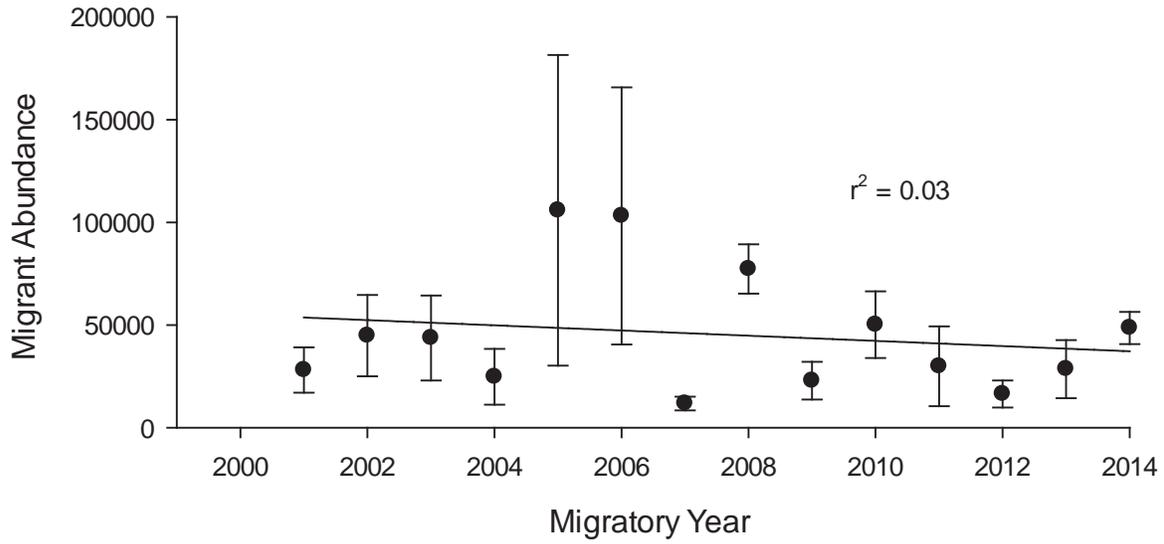


Figure 24. Steelhead migrant abundance estimates at the Minam River trap site by migratory year. Error bars are 95% confidence intervals.

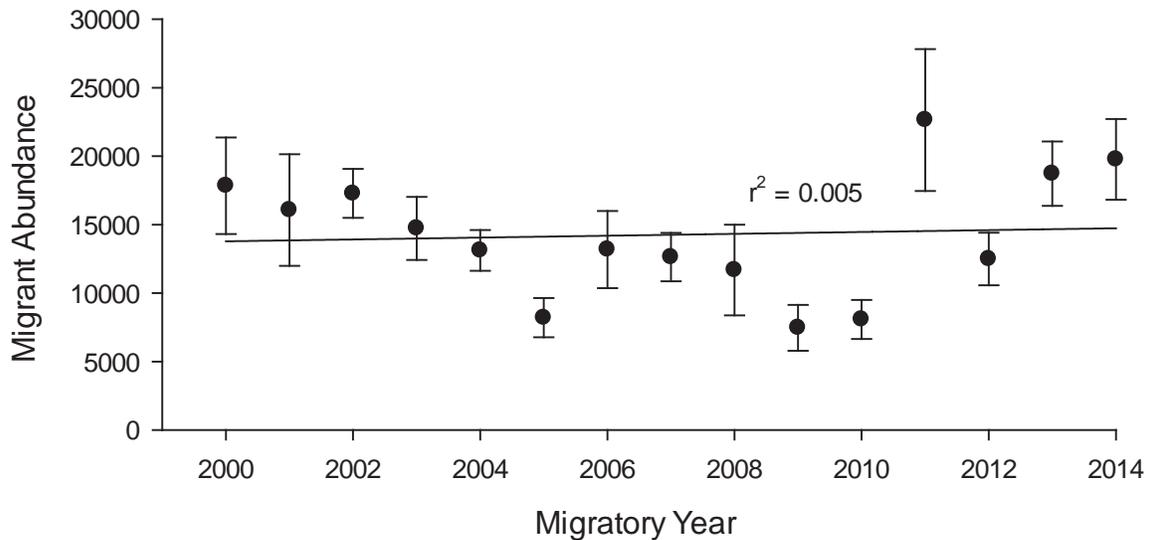


Figure 25. Steelhead migrant abundance estimates at the upper Grande Ronde River trap site by migratory year. Error bars are 95% confidence intervals.

Summer steelhead collected at trap sites during MY 2014 comprised five age-groups. Early migrants ranged from 0 to 4 years of age, while late migrants ranged from 1 to 4 years of age (Table 1). Majority of upper Grande Ronde river (51.5%) early migrants were age 1, while

majority of Catherine Creek (54.4%), Lostine River (65.1%), and Minam River (82.9%) early migrants were age 0. Majority of Catherine Creek (74.6%), Lostine River (57.6%), and Minam River (57.8%) late migrants were age 1, while majority of middle Grande Ronde River (64.7%) and upper Grande Ronde River (53.1%) late migrants were age 2 (Table 1).

Table 1. Age structure of early and late steelhead migrants collected at trap sites during MY 2014. The same four cohorts were represented in each migration period, but ages increased by one year from early migrants to late migrants (e.g., age-0 early migrants were same cohort as age-1 late migrants). Age structure was based on frequency distribution of sampled lengths and allocated using an age-length key. Means were weighted by migrant abundance at trap sites.

Emigrant type and trap site	Percent				
	Age-0	Age-1	Age-2	Age-3	Age-4
Early					
Catherine Creek	54.4	40.3	5.0	0.3	0.0
Lostine River	65.1	22.6	12.0	0.3	0.0
Minam River	82.9	10.3	6.5	0.2	0.0
Upper Grande Ronde River	28.3	51.5	19.9	0.3	0.0
Late					
Catherine Creek	0.0	74.6	23.6	1.7	0.0
Lostine River	0.0	57.6	35.0	7.4	0.0
Minam River	0.0	57.8	29.9	11.8	0.6
Upper Grande Ronde River	0.0	34.1	53.1	12.7	0.0
Early and Late ^a					
Middle Grande Ronde River	0.0	25.0	64.7	10.3	0.0

^a Middle Grande Ronde River trap was located downstream from Catherine Creek and upper Grande Ronde River overwinter rearing reaches resulting in early and late emigrants being sampled simultaneously during spring emigration.

Probability of surviving and migrating, during migration year of tagging, to Lower Granite Dam for steelhead tagged in fall 2013 ranged from 0.030 to 0.137 for all four spawning tributaries (Table 26). Probabilities of migration and survival, for larger steelhead (FL \geq 115 mm) tagged during spring 2014, ranged from 0.463 to 0.794 for all five populations studied (Table 26). Generally, probabilities of migration and survival, during spring 2014, were similar for all five populations studied compared to previous years.

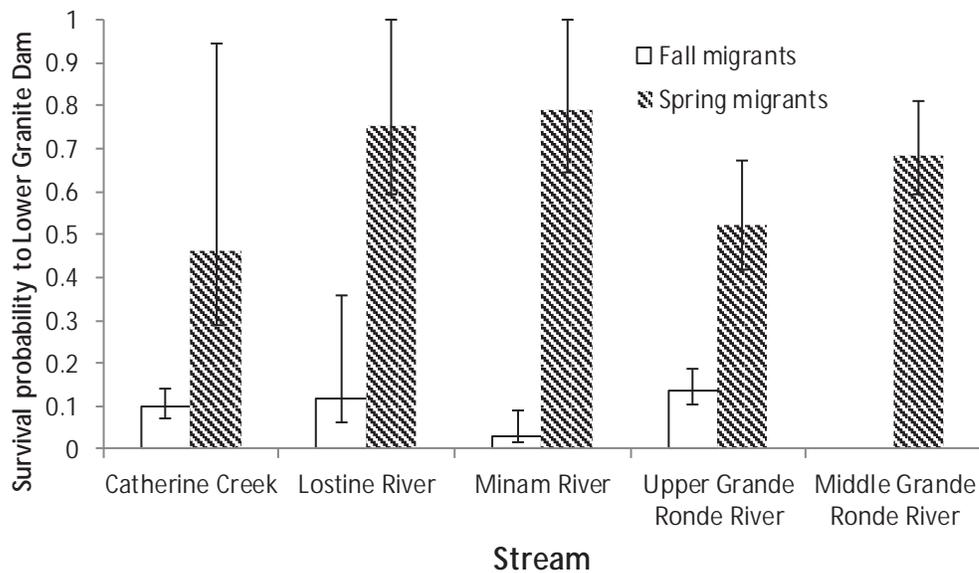


Figure 26. Probability of surviving and migrating, in the first year to Lower Granite Dam, for steelhead PIT-tagged at screw traps on Catherine Creek and Lostine, middle Grande Ronde, Minam, and upper Grande Ronde rivers during fall 2013 and spring 2014 (MY 2014). Catherine Creek and upper Grande Ronde River early migrants overwinter upstream of middle Grande Ronde River trap site, so no fall tag group was available for that site.

Conclusions

In 2014, we saw relatively high numbers of juvenile spring Chinook salmon from all of our study streams, resulting from the high number of spawners in 2012, continuing the increasing trend in juvenile migrants. We continue to see smaller juvenile spring Chinook salmon at higher spawner densities, which results in lower survival to Lower Granite Dam. The lower survival of the out-migrants results in low estimates of smolts/spawner, one indicator of the VSP parameter productivity. The higher number of spawners, whether of hatchery or natural origin, produced more total migrants but produced lower numbers of smolts per spawner, due to reduced survival rates of smolts. Habitat restoration projects funded by BPA and Bureau of Reclamation in the Upper Grande Ronde River watershed are addressing habitat capacity which should, in turn, result in an increase in productivity, such as smolts/spawner.

Steelhead emigrant abundance was above the trend line in all four streams we have been monitoring since 2000. In the future, this project will combine the out-migrant estimates, age structure, and survival rates to quantify the number of smolts by age and relate to the appropriate number of spawners to estimate smolts/spawner, a VSP indicator of productivity.

Steelhead Spawner Surveys

Introduction

Summer steelhead in the Grande Ronde River subbasin fall within the Snake River Distinct Population Segment (DPS) and are listed as threatened under the Endangered Species Act (62 FR 43937; August 18, 1997). The Upper Grande Ronde River (UGRR) and Joseph Creek watersheds (Figure 27) support two of the four Major Population Groups (MPG) in the Grande Ronde River subbasin. These populations are segregated based on topographic, genetic, and behavioral evidence of interactions. Historically, the Grande Ronde River was one of the more significant anadromous fish producing rivers in the Columbia River basin. Despite recovery efforts, these populations remain depressed relative to historic levels.

The goal of this project is to annually evaluate summer steelhead population abundance for the UGRR, and recently Joseph Creek, by conducting surveys of redds and spawning activity. These surveys provide those data needed to estimate adult steelhead escapement, improve our understanding of habitat utilization, and contribute to productivity and survival estimates for these populations.

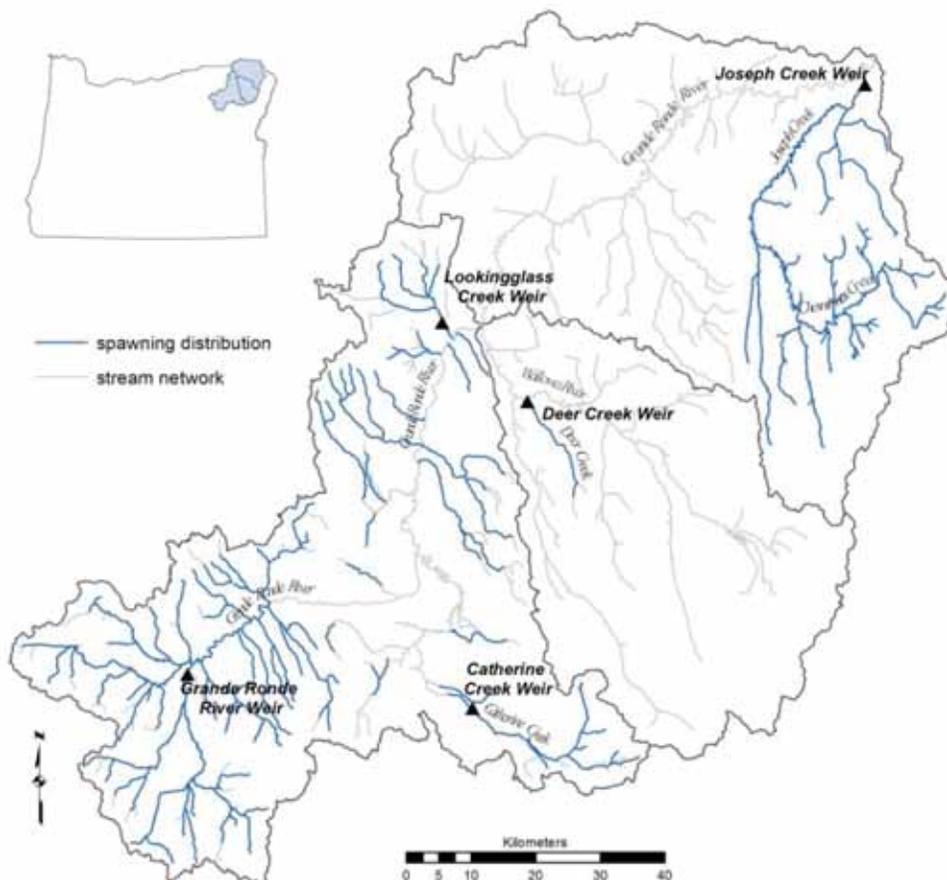


Figure 27. Grande Ronde River basin, divided by 4th order HUC. Steelhead distribution highlighted in blue for Joseph and UGRR subbasins.

Methods

Estimating Adult Summer Steelhead Escapement in North East Oregon

<https://www.monitoringmethods.org/Protocol/Details/757>

Results

We surveyed 29 sites in the UGRR (Figure 28) encompassing 61.3 km of an estimated 892 km (6.9 %) available steelhead spawning habitat (Appendix Table B-12). Two sites were not surveyed due to persistent high discharge and were not included in our calculations. Stream classification for the 29 surveyed sites was distributed evenly (10 sites in source classification, 9 in transport, and 10 in depositional). Four sites were located above the Grande Ronde River weir, two above the Catherine Creek weir, and one above the Lookingglass Creek weir.

Available spawning habitat was estimated at 897 km at the beginning of 2013 season, but we removed 5.2 km from Wright Slough, Orodell Ditch, and Conley Creek after determining this section of stream was ditched, had extremely low gradient, and little to no gravel available for spawning.

We conducted 119 surveys in the UGRR basin in 2014, with a mean interval of 16.6 days between surveys. A total of 65 steelhead redds were observed at 17 of the 29 sites (Appendix Table B-14). Redds were not evenly distributed among stream classifications: twelve (18%) were found in source areas, 31 (48%) in transport, and 22 (34%) in depositional reaches. A total of 19 live adult steelhead were observed in the UGRR (Appendix Table B-16). Of these fish three had an observable adipose fin clip, six were of wild origin, and 10 were of unknown origin. No carcasses were observed during our surveys in the UGRR basin.

Twenty-five sites were surveyed in Joseph Creek and tributaries (Figure 29), encompassing 51.8 km of an estimated 384 km (13.5 %) available spawning habitat (Appendix Table B-13), all of which were above the weir. Stream classification for the 25 sites was random with 10 sites surveyed in source classification, eight in transport, and seven in depositional.

A total of 73 surveys were completed in the Joseph Creek basin, with a mean interval of 10.5 days between surveys. We found 130 steelhead redds at 18 of the 25 sites (Appendix Table B-15). More redds were found in the depositional stream classification (n=53, 41%), than source or transport reaches (n=40 (31%) and 37 (28%) respectively). Eighteen live adult steelhead were observed at nine sites (Appendix Table B-17), while two dead, adult steelhead were found at two sites (Appendix Table B-18). No adipose-clipped hatchery fish were observed during our Joseph Creek surveys.

We conducted five surveys on Deer Creek encompassing 18.7 km of utilized spawning habitat from the weir to the USFS road 8270 bridge. In previous years, additional surveys were conducted upstream of these 18.7 km, and no redds or adult steelhead were observed.

We observed 18 redds on our visits to Deer Creek, 15 (83.3 %) of which were discovered in the lower 9.6 km. Seven live fish and three carcasses were observed on Deer Creek. Three adipose-clipped hatchery fish were also observed during our surveys.

Based on our redd observations, onset of spawn timing was similar between the UGRR and Joseph Creek basins, but a little later for Deer Creek. We observed the first redds on 25 March

in the UGRR, March 19 Joseph Creek basins (Appendix Figure B-21) and 17 April in Deer Creek (Appendix Figure B-22). The last redds were observed on 06 June in the UGRR, 03 June in Joseph Creek and 15 May in Deer Creek. By 12 May, 52% of the total redds in the UGRR basin were observed. By 05 May, 61% of the total redds in the Joseph Creek basin were observed. By the third survey on 17 April, 28% of the total redds were observed on Deer Creek. Although onset of redd building was similar among basins, peak redd observations occurred slightly later in Joseph Creek than UGRR (Appendix Figure B-21), which is similar to the pattern observed in 2012 and 2013 (Dobos et al. 2012, Fitzgerald et al. 2013). Most redds in the UGRR basin were first observed during the descending hydrographs of early May to late June. Surveys on Deer Creek coincided with low discharge periods.

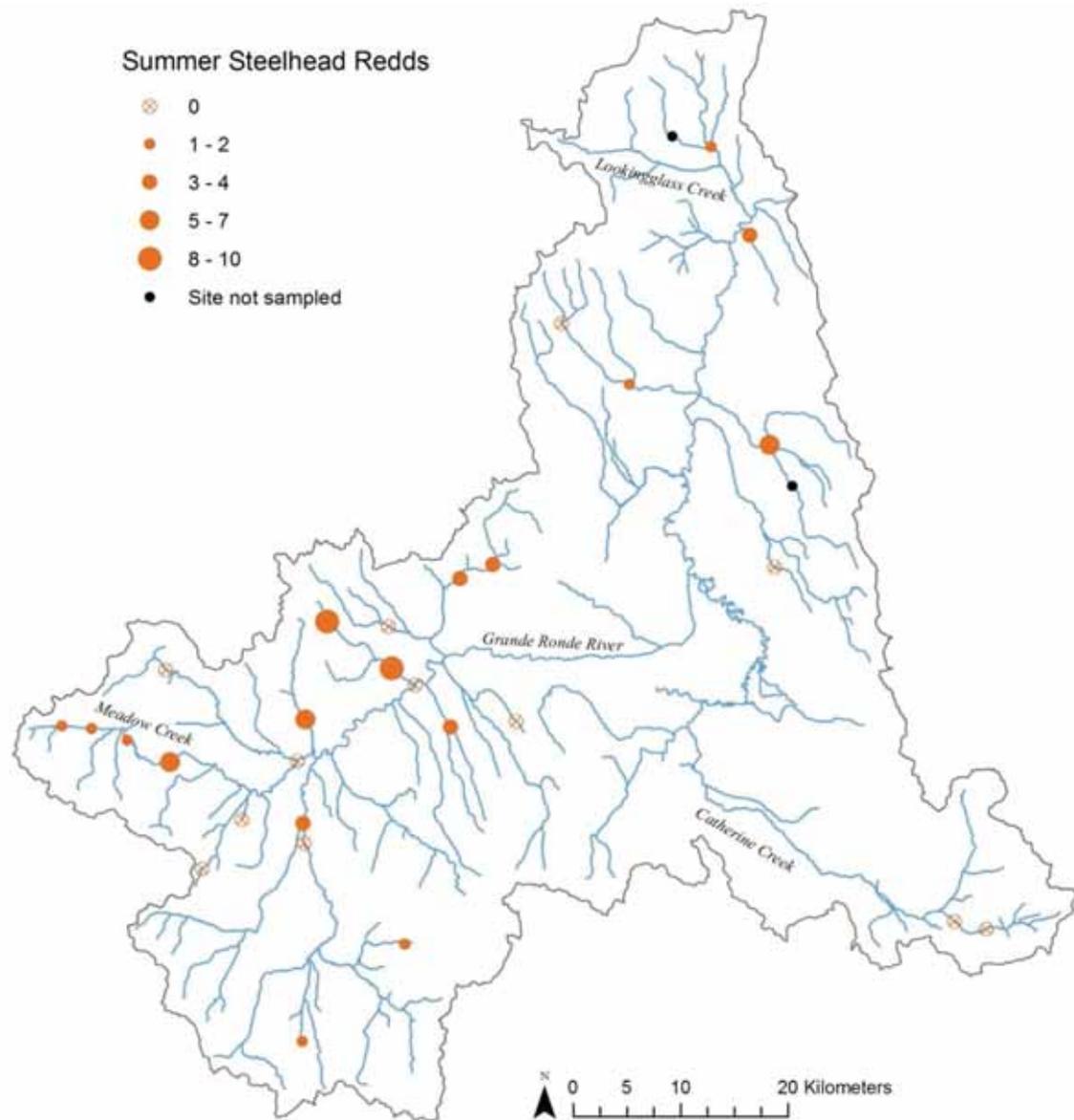


Figure 28. Map of the Upper Grande Ronde River basin displaying count of redds observed at each site in 2014. The two sites not surveyed were due to continual high flows and dangerous wading conditions.

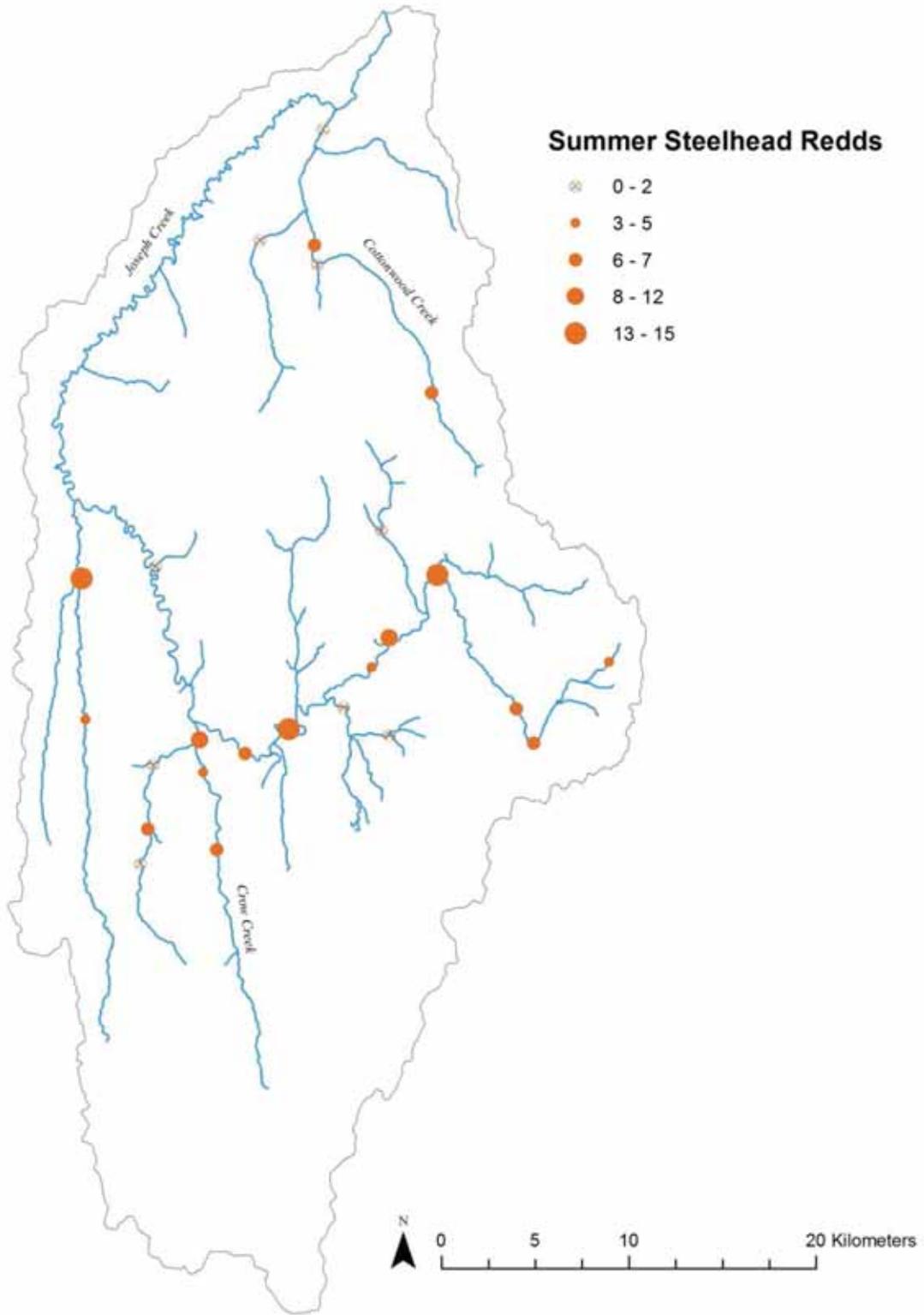


Figure 29. Map of the Joseph Creek basin showing count of redds observed at each site in 2014.
Conclusions

Most redds were first observed during descending limbs of the hydrograph. However, any relationship of spawning to stream flow may be obscured by artifacts of our sampling technique. Our ability to observe redds is strongly influenced by water clarity, which is generally better on the descending limb of hydrographs than on rising limbs. Even though our observations of redds were during these descending periods, they do not indicate exactly when the redd was made. Deer creek surveys illustrate this point. We were only able to survey during the low water periods between peaks in the hydrograph. However, redds were likely built during the high water periods between surveys. Our surveys cannot determine or estimate when redds were built (unless we observe fish actively spawning) limiting our ability to infer a relationship between flow and spawning activities.

Timing of initial redd observations was similar across both basins and in Deer Creek. However, the progression of redd building appeared to be slower in Joseph Creek. This seems counterintuitive, as Joseph Creek is lower in elevation, and generally warmer than UGRR or Deer Creek. We observed a two week lag (early April) between redd building in UGRR and Joseph Creek. This was also observed in 2012 and 2013 (Dobos et al. 2012, Fitzgerald et. al 2013), the first two years of Joseph Creek surveys. We were unable to determine if this is a real discrepancy in spawn timing, or an inability to effectively survey Joseph Creek tributaries during early April. Surveyors recorded water clarity (scale 1-3) at each survey event, and water clarity did improve substantially in Joseph Creek by mid- April. However, if water clarity/redd visibility was limiting our counts, one would expect a rapid increase in redd counts once water clarity improved. This was not the case, as redd observations climbed steadily after mid-April, but not faster than UGRR or Deer Creek.

Abundance of Steelhead Spawners at the Population Level

Introduction

Summer steelhead in the Grande Ronde River basin fall within the Snake River Distinct Population Segment (DPS) and are listed as threatened under the Endangered Species Act (62 FR 43937; August 18, 1997). The Upper Grande Ronde River (UGRR) and Joseph Creek watersheds support two of the four Major Population Groups (MPG) in the Grande Ronde River basin. These populations are segregated based on topographic, genetic, and behavioral evidence of interactions. Historically, the Grande Ronde River was one of the more significant anadromous fish producing rivers in the Columbia River Basin. Despite recovery efforts, these populations remain depressed relative to historic levels.

The goal of this project is to annually evaluate summer steelhead population abundance for the UGRR, and recently Joseph Creek, by conducting surveys of redds and spawning activity. These surveys provide the data needed to estimate adult steelhead escapement, improve our understanding of habitat utilization, and contribute to productivity and survival estimates for these populations.

Methods

Estimating Adult Summer Steelhead Escapement in North East Oregon

<https://www.monitoringmethods.org/Protocol/Details/757>

Results

A fish:redde ratio of 2.67 (48/18) was generated using the number of fish passed above the weir at Deer Creek and the number of redds observed there in 2014. Using this ratio and a single weight value for all stream classifications (30.8), 2,512 adult steelhead (95% C.I.: 1,538–3,487) escaped into the UGRR basin and naturally spawned (Appendix Table B-19; Figure 30). No adipose-clipped hatchery fish were observed during surveys on the UGRR. Using this same method with a weight value of 15.4, 2,522 adult steelhead (95% C.I.: 1,744–3,300) escaped into the Joseph Creek basin. No adipose-clipped hatchery fish were observed during surveys on Joseph Creek.

Using the weight values for each strata, source (50.1), transport (27.0), and depositional (19.7), we estimated that 2,305 (95% CI, 1,362–3,348) adult steelhead for the UGRR population (Appendix Table B-21). For Joseph Creek estimates changed by only one fish: using the weight values for each strata, source (15.9), transport (14.3), and depositional (15.8), we estimated that 2,253 (95% CI, 1,726–3,320) adult steelhead returned to spawn (Appendix Table B-22).

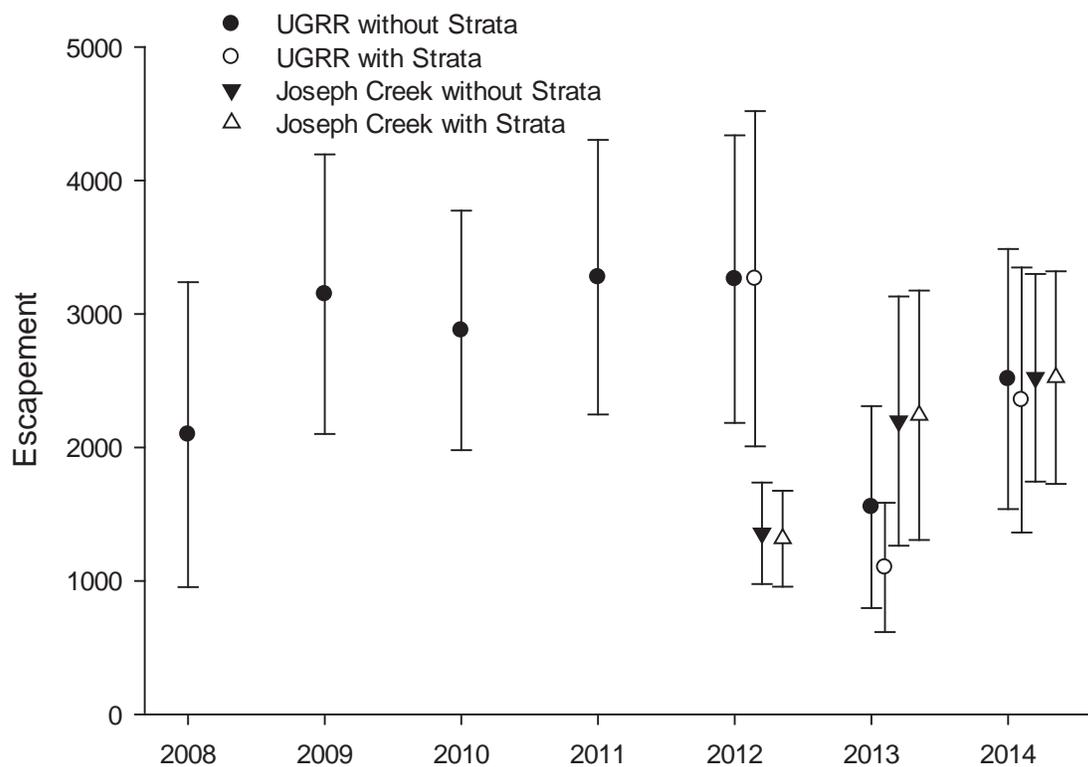


Figure 30. Escapement estimates with 95% confidence intervals for steelhead in the Upper Grande Ronde River basin using a single weight value, 2008–2014 and using strata weights for the three classifications of stream type for UGRR and Joseph Creek, 2012–2014.

Conclusions

Population-scale escapement estimates had relatively poor precision for both Joseph Creek and UGRR (95% CI ~38% of the estimate). This is better than last year's precision estimate of ~45% of estimate. Confidence intervals have consistently been 30–35% of the UGRR escapement estimate since 2009. This is despite our refinement of known steelhead spawning distribution, which has been reduced in length by 31% since 2008. It appears that the variable distribution of redds throughout the spawning distribution inflates the confidence intervals. In particular, observations of zero redds substantially increase the confidence interval, and certain streams are not likely to produce redds regardless of the number of adults returning. In 2014 we observed zero redds at 41% of our UGRR basin sites, and 28% of those in Joseph Creek. With continued observations of zero redds at some survey sites, it seems unlikely that precision will improve unless some other method of identifying appropriate spawning habitat can be found.

This is our third year of attempting to correlate redd locations with stream classifications. Redd observations were highest in transport reaches for UGRR and highest in depositional reaches for Joseph basins. This distribution is similar to Joseph Creek observations in 2012 and 2013, but far different for UGRR streams (Dobos et. al 2012, Fitzgerald et. al 2013). There seems to be only minor utility in attempting to relate stream classification generated from landscape level

variables to redd locations. Steelhead are likely not choosing appropriate spawning sites at the landscape scale. With the overlap of CHaMP sites and steelhead spawning ground surveys, we are exploring other potential relationships between redd building and small-scale habitat characteristics.

We will continue to define the extent of these identified stream reaches deemed unsuitable for spawning and locate similar reaches when they are selected in our sample draw. As the spawning distribution is refined, precision in our escapement estimates should increase. We will also continue to monitor trends of both methods and relate redd locations to immediate habitat to gain better understanding of how spawning habitat is utilized.

Steelhead and Chinook Salmon Parr Surveys, Parr Density, and Distribution

Introduction

Human impacts on fish populations are apparent in the Grande Ronde River basin, a tributary to the Lower Snake River. Historically, the Grande Ronde River supported several anadromous salmonid runs, including spring, summer and fall Chinook salmon, sockeye salmon, coho salmon and summer steelhead (ODFW 1990). During the past century numerous factors, including those mentioned above, have led to a reduction in salmonid stocks. Today, the only viable populations remaining are spring Chinook salmon and summer steelhead. Snake River spring/summer Chinook salmon, including Grande Ronde River spring Chinook salmon, were listed as threatened under the Endangered Species Act (ESA) in 1992; summer steelhead in 1997.

Numerous habitat restoration and protection projects have occurred within the Grande Ronde River basin, and other Columbia River sub-basins, over the past decades in attempt to improve native salmonid populations. The effectiveness of these projects at increasing native salmonid production and/or use has not been systematically evaluated. The CHaMP program systematically characterizes stream habitats in a spatially balanced manner and allows both status and trend monitoring (Bouwes et al. 2011). Coupling these habitat characterizations with salmonid presence and abundance will improve our understanding of the most important habitats for salmonid production, and allow appropriate targeting for restoration and protection actions.

Methods

Sixty habitat and fish monitoring locations were chosen within the UGRR sub-basin for 2014. Habitat monitoring locations were generated with the generalized random tessellation stratification (GRTS) design for the fourth year of the CHaMP (Bouwes et al. 2011). Only streams within the known (or assumed) anadromous fish spawning distribution were eligible for selection. Two crews completed these surveys, one from Oregon Department of Fish and Wildlife (ODFW) and the other from CRITFC. Site length varied based on stream size and was approximately 20 times the bankfull width (minimum 120 m, maximum 600 m).

All 60 CHaMP sites (Appendix Table B-23) were surveyed for juvenile salmonids via either a single-pass snorkel protocol (Juvenile Salmonid Density & Distribution in Northeast Oregon Watersheds, <http://www.monitoringmethods.org/Protocol/Details/370>) or single pass electrofishing. Fifty-three of the sites were surveyed snorkeling and most of those were only snorkeled once.

The remaining seven sites, small headwater streams, were sampled via electrofishing. These sites were electrofished with a single backpack electrofishing unit (Smith-Root model LR-20) during low flow periods (late June and July 2014). Direct current was used at all sites, with frequency and voltage adjusted to permit efficient capture of fish. Block nets were placed at the bottom and top of sites if the stream was flowing continuously. Some sites had only intermittent flow, and block nets were not used if fish were trapped within the sample reach by stretches of dry stream channel. A single electrofishing pass was completed in an upstream direction. Only salmonids were netted, while a visual estimate of non-salmonid relative abundance (abundant, common, or rare) was made throughout the survey. Netted fish were kept in a bucket until the entire channel unit had been sampled. All salmonids captured were identified to species, measured (fork length, mm), and released in the unit they were collected.

No marks or tags were placed on/in any fish. Metrics calculated from electrofishing surveys included: catch per unit effort (CPUE, no. fish/hour), mean length and relative density (fish per 100m²). Abundance estimates were calculated with a correction factor relating electrofishing catch to mark/recapture population estimates (Horn and Sedell 2012).

$$\text{Electrofishing Abundance Est. (all unit types): } N\hat{H}at = 1.7507 * E\text{fish Count}$$

Results

A significant change occurred in our snorkel methodologies in 2014. We began enumerating juveniles steelhead and Chinook salmon in the <50mm size class. In previous years (2011-2013) salmonids of this size were only noted for presence/absence. Thus, total estimates in 2014 will be inflated compared to any previous version of this report.

Salmonids were observed at all 60 surveyed CHaMP sites. Steelhead were found at 60 of the 60 sites, Chinook salmon at 29, and bull trout *Salvelinus confluentus* at only eight sites.

In the UGRR sub-basin, Chinook were usually the dominant salmonid in mainstem snorkel surveys (Figure 31), with counts in the hundreds, while counts were in the dozens for tributaries (Appendix Table B-24). A total of 4,586 juvenile Chinook were observed during snorkel surveys, and 90.1% were in the 50 – 90 mm size categories (age 0), while only 3% were in the <50mm size class. The remaining handful of Chinook salmon in the >90 mm size categories correspond to age 1 fish. Chinook were most abundant in mainstem UGRR and Catherine Creeks (Figure 32), with fewer observed in the larger tributaries like Sheep Creek, Meadow Creek, and the Catherine Creek Forks. There were fewer tributary observations of Chinook in 2014 than in previous years.

Steelhead were more widely distributed than Chinook (Figure 33), with individuals observed at all sites in 2014. Counts were higher than Chinook, with 5,563 individuals observed. Steelhead counts were much higher than in previous years, with many sites having counts over 100 individuals. However, 50.1% of the steelhead observed were in the size classes <50mm and 50-79mm. In past years the smallest steelhead size class available for enumeration was 70-130mm. Smaller individuals were noted as young-of-year and marked as present only. Thus, higher counts (and corresponding abundance estimates) do not reflect increased population levels. We made no differentiation between resident and anadromous individuals, and it is possible that many individuals observed in the smaller streams were resident rainbow trout, not steelhead. No adult steelhead were observed due to the timing of surveys.

Juvenile Chinook salmon and steelhead density estimates, were significantly higher (Kruskal-Wallis with Dunn's Test, $p < 0.05$) in pools than fastwater units or runs (Appendix Table B-25). There was no statistically significant difference between densities in fastwater units compared to runs. Catherine Creek and UGRR had the highest densities of Chinook, similar to previous years. Steelhead densities were highest in lower Fly Creek and Catherine Creek.

Other fish taxa observed during snorkeling were bull trout, mountain whitefish (*Prosopium williamsoni*), northern pikeminnow (*Ptychocheilus oregonensis*), redbside shiner (*Richardsonius balteatus*), speckled dace (*Rhinichthys osculus*), longnose dace (*Rhinichthys cataractae*), sculpin (*Cottus spp.*), bridgelip and unidentified suckers (*Catostomus spp.*), unidentified catfish (*Ictalurus spp.*) and sunfish (*Lepomis spp.*) (Appendix Table B-26). Bull trout were only observed

in Catherine Creek (mainstem, north and south forks) and the upper reaches of UGRR. Mountain whitefish, northern pikeminnow and suckers were generally seen in the mainstem Catherine Creek and UGRR sites, while dace, redbreast shiners and sculpins were observed in mainstem and lower gradient tributary sites, like Meadow Creek. In many cases, dace and shiners outnumbered salmonids in the same reaches. The smallest, high gradient sites generally produced only steelhead and sculpin. Catfish and sunfish were rarely observed in Meadow Creek and the UGRR mainstem.

Steelhead were the only salmonid captured via electrofishing at small stream sites. Juvenile steelhead were captured at all seven sampled sites. Steelhead CPUE ranged from 10.3 – 84.5 fish/hour (Appendix Table B-27), and densities ranged from 1.38 – 19.85 fish/100m².

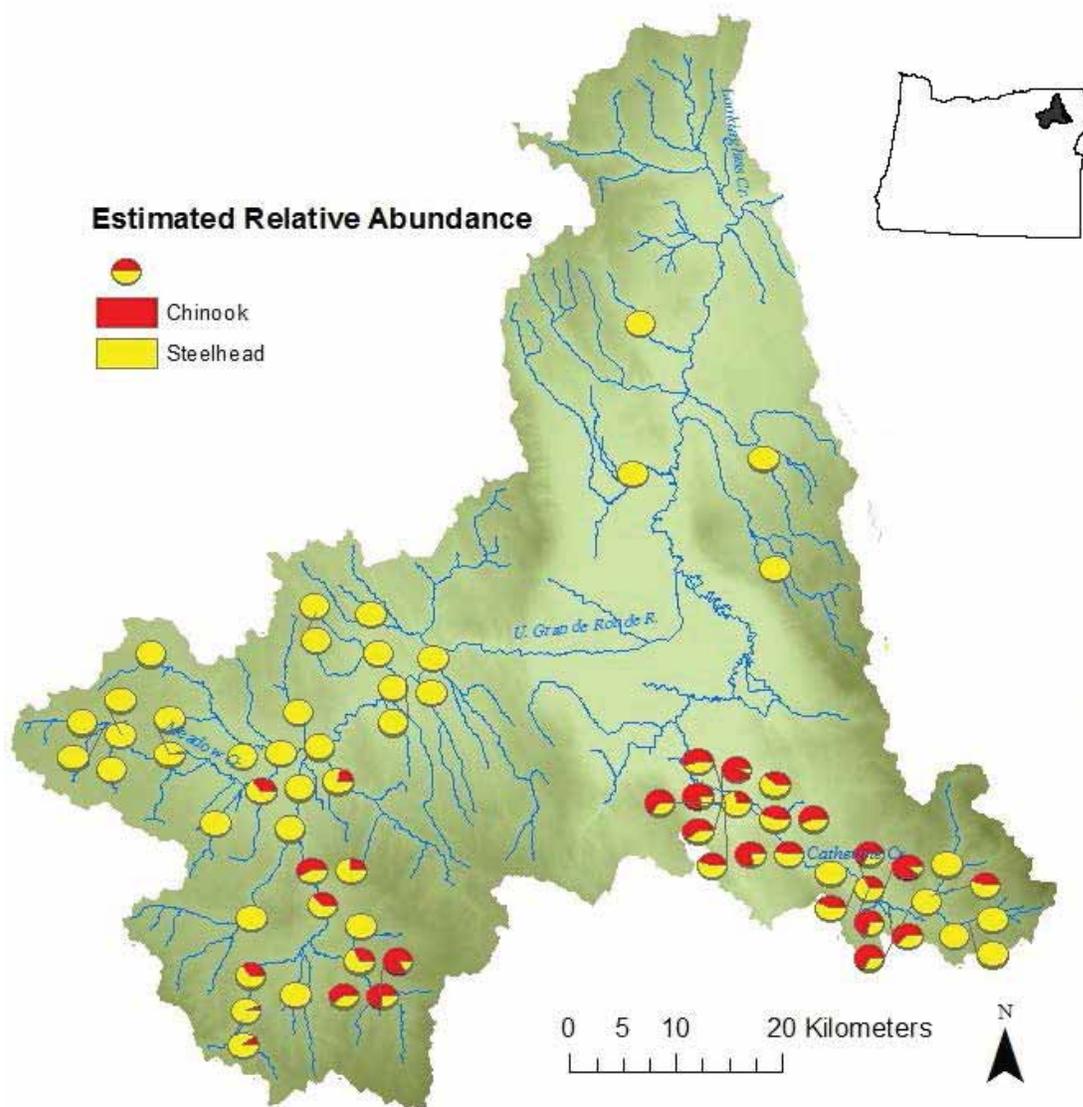


Figure 31. Proportional distribution of juvenile steelhead and Chinook salmon observed via snorkel and electrofishing surveys, 2014.

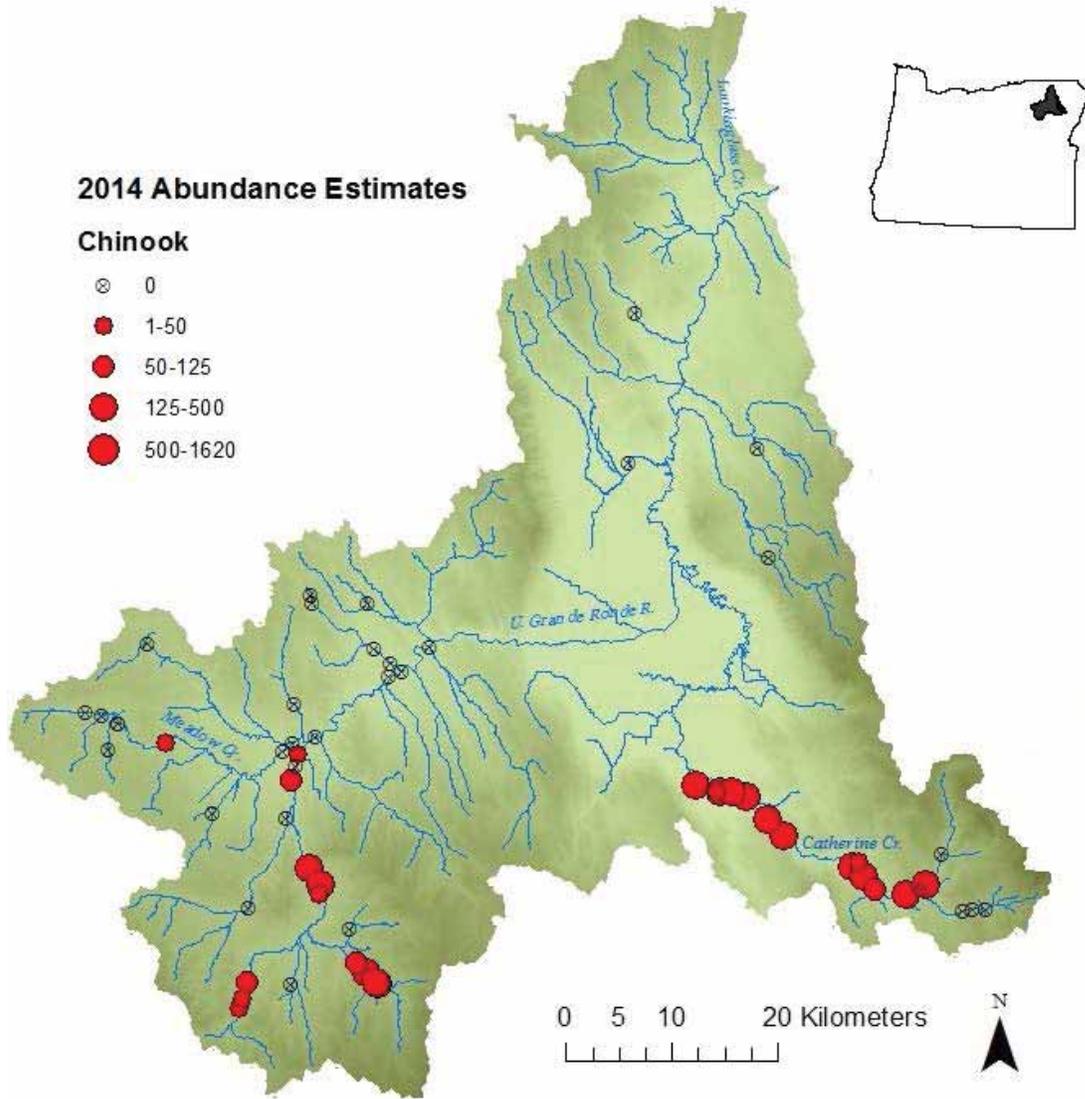


Figure 32. Spatial distribution and site level abundance estimates of Chinook salmon observed during snorkel and electrofishing surveys of the UGRR basin, 2014. Concentric circles indicate repeat snorkel surveys.

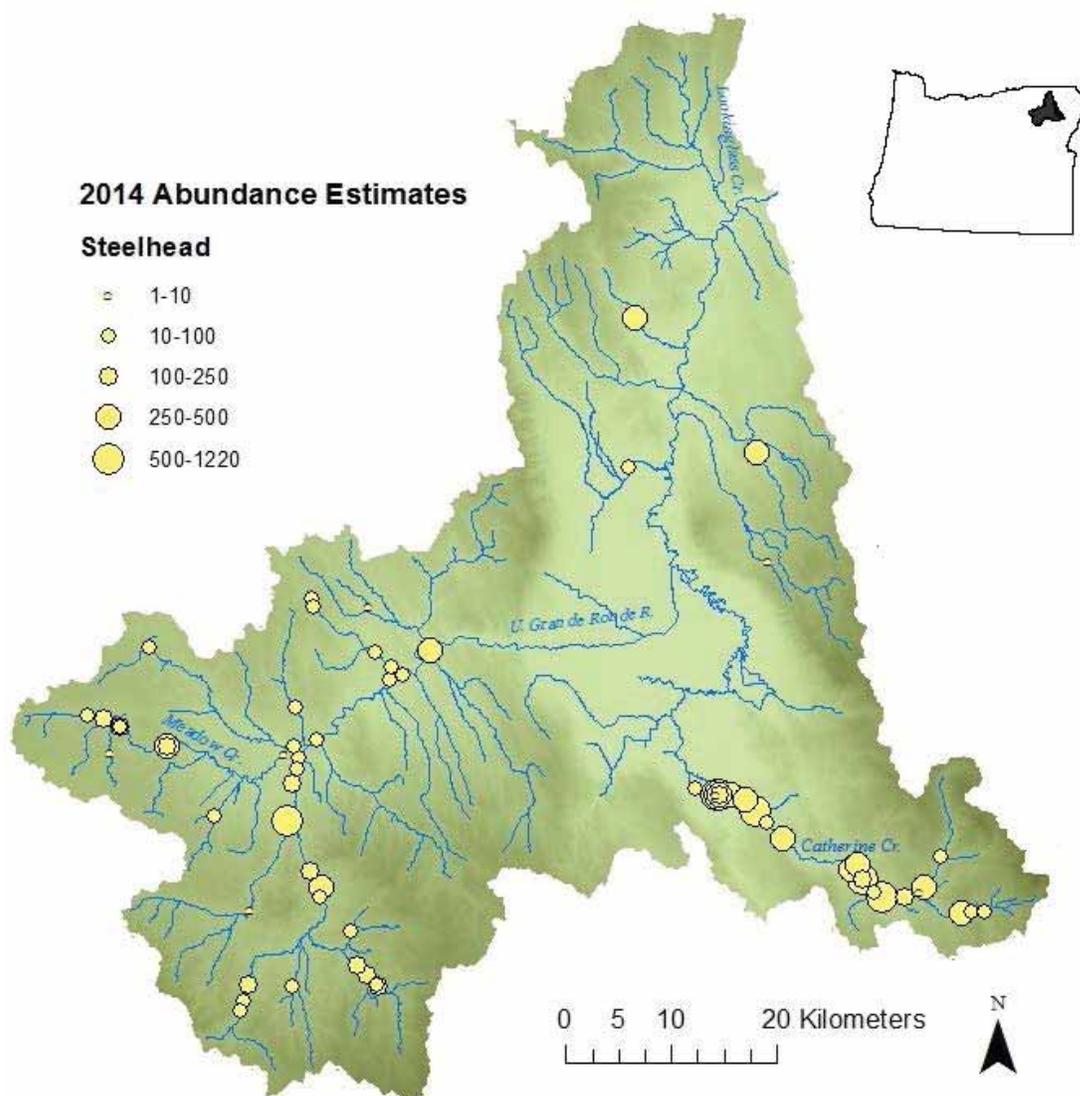


Figure 33. Spatial distribution and site level abundance estimates of steelhead observed during snorkel surveys of the UGRR basin, 2014. Concentric circles indicate repeat snorkel surveys.

Conclusions

The observed distribution of juvenile Chinook salmon was generally consistent with previous surveys and local, professional estimation of the Chinook rearing habitat. The majority of fish were using the mainstem Catherine Creek and Upper Grande Ronde River during their first summer. These areas are also the primary spawning grounds for UGRR Chinook salmon (Feldhaus et al. 2012). Additionally, a substantial number of Chinook were observed in Sheep Creek, which also has some spawning. The only other Chinook observed were in Meadow Creek. No Chinook salmon spawning is known to occur in this tributary, yet a few individuals were observed in the Starkey Experimental Range and Forest. These are likely stray juveniles seeking thermal refuge during hot summer months.

One of our goals is to constantly refine the known spawning and rearing distribution for steelhead in UGRR subbasin. This information is used by other ODFW research projects to define their sample space. As all sites contained *O. mykiss* in 2014, not sites are candidates for removal from the steelhead distribution.

This was the first year enumerating salmonids in the <50 mm size category. Steelhead were generally identifiable around the 45mm size when snorkeling, and a large portion of the steelhead counts were in this size class. A much smaller proportion of the Chinook salmon count were individuals <50mm, presumably due to earlier hatch dates and later snorkel dates for the larger, Chinook-dominated streams. Generally, crews found little difficulty with the addition of these smaller size classes, and we will continue to include them in our estimates. However, caution should be exercised when comparing these 2014 estimates to previous years', as the addition of smaller size classes has inflated the estimates.

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