

DAVID H. BECKER (OSB # 081507)
Law Office of David H. Becker, LLC
833 SE Main Street # 302
Portland, OR 97214
(503) 388-9160
davebeckerlaw@gmail.com

Attorney for Plaintiff Native Fish Society

PETER M.K. FROST (OSB # 91184)
Western Environmental Law Center
1216 Lincoln Street
Eugene, OR 97401
Tel: (541) 359-3238
Fax: (541) 485-2457
frost@westernlaw.org

Attorney for Plaintiff McKenzie Flyfishers

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF OREGON
PORTLAND DIVISION

NATIVE FISH SOCIETY,
MCKENZIE FLYFISHERS,

Plaintiffs,

v.

Case No.: 3:12-cv-431-HA

DECLARATION OF
GORDON LUIKART, Ph.D.

NATIONAL MARINE FISHERIES
SERVICE, REBECCA BLANK, Acting
Secretary of Commerce, **WILLIAM STELLE,**
Regional Administrator, NMFS, **OREGON**
DEPARTMENT OF FISH & WILDLIFE,
ROY ELICKER, Director, ODFW,
BRUCE McINTOSH, Acting Fish
Division Administrator, ODFW, **CHRIS**
WHEATON, Northwest Region Manager,
ODFW,

DECLARATION OF GORDON LUIKART, Ph.D.

Defendants.

I, Gordon Luikart, declare the following to which I am competent to testify under penalty of perjury of the laws of the United States:

1. My address is 41229 Haystack Mountain Lane, Polson, Montana 59860. I have been retained as an expert on salmonid genetics by the Plaintiffs in this matter.

PROFESSIONAL QUALIFICATIONS

2. I have 20 years of professional experience researching and teaching at the college and university level. Since 2000, I have specialized in research and teaching in the area of animal conservation and population genetics.

3. From 1997-2000, I was a postdoctoral researcher in Europe working on large (five country) animal genetics projects funded by the European Union and also NSF-NATO. I received a Ph.D. in Organismal Biology and Ecology in 1997 and a M.S. in Zoology in 1992, both from the University of Montana (but including a year in Australia on a Fulbright fellowship). I received a Bachelor of Science degree in Biology from Iowa State University in 1988, with a minor in Animal Ecology.

4. Since 2005 I have spent part of each year researching and teaching as a visiting professor and senior research scientist with the Center for Investigation of Biodiversity and Genetic Resources at the University of Porto, in Portugal. For the last three years, I have spent the majority of each year researching and teaching as an associate professor at the University of Montana's Flathead Lake Biological Station. Courses I teach include undergraduate and graduate level fish and wildlife genetics classes.

5. I have conducted genetic research on fish and wildlife populations in several different countries in addition to the United States and Portugal, including in Australia as a Fulbright Fellow, and in France as a government scientist where I won the bronze medal as a top researcher with the Centre National de la Recherche Scientifique. I have conducted research on a wide range of species, including goats and other domestic and wild ungulates, carnivores, fish, and other aquatic species.

6. My research and teaching embraces various topics related to animal genetics/genomics, including disease-diagnostics (via pathogen DNA detection), population modeling, captive and domesticated populations, endangered and threatened species recovery, gene flow effects on individual fitness and adaptation, population size and structure, and monitoring of the genetically-effective population size and the effective number of breeders (spawners) using genetic markers in natural and captive populations.

7. I have conducted numerous research investigations on these subjects. Serving as a principal or co-principal investigator on more than 40 scientific research projects, my work has produced chapters in four books, all relating to wildlife and conservation genetics (one on animal domestication), and over 110 scientific papers in peer-reviewed international journals. Also, I recently (2007) co-authored a major textbook on conservation genetics (the second edition was published in 2013).

8. My recent research projects involved developing a computer program simulator to model gene flow among populations within aquatic species in complex river systems. My recent papers include the genetic/genomic sequencing to quantify gene flow and introgression in trout and in wild and domestic populations; they also include development of novel estimators of the number of breeders (spawners per generation) from genetic marker data.

9. My scholarship includes service on the editorial board of the journal Conservation Biology and as an associate editor for both Molecular Ecology Resources and the Journal of Heredity.

10. In the last five years I was recruited as an advisor for the Swan Ecosystem Center Native Fish Committee, and I am a member of the American Fisheries Society, the Ecological Society of America, the Society for Conservation Biology, the Wildlife Disease Association, and the Wildlife Society.

11. Attached hereto as Exhibit 1 are my curriculum vitae, which include a list of all peer-reviewed publications I have authored since 1996.

12. I have substantial familiarity with the genetics of animal domestication, adaptation to captivity, the effects of gene flow on fitness and population persistence in fish and wildlife, admixture and local adaptation in salmonids, and statistical and molecular empirical genomics.

13. I am being compensated for my work on this matter. The reasonable rate for my work is \$150 per hour. I have worked for approximately 16 hours at this point.

14. In addition to drawing upon my knowledge and experience, I have reviewed and considered the following documents in developing my opinions expressed herein: the Opinion and Order on Preliminary Injunction; the NMFS ESA Section 7 Biological Opinion and Magnuson-Stevens Fishery Conservation and Management Act Essential Fish Habitat (EFH) Consultation (BiOp) (NMFS Consultation Number 2011/02491, dated September 28, 2012); the NMFS Final Environmental Assessment (EA) (dated September 2012); the versions of the Final Sandy River Spring Chinook Hatchery Genetic Management Plan (HGMP) (dated May 31, 2011), Final Sandy River Summer Steelhead HGMP (May 10, 2011), Final Sandy River Winter

Steelhead HGMP (May 31, 2011) and Final Sandy River Coho HGMP (May 10, 2011) that were approved by NMFS; and Ford, Status Review Update for Pacific Salmon and Steelhead Listed under the Endangered Species Act: Pacific Northwest (November 2011). I have also spoken with individuals familiar with the Sandy River watershed and salmon genetics, including Aquatic Ecologists Dr. Chris Frissell and Dr. Jack Stanford, and salmonid geneticists Dr. Fred Allendorf.

SUMMARY OF OPINIONS

15. In summary, it is my professional opinion that the Spring Chinook, winter steelhead and coho artificial production programs described in the winter steelhead HGMP, spring Chinook HGMP, and coho HGMP: (a) will almost certainly result in the spreading of maladaptive genes from the hatchery fish to the wild population via interbreeding and introgression into the wild, which will very likely result in lower fitness and reduced local adaptation; (b) that the negative effects of introgression (e.g., even from only ~ 1% hatchery spawners among the naturally-spawning population) each year will accumulate over several years to cause high long-term introgression rates; and (c) that the negative effects of introgression of maladaptive genes into wild fish will likely persist for multiple generations (decades); and (d) that hatchery fish introgression will likely lead to loss of genome-wide genetic variation and reduction of the effective population size of the wild population. It is also my opinion that the 10% annual stray rate allowed in the HGMPs is arbitrary, and unacceptably high. Even a 5% stray rate would be unacceptably high because it would likely result in the decline, rather than the recovery, of the wild populations of winter steelhead, spring Chinook, and coho in the Sandy River, if the straying continued for several years. By extension, an unacceptably high stray rate (i.e., 5% to 10%) will likely lead to a reduction in the likelihood of recovery of the Lower Columbia River species to which these populations belong. I would

strongly advise that if protection of the genetic integrity of Sandy River salmon and steelhead is to remain a management priority, more research and a monitoring program are needed to determine the actual stray rate, the introgression rate, and the fitness effects of introgression, before any more releases are allowed.

THREATENED SANDY CHINOOK, STEELHEAD AND COHO

16. The Lower Columbia River Chinook and Lower Columbia River Coho Evolutionarily Significant Units (ESUs) and Lower Columbia River Steelhead Distinct Population Segment (DPS) are each listed as a “threatened” species under the Endangered Species Act (“ESA”). The wild populations of Sandy River spring Chinook, winter steelhead, and coho are among the very few wild populations in the Lower Columbia River ESUs and DPS that have not been extirpated (e.g., Ford 2011).

ADVERSE EFFECTS FROM HATCHERY DOMESTICATION

17. Hatchery domestication is caused by a process analogous to natural selection, but occurring under unnatural conditions—the individual fish “selected” are those better adapted to live in unnatural conditions (high density, no predators, no disease or different disease, unnatural food, artificial spawning, artificial flow and unnatural habitat conditions, unnatural densities). The process results in loss of the ability to avoid predation, loss of disease resistance, loss of ability to forage and spawn efficiently, and reduced reproductive success (Reisenbichler and Rubin 1999; Chilcote 2003; Kostow and Zhou 2006; Kostow 2009; Araki 2010; Seamons et al. 2012; Allendorf et al. 2013). This artificial selection pressure is strong; it results in rapid adaptation to captivity with loss of the ability to survive and reproduce effectively in the wild. The genes underlying these maladaptive traits will be fixed (or at high frequency) in hatcheries (even after only a few months of differential survival of embryos to smolts). These

domestication effects occur even when the hatchery fish were originally derived from the local wild population, and is exacerbated by the sort of segregated hatchery programs described in the HGMPs.

18. Maladaptive (deleterious) genes from hatchery fish will likely be transmitted (via cross-breeding and introgression) into wild fish and thereby reduce the fitness of wild fish. This reduced fitness will happen if the hatchery fish are allowed to spawn in the wild. The negative fitness effects of hatchery fish on natural populations are widely documented in the scientific literature (e.g., Araki et al., 2007, Araki et al. 2009, Christie et al. 2011, Christie et al. 2012, Normandeau et al. 2009; Theriault et al. 2011; Waples 2011). The negative effects from hatchery gene introgression would likely persist for many years (generations), however few empirical data exist on duration of effects (Loder 2005; Allendorf et al. 2008).

19. As one of a growing (and large) number of examples of negative effects of hatchery introgression, a wild winter-run steelhead supplementation program in the Hood River, Oregon was started in 1991 and has continued to the present. The success of the Hood River program has been studied intensively by researchers at Oregon State University, with results reported in numerous peer-reviewed scientific publications (including Araki et al. 2007a,b, Araki et al. 2009, Christie et al. PNAS 2011, and Christie et al. Heredity 2012). Araki et al. have shown that on average first-generation hatchery fish produced from native wild broodstock have only 60% to 80% of the reproductive success in the wild compared to the native wild fish themselves. Araki et al. have also shown that when second-generation hatchery fish (i.e., the offspring of wild-spawning first-generation hatchery fish) spawn in the wild, they also produce fewer surviving adult offspring than pure wild fish (W x W). If two second generation hatchery fish spawn together, they have less than 40% of the reproductive success of two wild fish

spawning together; spawning between a pure wild and a second generation hatchery fish (H x W) have less than 90% the success of two wild fish.

20. In a follow-up analysis of this same long-term data, Christie et al. (2011) have shown that the majority of offspring from matings in the hatchery between two wild parents (W x W) that survive to return and spawn in the wild will be produced by a few large families. Progeny from these few families are those that adapt best to the hatchery rearing environment and thus produce the majority of the migrating (released) smolts. It will be these hatchery progeny with lower relative fitness in the wild that will constitute the majority of hatchery-origin spawners each year. In other words, the majority of returning adults from a hatchery program will be made up of individuals with the lowest fitness in the wild of all returning hatchery adults. This was demonstrated as was the fact that the loss of fitness is a genetic effect (i.e., has a genetic basis), and was not an effect of the hatchery rearing environment.

21. In a recent publication, Christie et al. (2012) further showed that these phenomena result in the genetically effective population size of wild steelhead populations subjected to such hatchery supplementation programs is significantly reduced compared to a similar size wild population that is not subject to supplementation. This effect significantly increases the rate at which adaptive genetic material will be lost from the wild population under supplementation. The 10% percentage of hatchery fish spawning among the naturally spawning population allowed in the HGMPs for the segregated Sandy River hatchery programs will cause effects similar to those identified in the Araki and Christie studies of hatchery supplementation programs because the Sandy River hatchery programs will suffer from adaptation to captivity (e.g., increased frequency of maladaptive genes) and a reduction of genetic variation in the wild populations. In fact, segregated hatchery programs with low introgression (5% - 10%) into the

wild population are likely to cause more harmful genetic effects (reduction of fitness) than are nonsegregated hatchery programs (e.g., Laikra et al. 2010; Naish et al. 2010; Baskett and Waples, 2013). This is because the isolation of a segregated program population from the wild populations exacerbates the genetic problems (e.g., adaptation to captivity) associated with captive rearing as there is not high gene flow with the wild population to keep the captive population from experiencing rapid maladaptive genetic change.

22. The reduction in reproductive success that is expected from the hatchery programs described in the spring Chinook, coho, and winter steelhead HGMPs is likely to have serious and long-lasting harmful effects on the rate that the native steelhead population can rebuild and recolonize the newly accessible habitat made available by the removal of the two dams. Araki and colleagues (Araki et al. 2009) estimated that the net negative effect on the whole naturally spawning winter-run steelhead population in Hood River resulting from the reduced reproductive success of fish from the supplementation program was 8% relative to a purely wild population of the same size. This is a significant amount. For example, if the size of the population that included the supplementation hatchery fish was 100 and this population had an annual growth rate of 1.0 (meaning that it just replaced itself every year), a purely wild population of 100 would have an annual growth rate of 1.087 ($1/0.92$). At this growth rate the purely wild population would double in approximately 8.5 years. Conversely, if the purely wild population was 8% less productive (annual growth rate of 0.92), it would decline to one-half of its initial size (50) in about 8.5 years. The Sandy River wild fish populations will likely suffer a reduced annual growth rate (e.g., 5% -10%) and thus a decline in population abundance, given the 10% stray rate that is allowable in the Sandy River HGMPs. The harmful effects on the fitness of wild spawning spring Chinook, coho and winter steelhead caused by the hatchery

programs (described in the spring Chinook, coho, and winter steelhead HGMPs) are highly likely to cause significant impairment to the fitness of the Sandy River wild spring Chinook, coho, and winter steelhead populations and thereby to the Chinook ESU, Coho ESU, and Steelhead DPS.

23. The Hood River studies described herein show that the domestication effect causing loss of fitness unequivocally contains a genetic component. Consequently, the lower reproductive success of hatchery spawners in the wild, which will include spawning between hatchery and wild fish, will result in the spread of maladaptive genes to the already depressed wild populations. This risk to the genetic integrity of the wild populations will therefore assuredly not be offset by the reduced spawning success of hatchery origin adults. Further, as noted herein, the circumstances on the Hood River provided precisely the (rare) conditions needed for creating an experimental design capable of distinguishing the effects of genetics from those of the rearing environment and this is precisely what Dr. Araki and his colleagues achieved. The serious risks that are thus known to attend hatchery-origin fish spawning among wild populations of spring Chinook, coho and winter steelhead appear to be largely dismissed or ignored by those implementing the hatchery programs and by NMFS in its EA and BiOp.

24. The domestication effects and resulting loss of fitness in the wild due to hatchery supplementation shown by the Oregon State University colleagues in Hood River occur under nearly ideal conditions that permit only wild, non-first-generation hatchery progeny, to be used for hatchery broodstock. These effects will be worse, fitness in the wild even lower, when returning adults produced by the captive brood are taken back into the hatchery for broodstock, as will occur in the Sandy River programs.

25. The risks posed by the spring Chinook, coho and winter steelhead hatchery programs are exacerbated by reliance on plans for monitoring, evaluation, and modification that

either did not exist or had not been implemented at the time the EA and BiOp were prepared and which were of unknown efficacy. Thus, it is not clear whether or not the hatchery programs will be properly monitored or if sufficient funding exists for timely monitoring and evaluation of likely harmful effects of the proposed hatchery actions. This is a major deficiency. Rigorous monitoring and evaluation of the impact of hatchery fish on wild salmonids, along with clearly defined adaptive management protocols, are essential to preventing unwarranted and severe harm to wild fish populations. It is not possible to adequately evaluate the risks the hatchery programs pose to wild salmonids and their recovery without knowing how those programs will be monitored, evaluated, and modified in response to changing conditions. A monitoring and evaluation program is especially important given the rapidly improving ability of biologists to use molecular and computational tools to monitor gene flow and the effects of hatchery introgression on individual fitness and population performance (i.e., growth rate and probability of persistence).

26. In order to contain and minimize significant genetic risks, both the total numbers of hatchery adults on the spawning grounds in the wild annually and the proportion of these fish to the total naturally-spawning population must be limited. In my professional opinion, the percentage of hatchery fish spawning (each year) should not be more than 1% because over multiple years the cumulative effects would likely grow to a larger percent (of genetic contribution to wild) which would likely reduce fitness and population growth, persistence, and recovery.

27. I have reviewed the EA and BiOp to attempt to identify where and how NMFS justified approving the 10% percentage of hatchery origin spawners allowed in the HGMPs. In both documents, the justification is sparse or non-existent. In the EA, NMFS states on pages 97

and 111 that the 10% figure for spring Chinook and winter steelhead “reflects the similarity between the hatchery” and natural-origin fish. NMFS does not seem to include any justification for the 10% figure for coho in the EA in its discussion of genetics on page 104. In the general discussion of genetic and biological effects at page 74, NMFS indicates that the agency applies a standard of 5% maximum hatchery strays into naturally spawning populations, and that its goal is that “the number of non-local or hatchery-produced strays in a particular population should be as low as possible to minimize the potential for genetic introgression.” NMFS then arbitrarily selected the 10% stray rate based on the similarity of hatchery and wild fish. NMFS and the ODFW Recover Plan discuss a salmon population viability model that could potentially estimate the negative impacts of a 10% stray rate however the model does not take into account the multi-year accumulating genetic introgression effects from setting the stray rate at 10% (per year); the discussion and model also do not evaluate the level of "similarity" from which the the populations start. The viability model and Recovery Plan was apparently premised on a continuation of an integrated hatchery program using wild broodstock. .

28. The BiOp, at page 46, states that “Information that NMFS is particularly interested in and that should be included in an HGMP includes the number, location and timing of naturally spawning hatchery fish, the estimated level of gene-flow between hatchery fish and fish from natural populations, the origin of the hatchery stock, the more distant the origin, compared to the affected natural population, the greater the threat, the level and intensity of hatchery selection, and the duration of gene flow.” There is no evidence that there is any estimate of the level of gene-flow, duration of gene flow, or any indication that NMFS evaluated any evidence of the genetic divergence between the hatchery origin and natural origin populations of the species in the Sandy River in making its conclusion statements that the hatchery origin and

wild fish populations are similar. It seems that NMFS had no genetic data or evidence that supports its surrogate for inferring the gene flow or the stray rate. At least base line genetic data on the hatchery and wild populations and introgression rates are required for choosing a stray rate that is not likely to lead to introgression and loss of fitness in wild fish. NMFS also failed to consider or discuss the fact that a 10% annual stray rate will lead to a much higher introgression rate over time (fish generations) as hatchery fish in these segregated programs diverge more genetically from the wild fish in the Sandy River with each generation. NMFS also ignored the fact that any strong similarity that might exist between the hatchery and wild populations will likely be reduced significantly after as little as one generation of returns of hatchery fish that were bred from hatchery parents.

29. As discussed above, the current scientific consensus is that serious adverse genetic effects and population declines can occur at a 10% stray rate, and even at lower stray rates of hatchery-origin spawners. There is no documentation in the EA or BiOp of why NMFS considers the hatchery and wild populations in the Sandy River to be similar genetically. ODFW has noted that there has never been a comprehensive genetic analysis of the hatchery and wild populations of coho in the Sandy River, and that the broodstock which originated from wild adult fish may have developed genetic differences over time (Coho HGMP page 40-41). The conclusion in the spring Chinook HGMP (pg. 56) “Due to the recent development of this broodstock from the wild spring Chinook population, the hatchery and wild populations are not thought to have diverged to any significant extent” is flawed because of the fact that genetic divergence can occur in just one generation; NMFS did not evaluate these factors in the EA and BiOp.

30. In addition, NMFS does not consider whether the 10% percentage of hatchery origin spawners allowed in the spring Chinook HGMP is justified based on the recent spikes in hatchery origin fish spawning among the wild population. The EA notes at pages 97 and 98 that the percentage of hatchery origin spring Chinook spawning among the natural population was 61% in 2011 and 75.7% in 2010.

31. The extremely high rate of hatchery origin spawners makes a 10% stray rate insufficiently likely to protect wild fish. NMFS apparently ignores that these stray rates have already likely caused significant introgression of maladaptive hatchery genes into the wild populations. NMFS apparently chose the 10% stray rate without considering introgression and harm has very likely already occurred. The 10% rate seems based on similarity between the local origin brood stock and the wild fish, whereas the similarity between brood stock and wild fish cannot be known because the ODFW ceased using wild fish for brood stock after 2010 and there was massive straying in 2010 and 2011.

32. NMFS appears not to have considered whether a 10% stray rate, given the accumulating negative effects on wild populations of the Sandy River species, will lead to the recovery of these populations and hence these species. For example, the EA states (page 74) only that the 10% stray rate performance standard was identified by ODFW in its Recovery Plan as the level necessary for delisting. Similar statements appear in the BiOp at pages 25, 33, 46, 53, and 97. Neither NMFS nor ODFW in the Recovery Plan considered that a 10% stray rate, over time, would lead to the decline, rather than recovery, of these populations.

33. In the BiOp at page 53, NMFS states that “Gene-flow and competition on the spawning grounds is not a threat because the HGMPs impose strict limits on pHOS. The hatchery programs using broodstocks derived from local natural populations (the spring Chinook

salmon, coho salmon, and winter steelhead hatchery programs) require that pHOS may not exceed 0.10. Changes in the Hatchery Program: For comparison purposes, the HSRG recommendation for this situation is 0.30.” This is incorrect because the HSRG recommendation for 30% hatchery-origin fish only applies to integrated hatchery programs, not segregated programs such as in the Sandy River. But, like the statements in the EA, it also ignores that the hatchery population will begin to diverge genetically from the wild population after even one generation, about two to four years after the discontinuation of use of wild fish for broodstock after 2010, and ignores that that the 10% annual stray rate will lead to a much higher introgression rate over time (multiple yearss).

34. Another problem caused by hatcheries and the release of hatchery fish is that they greatly increase risks of disease transmission to wild fish. This occurs because of the unnaturally high densities of fish maintained in captivity leads to increased risk of infection and thus subsequent transmission through water or directly from fish released by hatcheries into wild native populations.

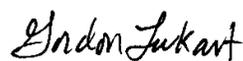
35. It is my professional opinion that, the hatchery programs described in the spring Chinook HGMP, winter steelhead HGMP, and coho HGMP should be immediately discontinued (or at least severely limited to <1% returning spawners until introgression and its effects on fitness can be thoroughly evaluated). Any introgression of maladapted genes from hatchery fish into the wild fish population will likely have long-lasting adverse effects on that population and its ability to fully recover. Any potential future hatchery releases will return and some fish will most likely cross-breed with wild steelhead, spring Chinook, and coho, and it is highly likely that the resultant offspring will have reduce fitness (survival and reproduction) in the wild. Maladapted genes introduced into the wild populations will likely persist for many generations

even after the returns of hatchery fish have ceased, thereby causing long-lasting harm to the population. Any reduction in the spawning success will harm the depressed wild Chinook, coho and wild steelhead populations and their ability to persist and recover.

36. The growth, persistence, and recovery of the Sandy River spring Chinook, coho, and winter steelhead is essential to the recovery of the respective Chinook and coho ESUs and steelhead DPS. The steelhead hatchery programs pose a threat to the persistence and recovery and de-listing of the species. The 10% stray rates selected for these programs was apparently arbitrary. NMFS did not consider the short and long term dangers from genetic introgression that such a high rate would cause, nor the likelihood that it would lead to the decline, rather than the recovery, of these species. These programs should be terminated or, at a minimum, reduced (and effects monitored) to prevent severe and lasting harm to this species.

I declare under penalty of perjury under the laws of the United States of America that the foregoing is true and correct.

Executed this 2nd day of July, 2013.



Gordon Luikart, Associate Professor
Flathead Lake Biological Station, University of Montana

LITERATURE CITED

Allendorf, F.W., G. Luikart, S. Aitken. 2013. Conservation and the Genetics of Populations [Second Edition]. Wiley-Blackwell. Pp. 642.

Allendorf, F.W., P.R. England, G. Luikart, G.A. Ritchie, and N. Ryman. 2008. Genetic effects of harvest on wild animal populations. Trends in Ecology and Evolution, 6:327-337.

Araki. H., B.A. Berejikian, M.J. Ford, and M.S. Blouin. 2008. Fitness of hatchery-reared

salmonids in the wild. *Evolutionary Applications* 2008 May; 1(2):342–355.

Araki, H., B. Cooper, and M.S. Blouin. 2007. Genetic effects of captive breeding cause a rapid, cumulative fitness decline in the wild. *Science* 318:100-103.

Baskett M.L, and R.S. Waples. 2013. Evaluating alternative strategies for minimizing unintended fitness consequences of cultured individuals on wild populations. *Conservation Biology* 27: 83-94.

Chilcote, M. W. 2003. Relationship between natural productivity and the frequency of wild fish in mixed spawning populations of wild and hatchery steelhead (*Oncorhynchus mykiss*). *Canadian Journal of Fisheries and Aquatic Sciences* 60:1057–1067.

Chandler, G.L., Bjornn, T.C., 1988. Abundance, growth, and interactions of juvenile steelhead relative to time of emergence. *Transactions of the American Fisheries Society* 117:432–443.

Christie M.R., M.L. Marine, R.A. French, R.S. Waples, and M.S. Blouin. 2012a. Effective size of a wild salmonid population is greatly reduced by hatchery supplementation. *Heredity* 109, 254-260.

Christie M.R., M.L. Marine, R.A. French, and M.S. Blouin (2012b) Genetic adaptation to captivity can occur in a single generation. *Proceedings of the National Academy of Sciences, USA* 109:238-242.

Ford, M.J., 2011, Status Review Update for Pacific Salmon and Steelhead Listed under the Endangered Species Act: Pacific Northwest (November 2011).

Kostow, K.E., and S. Zhou. 2006. The effect of an introduced summer steelhead hatchery stock on the productivity of a wild winter steelhead population. *Transactions of the American Fisheries Society* 135:825–841.

Kostow, K. 2009. Factors that contribute to the ecological risks of salmon and steelhead hatchery programs and some mitigating strategies. *Reviews in Fish Biology and Fisheries* 19:9-31.

Laikre, L., M. K. Schwartz, R. S. Waples, and N. Ryman. 2010. Compromising genetic diversity in the wild: unmonitored large-scale release of plants and animals. *Trends in Ecology&Evolution* 25:520–529.

Loder, N. 2005. Point of no return. *Conserv. Pract.* 6:29–34.

Naish, K. A., I. J. E. Taylor, P. S. Levin, T. P. Quinn, J. R. Winton, D. Huppert, and R. Hilborn. 2007. An evaluation of the effects of conservation and fishery enhancement hatcheries on wild populations of salmon. *Advances in Marine Biology* 53:61–194.

Normandeau E., Hutchings J.A., Fraser D. J., Bernatchez L. 2009. Population-specific gene

expression responses to hybridization between farm and wild Atlantic salmon. *Evol Appl* 2: 489–503.

Reisenbichler, R.R., Rubin, S.P. 1999. Genetic changes from artificial propagation of Pacific salmon affect the productivity and viability of supplemented populations. *ICES Journal of Marine Sciences* 56:459–466.

Seamons T.R., L. Hauser, K.A. Naish, and T.P. Quinn. 2012. Can interbreeding of wild and artificially propagated animals be prevented by using broodstock selection for divergent life history. *Evolutionary Applications* 5(7): 705-719.

Theriault V. et al. 2011. Reduced reproductive success of hatchery coho salmon in the wild: insights into most likely mechanisms. *Molecular Ecology* 1860–1869.

Waples R.S. 2011. Genetic interactions between hatchery and wild salmonids: Lessons from the Pacific Northwest. *Canadian Journal of Fisheries and Aquatic Sciences*, 48:124-133.