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**Conceptual Approach to Monitoring and  
Evaluation for Hatchery Programs**  
**funded by Douglas County Public Utility District**

*Prepared for:*  
**Douglas PUD Habitat Conservation Plan Hatchery Committee**

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## **Abstract**

Public Utility District No. 1 of Douglas County (Douglas PUD) implements hatchery programs as part of the Habitat Conservation Plan (HCP) agreement relating to the operation of the Wells Hydroelectric Project. The HCP defines the goal of achieving no net impact (NNI) to anadromous fish species affected by operation of Wells Dam. The HCP identifies general program objectives as “contributing to the rebuilding and recovery of naturally reproducing populations in their native habitats, while maintaining genetic and ecologic integrity, and supporting harvest. The HCP further establishes a Hatchery Committee charged with defining specific hatchery program objectives and developing a monitoring and evaluation (M & E) program to determine if the hatchery objectives are being met. The HCP specifies that this plan will be reevaluated and adjusted, if need be, every five years. The purpose of this plan is to provide the conceptual framework to monitor and evaluate the success of the hatchery programs. This will in turn provide information to the HCP Hatchery Committee to manage these programs.

## **Introduction**

In April 2002, negotiations on the Wells Habitat Conservation Plan (HCP) were concluded (DPUD 2002). The HCP is a long-term agreement between Douglas PUD, National Marine Fisheries Service (NOAA Fisheries), the Washington Department of Fish and Wildlife (WDFW), the U. S. Fish and Wildlife Service (USFWS), the Confederated Tribes of the Colville Reservation (Colville Tribes) and the Confederated Tribes and Bands of the Yakama Nation (Yakama Nation)<sup>1</sup>. The HCP objective is to achieve No Net Impact (NNI) for each plan species (spring Chinook salmon, summer/fall Chinook salmon, sockeye salmon, steelhead, and coho salmon of upper Columbia River (UCR) Basin) affected by the hydroelectric project. NNI consists of two components: (1) 91% combined adult and juvenile project survival achieved by project passage improvements implemented within the geographic area of the Project, (2) up to 9% compensation for unavoidable project mortality provided through hatchery and tributary programs, with a maximum 7% compensation provided through hatchery programs and 2% compensation provided through tributary programs. The signatory parties intend these actions to contribute to the rebuilding of tributary habitat production capacity and basic productivity and numerical abundance of plan species. Previous artificial propagation commitments to compensate for habitat inundation are carried forth in the HCP<sup>2</sup>.

The Joint Fisheries Parties (JFP) include fishery resource managing agencies that are signatories to the HCP agreements and responsible for developing species-specific hatchery program goals. At this time, the WDFW, the USFWS, the Colville Tribes, the Yakama Nation and NOAA Fisheries constitute the JFP in regards to the HCP agreements. The JFP has agreed that hatchery programs for anadromous salmonid tributary populations (Methow and Okanogan) will attempt to follow the concepts and

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<sup>1</sup> The Yakama Nation signed the HCP on March 24, 2005.

<sup>2</sup> For further information on the HCPs, and the creation and role of the Hatchery Committees, please see the HCP (DPUD 2002).

strategies of supplementation as defined and outlined in RASP (1992) and Cuenco et al. (1993). While hatchery programs for those salmonid population(s) that are released directly into the Columbia River will follow conventional hatchery practices associated with harvest augmentation. The Entiat River has been selected as a potential reference stream (population) for hatchery evaluations purposes, and as such, no new HCP hatchery supplementation programs will be initiated in that watershed. Conversely, conventional hatchery practices will continue to be utilized for plan species released into the mainstem Columbia River. The primary goal of these hatchery programs continues to be both inundation compensation and harvest augmentation.

The HCP Hatchery Committee (HCP HC) is responsible for developing a monitoring and evaluation (M&E) plan to assess overall performance of Douglas PUD's hatchery programs in achieving the general program objective of *“contributing to the rebuilding and recovery of naturally reproducing populations in their native habitats, while maintaining genetic and ecologic integrity, and supporting harvest as well as defining and monitoring specific hatchery program objectives”*. The HCP HC has developed and adopted goals for specific hatchery programs. The various goals of those programs are outlined below:

1. Support the recovery of ESA listed species<sup>3</sup> by increasing the abundance of the natural adult population, while ensuring appropriate spatial distribution, genetic stock integrity, and adult spawner productivity.

Hatchery Programs: Methow spring Chinook; Methow steelhead; and Okanogan steelhead

2. Increase the abundance of the natural adult population of unlisted plan species, while ensuring appropriate spatial distribution, genetic stock integrity, and adult spawner productivity. In addition, provide harvest opportunities in years when **spawning escapement** is sufficient to support harvest.

Hatchery Programs: Methow summer/fall Chinook; Okanogan sockeye<sup>4</sup>

3. Provide salmon for harvest and increase harvest opportunities, while segregating returning adults from natural spawning populations.

Hatchery Programs: Wells summer/fall Chinook

As previously mentioned, Douglas PUD's hatchery program encompasses two different hatchery strategies that address different goals due in part to the purpose in which the program was created. The main focus and an important goal of the hatchery program is to increase the natural production of fish in the tributaries that will aid in the achievement of no net impact (NNI) and in the recovery of ESA listed stocks. This is

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<sup>3</sup> While the HCP is not a recovery plan into itself, the hatchery component of it must be consistent with hatchery goals and objectives through the ESA, and as such should aid in the recovery of listed fish.

<sup>4</sup> Evaluation of the Douglas PUD Okanogan Sockeye obligation is conducted through the implementation of the Fish-Water Management Tool Program.

accomplished through the strategy of supplementation. Simple put, supplementation uses broodstock for the hatchery program from a target stream or area, the offspring of which are reared in a hatchery and released back to the target stream or area. Fish will be reared and released in a manner that ensures appropriate spatial distribution and genetic integrity of the populations being supplemented. Subsequently, these juvenile hatchery fish will return as adults to supplement the natural spawning population with the intent of increasing the natural production of the population.

The fundamental assumption behind the theory of supplementation is that hatchery fish returning to the spawning grounds are “reproductively similar” to naturally produced fish. There is some information that suggests that this may not be true. Therefore, one of the questions that will be answered through this M&E plan is how effective are hatchery-origin salmon and steelhead at reproducing in the natural environment.

One of the important aspects of this Plan is to compare changes in productivity of a supplemented population to a non-supplemented population. Potential reference streams (e.g., Entiat) should have similar biotic and abiotic components as experimental streams. Preliminary determinations regarding the suitability of potential reference streams or areas within streams will be made based on the following criteria (these criteria are not considered all inclusive at this time):

- No recent (within last 5-10 years; two generations) hatchery releases directed at target species
- Similar information of hatchery contribution on the spawning grounds
- Similar fluvial-geomorphologic characteristics
- Similar out of subbasin effects
- Similar historic records of productivity
- Appropriate scale for comparison
- Similar in-basin biological components, based on analysis of empirical information

The question of how effective hatchery-origin salmon and steelhead are at reproducing in the natural environment will be answered in separate studies (i.e., DNA pedigree) that will eventually be added to this plan. Results from ongoing reproductive success studies (Wenatchee spring Chinook) as well as future studies (Upper Columbia steelhead) will be incorporated into the Plan on a continual basis. This plan recognizes that it is important to manage the numbers of hatchery fish spawning in the wild and the proportion of naturally produced fish in the broodstock. The further development of goals to achieve these mutual management actions will be developed by the HCP HC in the future and will be incorporated within the M&E plan at that time.

The second strategy is intended to increase harvest opportunities. This is accomplished primarily with releases of hatchery fish into the mainstem of the Columbia River or other terminal areas with the intent that the returning adults be harvested. Additionally non harvest fish should remain segregated, from the naturally spawning populations.

## **Conceptual Framework of the Monitoring and Evaluation Plan**

It is important that the M&E Plan has obtainable goals, and that the objectives and strategies are clearly linked to those goals. Figure 1 depicts the generalized conceptual model that this M&E Plan will follow. The hypotheses that will be tested under the objectives will be based on previous monitoring and evaluation information (i.e., key findings), and from the Biological Assessment and Management Plan (BAMP, 1998). Strategies, and the subsequent research, monitoring and evaluation, will clearly link to and provide feedback for the objectives.

The HCP specifies that the M&E Plan will be reevaluated, and revised if necessary every five years. It is important that information is collected through the evaluation plan that will enable the committee to make changes if needed. One of the challenges presented in developing the M&E Plan is to develop quantifiable metrics that support the goals of the hatchery programs. As such, it will be necessary to develop a conceptual framework for not only the M&E Plan, but for each objective to determine what types of information is required. A hierarchal approach to accomplishing the objectives would optimize data collection, analysis, and resources required to implement the Plan. Some of the data collection tasks will not need to be performed unless a data gap appears from other monitoring efforts.

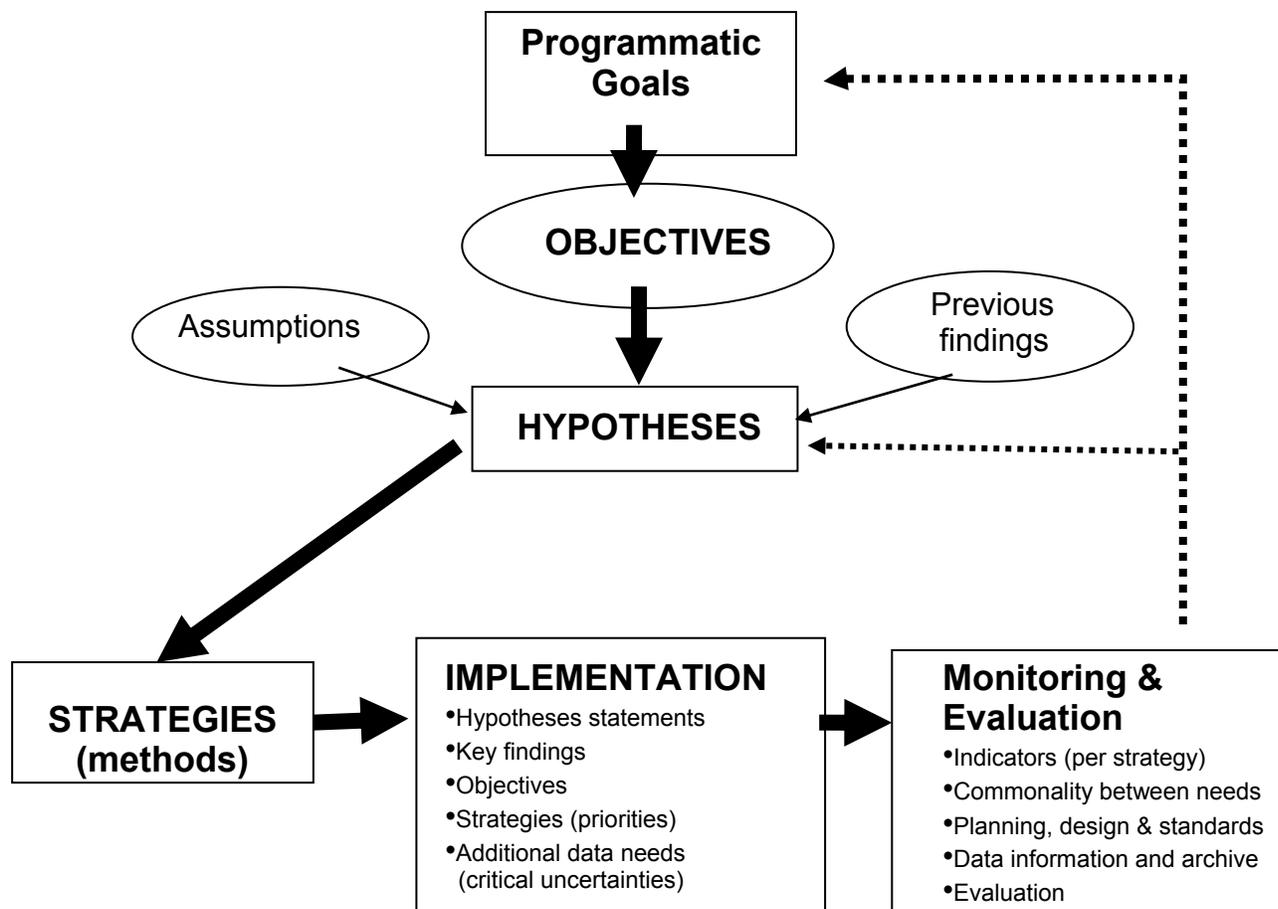


Figure 1. Conceptual model of how goals, objectives, strategies, and monitoring and research interrelate.

### Monitoring and Evaluation Plan Objectives

The objectives (and subsequent hypotheses) of the Plan are generated in part from existing evaluations plans, the BAMP, and support the Hatchery Program Goals as defined by the HCP HC.

**Objective 1:** Determine if supplementation programs have increased the number of naturally spawning and naturally produced adults of the target population relative to a non-supplemented population (i.e., reference stream) and the changes in the natural replacement rate (NRR) of the supplemented population is similar to that of the non-supplemented population.

Hypotheses:

- Ho:  $\Delta \text{Total spawners}_{\text{Supplemented population}} > \Delta \text{Total spawners}_{\text{Non-supplemented population}}$

- Ho:  $\Delta \text{NOR}^5_{\text{Supplemented population}} \geq \Delta \text{NOR}_{\text{Non-supplemented population}}$
- Ho:  $\Delta \text{NRR}_{\text{Supplemented population}} \geq \Delta \text{NRR}_{\text{Non-supplemented population}}$

**Objective 2:** Determine if the run timing, spawn timing, and spawning distribution of both the natural and hatchery components of the target population are similar.

Hypotheses:

- Ho: Migration timing<sub>Hatchery</sub> = Migration timing<sub>Naturally produced</sub>
- Ho: Spawn timing<sub>Hatchery</sub> = Spawn timing<sub>Naturally produced</sub>
- Ho: Redd distribution<sub>Hatchery</sub> = Redd distribution<sub>Naturally produced</sub>

**Objective 3:** Determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery program. Additionally, determine if hatchery programs have caused changes in phenotypic characteristics of natural populations.

Hypotheses:

- Ho: Allele frequency<sub>Donor</sub> = Allele frequency<sub>Naturally produced</sub> = Allele frequency<sub>Hatchery</sub>
- Ho: Genetic distance between subpopulations<sub>Year x</sub> = Genetic distance between subpopulations<sub>Year y</sub>
- Ho:  $\Delta$  Spawning Population =  $\Delta$  Effective Spawning Population
- Ho: Ho: Age at Maturity<sub>Hatchery</sub> = Age at Maturity<sub>Naturally produced</sub>
- Ho: Size at Maturity<sub>Hatchery</sub> = Size at Maturity<sub>Naturally produced</sub>

**Objective 4:** Determine if the hatchery adult-to-adult survival (i.e., hatchery replacement rate, HRR)<sup>6</sup> is greater than the natural adult-to-adult survival (i.e., natural replacement rate, NRR) and equal to or greater than the program specific HRR expected value (BAMP1998).

<sup>5</sup> Natural Origin Recruits.

<sup>6</sup> See Table 1 for HRR.

Hypotheses:

- Ho:  $HRR_{Year\ x} \geq NRR_{Year\ x}$
- Ho:  $HRR \geq$  Expected value per assumptions in BAMP

**Objective 5:** Determine if the stray rate of hatchery fish is below the acceptable levels to maintain genetic variation between stocks.

Hypotheses:

- Ho: Stray rate Hatchery fish  $< 5\%$  total brood return
- Ho: Stray hatchery fish  $< 5\%$  of spawning escapement of other independent populations<sup>7</sup>
- Ho: Stray rate Hatchery fish  $< 10\%$  total within independent populations<sup>8</sup>

**Objective 6:** Determine if hatchery fish were released at the programmed size and number.

Hypotheses:

- Ho: Hatchery fish Size = Programmed Size
- Ho: Hatchery fish Number = Programmed Number

**Objective 7:** Determine if the proportion of hatchery fish on the spawning grounds affects the freshwater productivity (i.e., number of smolts per redd) of supplemented streams when compared to non-supplemented streams.

Hypotheses:

- Ho:  $\Delta$  smolts/redd Supplemented population  $>$   $\Delta$  smolts/redd Non-supplemented population

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<sup>7</sup> This stray rate is suggested based on a literature review and recommendations by the ICTRT. It can be re-evaluated as more information on naturally-produced Upper Columbia salmonids becomes available. This will be evaluated on a species and program specific basis and decisions made by the HCP HC. It is important to understand the actual spawner composition of the population to determine the potential effect of straying.

<sup>8</sup> This stray rate is suggested based upon a literature review. It can be re-evaluated as more information on naturally produced Upper Columbia salmonids becomes available. The selected values will be evaluated on a species and program specific basis and decision.

**Objective 8: Determine if harvest opportunities have been provided using hatchery returning adults where appropriate.**

Hypotheses:

- Ho: Harvest rate  $\leq$  Maximum level to meet program goals

**Regional Objectives**

Two additional objectives will be included within the total framework of this plan because they are related to the goals of the programs funded by Douglas PUD and other hatchery programs throughout the region. These regional objectives will be implemented at various levels into all M&E plans in the upper Columbia Basin region (Douglas PUD, Chelan PUD, Grant PUD, USFWS, and CCT). These objectives may be more suitable for a specific hatchery or subbasin, the results of which could be transferred to other locations. As such, the HCP HC should ensure that these efforts are coordinated throughout the region so resources are used efficiently. Other objectives that are deemed more regional in nature, per HCP HC, could also be included in the section.

**Objective 9: Determine if the incidence of disease has increased in the natural and hatchery populations.**

Hypotheses:

- Ho: Disease supplemented pop.  $_{Year\ x} =$  Disease non-supplemented pop.  $_{Year\ x}$
- Ho: Naturally produced disease  $_{Year\ x} =$  Naturally produced disease  $_{Year\ y}$
- Ho: Hatchery disease  $_{Year\ x} =$  Hatchery disease  $_{Year\ y}$

**Objective 10: Determine if the release of hatchery fish impact non-target taxa of concern (NTTOC) within acceptable limits.**

Hypotheses:

- Ho: NTTOC abundance  $_{Year\ x} =$  NTTOC abundance  $_{Year\ y}$
- Ho: NTTOC distribution  $_{Year\ x} =$  NTTOC distribution  $_{Year\ y}$
- Ho: NTTOC size  $_{Year\ x} =$  NTTOC size  $_{Year\ y}$

## Detailed Objectives

Below, we detail the objectives, generate hypotheses, and describe the importance of each objective in accomplishing goals of the plan.

### **Objective 1: Determine if supplementation programs have increased the number of naturally spawning adults of the target population relative to a non-supplemented population**

At the core of a supplementation program is the objective of increasing the number of spawning adults (both naturally produced and hatchery fish) in order to affect a subsequent increase in the number of returning naturally produced fish or natural origin recruits (NOR). This is measured as the Natural Replacement Rate (NRR). All other objectives of the M&E Plan either directly support this objective or minimize impacts of the supplementation program to non-supplemented population. Specific hypotheses tested under this objective are:

Ho:  $\Delta \text{Total spawners}_{\text{Supplemented population}} > \Delta \text{Total spawners}_{\text{Non-supplemented population}}$

Ho:  $\Delta \text{NOR}_{\text{Supplemented population}} \geq \Delta \text{NOR}_{\text{Non-supplemented population}}$

Ho:  $\Delta \text{NRR}_{\text{Supplemented population}} > \Delta \text{NRR}_{\text{Non-supplemented population}}$

The supplementation program should in all cases increase the number of spawning adults (i.e., hatchery origin). If the supplementation program does not increase the number of spawners, the subsequent increase in natural produced fish cannot occur. Under this scenario, poor survival or high stray rates of the hatchery fish will prevent the objectives and goals of the hatchery program from being met.

When an increase in the spawning population has been observed, the subsequent increase in naturally produced returning adults is determined by comparing the natural replacement rate of the treatment population to a reference population (i.e., non-supplementation fish). If supplementation fish do have a similar reproductive success as naturally produced fish, then the trend of the NRR of both populations should not differ over time. Should divergence of the NRRs occur and the treatment population NRR does decline over time, the level or strategy of supplementation will be reevaluated by the HCP HC and appropriate adjustments to the program would be recommended.

If reference streams are not available for all hatchery programs or are not suitable due to 1) effects of other hatchery programs or 2) biotic or abiotic conditions are different from the treatment stream, an alternate experimental design needs to be considered to examine this important aspect of the Plan. Relative productivity of hatchery and naturally produced fish can be empirically measured using DNA pedigree approach study design. This approach may not be logistically feasible for all programs (i.e., too many fish to sample or poor trap efficiency). Alternatively, a temporal rather than a

spatial reference stream can be used. This approach would involve not releasing hatchery fish in a specific stream for at least one generation and determine if a change in the NNR is observed without hatchery fish present on the spawning grounds. Regardless of the approach or experimental design used, this component of the Plan is crucial and must be examined in order to determine if supplementation will result in an increased number of naturally produced adults.

Another important comparison, with or without reference streams, can be made by looking at different parental crosses (treatments) and what affects these crosses may have on NRR and HRR.

**Objective 2: Determine if the run timing, spawn timing, and spawning distribution of both the natural and hatchery components of the target population are similar.**

Supplementation is an integrated hatchery program. Hatchery and naturally produced fish are intended to spawn together and in similar locations. Run timing, spawn timing, and spawning distribution may be affected through the hatchery environment (i.e., domestication). If supplemented fish are not fully integrated into the naturally produced spawning population, the goals of supplementation may not be achieved. Hatchery adults that migrate at different times than naturally produced fish may be subject to differential survival. Hatchery adults that spawn at different times or locations than naturally produced fish would not be integrated into the naturally produced spawning population (i.e., segregated stock). Specific hypotheses tested under this objective are:

Ho: Migration timing<sub>Hatchery</sub> = Migration timing<sub>Naturally produced</sub>

Ho: Spawn timing<sub>Hatchery</sub> = Spawn timing<sub>Naturally produced</sub>

Ho: Redd distribution<sub>Hatchery</sub> = Redd distribution<sub>Naturally produced</sub>

Broodstock collection and spawning protocols should ensure appropriate run timing and spawn timing of the supplemented fish, respectively. Observed differences in these indicators would suggest that protocols be reevaluated. Differences in redd distributions will be evaluated based upon the location that carcasses were recovered during spawning ground surveys. However, freshets or fall floods may limit the utility of these data. If the accuracy of carcass recovery location is questionable (i.e., floods), a more precise, although more labor intensive, indicator for redd distribution would involve determining the origin of actively spawning fish.

**Objective 3: Determine if genetic diversity, population structure, and effective population size have changed in natural spawning populations as a result of the hatchery program. Additionally, determine if hatchery programs have caused changes in phenotypic characteristics of natural populations.**

The genetic component of the Plan specifically addresses the long-term fitness of supplemented populations. Fitness, or the ability of individuals to survive and pass on their genes to the next generation in a given environment, includes genetic, physiological, and behavioral components. Maintaining the long-term fitness of

supplemented populations, per the HCP Hatchery Program goals, requires a comprehensive evaluation of genetic and phenotypic characteristics. Evaluation of some phenotypic traits (i.e., run timing, spawn timing, spawning location and stray rates) is already addressed under other objectives.

Theoretically, a supplementation program should maintain genetic variation present in the original donor population, and as a program proceeds, genetic variability in hatchery- and naturally-produced fish in the supplemented population should be similar. Loss of within-population variation is a genetic risk of artificial production programs, and genetic divergence between hatchery and natural components of a supplemented population may lead to a loss of long-term fitness.

Differences in genetic variation among neighboring populations maintain the genetic population structure of drainages, basins, and regions. Mixing of populations in the hatchery (e.g., improper broodstock collection) or in the natural environment (e.g., excessive straying of hatchery fish) may lead to outbreeding depression and a loss of long-term fitness. Loss of between-population variation is also a genetic risk of artificial production programs, and can lead to long-term fitness loss at a scale larger than the population targeted for supplementation. Specific hypotheses tested under this objective for these issues are:

$H_0$ : Allele frequency<sub>Hatchery</sub> = Allele frequency<sub>Natural</sub> = Allele frequency<sub>Donor</sub>

$H_0$ : Genetic distance between subpopulations<sub>Year x</sub> = Genetic distance between subpopulations<sub>Year y</sub>

Supplementation should increase spawning population abundance as a result of high juvenile survival in the hatchery. Associated with an increase in returning spawner abundance should be an increase in effective population size (i.e., the number of actual breeders that produce successful offspring;  $N_e$ ). The relative proportion of hatchery-origin spawners that participate in natural spawning is an important factor in realizing improvements in  $N_e$ . A disproportionate number of hatchery spawners may cause inbreeding depression if their level of relatedness is relatively high due to expected high juvenile survival. A decrease in reproductive success and thus lowered  $N_e$  is an expected result of inbreeding. Lowered genetic variability is also expected. Achieving a larger  $N_e$  in a supplemented population should improve long-term fitness. The specific hypothesis tested under this objective for this issue is:

$H_0$ : Spawning Population Size Change = Effective Population Size Change

Results of domestication selection may be expressed through changes in life history patterns. Changes in phenotypic traits can result from inadvertent selection during artificial propagation and rearing. Persistence of selection effects will be influenced by the genetic basis of a trait. Age and size at maturity are two important phenotypic traits that have not been already addressed in the Plan. Should domestication selection be found, changes in broodstock collection protocols and hatchery operations would be required. Specific hypotheses tested under this objective for this issue are:

H<sub>0</sub>: Age at Maturity<sub>Hatchery</sub> = Age at Maturity<sub>Naturally produced</sub>

H<sub>0</sub>: Size at Maturity<sub>Hatchery</sub> = Size at Maturity<sub>Naturally produced</sub>

**Objective 4:** Determine if the hatchery adult-to-adult survival (i.e., hatchery replacement rate) is greater than the natural adult-to-adult survival (i.e., natural replacement rate) and equal to or greater than the program specific expected value (BAMP 1998).

The survival advantage from the hatchery (i.e., egg-to-smolt) must be sufficient to overcome the survival disadvantage after release (i.e., smolt-to-adult) in order to produce a greater number of returning adults than if broodstock were left to spawn naturally. If a hatchery program cannot produce a greater number of adults than naturally spawning fish the program should be modified or discontinued. Production levels were initially developed using historical run sizes and smolt-to-adult survival rates (BAMP 1998). Using the stock specific NRR and the values listed in the BAMP, comparisons to actual survival rates will be made to ensure the expected level of survival has been achieved. Specific hypotheses for this objective are:

H<sub>0</sub>:  $HRR_{year\ x} \geq NRR_{year\ x}$

H<sub>0</sub>:  $HRR \geq$  Expected value per assumptions in BAMP

Using five-year mean and determining trends in survival of specific programs would address interannual variability in survival. Although annual differences among programs would still be analyzed to detect within year differences, which could explain some the variability among programs. Specific recommendations to increase survival would be provided for programs in which the HRR do not exceed the NRR or the expected values.

Table 1. The expected smolt to adult (SAR) and hatchery replacement rates (HRR) for Wells Complex programs based on assumptions provided in BAMP (1998).

Program	SAR	HRR
Methow spring Chinook	0.0030	4.5
Chewuch spring Chinook	0.0030	4.5
Twisp spring Chinook	0.0030	4.5
Wells summer Chinook (yearlings)	0.0030	4.9
Wells summer Chinook (subyearlings)	0.0012	3.0
Wells steelhead	0.0100	19.5

**Objective 5:** Determine if the stray rate of hatchery fish is below the acceptable levels to maintain genetic variation between stocks

Maintaining locally adapted traits of fish populations requires that returning hatchery fish have a high rate of site fidelity to the target stream. Hatchery practices (e.g., acclimation, release methodology and location) are the main variables that affect stray rates. Regardless of the adult returns, if adult hatchery fish do not contribute to the donor population the program will not meet the basic condition of a supplementation program. Fish that do stray to other independent populations should not comprise greater than 5% of the spawning population. Likewise, fish that stray within an independent population should not comprise greater than 10% of the spawning population. Specific hypothesis for this objective is:

Ho: Stray rate  $\text{Hatchery fish} < 5\%$  total brood.

Ho: Stray rate  $\text{Hatchery fish} < 10\%$  within independent populations

Stray rates should be calculated using the estimated number of hatchery fish that spawned in a stream and CWTs were recovered. Recovery of CWT from hatchery traps or broodstock may include “wandering fish” and may not include actual fish that spawned. Special consideration will be given to fish recovered from non-target streams in which the sample rate was very low (i.e., sample rate  $< 10\%$ ). Expansion of strays from spawning ground surveys with low sample rates may overestimate the number of strays (i.e., random encounter).

The rate and trend in strays from hatchery programs will be used to provide recommendations that would lead to a reduction in strays. Depending on the severity, hatchery programs with fish straying out of basin will be given high priority, followed by strays among independent populations, and finally strays within an independent population.

**Objective 6: Determine if hatchery fish were released at the programmed size and number.**

The HCP outlines the number and size of fish that are to be released to meet NNI compensation levels. Although many factors can influence both the size and number of fish released, past experience with these stocks should assist in minimizing impacts to the program. Specific hypotheses for this objective are:

Ho: Hatchery fish  $\text{Size} = \text{Programmed Size}$

Ho: Hatchery fish  $\text{Number} = \text{Programmed Number}$

Understanding causes of not meeting programmed release size or goal is important for the continued success of the program. Systematic problems must be identified and managed properly to achieve the objective(s) and goal of the program. Annual and some stock specific issues may be addressed via changes in hatchery operations.

A review of broodstock collection protocols every five years should occur concurrently with an evaluation of the number of fish released from each hatchery. In addition, the

assumptions under pinning the HCP size at release goals should be evaluated and if necessary should be adjusted based upon the best scientifically based conclusions. In the absence of such studies, the HCP size at release goal should be the target for each hatchery program.

**Objective 7: Determine if the proportion of hatchery fish on the spawning grounds affect the freshwater productivity (i.e., number of smolts per redd) of supplemented streams when compared to non-supplemented streams.**

Out of basin effects (e.g., smolt passage and ocean productivity) have a strong influence on survival of smolts after they migrate from the tributaries. These effects introduce substantial variability into the adult-to-adult survival rates (NRR and HRR), which may mask in-basin effects (e.g., habitat quality, density related mortality, and differential reproductive success of hatchery and naturally produced fish). The objective of smolt monitoring programs in the Upper Columbia ESU is to determine the egg-to-smolt survival of target stocks. Smolt production models generated from the information obtained through these programs will provide a level of predictability with greater sensitivity to in-basin effects than spawner-recruitment models that take into account all effects.

A critical uncertainty with the theory of supplementation is the reproductive success of hatchery fish. Given the dependence of hatchery fish to assist in achieving program and recovery goals, monitoring smolt production with respect to the proportion of hatchery fish on the spawning grounds is critical in understanding subsequent adult-to-adult survival. While some factors that affect freshwater production require years or decades to detect change in productivity (e.g., habitat quality and quantity), other factors (e.g., spawner density and number of hatchery fish) can be adjusted annually in most tributaries.

The number of smolts per redd (i.e., smolt production estimate divided by total number of redds) will be used as an index of freshwater productivity. While compensatory mortality in salmonid populations cause survival rates to decrease as the population size increases, inferences regarding the reproductive success of hatchery fish may be possible by carefully examining and understanding this relationship. Inherent differences in productivity are expected among tributaries (spatial), changes in relative differences among years (temporal) would suggest differences in spawner productivity. Negative effects could then be minimized through actions take by the management agencies. Specific hypothesis for this objective is:

Ho:  $\Delta \text{ smolts/redd}_{\text{Supplemented pop.}} > \Delta \text{ smolts/redd}_{\text{Non-supplemented pop.}}$

Robust smolt production models derived from basin specific data are critical to this objective. In addition, accurate estimates of the proportion of hatchery fish on the spawning grounds will be needed. Inferences regarding the freshwater productivity cannot be made until both of these requirements are satisfied. Alternatively, DNA pedigree studies can be used to assess the relative freshwater production of hatchery and naturally produced fish within a tributary.

**Objective 8: Determine if harvest opportunities have been provided using hatchery returning adults where appropriate.**

In years when the expected returns of hatchery adults are above the level required to meet program goals (i.e., supplementation of spawning populations and/or broodstock requirements), surplus fish are available for harvest (i.e., target population). Harvest or removal of surplus hatchery fish from the spawning grounds would also assist in reducing genetic impacts to naturally produced populations (loss of genetic variation within and between populations). Specific hypotheses for this objective are:

Ho: Harvest rate  $\leq$  Maximum level to meet program goals

A robust creel program on any fishery would provide the precision needed to ensure program goals are met. In addition, creel surveys would be used to assess impacts to non-target stocks.

**Regional Objectives**

**Objective 9: Determine if the incidence of disease has increased in the natural and hatchery populations.**

The hatchery environment has the potential to amplify diseases that are typically found at low levels in the natural environment. Amplification could occur within the hatchery population (i.e., vertical and horizontal transmission) or indirectly from the hatchery effluent or commingling between infected and non-infected fish (i.e., horizontal transmission). Impacts to natural populations have not been extensively studied and must be considered if recovery of listed species is an objective. This is particularly important for supplementation type programs. Specifically, the causative agent of bacterial kidney disease (BKD), *Renibacterium salmoninarum* (Rs), could be monitored at selected acclimation ponds, both in the water and fish, in which the risk and potential for transmission from the hatchery is highest. While various diseases are common in hatchery populations, the most important and frequently occurring disease for Chinook is BKD. Specific hypotheses for this objective are:

Ho: Disease supplemented stream<sub>Year x</sub> = Disease non-supplemented stream<sub>Year x</sub>

Ho: Naturally produced disease<sub>Year x</sub> = Naturally produced disease<sub>Year y</sub>

Ho: Hatchery disease<sub>Year x</sub> = Hatchery disease<sub>Year y</sub>

Ho: Supplementation Stream Upstream<sub>Year x</sub> = Hatchery Effluent<sub>Year X</sub> =  
Supplementation Stream Downstream<sub>Year X</sub>

**Objective 10: Determine if the release of hatchery fish impact non-target taxa of concern (NTTOC) within acceptable limits.**

Supplementation of any stock or species will increase demand for resources and the potential of species interactions. The benefits gained from supplementation must be balanced with the ecological costs of the releasing hatchery fish into the ecosystem. Resource managers must be aware of and monitor potential impacts of supplementation related activities to non-target taxa. This is more important when supplementation activities involving more than one taxon are occurring simultaneously. For example, within the Methow Basin supplementation programs (i.e., spring Chinook, summer/fall Chinook, and steelhead), a spring Chinook harvest augmentation program and a coho reintroduction program release fish annually. At full program, the number of hatchery fish released into the Methow Basin would be approximately 2.4 million. Theoretical or realized benefits from supplementation activities may be at a cost to other taxa that are too great for the program to be deemed successful. In extreme cases, the costs of such activities may negate benefits of similar activities within the same subbasin. For example, predation by residualized hatchery steelhead may reduce the abundance of naturally produced spring Chinook fry that may subsequently result in a lower number of naturally produced adult spring Chinook.

In the Upper Columbia River ESU, a target species in one program is likely a non-target species in another program. The extent of spatial overlap is a decisive factor in determining the potential for ecological interactions and the associated risk. Consideration must be given to those fish that pose the greatest risk to NTT. Busack et al. (1997) categorized NTT into two classes. Strong interactor taxa (SIT) are those species that potentially could influence the success of the program through predation, competition, disease transmission or mutualistic relationships. Other NTT are classified as stewardship or utilization taxa (SUT), which are important ecologically or have high societal value.

Monitoring and evaluation plans concentrate efforts on the target species with little effort pertaining to the direct or indirect impacts to non-target species. In the Upper Columbia River ESU, a target species in one program is likely a non-target species in another program. There are also some stocks and species in which no artificial propagation programs have been initiated and as a result are non-target for all existing hatchery programs. While impacts to non-target taxa are often preconceived to be negative (e.g., competition, predation, behavioral, and pathogenic), positive impacts may also occur (e.g., nutrient enhancement and prey). Monitoring efforts will be concentrated on those interactions that pose the highest risk of limiting the success of the programs and deemed important for ecological reasons. Specific hypotheses for this objective are:

Ho: NTTOC abundance<sub>Year x</sub> = NTTOC abundance<sub>Year y</sub>

Ho: NTTOC distribution<sub>Year x</sub> = NTTOC distribution<sub>Year y</sub>

Ho: NTTOC size<sub>Year x</sub> = NTTOC size<sub>Year y</sub>

If changes in abundance, distribution, and size of NTTOC occur, other information will need to be considered before attributing the changes to the hatchery program.

## Strategies

The hypotheses and strategies that have been created in this plan were developed from the objectives of the hatchery program (Figure 1). As such, it is important to consider the goals and how they relate to the overall vision of the hatchery program, which is to meet NNI. The strategies outlined in this plan form the basis for how information will be collected and analyzed.

Commonalities among certain strategies and hypotheses will provide efficiencies in data collection and analysis. A detailed explanation of each strategy employed in the Plan is provided in the appendices to ensure repeatability in protocols, data collection, and analysis.

Other strategies and potentially hypotheses may be developed after information is collected and analyzed through the five-year review as specified in the HCP.

## Indicators

An important function of the Plan is to define the indicators and methods used to measure the effect of hatchery fish on naturally spawning populations, guide hatchery operations and subsequent M&E activities. The indicators in the M&E Plan describe the biological data of interest. The protocols describe the strategy or methodologies used to measure or calculate the indicator. These are found in the appendices. The M&E Plan will also enable the hatchery committee to assess the progress toward meeting the goals and objectives of the hatchery program. The plan will be used to assure that the proper information is collected, and can be used to reevaluate hatchery production levels in 2013. In order to do this, each objective must have a:

- **Indicator:** A description of the biological data of interest. Each indicator must have a standardized methodology or protocol to ensure accuracy and precision are consistent spatially and temporally.
- **Baseline condition:** Each indicator must have a measurement or range of measurements (spatially and temporally) against which future conditions will be compared.
- **Target:** A scientifically defensible value that when obtained would lead to meeting the objective(s).
- **Performance Gap:** The difference in the baseline condition of an indicator and the target.

In order to refine the monitoring and evaluation plan with an appropriate detail, indicators are distributed into three categories: 1) the primary indicators that will be used initially to quantitatively assess if the objectives of the programs are being achieved (i.e., was the target reached or exceeded); 2) secondary indicators that will be used to collect information annually and may be used to calculate the primary indicator or assess whether the objectives are being reached in conjunction with the primary indicators; and 3) tertiary indicators that will be used when secondary indicators fail to explain some critical uncertainties in reaching the target. Primary indicators may reflect performance on a longer (temporal) or larger (spatial) scale where secondary and tertiary indicators are often used to drive smaller scale adjustments and refinements in operations to improve the likelihood of meeting the target.

To the extent possible, the objectives of this Plan must be quantifiable. The HC specified the capability to assess if the goals are being achieved. To assess this, indicators were developed that have targets associated with them that enable the HC to determine if the hatchery program is meeting objectives (see Tables 3 and 4).

Due to the variability in survival, monitoring and reporting will be conducted annually but evaluation of most objectives will be conducted over a five-year period. Measurements will center on the established indicators and whether the targets are being met. Trends in the primary indicators rather than simply the five-year mean will be important in determining if objectives are being achieved. Primary and secondary indicators will be calculated when needed (as dictated by the information obtained). However, in the event that these indicators fall below the agreed to target values, tertiary indicators may be required to explain the differences observed (uncertainty) and also a possible course of action.

Realistic targets for the indicators need to be identified. Targets set too low may lead to a perceived short-term success, but may ultimately result in the long-term failure of the hatchery program. Conversely, targets that are too high may lead to an unnecessary use of resources and a low cost-benefit ratio. The proposed initial targets for indicators appear in Table 3.

Supplementation is a strategy used in most of the hatchery programs (except Wells summer/fall Chinook) and will be the focus of discussion. As mentioned earlier, supplementation by definition implies that naturally spawning hatchery fish possess a similar reproductive potential as naturally produced fish. This critical uncertainty associated with the theory of supplementation is a primary focus of the M&E Plan and logically a majority of the primary indicators in this plan are related to testing this uncertainty. Thus, the targets of many of the indicators are based on measurements taken from naturally produced populations, both temporally and spatially (i.e., Before-After-Control-Impact Design or BACI). Under this statistical design, inferences can be made regarding the effectiveness of supplementation in achieving the goals of the hatchery program. Without the use of a control or reference population, changes in the indicators over time could not be attributed to the supplementation fish. Due to potential multiple treatment effects, a direct comparison of the indicators may be invalid. Instead, a comparison in the change of the indicators over time may be more appropriate. For

example, if indicator A showed a 15% increase in the reference population in the first five years, a similar 15% increase in the treatment population would also be expected. Thus, any decrease in the change of the treatment population relative to the reference population could be attributed to the presence or abundance supplementation fish.

All primary and a proportion of the secondary indicators have a target. Those indicators that are influenced by out of basin causes (e.g., ocean productivity) or density dependent factors (e.g., egg-to-smolt survival) do not have a target identified in this Plan because the ability to change these indicators fall outside the control of the HC. All primary and secondary indicators will be calculated on an annual basis. Tertiary indicators would only be measured or calculated when required. Most primary indicators will be analyzed at the five-year scale. All secondary and tertiary indicators would be analyzed on an annual basis. The relationship between indicators and the methods used to calculate them is listed in Table 4. A list of appendices with detailed methodologies for each strategy is listed in Table 5.

Table 2. Relationship of hypotheses and strategies (methods) used in monitoring and evaluation plan.

<i>Methods</i>	<i>Relative increase in spawners of supplemented stream is greater than non-supplemented stream</i>	<i>NRR of supplemented stream is equal to that of non-supplemented stream</i>	<i>Run timing, spawn timing, and redd distribution of supplemented fish is equal to that of naturally produced fish</i>	<i>No loss of within or between genetic variability</i> <i>Size and age at maturity of hatchery fish is equal to that of naturally produced fish</i>	<i>Effective population size of supplemented stream increases in relation to spawning population</i>	<i>HHR is greater than NRR</i> <i>HRR is equal or greater than expected value</i>
Spawning ground survey	X	X	X	X	X	X
Creel surveys	X	X	X	X	X	X
Broodstock sampling	X	X	X	X	X	X
Hatchery juvenile sampling				X	X	X
Smolt trapping				X	X	X
Residual sampling				X	X	X
Precocity sampling				X	X	X
PIT tagging	X		X	X	X	X
CWT tagging	X	X	X	X	X	X
Radio tagging	X	X	X			
Genetic sampling	X			X	X	
Disease sampling						
Snorkel surveys		X	X			
Redd capping		X				
	<i>Stray rates of hatchery fish are less than 5%</i>	<i>Hatchery fish are released at programmed number and size</i>	<i>Hatchery fish have not increased the prevalence of disease in the supplemented stream or hatchery and naturally produced populations</i>	<i>Impacts to NTTOC (size, abundance, and distribution) are within acceptable levels</i>	<i>Supplemented streams have equal ratio of smolts/redd than non-supplemented streams</i>	<i>Harvest of hatchery fish is at or below the desired level to meet program goals</i>
Spawning ground surveys	X		X		X	X
Creel surveys	X					X
Broodstock sampling	X	X	X			X
Hatchery juvenile sampling		X	X			
Smolt trapping		X	X	X	X	
Residual sampling		X	X	X	X	
Precocity sampling		X	X	X	X	
PIT tagging		X		X	X	
CWT tagging	X	X	X			
Radio tagging	X					
Genetic sampling						
Disease sampling			X	X	X	
Snorkel surveys				X	X	
Redd capping				X	X	

Table 3. A list of primary indicators and targets used in the M&E Plan (S=supplementation; H=harvest augmentation). Data will be collected annually and analyzed when required (minimum every 5 years). The HC will reevaluate objectives and results and make recommendations. See Glossary for definition of indicators.

<sup>1</sup> Derived from plug numbers in BAMP

Objective #	Program	Indicator	Target	Preliminary results
1	S	Natural replacement rate	≥ Non-supplemented pop.	> 10 yrs
2/3	S	Run timing	= Naturally produced run timing	5 yrs
2/3	S	Spawn timing	= Naturally produced spawn timing	5 yrs
2/3	S	Redd distribution	= Naturally produced spawning distribution	5 yrs
3	S	Genetic variation	= Donor population	5 yrs
3	S	Genetic structure	= Baseline condition	5 yrs
3	S	Effective population size	Δ Spawning population size	5 yrs
3	S	Size and age at maturity	= Naturally produced fish	5 yrs
4	S/H	Hatchery replacement rate	≥ Expected value <sup>1</sup>	5 yrs
5	S/H	Stray rate	< 5% of adult returns	5 yrs
6	S/H	Number and size of fish	± 10% of production level	5 yrs
7	S	Smolts/redd	≥ Non-supplemented pop.	> 10 yrs
8	H	Harvest	≤ Maximum level	5 yrs
9	S/H	Disease	< Baseline values	> 5 yrs
10	S/H	NTTOC	Various (0-40%)	> 5 yrs

Table 4. Indicators that will be used in the monitoring and evaluation plan, indicator level (primary, secondary, and tertiary), and the strategies used to calculate the indicator.

Specific Indicators	Level	Strategies														
		Spawning ground surveys	Creel surveys	Broodstock collection	Hatchery spawning	Hatchery juvenile sampling	Smolt trapping	Residual sampling	Precocity sampling	PIT tagging	CWT tagging	Radio tagging	Genetic sampling	Disease sampling	Snorkel surveys	Redd capping
Natural replacement rate	1	X	X	X	X					X	X					
Spawning escapement	2	X						X	X	X	X	X	X	X	X	X
Spawning composition	2	X		X	X											
Sex ratio	2	X	X	X	X											
Recruits	2	X	X	X	X					X	X					
Number of redds	2	X														
Run timing	1			X						X		X				
Spawn Timing	1	X														
Redd Distribution	1	X														
Genetics variation/structure	1	X		X	X	X	X						X			
Effective pop. Size	1	X		X	X								X			
Broodstock composition	2			X	X											
Age at maturity	1	X	X	X	X											
Size at maturity	1	X	X	X	X											
Hatchery replacement rate	1	X	X	X	X	X		X	X	X	X			X		

Table 4. Continued.

Specific indicators	Level	Strategies														
		Spawning ground surveys	Creel surveys	Broodstock collection	Hatchery spawning	Hatchery juvenile sampling	Smolt trapping	Residual sampling	Precocity sampling	PIT tagging	CWT tagging	Radio tagging	Genetic sampling	Disease sampling	Snorkel surveys	Redd capping
Smolt-to-adult	2	X	X	X	X	X	X	X	X	X	X			X		
Number of broodstock	2			X	X											
Precocity rates	2					X	X		X							
Residualism rates	2						X	X	X	X	X					
Stray rate	1	X	X	X	X					X		X	X			
Days of acclimation	2					X				X	X					
Number juveniles released	1			X	X	X				X				X	X	
Fecundity	2			X	X											
Broodstock survival	2			X	X											
In-hatchery survival	2					X				X	X			X		
Size of juveniles released	1			X	X	X		X	X	X	X			X	X	
Growth rates	2				X	X										
Incubation timing	3				X	X										
Disease	1					X								X		
Density index	2					X										
Flow index	2					X										

Table 4. Continued.

Specific Indicators	Level	Strategies														
		Spawning ground surveys	Creel surveys	Broodstock collection	Hatchery spawning	Hatchery juvenile sampling	Smolt trapping	Residual sampling	Precocity sampling	PIT tagging	CWT tagging	Radio tagging	Genetic sampling	Disease sampling	Snorkel surveys	Redd capping
Pathogen values	2					X								X		
Hatchery effluent	2					X								X		
Smolts per redd	1	X					X								X	X
Egg-to-smolt	2	X					X								X	X
Egg-to-parr	3	X					X								X	X
Parr-to-smolt	3	X					X								X	X
Smolt-to-smolt	3	X					X			X						
Egg-to-fry	3	X														X
NTTOC (A,S,D)	1						X	X	X	X					X	
Harvest rate	1	X	X	X	X						X					

Table 5. List of appendices outlining the methodologies for calculating indicators used in the M & E plan.

Appendix	Strategy	Indicator(s)	
		Primary	Secondary and/or tertiary
A	Broodstock protocols	Not applicable	Broodstock number
B	Broodstock collection	Run timing	Broodstock number, male to female ratio, run composition, run timing, trap efficiency, extraction rate
C	Hatchery evaluations	Number and size of fish released	Age at maturity, length at maturity, spawn timing, fecundity, broodstock survival, juvenile hatchery survival, rearing density index, incidence of disease
D	Post-release survival and harvest	HHR Exploitation rate	SAR, harvest rates
E	Smolt trapping	Smolts per redd	Smolt production, egg-to-smolt survival, overwinter survival, size at emigration
F	Spawning ground surveys	NRR Spawn timing Redd Distribution	Spawning escapement, redd count, spawning composition, age structure, size at maturity, stray rates,
G	Relative abundance	NRR	Recruits
H	Genetics	Genetic variation Stock structure Effective pop. size	Broodstock composition, spawning composition, stray rates
I	NTTOC	NTTOC	Size, abundance, and distribution
J	Disease sampling	Naturally produced fish incidence of disease Hatchery fish incidence of disease	Flow index, hatchery effluent

## Implementation

A statement of work based on this document will be developed annually that outlines and prioritizes proposed M&E activities for the upcoming field season. This document will be reviewed by the HCP HC for approval before being finalized prior to the field season. The draft statement of work should be completed no later than July 1 and approved by the HCP HC no later than September 1, unless otherwise agreed to by the HCP HC.

The annual plan will serve two purposes; allow the HCP HC to determine whether the monitoring efforts are prioritized correctly and to determine costs of the program for budgeting.

### **Reporting**

A yearly comprehensive report, in the form of a technical memorandum, will be completed for HC review. A draft of the report will be ready for distribution by March 1 of the year following the monitoring efforts. A final report will be completed by the middle of May of the same year.

Within the annual report, all indicators that were measured for that particular year will be displayed. This will include topics such as smolt trapping information, run timing, spawn timing, redd distribution, stray rates, and all other information that is generated by additional analyses, like smolt-to-adult survival, NRR, HRR, etc. Tables 3 and 4 should be used as guidance on what indicators are reported, as well as the yearly statement of work that is agreed upon by the HC.

It will also be important to maintain cumulative information that is updated yearly as appendices to the technical memorandum.

### **Glossary**

The following is a definition of terms used throughout the M&E Plan:

Age at maturity: the age of fish at the time of spawning (hatchery or naturally)

Augmentation: a hatchery strategy where fish are released for the sole purpose of providing harvest opportunities.

Adult-to-Adult survival (Ratio): the number of parent broodstock relative to the number of returning adults.

Broodstock: adult salmon and steelhead collected for hatchery fish egg harvest and fertilization.

Donor population: the source population for supplementation programs before hatchery fish spawned naturally.

Effective population size (Ne): the number of reproducing individuals in an ideal population (i.e.,  $N_e = N$ ) that would lose genetic variation due to genetic drift or

inbreeding at the same rate as the number of reproducing adults in the real population under consideration (Hallerman 2003).

ESA: Endangered Species Act passed in 1973. The ESA-listed species refers to fish species added to the ESA list of endangered or threatened species and are covered by the ESA.

Expected value: a number of smolts or adults derived from survival rates agreed to in the Biological Assessment and Management Plan (BAMP 1998).

Extraction rate: the proportion of the spawning population collected for broodstock.

Genetic Diversity: all the genetic variation within a species of interest, including both within and between population components (Hallerman 2003).

Genetic variation: all the variation due to different alleles and genes in an individual, population, or species (Hallerman 2003).

Genetic stock structure: a type of assortative mating, in which the gene pool of a species is composed of a group of subpopulations, or stocks, that mate panmictically within themselves (Hallerman 2003).

HCP: Habitat Conservation Plan is a plan that enables an individual or organization to obtain a Section 10 Permit which outlines what will be done to “minimize and mitigate” the impact of the permitted take on a listed species.

HCP-HC Habitat Conservation Plan Hatchery Committee is the committee that directs actions under the hatchery program section of the HCP’s for Chelan and Douglas PUDs.

HRR: Hatchery Replacement Rate is the ratio of the number of returning hatchery adults relative to the number of adults taken as broodstock, both hatchery and naturally produced fish (i.e., adult-to-adult replacement rate).

Long-term fitness: Long-term fitness is the ability of a population to self-perpetuate over successive generation.

Naturally produced: progeny of fish that spawned in the natural environment, regardless of the origin of the parents.

NRR: Natural replacement rate is the ratio of the number of returning naturally produced adults relative to the number of adults that naturally spawned, both hatchery and naturally produced.

(NTTOC) Non-target taxa of concern: species, stocks, or components of a stock with high value (e.g., stewardship or utilization) that may suffer negative impacts as a result of a hatchery program.

Productivity: the capacity in which juvenile fish or adults can be produced.

Reference population: a population in which no directed artificial propagation is currently directed, although may have occurred in the past. Reference populations are used to monitor the natural variability in survival rates and out of basin impacts on survival.

Segregated: a type of hatchery program in which returning adults are spatially or temporally isolated from other populations.

(SAR) Smolt-to-adult survival rate: smolt-to-adult survival rate is a measure of the number of adults that return from a given smolt population.

Size-at-maturity: the length or weight of a fish at a point in time during the year in which spawning will occur.

Smolts per redd: the total number of smolts produced from a stream divided by the total number of redds from which they were produced.

Spawning Escapement: the number of adult fish that survive to spawn.

Stray rate: the rate at which fish spawn outside of natal rivers or the stream in which they were released.

Supplementation: a hatchery strategy where the main purpose is to increase the relative abundance of natural spawning fish without reducing the long-term fitness of the population.

Target population: a specific population in which management actions are directed (e.g., artificial propagation, harvest, or conservation).

## Literature

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## Appendices

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## APPENDIX A

### Broodstock Collection Protocols

The Broodstock Collection Protocol is intended to be implemented over a five-year period, consistent with the M & E plan. This protocol will be updated annually based on the yearly run size estimates by the HCP-HC. This appendix provides the methodology to determine where and when the actual broodstock would be collected and allows for in-season escapement estimates. Appendix B (broodstock collection) provides the broodstock composition and numbers and will be used annually to adjust the broodstock collection composition.

This protocol was developed for hatchery programs associated with the Wells Habitat Conservation Plan. Hatchery programs or facilities operated by other agencies or tribes are not addressed in the document. Trapping facilities associated with these programs have been operated in a similar manner without modifications for an adequate period of time to allow baseline data collection. Using the actual trap extraction efficiencies broodstock collection protocols could be developed under a large range of run escapement scenarios. This adult broodstock collection protocol is intended for implementation over a five-year period, consistent with the M & E plan. After which, the Hatchery Committee could modify the protocol where appropriate to ensure collection goals are met while maintaining consistency with the overall program goals. As trap modifications are completed in the Methow Basin (Twisp trap in 2005, Chewuch trap in 2006), trap efficiencies and extraction rates for the new facilities would be calculated.

The general approach in developing this protocol involved analyzing the last five years of run timing and trapping data. Using the trapping period outlined in the 2004 protocol, stock specific daily and cumulative passage dates (i.e. 25%, 50%, 75%) were calculated (Table 1). Weekly collection goals were calculated based on the proportion of the broodstock goal expected to migrate upstream of the collection location (Table 2). Weekly collection values would differ if the broodstock goal was not expected to be obtained for a given stock. Using pre-season escapement estimates and the five-year trap extraction efficiencies (Table 3), the probability of achieving the broodstock collection goal can be estimated assuming the following general guidelines:

- **Very high probability** - If the required trap extraction efficiency (broodstock goal/estimated escapement) is below the observed five-year minimum trap extraction efficiency.
- **High probability** - If the required trap extraction efficiency (broodstock goal/estimated escapement) is below the observed five-year average trap extraction efficiency.
- **Moderate probability** - If the required trap extraction efficiency (broodstock goal/estimated escapement) is below the observed five-year maximum trap extraction efficiency.

- **Low probability** - If the required trap extraction efficiency (broodstock goal/estimated escapement) is above the observed five-year maximum trap extraction efficiency.

As previously mentioned, in-season escapement estimates will also be used to estimate the probability of achieving broodstock collection goals. When the probability of achieving the broodstock goal is estimated to be moderate or low, modifications to the collection protocol, broodstock composition, or production level would occur on a stock specific basis (See flow charts).

Table 1. Cumulative passage dates of salmon and steelhead stocks based on the trapping period.

Stock	Cumulative passage dates during trapping period <sup>1</sup>			
	25%	50%	75%	100%
MEOK summer	12 Jul	22 Jul	08 Aug	14 Sept
MEOK steelhead	29 Aug	15 Sep	28 Sep	31 Oct
Met comp. spring	10 May	21 May	2 Jun	28 Jun
Twisp spring <sup>1</sup>	10 May	21 May	2 Jun	28 Jun

<sup>1</sup> To be determined at Twisp Weir following operation of new weir.

Table 2. Weekly collection quotas for spring Chinook, summer Chinook and steelhead.

Week	MetComp <sup>1</sup>	Twisp spring		Wells Summer		MEOK Steelhead	
		H	NP	H	NP	H	NP
07 May	24		12				
14 May	32		16				
21 May	42		21				
28 May	44		22				
04 Jun	24		12				
11 Jun	20		10				
18 Jun	16		8				
25 Jun	14		7				
02 Jul	10		5				
09 Jul	8		4				
16 Jul	4		2	232	26		
23 Jul	2		1	195	22		
30 Jul	1		1	195	22		
06 Aug				195	22	15	6
13 Aug				154	17	20	8
20 Aug				69	8	32	11
27 Aug				37	4	32	11
03 Sep						32	11
10 Sep						32	11
17 Sep						51	21
24 Sep						36	12
01 Oct						28	11
08 Oct						25	10
15 Oct						15	6
22 Oct						5	4
29 Oct						3	1
31 Oct							
07 Nov							
Total	242	0	121	1077	121	326	123

<sup>1</sup> A combination of hatchery and wild fish collected at Methow FH, Foghorn and Chewuch weir.

Table 3. Historical trap extraction rates and required escapement levels to achieve broodstock goal under average extraction rates.

Stock	Broodstock goal		Required escapement		Observed extraction rate <sup>1</sup>		
	W	H	W	H	Mean	Min	Max
Wells summer	121	1077					
MEOK steelhead	123	326					
Twisp spring	121	0					
Met comp	121	121					

### Methow River Basin Spring Chinook

The spring Chinook collection protocols will target specific populations of fish in the Methow Basin through broodstock collections in tributary locations and the remainder collected at Methow Hatchery. Fish will be collected from tributaries in an attempt to increase the number of natural origin fish incorporated into the broodstock and to improve local tributary survival attributes.

Consistent with the BAMP (1998), Biological Opinion for ESA Section 10 Permit 1196; Permit 1196; and the Biological Opinion for Section 7 Consultation on the Interim Operations for the Priest Rapids Hydroelectric Project (FERC N0. 2114), WDFW proposes to collect broodstock consistent with the production level of 550,000 smolts, development of local tributary attributes and in a manner that reduces the Carson lineage within the supplementation production.

The collection protocol outlines trapping at the Methow FH outfall and tributary trapping on the Methow, Chewuch, and Twisp rivers. Site specific broodstock collection numbers and origin may vary due to unknown tributary trap efficiency, origin composition and extent of the return; however, the maximum number of broodstock spawned will not exceed 363 fish (assuming a 50:50 sex ratio). If sex ratios are skewed toward the male component, additional females may be targeted for broodstock collection. Accurate sex determination is difficult early in the collection period; therefore, any shortfall in the number of females required for full production will likely be known toward the latter stages of broodstock collection. Additional collection at this time will require release of excess males in an effort to maintain a total spawning population no greater than 363 fish. All fish released will be returned to the tributary of collection. Three hundred and sixty-three fish (182 females) accounts for a 15% reduction expected due to ELISA culling, 5% pre-spawn mortality and maximum facility production of 550,000 smolts. The number of natural origin fish available for broodstocking purposes will be revised “in-season” and will be proportional, based on the initial forecast provided in Table 2 of the 2005 upper Columbia River Salmon and Steelhead Escapement and Broodstock Forecast.

Current estimates have 4,573 Chinook destined above Wells Dam, 33% or 1,528 are expected to be natural origin (TAC forecast has no effect on this estimate, since the estimate was derived from hatchery releases, hatchery SARs, and natural production (R/S estimates) and not based on the TAC estimate). “In-season” estimates of natural origin Chinook to individual tributaries will be estimated based on proportion natural origin returns to Twisp, Chewuch and upper Methow (Table 2 of the 2004 upper Columbia River Salmon and Steelhead Escapement and Broodstock Forecast) and 33% proportion of natural origin fish in the total return past Wells Dam. Natural origin fish inclusion into the broodstock will be a priority, with natural origin fish specifically being targeted; however, natural origin fish collections will not exceed 33% of the projected or in-season estimated return to any tributary spawning population.

## **Methow FH Spring Chinook**

### **Biological Assumptions**

Production level	550,000 yearling smolts
Propagation survival	90% fertilization to release
Maximum broodstock require	363
Natural origin/hatchery broodstock composition	90% / 10%
Pre-spawn survival	95%
Female to male ratio	1 to 1
Fecundity	4,200 eggs/female
ELISA cull rate	15%

### **Winthrop NFH spring Chinook program (BAMP):**

Production Objective	600,000 yearling smolts
Broodstock required	352 (BAMP)

### **Trapping Locations**

#### **Methow River**

##### **Foghorn Dam      1 May – 30 July**

Trap 7-days/week- Operated by WDFW personnel. Adipose present Chinook will be retained at this site. All fish collected at this site will be held at the Methow FH. Up to 121 fish (9.9% of the 1,228 fish projected to return to the mainstem Methow River) may be retained for broodstock purposes. One hundred percent (121 fish) may be natural origin (29.5% of the 410 natural origin fish projected to return to the mainstem Methow River). If other trap locations at the Methow FH, and Fulton Dam experience collection shortfalls, additional fish may be collected over and above the 121 fish to effectively minimize the shortfall.

In-season estimates of natural origin fish returning to the upper Methow River will be provided through initial estimates provided in Table 2 of the 2005 escapement and broodstock forecast and observed passage at Wells Dam. Overall broodstock collection

and number of natural origin fish retained will be modified, in-season, as necessary to maintain a collection protocol that removes no more than 33% of the return. Fish collected at from the Methow River will be held at the Methow FH.

## **Chewuch River**

### **Fulton Dam Trap                      1 May – 30 July**

Trap 7-days/week- Operated by WDFW personnel. The WDFW will also attempt to seine broodstock once a week at locations determined to be effective and where fish can be safely transported to Methow Hatchery. Angling will be used as a last resort if all other methods do not provide adequate broodstock.

Adipose present spring Chinook will be retained from the Chewuch River. Up to 121 fish (7.9% of the 1,524 fish projected to return to the Chewuch River) may be retained for broodstock purposes, of which, up to 121 natural origin fish (17% of the 680 natural origin fish projected to return to the Chewuch River) may be retained for broodstock purposes. If other trap locations at the Methow FH and Foghorn Dam experience collection shortfalls, additional fish may be collected over and above the 121 fish to effectively minimize the shortfall.

In-season estimates of run size and origin of spring Chinook to the Chewuch River will be made, similar to that described for the Methow River. The collection protocols will be modified as necessary to maintain an extraction of no more than 33% of the projected return. Fish collected at the Chewuch trap will be held at the Methow FH.

The trapping efficiency of the Fulton facility averaged 30% between 1992 and 1994, ranging from a low of 9.2 in 1992 to a high of 58.2% in 1993. Significant river flows in 1996 and 1997 disrupted the configuration of the dam, likely reducing the potential trapping efficiencies from those observed between 1992 and 1994. Maintenance work completed in the spring of 2001 was expected to return trapping efficiencies to approximately 60%. Unfortunately, the 2001 trapping efficiencies were approximately 3.5%, significantly less than anticipated. During the late winter/early spring of 2002, minor construction was again performed at the Fulton Dam site, seeking improvements to trapping efficiencies. Trapping efficiencies during the 2002 broodstock collection fell to just 0.3%, a clear indication that the modifications completed in 2001 and 2002 failed to return the trap to pre-1994 trapping efficiencies.

Current snow-pack in the Methow River Basin is low and reminiscent of conditions in 2001. Based on current snow-pack conditions, WDFW expects flow in the Chewuch basin to be similar to 2001 and therefore, expects trap extraction rates to be similar to 2001 (approximately 3.5%). WDFW anticipates the Fulton Dam trap to provide approximately 24 natural origin and 29 hatchery origin fish. Based on the anticipated collection at Fulton Dam, collections at the Methow FH will be required to address the shortfall in adult collections at Fulton Dam.

## **Twisp River**

### **Twisp Weir 1 May – 30 July**

Trap 7-days/week- Operated by WDFW personnel. A floating weir on the Twisp River provides for collection of Twisp stock spring Chinook. Historically, trap efficiency at this facility has been low, averaging 16% (range 10.4% – 23.7%) between 1992 and 1994. During the 2001 trapping season, the trap efficiency was just 6% and fell to just 0.2% in 2002. A modified V-trap installed along the weir sill, adjacent to the trap entrance, increased the trap efficiency in 2003 to 42%; however the 2004 trap efficiency was estimated at 19.2%. The installation of the permanent V-trap will allow trapping over a greater range of stream flows and should provide greater extraction potential than observed in 2004. To guard against extracting more than 33% of the natural origin return, WDFW assumes the weir to have 100% extraction potential. Based on an assumed 100% extraction potential, one of three natural origin fish captured will be retained for broodstock, effectively limiting the extraction to 33%.

Based on an escapement estimate of 1,167 fish, including 445 natural origin and 722 hatchery origin fish (2005 escapement and broodstock forecast), up to 121 fish (10.4% of the projected return to the Twisp River.) may be retained for broodstock purposes, of which a collection goal of 121 fish (27% of the projected natural origin return to the Twisp River) may be natural origin. In-season estimates of run size and origin of spring Chinook to the Twisp River will be made, similar to that described for the Methow River. The collection protocols will be modified as necessary to maintain an extraction of no more than 33% of the projected return. Twisp origin spring Chinook trapped at this site will be held at the Methow FH.

The Twisp weir poses several operating constraints, including stranding of steelhead and spring Chinook on the weir pickets during upstream and downstream movement. The new weir design is capable of submerging the pickets to allow stranded fish to swim off the pickets. The weir will be manned 24-hours/day to facilitate operation to minimize impact to steelhead kelts and spring Chinook fallback. If the new weir design and operation cannot adequately address kelt migration or spring Chinook fallback, trapping will cease and the weir removed (pending appropriate flow conditions).

## **Methow FH**

### **Methow FH Outfall Trap 01 May – 30 July**

Collection at the Methow Fish Hatchery outfall will be variable and dependent upon success of tributary collections. Outfall trapping will be used in conjunction with tributary traps, seining and angling to achieve a production level of 550,000 ESA-listed upper Columbia River spring Chinook smolts.

## **Winthrop NFH**

Trapping is expected to occur at the Winthrop NFH and will be consistent with collection protocols provided by the USFWS. Additional adult collection at Winthrop NHF may occur, if required to meet broodstock collection shortfalls at the Methow FH, Foghorn Dam and Fulton Dam.

## **Wells Dam**

No spring Chinook trapping at Wells Dam will occur unless the total annual adult return to Wells Dam is predicted to be 668 or less as identified in Section 10 Permit 1196.

### **Columbia River Mainstem below Wells Dam**

#### **Wells Hatchery Summer Chinook**

##### **Biological Assumptions**

Wells program	320,000 yearling smolts (182 adults) 484,000 subyearlings (266 adults)
Lake Chelan program	100,000 green eggs (44 adults)
Rocky Reach program	200,000 yearling smolts (114 adults) 628,000 subyearlings (345 adults) 450,000 accel. subyearling (247 adults)
Broodstock required	1,198
Broodstock composition	10% natural origin from west ladder
Pre-spawn survival	90%
Female to male ratio	1 to 1
Fecundity	5,000 eggs per female
Propagation survival	81% unfertilized egg to 0+ release 78% unfertilized egg to 1+ release

##### **Trapping Assumptions**

Trapping period	14 July – 28 August (hatchery origin) 01 July – 14 September (natural origin)
# Days/week	3
# Hours/day	16 (Monday-Wednesday)
Broodstock composition	10% natural origin from west ladder
Broodstock number	Not to exceed 33% of the population

The goal of the Wells/Turtle Rock summer Chinook program is to provide harvest augmentation. Those fish that are not harvested have the potential and have been documented to spawn in tributaries where supplementation is currently ongoing. Until a terminal fishery is developed or methods to reduce the number of Wells/Turtle Rock fish that spawn in tributaries are found, infusing natural origin genes into the broodstock will minimize the risk of inbreeding depression, genetic drift, and domestication selection.

This is consistent with the objectives of the Harvest and Genetic Reserve program as outlined by NOAA Fisheries (Rob Jones, NOAA Fisheries, personal communication).

Collect 1,198 run-at-large summer Chinook from the volunteer ladder trap at Wells Fish Hatchery outfall (1,077 hatchery fish) and west ladder (121 natural origin fish). The 3-year old component will be limited to 10% of the broodstock collection to minimize the potential of reduced production as a result of a strong 3-year-old age class, as was the case in 2001. In the event excess fish are collected, they will be returned to the Columbia River below Wells Dam.

## **Methow / Okanogan River Basins**

### **Wells Hatchery Steelhead**

#### **Biological Assumptions**

Wells HCP (Methow/Okanogan)	349,000 yearling smolts (178 adults)
Grant PUD BiOp (Methow/Okanogan)	100,000 yearling smolts (52 adults)
WNFH transfer (Methow River)	100,000 smolts (55 adults)
Ringold transfer (Columbia River)	180,000 smolts (88 adults)
Grant PUD Survival Studies	150,000 yearling smolts (76 adults)
Broodstock required	449 Adults
Natural origin/hatchery broodstock composition	
Wells Production <sup>1/</sup>	33% / 67%
Survival Studies	0% / 100%
Pre-spawn survival	97%
Female to male ratio	1 to 1
Fecundity	5,400 eggs per female
Propagation survival	87% fertilization to eyed egg 86% eyed egg to yearling release 75% fertilization to yearling release

<sup>1/</sup>- Includes Wells HCP, Grant PUD BiOp, Winthrop NFH and Ringold production.

#### **Trapping Assumptions**

Trapping period	01 July – 29 October
# Days/week	3
# Hours/day	16
Broodstock number/composition	
Wells Production	373 - (33% natural / 67% hatchery)
Survival Studies	76 - (0% natural / 100% hatchery)
Total Broodstock	449 – (27% natural / 735 hatchery)

Trapping efforts will selectively retain 449- steelhead at Wells Dam (East and West ladder collection), to attain a 33% natural origin component within the “Wells production” broodstock (123 natural origin steelhead) and 100% hatchery origin within the survival

study production components. Overall collection will not exceed 33% of the expected return (hatchery or natural origin). Increasing the natural origin component within the broodstock to near 33% will provide opportunities to increase the HxW and WxW parental cross proportion from what has occurred previously under random run-at-large collections. Increasing the number of HxW and WxW parental crosses within the Wells Program is consistent with management objectives described in WDFW's ESA Section 10 Permit 1395 Application and consistent with other upper Columbia River summer steelhead supplementation efforts. Collection within the "Wells Production" component will also be selective for adipose present hatchery origin steelhead (HxW parental crosses), consistent with production objectives. The east and west ladder traps at Wells Dam will be operated concurrently, three days per week, up to 16 hours per day. Trapping on the east ladder will be commensurate with summer Chinook brood stocking efforts through 14 September and will continue through 29 October, concurrent with west ladder collections. All steelhead excluded from the broodstock will be directly passed upstream at the trapping site or captured, examined and released upstream from the trap site.

Adult return composition including number, origin, age structure, and sex ratio will be assessed in-season at Priest Rapids and Wells dams. Broodstock collection adjustments will be made consistent with the estimated return of natural origin steelhead to Wells Dam and production objectives

## APPENDIX B

### Broodstock Collection

Task 1: Collect the required number of broodstock that represent the demographics of the donor population with minimal injuries and stress to target and non-target fish. (*Broodstock number, male to female ratio, run composition, run timing, trap efficiency, extraction rate*)

Task 1-1. Develop broodstock trapping protocol based on program goal, estimated escapement, number and age classes of returning wild fish, minimum proportion of wild fish required in the broodstock, and demographics of the donor population to achieve production levels (Table 1).

- a. Ensure broodstock collection protocols are consistent with Section 10 Permits.
- b. Reexamine and modify assumptions of the broodstock protocol to reflect recent data (e.g., male to female ratio, fecundity, prespawn survival, egg to smolt survival).

Table 1. Annual broodstock collection worksheet for Wells Complex programs.

Stock	Estimated escapement		Broodstock goal		Required extraction rate		Observed extraction rate			Estimated broodstock	
	W	H	W	H	W	H	Avg	Min	Max	W	H
Wells summer			121	1,077							
Wells steelhead			76	153							
Met comp. spring			242	0							
Twisp spring			121	0							

Task 1-2. Monitor operation of adult traps in the Twisp River, Chewuch River, Fulton Dam, Methow Hatchery, Wells Hatchery and Wells Dam. Ensure compliance with established broodstock collection protocols and Section 10 permits for each station.

- a. Record date, start time, and stop time of trapping operations.

Task 1-3. Conduct in-season run forecasts and modify broodstock protocols accordingly (Table 2).

- a. Monitor run timing at Columbia River dams and make comparisons using previous years data.

- b. Determine run timing and size using PIT tag detections at Columbia River Dams.
- c. Make recommendations to broodstock collection protocols to increase probability of collecting broodstock goal.

Table 2. In-season Chinook and steelhead escapement worksheet.

Stock	Pre-season run estimate	Cumulative passage dates during trapping period <sup>1</sup>				In-season run estimate
		25%	50%	75%	100%	
MEOK summer		12 Jul	22 Jul	08 Aug	14 Sept	
MEOK steelhead		29 Aug	15 Sep	28 Sep	31 Oct	
Met comp. springer		10 May	21 May	2 Jun	28 Jun	
Twisp spring <sup>1</sup>		10 May	21 May	2 Jun	28 Jun	

<sup>1</sup> To be determined at Twisp Weir following operation of new weir.

Task 1-4. Monitor timing, duration, composition, and magnitude of the salmon and steelhead runs at adult collection sites.

- a. Maintain daily records of trap operation and maintenance, number and condition of fish trapped, and river stage.
- b. Record species, origin, and sex of all fish collected for broodstock.
- c. Record species, origin, and sex of all fish not collected for broodstock (i.e., passed upstream).
- d. Collect biological information on trap-related mortalities. Determine the cause of mortality if possible.

Task 1-5. Evaluate the efficacy of the broodstock protocol in achieving collection goals.

- a. Summarize results and review assumptions, escapement estimates, extraction rates, and broodstock goals.
- b. Calculate trapping efficiency (TE).

$$TE = \text{Number of fish trapped} / \text{Estimated spawning escapement}$$

- c. Calculate extraction rate (ER).

ER = Number of fish collected/Estimated spawning escapement

- d. Ensure broodstock collections follow weekly collections quotas.
- e. Calculate trap operation effectiveness (TOE).

$$\text{TOE} = \frac{\text{Number of hours trap operated}}{\text{Maximum number of hours trap could operate per protocol}}$$

- f. Calculate estimated maximum trap efficiency (i.e., TOE = 1).

$$\text{Estimated Max. TE} = \frac{\text{Number of fish trapped/TOE}}{\text{Estimated spawning escapement}}$$

- g. Provide recommendations on means to improve adult trapping and refinements to broodstock collection protocols for each stock.

## APPENDIX C

### Hatchery Evaluation

Task 2: Conduct spawning operations and collect biological data from broodstock (*Age at maturity, length at maturity, spawn timing, fecundity*)

Task 2-1. Collect biological data from all broodstock during spawning including mortality (i.e., date, origin, scales, fork length and POH, DNA, CWT, and PIT tags).

- a. All females are sampled for disease (i.e., kidney, spleen, ovarian fluid).

Task 2-2. Ensure proper mating schemes are followed that is consistent with the program objectives and per broodstock protocol.

- a. One female per incubation tray unless physically separated within tray.
- b. All egg lots will be run through an egg counter to determine fecundity

Task 3: Monitor growth and health during rearing and determine life stage survival rates for each stock at each of the Wells Hatchery Complex facilities. (*Broodstock survival, juvenile hatchery survival, rearing density index, size at release, incidence of disease*)

Task 3-1. Monitor growth of juvenile fish during rearing and prior to release.

- a. Collect end of month length and weight data.
  1. Whenever possible, crowd fish and dip net into 500-1000 fish into a net pen.
  2. Measure and record fork length on 100 fish to the nearest millimeter.
  3. Dip net approximately 200 fish into a bucket and record weight. Calculate grams/fish by dividing total weight by number.
  4. Repeat weight sample three times and calculate average weight of fish.
- b. Collect length and weight data prior to release.
  1. Whenever possible, crowd fish and dip net into 500-1000 fish into a net pen.
  2. Measure and record fork length (nearest millimeter) and weight (nearest 0.1 g) on 200 fish.
- c. Analyze data to ensure fish were released at the proper fork length, condition factor, and size distribution (i.e., CV of fork length).

Task 3-2. Calculate end of month density indices for juvenile fish.

- a. Use end of month length and weight data and the total rearing volume to calculate rearing density index (DI).

$$DI = \frac{\text{Population size} * \text{mean weight (lbs)}}{\text{total rearing volume (ft}^3\text{)}} \\ \text{Mean fork length (inches)}$$

Task 3-3. Monitor fish health, specifically as related to cultural practices that can be adapted to prevent fish health problems.

- a. Standard hatchery fish health monitoring will be conducted monthly by fish health specialist, with intensified efforts to monitor presence of specific pathogens that are known to occur in the donor populations. Significant fish mortality of unknown cause(s) will be sampled for histopathological study.
- b. Collect biological information on all adult broodstock mortalities. Determine the cause of mortality whenever possible.
- c. The incidence of viral pathogens in salmon and steelhead broodstock will be determined by sampling fish at spawning in accordance with the Salmonid Disease Control Policy of the Fisheries Co-Managers of Washington State. Stocks of particular concern may be sampled at the 100% level and may require segregation of eggs/progeny in early incubation or rearing.
- d. Determine antigen levels of *Renibacterium salmoninarum* (Rs, causative agent of bacterial kidney disease) in Chinook salmon broodstock by sampling fish at spawning using the enzyme-linked immunosorbent assay (ELISA).
- e. If required, provide recommendations to hatchery staff on means to segregate eggs/progeny based on levels of Rs antigen, protecting “low/negative” progeny from the potential horizontal transmission of Rs bacteria from “high” progeny.
- f. Autopsy-based condition assessments (OSI) or other physiological assessments deemed valuable would be used to assess hatchery-reared salmon smolts at release. If needed, perform assessments at other key times during hatchery rearing.
- g. Provide recommendations on fish cultural practices at Wells Complex hatcheries and satellite stations on monthly basis. Summarize results for presentation in annual report or technical memorandum if applicable.

Task 3-4. Calculate various life stage survival rates for broodstock and juvenile fish (Table 3).

- a. Use the stock inventory at time of tagging to recalculate population sizes and life stage survival rates.

Task 3-5. Summarize broodstock collection, spawning, rearing survival, and release information in an annual technical memorandum.

- a. Where applicable, provide recommendations to increase survival rates of life stages that were lower than the survival standard or recommend studies to investigate causes of poor survival.

Task 4: Determine if broodstock collections and hatchery survival was adequate to achieve smolts releases at the programmed production levels (*Number of fish released, size at release*).

Task 4-1. Calculate the number of fish released from Wells FH Complex facilities.

- a. If release numbers are within  $\pm 10\%$  of the production levels no further action required (Table 4).
- b. If release numbers are not within  $\pm 10\%$  of the production levels determine what factors contributed to the shortage/overage.

Task 4-2. Calculate the size of fish released from Wells FH Complex facilities.

- a. If size at release numbers is within  $\pm 10\%$  of the target no further action required (Table 5).
- b. If size at release is not within  $\pm 10\%$  of the target determine what factors contributed to the shortage/overage.

Table 3. Hatchery life stage survival rate standards, 5 year mean (SD), and survival achieved for current brood year.

Life stage	Survival standard	Wells steelhead		Wells summer Chinook		Methow spring Chinook		Chewuch spring Chinook		Twisp spring Chinook	
		Mean (95%)	Survival achieved	Mean (95%)	Survival achieved	Mean (95%)	Survival achieved	Mean (95%)	Survival achieved	Mean (95%)	Survival achieved
Collection-to-spawning	<i>90.0</i> <i>Female</i>										
Collection-to-spawning	<i>85.0</i> <i>Male</i>										
Unfertilized egg-to-eyed	92.0										
Eyed egg-to-ponding	98.0										
30 d after ponding	97.0										
100 d after ponding	93.0										
Ponding-to-release	90.0										
Transport-to-release	95.0										
Unfertilized egg-to-release	<i>81.0</i>										

*Italics are revised survival standards*

Table 4. Summary of the number of fish released from Wells FH Complex.

Stock	Target	5-year min.	5-year max.	5-year mean	Number released
Wells yearling summer Chinook	320,000	185,200	45,770	321,060	
Wells subyearling summer Chinook	484,000	370,617	498,500	416,369	
Methow spring Chinook	183,024	66,454	218,499	155,570	
Chewuch spring Chinook	183,023	0	261,284	143,092	
Twisp spring Chinook	183,024	15,470	75,704	53,668	
Wells steelhead	348,858	390,965	694,765	539,768	

Table 5. Size at release targets for fish released from Wells FH Complex.

Stock	Target		Actual	
	Fork length (CV)	Weight	Fork length (CV)	Weight
Wells yearling summer	176 (9.0)	45.4		
Wells subyearling summer	140 (9.0)	22.7		
Methow spring Chinook	154 (9.0)	30.2		
Chewuch spring Chinook	154 (9.0)	30.2		
Twisp spring Chinook	154 (9.0)	30.2		
Wells steelhead	198 (9.0)	75.6		

## APPENDIX D

### Post-release Survival and Harvest

Task 5: Determine whether the survival from release-to-adult of fish from the Wells Hatchery Complex is sufficient to achieve the program goal. (*Smolt to adult survival, hatchery replacement rate, exploitation rate, harvest rate*)

Task 5-1. Mark (i.e., adipose fin clip) and tag (i.e., coded-wire tag or elastomer) each stock subjected to ocean fisheries or mainstem Columbia River commercial, sport, or tribal fisheries with sufficient coded-wire tags (CWT) to estimate harvest contribution.

- a. Provide summary of marked and unmarked smolt releases from the Wells Hatchery Complex.
- b. Determine the statistical requirements to provide reliable estimates of escapement and harvest contribution. Determine the number of coded-wire tags and other marks needed in relation to the number of recoveries expected.

Task 5-2. Summarize information at time of release that may influence post-release survival and performance.

- a. Calculate mean fork length (FL) at release, FL coefficient of variation (CV), and condition factor (K) for all stocks released from Wells Complex.
- b. Summarize fish health information (e.g., reports, OSI, precocity rates).
- c. Calculate the number of days rearing on well and river water. Calculate the number of days reared at acclimation sites.

Task 5-3. When applicable, estimate travel time and smolt-to-smolt survival rates of hatchery and wild fish using PIT tag recaptures.

- a. Compare smolt-to-smolt survival, emigration rate, and duration with rearing water source, duration of acclimation, and size at emigration.

Task 5-4. Estimate the harvest contribution for each stock released from the Wells Hatchery Complex.

- a. Compile CWT recovery data from Wells Hatchery releases for inclusion in reports.
- b. Recover heads from marked (adipose fin clipped) returns to Wells Fish Hatchery Facilities during routine spawning operations. Transfer heads to WDFW tag recovery lab in Olympia, Washington.

- c. Conduct statistically valid creel surveys during sport fisheries in the mid-Columbia River to estimate harvest and adult returns of hatchery stocks from Wells Complex releases.
- d. For each brood year and run year, calculate exploitation rate and harvest rates in commercial, tribal, and sport fisheries.

Task 5-5. Estimate the contribution to spawning escapement for each stock released from the Wells Hatchery Complex.

- a. Provide a summary of the number of fish contributing to spawning escapement, broodstock, commercial, sport, and tribal fisheries.
- b. Calculate stray rates for all stocks released from Wells FH Complex facilities and compare with rearing water source and duration.

Task 5-6. Determine the smolt to adult survival rates (SAR) for each stock.

- a. Determine the total estimated the number of hatchery adults recovered in all fisheries, hatcheries, and spawning ground surveys using CWT data.
- b. To calculate SAR for salmon, use the estimated number of smolts released divided by the estimated number of hatchery adults.
- c. To calculate SAR for steelhead, use the estimated number of smolts released divided by the estimated number of adults migrating pass Priest Rapids Dam
- d. Examine the influence of size, fish health, rearing location, and acclimation on survival and straying.
- e. Compare SARs using CWT recoveries and PIT tag recaptures of adults, when applicable.

Task 5-7. Determine the expected and actual hatchery replacement rate for each brood year (Table 6).

- a. Calculate HRR by dividing the number of broodstock collected by the estimated number of returning adults.
- b. For stocks that fail to meet or exceed the expected hatchery replacement rate determine the life history stage that limited survival.

Table 6. The expected and actual smolt to adult (SAR) and hatchery replacement rates (HRR) or adult to adult survival rates for Wells FH Complex programs.

Program	Number of broodstock	Smolts released	SAR	Adult equivalents	# smolts/ adult	HRR
Wells yearling summer Chinook						
Expected	182	320,000	0.003	960	333	5.3
Actual						
Wells subyearling summer Chinook						
Expected	266	484,000	0.0012	581	833	2.2
Actual						
Twisp spring Chinook						
Expected	121	183,024	0.003	549	333	4.5
Actual						
Methow spring Chinook						
Expected	121	183,024	0.003	549	333	4.5
Actual						
Chewuch spring Chinook						
Expected	121	183,023	0.003	549	333	4.5
Actual						
Wells steelhead						
Expected	229	348,858	0.010	3,489	100	15.2
Actual						

## Appendix E

### Smolt Production

Task 6: Calculate freshwater production estimates of anadromous salmonids from selected river systems (*Egg-to-smolt survival, smolts per redd, emigration timing, size at emigration*)

Task 6-1. Install and operate a rotary smolt trap(s) in a location downstream from the majority of the spawning areas and that allows operation throughout the emigration period.

Task 6-1-1. Identify potential trap positions based on variation in flows. Large variations in discharge may require alternate trap locations.

Task 6-1-2. Operate trap continuously throughout the emigration period.

- a. During the first year of operation at a new location determine the extent of emigration during daylight hours. Significant emigration during the daylight hours will require trap efficiency trials to be conducted during both the day and night.
- b. Trap should be checked at a minimum every morning of operation. Remove fish from the live box and place in an anesthetic solution of MS-222. Identify fish to species and enumerate.
- c. Determine sample size requirements of target and nontarget species for biological sampling.
- d. All fish should be allowed to fully recover in fresh water prior to being released in an area of calm water downstream from the smolt trap.
- e. Pressure wash trap and clean debris from cone and live box prior to leaving.

Task 6-2. Collect daily environmental and biological data.

- a. Record the time the trap was checked, water temperature, river discharge, and trap position, if applicable.
- b. Identify species and enumerate all fish captured to include life stage for non-anadromous species (e.g., fry, juvenile, and adult) or degree of smoltification for anadromous species (i.e., parr, transitional, or smolt). Parr have distinct parr marks, transitional fish have parr marks that are fading and not distinct, and smolts do not have parr marks and exhibit a silvery appearance, often with a black band on the posterior edge of the caudal fin.

- c. Examine all fish for external marks as a result of trap efficiency trials and record them as recaptures.
- d. Record fork length and weight measurements for all fish, or per designated sample size. All fish to be used in mark/recapture efficiency trials will be measured and weighed, and again as subsequent recaptures. Fork length is measured to the nearest millimeter and weight to the nearest 0.1 g.
- e. Scales samples should be randomly collected throughout the emigration period from species with multiple year class smolts (i.e., steelhead and sockeye).

Task 6-3. Conduct mark-recapture trials for target species to develop a discharge-trap efficiency linear regression model to estimate daily trap efficiency.

Task 6-3-1. Conduct mark/recapture efficiency trials throughout the trapping season at the largest range of discharge possible.

- a. No less than 100 fish should be used for each trial.
- b. Parr and smolts can be marked by clipping the tip of either the upper or lower lobe of the caudal fin. Alternate fin clip location for each trial. Fry should be marked with dye.
- c. All marked fish should be allowed to recover in a live pen for at least 8 h before being transported to a release site at least 1 km upstream of the trap. Release marked fish across the width of the river, when possible, or equally along each bank in pools or calm pockets of water.
- d. Nighttime efficiency trials should be conducted after sunset. Daytime efficiency trials should be conducted after sunrise.
- e. The following assumptions should be valid for all mark-recapture trials:
  - 1. All marked fish passed the trap or were recaptured during time period  $i$ .
  - 2. The probability of capturing a marked or unmarked fish is equal.
  - 3. All marked fish recaptured were identified.
  - 4. Marks were not lost between the time of release and recapture.
- f. Calculate trap efficiency using the following formula.

$$\text{Trap efficiency} = E_i = R_i / M_i$$

Where  $E_i$  is the trap efficiency during time period  $i$ ;  $M_i$  is the number of marked fish released during time period  $i$ ; and  $R_i$  is the number of marked fish recaptured during time period  $i$ .

Task 6-3-2. Perform linear regression analysis using discharge (independent variable) and trap efficiency (dependent variable) data from the mark-recapture trails to develop a model to estimate trap efficiency on days when no mark-recapture trials were conducted. Separate models should be developed for each trap position and target species.

Task 6-4. Estimate daily migration population by dividing the number of fish captured by the estimated daily trap efficiency using the following formula:

$$\text{Estimated daily migration} = \hat{N}_i = C_i / \hat{e}_i$$

where  $N_i$  is the estimated number of fish passing the trap during time period  $i$ ;  $C_i$  is the number of unmarked fish captured during time period  $i$ ; and  $e_i$  is the estimated trap efficiency for time period  $i$  based on the regression equation.

Task 6-5. Calculate the variance for the total daily number of fish migrating past the trap using the following formulas:

$$\text{Variance of daily migration estimate} = \text{var}[\hat{N}_i] = \hat{N}_i^2 \frac{\text{MSE} \left( 1 + \frac{1}{n} + \frac{(X_i - \bar{X})^2}{(n-1)s_X^2} \right)}{\hat{e}_i^2}$$

where  $X_i$  is the discharge for time period  $i$ , and  $n$  is the sample size. If a relationship between discharge and trap efficiency was not present (i.e.,  $P < 0.05$ ;  $r^2 \lesssim 0.5$ ), a pooled trap efficiency was used to estimate daily emigration:

$$\text{Pooled trap efficiency} = E_p = \sum R / \sum M$$

The daily emigration estimate was calculated using the formula:

$$\text{Daily emigration estimate} = \hat{N}_i = C_i / E_p$$

The variance for daily emigration estimates using the pooled trap efficiency was calculated using the formula:

$$\text{Variance for daily emigration estimate} = \text{var}[\hat{N}_i] = \hat{N}_i^2 \frac{E_p(1 - E_p) / \sum M}{E_p^2}$$

Task 6-6. Estimate the total emigration population and confidence interval using the following formulas:

$$\text{Total emigration estimate} = \sum \hat{N}_i$$

$$95\% \text{ confidence interval} = 1.96 \times \sqrt{\sum \text{var}[\hat{N}_i]}$$

Task 7: Calculate survival rates at various life stage for target species.

Task 7-1. Calculate the total estimated egg deposition for the selected river.

- a. When possible, estimated egg deposition should be based on the average fecundity of the spawning population. Hatchery broodstock randomly collected from the run should provide a representative sample of the spawning population.
- b. Multiply the average fecundity by the total number of redds upstream of the trap location to estimate the total egg deposition.

Task 7-2. Calculate the egg-to-emigrant or egg-to-smolt survival of the target species, dependent on the trap location in the watershed and life history of the target species.

- a. Egg-to-emigrant survival rates are calculated by dividing the total estimated number of subyearling and yearling fish of the same brood year by the total estimated number of eggs deposited.
- b. Egg-to-smolt survival rates are calculated by dividing the total estimated number of smolts of the same brood year by the total estimated number of eggs deposited. For species with multiple year class smolts, the egg-to-smolt survival may require several years of trapping data.

Task 7-3. Calculate egg-to-parr and parr-to-smolt (i.e., overwinter) survival for target species.

- a. Egg-to-parr survival rates are calculated by dividing the total estimated number of parr the total estimated number of eggs deposited. Parr estimated are derived independently using snorkel methodologies described in Hillman and Miller (2002).
- b. Parr-to-smolt survival rates are calculated by dividing the overwinter population by the total estimated number of smolts that emigrated that following spring. The overwinter population is calculated by subtracting the estimated number of parr that emigrated following the completion of the summer parr estimate.
- c. To estimate the parr-to-smolt survival rate of those parr that emigrated, representative samples of subyearling and yearling emigrants should be PIT tagged ( $N = 5,000/\text{group}$ ). Subsequent PIT tag survival analysis would provide the relative survival of the two groups. The estimated number of parr could be converted to smolts based on the reduced survival. Subsequently, an egg-to-smolt survival estimate (versus and egg-to-emigrant) could be calculated.

## Appendix F

### Spawner Escapement and Distribution

Task 7: Determine the stock demographics, spawn timing, redd distribution, redd abundance, and estimate the spawning escapement of selected streams (*spawner escapement, proportion of hatchery fish, fish per redd, number of precocial fish, sex ratio, redd distribution, spawn timing, stray rate*).

Task 7-1. Delineate survey reaches of all available spawning habitat. Whenever possible, use historical reaches for comparisons across years.

- a. Reaches should not take longer than one day to survey.
- b. Historical reaches can be subdivided if required.
- c. Beginning and end points of reaches should be fixed locations (e.g., confluence with a stream or bridge).

Task 7-2: Conduct comprehensive spawning ground surveys of all available spawning habitat and count all redds within a selected stream (i.e., total redd count).

- a. Conduct weekly surveys of all reaches by foot or raft. The survey period should begin at the earliest known date of spawning and continue until no new redds have been observed within a reach.
  1. One person can conduct surveys on small stream where both stream margins are easily observed. Two people should conduct surveys whenever both stream margins cannot be easily observed from a location.
  2. When a raft is used to conduct surveys, two observers should be in an elevated position at the front of the raft while one person navigates the raft.
- b. Individually number all completed redds.
  1. In areas with low spawner density, flagging can be placed on the nearest vegetation. Data on flag should include unique redd number, distance from flag to redd, and date. Data recorded in field notes should include date, water temperature, reach, and redd number. If applicable, the number and origin of the fish on the redd should be recorded.
  2. In areas with medium and high spawner density, mapping of redds is required. Site specific (e.g., a single riffle), area specific (e.g., section of stream between two power lines), or aerial photographs can be used to annotate redds. Redds should be uniquely numbered on the map(s). Different symbols should be used for complete, incomplete, and test redds.

3. All completed redds should have the correct redd morphology (i.e., well developed tailspill and pit or the appropriate size for the target species). Incomplete redds have fish actively constructing a redd, but no completed. Test digs are disturbed areas of substrate that do not have the correct morphological characteristics for the target species.

Task 7-3: Conduct index spawning ground counts and estimate the total number of redds in a selected stream.

Task 7-3-1: Identify index reaches in selected tributaries.

- a. Index reaches should overlap historical reaches whenever possible.
- b. Index reaches should be identified in streams with known or suspected spawning populations.
- c. Index reaches should be located in the core spawning locations of the stream.
- d. Multiple index areas should be identified for streams when any of the following apply:
  1. Potential spawning habitat of target species cannot be surveyed in one day for any reason.
  2. Large tributaries enter the stream that may affect visibility.
  3. Significant gradient changes that may affect visibility.

Task 7-3-2: Conduct comprehensive spawning ground surveys and count all redds within an index area (See Task 5-2).

Task 7-3-3: Conduct a final survey of the entire reach(s) at the end of spawning or after peak spawning if poor water conditions are expected ( $n_{total}$ ).

- a. Count all redds in each reach. Marking redds is not required.
- b. A different surveyor should survey within the index area. Count only redds that are visible.
- c. Calculate an index expansion factor ( $IF$ ) by dividing the number of visible redds in the index by the total number of redds in the index area.

$$IF = \frac{n_{visible}}{n_{total}}$$

- d. Expand the non-index area redd counts by the proportion of visible redds in the index to estimate the total number of redds in the entire reach ( $RT$ ).

$$RT = n_{non-index} / IF$$

- e. Estimate the total number of redds ( $TR$ ) by summing the reach totals.

$$TR = \sum RT$$

Task 7-4: Conduct comprehensive modified-peak spawning ground surveys and estimate the total number of redds in a selected stream.

Task 7-4-1: Establish index areas per Task 5-3-1.

Task 7-4-2: Conduct comprehensive spawning ground surveys and count all redds within an index area (See Task 5-2).

Task 7-4-3: Conduct comprehensive peak spawning ground surveys within non-index and index areas.

- a. Different survey crew must perform the index area total counts and the index area peak counts.
- b. Count all visible redds within the non-index area, but do not individually mark the redds.

Task 7-4-4: Calculate an index peak expansion factor ( $IP$ ) by dividing the peak number of redds in the index by the total number of redds in the index area.

$$IP = n_{peak} / n_{total}$$

Task 7-4-5: Expand the non-index area peak redd counts by the  $IP$  to estimate the total number of redds in the entire reach ( $RT$ ).

$$RT = n_{peak} / IP$$

Task 7-4-6: Estimate the total number of redds ( $TR$ ) by summing the reach totals.

$$TR = \sum RT$$

Task 7-5: Conduct carcass surveys on selected streams and collect biological data from a representative sample (i.e., 20%) of the spawners.

- a. Determine the sampling protocol based on escapement and effort. A sampling rate of 100% of all carcasses encountered is normally required, the exception is for sockeye.
- b. Collect biological data from all carcasses sampled, including:
  1. Sex.
  2. Fork and post orbital-to-hypural length (cm).
  3. Scales.
  4. Remove snout including the eyes for CWT analysis is adipose fin-clipped or if origin is undetermined.
  5. Number of eggs in body cavity, if body cavity is intact.
  6. DNA tissue (5 hole punches from opercle) if applicable.
- c. All biological information should be recorded on the scale card to include:
  1. Date.
  2. Stream.
  3. Reach.
  4. Stream survey tag number if snout was collected.
  5. DNA sample number if tissue was collected.
- d. All sampled carcasses must have the tail removed (posterior of the adipose fin) and placed back into the stream after data have been recorded.

Task 7-6: Conduct snorkel surveys on redd to determine the incidence of precocial fish spawning in the wild.

- a. Determine sampling protocol based on escapement and personnel.
- b. Survey crews should consist of two snorkelers.
- c. Snorkel surveys should be conducted only on active redds (i.e., presence of spawning female).
- d. Snorkel surveys should be conducted in an upstream direction.
- e. Record the number of males by size (e.g., adult, jack, or precocial) and origin (e.g., wild or hatchery).

Task 7-7: Determine the spawning distribution of wild and hatchery fish in a selected stream.

- a. Assume the carcass recovery location (i.e., reach) is also the spawning location.

- b. Calculated the proportion of the spawning population that spawned in each reach and compare with historical values (i.e., before supplementation).
- c. Compare the proportion of each component (i.e., wild and hatchery) that spawned in each reach.

Task 7-8: Calculate a sex ratio and fish per redd ratio (i.e., redd expansion factor) for a selected stream.

- a. Sex ratios for spawning populations should be calculated for the hatchery broodstock if the broodstock was randomly collected from the run-at-large.
- b. If broodstock stock was not collected randomly from the run-at-large, trapping records can be used in conjunction with the broodstock to develop a random sample provided sex was recorded for those fish trapped and released.
- c. Once a sex ratio has been determined for a stock (e.g., 1 female: 1.5 males) a redd expansion factor can be calculated by summing the ratio (e.g., 1 female: 1.5 males = 2.5 fish per redd).
  - 1. Assumptions associated with this methodology include: a female constructs only one redd and male fish only spawn with one female.
- d. This redd expansion factor can be applied to stocks without a hatchery broodstock, but have similar age compositions.
- e. An alternative method (Meekin 1967) involves using previously calculated adults per redd values (i.e., 2.2 adults/redd for spring Chinook and 3.1 adults/redd for summer Chinook) and adjusting for the proportion of jacks in the run (e.g., jack spring Chinook comprise 10% of the run. The redd expansion factor =  $2.2 \times 1.1 = 2.4$  fish/redd).

Task 7-9: Calculate the proportion of hatchery fish (target and non-target or strays) on the spawning grounds.

- a. The proportion of hatchery on the spawning grounds is determined via scale analysis from carcasses randomly collected over the spawning period and all available habitat.
- b. Stray rates are calculated from CWT recoveries divided by tag rate and sample rate.

Task 7-10: Summarize length-at-age and age-at-maturity data for the spawning population.

## Appendix G

### Relative Spawner Abundance Monitoring

Task 8: Determine if the relative abundance of supplemented populations is greater than non-supplemented populations and the influence the relative proportion of hatchery origin spawners may have on the abundance (*NRR*, *recruits*).

Task 8-1. Calculate the adult-to-adult survival rates or natural replacement rate (NRR) for selected stocks using the formula

$$NRR = r_{i+1} + r_{i+2} + r_{i+3} + \dots / S_i$$

- a. Estimate the number of spawners (*S*) from redd counts during year *i* by expanding the total redd count by a redd expansion value. When comparing across years, the number of spawners should be calculated using the same methodologies.
  1. When available, use the sex ratio of broodstock randomly collected from the run as the redd expansion factor.
  2. The alternate method would be the modified Meekin method that is calculated using a 2.2 adults/redd values expanded for the proportion of jacks within the run.
- b. Estimate the number of recruits (*r*). When applicable, use the age composition derived from broodstock randomly collected from the run in stock reconstruction. Age composition data derived from spawning round surveys may bias towards larger and older fish.
  1. Exploitation rate of hatchery fish (indicator stock) may be used for naturally produced fish provided the stock was not subjected to selected fisheries. In which case, a hooking mortality should be applied and recruits adjusted accordingly.
  2. Stocks without a hatchery component (i.e., reference streams) may use exploitation rate of supplemented stock provide there is no difference in run timing or probability of harvest.
- c. Conduct spawner-recruit analysis to explain density dependent effects within each of the supplemented and reference stream and correlate with the proportion of hatchery spawners for each brood year.

Task 8-2. Compare NNR of supplemented stream and reference stream to detect differences due to supplementation program.

- a. When possible, establish baseline conditions (i.e., before supplementation) for supplemented and reference streams. Ensure spawning data is comparable across years and calculated using similar methodologies for each stream, preferably both streams.
- b. High variability in SAR may preclude use of NRR.

Task 8-3. Compare the relationships of the number of smolts per redd (independent variable) and NRR (dependent variable) of the supplemented and reference streams.

- a. Conduct regression analysis using number of smolts per redd and NRR of both the supplemented stream and reference stream. Adjust the number of smolts per redd variable for differences in the number of Columbia River hydro projects between the supplemented and reference streams.
- b. Perform statistical analysis to determine if the slope of the two regression equations is similar.

Task 8-4. Conduct statistical analysis to determine what influence hatchery fish may have on relative abundance.

- a. Examine the relationship between the proportion of hatchery fish on the spawning grounds and NRR.
- b. Examine the relationship between the proportion of hatchery fish on the spawning grounds and egg-to-emigrant survival.
- c. Examine the relationship between the proportion of hatchery fish on the spawning grounds and the number of smolts per redd.
- d. Examine the relationship between the proportion of hatchery fish on the spawning grounds and smolt-to-adult survival.

## Appendix H

### Genetics

Task 9: Determine if genetic variation of hatchery-origin fish is similar to that of donor population and naturally produced fish in supplemented populations (*Genetic variation, proportionate natural influence*).

Task 9-1. Establish a genetic sampling and analysis schedule for programs in the Wells FH Complex.

- a. Prioritize programs for evaluation relative to recovery monitoring needs. An example scheme is shown in Table 7.
- b. Determine if adequate genetic samples (N= 50 to 100 per year for at least 2 years) of donor population per program have been collected.
- c. If necessary, design a sampling plan to collect additional donor population samples.
- d. Determine whether suitable DNA markers are available or need to be developed for target species.
- e. Determine the number of genetic samples from current wild population(s) and hatchery-origin adults that need to be collected each year of an evaluation period (period length depends on species).
- f. Develop annual schedule of laboratory analysis and reporting with agency genetics staff.
- g. Conduct analyses and evaluate results.
- h. Determine the frequency of analysis necessary for long-term monitoring of genetic variation in naturally produced and hatchery-origin populations.

Table 7. Example of prioritized genetic sampling and analysis scheme for evaluation of Wells FH programs (D=Donor population pre-hatchery program, H=hatchery, NP=naturally produced).

Stock	Origin	Last samples collected			Priority	Start year
		Year(s)	N	Stage		
Twisp spring Chinook	D				1	2006
	H				1	2006
	NP				1	2006
MetComp spring Chinook	D				2	2007
	H				2	2007
	NP				2	2007
Wells Steelhead	D				3	2008
	H				3	2008
	NP				3	2008
Wells summer Chinook	D				4	2009
	H				4	2009
	NP				4	2009

Task 9-2. In conjunction with genetic sampling schedule, conduct evaluation of phenotypic traits that serve as indicators of potential domestication impacts of hatchery programs

- a. Determine availability and applicability of historical phenotypic data from donor populations. If data are not adequate, develop plan to acquire appropriate contemporary data.
- b. Determine availability and extent of phenotypic data from current hatchery and natural populations and whether sample sizes from annual samples are adequate. Phenotypic data sets should extend over a series of years to account for effects of environmental variability. Plan data collection schedule if necessary for current populations.
- c. Conduct data analysis using appropriate statistical methods.
- d. Where available spawning ground survey data are suitable, calculate recent and historical proportionate natural influence (PNI; formula shown below) for target stocks. Develop survey protocol where data are unavailable, and collect spawning ground data for target stocks throughout evaluation period in order to calculate PNI.

$$PNI = \frac{\text{proportion of natural produced fish in the broodstock (pNOB)}}{\text{pNOB} + \text{proportion of hatchery fish on the spawning grounds (pHOS)}}$$

Task 10: Determine if genetic stock structure of within-basin natural populations has changed due to effects of hatchery programs.

Task 10-1. Establish a sampling and analysis schedule for potentially affected populations in the Upper Columbia Basin.

- a. Based on program prioritization established in Task 9-1, determine if adequate historical genetic samples (N= 50 to 100 per year for at least 2 years) of potentially affected populations are available.
- b. If necessary, design and conduct a sampling plan to collect appropriate within-basin population samples. An example scheme is shown in Table 8 relative to the Chiwawa spring Chinook program.
- c. Depending on baseline data available (historical and/or recent), develop data analysis plan to assess temporal variability of with-in basin genetic population structure over meaningful time frames.
- d. Develop schedule of laboratory analysis and reporting with agency genetics staff.
- e. Conduct analyses and use results to determine subsequent evaluation needs.

Task 10-2. Establish a field sampling and data analysis program to verify and monitor impacts from hatchery programs on affected within-basin populations.

- a. Based on genetic results from Task 10-1, design a sampling plan to enumerate hatchery-origin strays within non-target, affected populations and to collect genetic samples of naturally produced fish of pertinent brood years from these populations.
- b. Conduct genetic laboratory and statistical analyses and evaluate results.
- c. Determine the frequency of analysis necessary for long-term monitoring of genetic effects of hatchery supplementation fish on non-target natural populations.

Table 8. Example of genetic sampling and analysis scheme for evaluation of effect of Methow spring Chinook supplementation program on within-basin population structure (NP=naturally produced).

Stock	Origin	Last samples collected			Priority	Year
		Year	N	Stage		
Twisp spring Chinook	NP				1	2006
Methow spring Chinook	NP				1	2006
Chewuch spring Chinook	NP				1	2006
Entiat R. spring Chinook	NP				1	2006

Task 11: Determine if effective population size ( $N_e$ ) of target natural spawning populations increases at rate expected given an increase in hatchery-origin fish on the spawning grounds.

- a. In order to estimate current or baseline  $N_e$ , assess whether temporal samples of naturally spawning populations planned in Task 9-1(e) provided the necessary genetic data from natural-origin adults of same brood year from at least three brood years. (Indirect estimates of  $N_e$  are made from temporal variation of gene frequencies or genetic linkage disequilibrium in cohorts).
- b. If adult (by brood year) sample sizes are adequate, estimate  $N_e$  for the base period using genetic methods.
- c. If adult (by brood year) sample sizes are not adequate, design and conduct genetic sampling of same brood year naturally produced juveniles for at least a three year period.
- d. Conduct laboratory analyses to collect genetic data from juvenile samples and estimate  $N_e$ .
- e. Compare  $N_e$  results to spawning ground survey estimates of annual spawner population census sizes, and proportions of naturally spawning hatchery- and wild-origin fish.
- f. At least one generation later, assuming supplementation program is providing large proportions of hatchery-origin fish and their natural adult progeny on spawning grounds, ensure that sampling for other evaluation and monitoring purposes includes adequate temporal genetic samples of same-brood year natural adults.

- g. Conduct laboratory analyses to collect genetic data from adult samples *if* these data are not being collected to accomplish another evaluation task.
- h. Estimate  $N_e$  for the later period using genetic methods and compare results to survey data on census size and hatchery/wild proportions.

## Appendix I

### Monitoring non-target taxa of concern

Task 12: Monitor non-target taxa of concern (NTTOC) to determine if impacts are within acceptable levels.

Task 12-1. Identify NTTOC for each target stock and define acceptable level of impact associated with hatchery program (Table 9).

Task 12-2. Identified the most probable interactions (Table 10) that would impact NTTOC as described by Pearsons et al. (19XX).

Task 12-3. Conduct risk assessment to prioritize monitoring effort (Table 11).

Task 12-4. Monitor size, distribution, and abundance of NTTOC as it relates to target stock and determine impact levels.

- a. Monitor size and abundance of NTTOC using smolt traps.
- b. Monitor distribution of NTTOC using snorkel surveys.
- c. If impact levels exceed acceptable levels determine if changes in NTTOC are correlated to changes in production levels, size of fish released from hatchery, or location hatchery fish are released.
  1. Determine if changes in abundance are a result from predation, disease, or competition.
  2. Determine if changes in size are a result of competition.
  3. Determine if changes in distribution are a result of predation, disease, or competition.

Task 12-5. Develop and implement specific research studies to determine causation of impacts to NTTOC.

Table 9. NTTOC containment objectives for hatchery programs in the Upper Columbia River ESU. Impacts are defined as the decline in one or more variables (size, abundance, and distribution) that can be attributed to hatchery fish.

Target Species/Stock	NTTOC	Containment Objective
Common to all programs	Bull trout	No impact (0%)
	Pacific lamprey	No impact (0%)
	Mountain sucker	Very low impact ( $\leq 5\%$ )
	Leopard dace	Very low impact ( $\leq 5\%$ )
	Westslope cutthroat	Low impact ( $\leq 10\%$ )
	Resident <i>O. mykiss</i>	Low impact ( $\leq 10\%$ )
	Mountain whitefish	Moderate impact ( $\leq 40\%$ )
	Other native species <sup>1</sup>	High impact ( $\leq$ Maximum)
Twisp spring Chinook	Methow steelhead	No impact (0%)
	Twisp spring Chinook	No impact (0%)
	Methow summer Chinook	Low impact ( $\leq 10\%$ )
Metcomp spring Chinook	Methow spring Chinook	No impact (0%)
	Chewuch spring Chinook	No impact (0%)
	Methow steelhead	No impact (0%)
	Methow summer Chinook	Low impact ( $\leq 10\%$ )
Methow steelhead	Methow spring Chinook	No impact (0%)
	Chewuch spring Chinook	No impact (0%)
	Twisp spring Chinook	No impact (0%)
	Methow steelhead	No impact (0%)
	Methow summer Chinook	Low impact ( $\leq 10\%$ )
Methow summer Chinook	Methow spring Chinook	No impact (0%)
	Methow steelhead	No impact (0%)
	Methow summer Chinook	Low impact ( $\leq 10\%$ )
Okanogan summer Chinook	Okanogan steelhead	No impact (0%)
	Okanogan summer Chinook	Low impact ( $\leq 10\%$ )
Wells summer Chinook	Methow spring Chinook	No impact (0%)
	Methow steelhead	No impact (0%)
	Okanogan steelhead	No impact (0%)
	Methow summer Chinook	Low impact ( $\leq 10\%$ )
	Okanogan summer Chinook	Low impact ( $\leq 10\%$ )

1/ Native species refers to all other species endemic to the subbasin. Impacts to should not exceed a level required to maintain a sustainable population.

Table 10. Species interactions between hatchery programs and NTTOC (C=competition, F=Prey for predators, P=Predation, D=disease).

Hatchery program	NTTOC	Interaction			
		Type	Risk	Potential	Uncertainty
Methow/Twisp spring Chinook	Steelhead	C, F, D	Low	Low	Mod.
	Spring Chinook	C, F, D	High	Mod	High
	Bull trout	C, F, D	Low	Low	Low
	WCT	C, F, D	Low	Low	Low
	Resident <i>O. mykiss</i>	C, F, D	Mod	Mod	Mod
	Mountain sucker	C, F, D	Low	Low	Low
Wells steelhead	Spring Chinook	C, P, D	Mod	Mod	Low
	Summer Chinook	C, P, D	Mod	Mod	Low
	Sockeye	C, P, D	Low	Low	Low
	Bull trout	C, P, D	Low	Low	Low
	WCT	C, P, D	Mod	Mod	Low
	Resident <i>O. mykiss</i>	C, P, D	Mod	High	Mod
	Mountain sucker	C, P, D	Low	Low	Low
	Pacific lamprey	C, P, D	Low	Low	Low
	Leopard dace	C, P, D	Low	Low	Low
Wells summer Chinook	Spring Chinook	C, F, D	High	Mod	Mod
	Steelhead	C, F, D	Low	Low	Low
	Bull trout	C, F, D	Low	Low	Low
	WCT	C, F, D	Low	Low	Low
	Resident <i>O. mykiss</i>	C, F, D	Low	Low	Low
	Mountain sucker	C, F, D	Low	Low	Low
	Pacific lamprey	C, F, D	Low	Low	Low
	Leopard dace	C, F, D	Low	Low	Low

Table 11. Risk assessment of target and nontarget taxa for hatchery programs.

Target species	Interactors	Life stage	Interaction	Risk Assessment
Spring Chinook	Steelhead	Fry, parr	F, C	Low
	Spring Chinook	Fry, parr, smolt	C, D	Low
	Bull trout	Fry, parr	F, C	Low
Steelhead	Spring Chinook	Fry, parr, smolt	P, C, D	High
	Summer Chinook	Fry, parr, smolt	P, C, D	High
	Steelhead	Fry, parr, smolt	P, C, D	Mod
Summer Chinook	Spring Chinook	Smolt	C, D	Low
	Steelhead	Fry, parr, smolt	P, C, D	Mod

## Appendix J

### Disease monitoring of hatchery programs

Task 13: Determine if hatchery programs have influenced incidence or magnitude of disease in hatchery and naturally produced fish.

Task 13-1. Monitor disease in broodstock and juvenile fish.

- a. Sample all female broodstock for disease per WDFW Fish Health protocols.
  1. Monitor density and flow index in adult holding pond.
  2. Examine relationship between holding conditions and disease.
- b. Sample juvenile fish monthly and prior to release to develop disease profile ( $N=30$ ).
  1. Monitor density and flow index during rearing.
  2. Examine relationship between holding conditions and disease.
- c. Sample naturally produced fish monthly, both upstream and downstream of acclimation ponds or release sites ( $N=30$ ).
- d. Sample naturally produced fish monthly from a population without hatchery program ( $N=30$ ).

Task 13-2. Examine the influence between the incidence of disease in the broodstock and progeny.

Task 13-3. Monitor incidence of disease in hatchery effluent and natural environment.

- a. Collect monthly water samples from hatchery effluent and upstream and downstream of acclimation ponds.
- b. Determine if acclimation ponds increase disease load in river.