

• **Columbia River spring chinook gill-net fishery**

An example of the power of genetic stock identification is provided by the management of the lower Columbia River winter gill-net fishery for spring-run chinook salmon. This fishery targets the abundant hatchery stocks from the Willamette River and other lower Columbia River tributaries, but is constrained by both management intent and federal court mandate from harvesting excessive numbers of fish from both mid-Columbia and Snake River stocks (Fig. 1). The recent U.S. government listing of Snake River spring- and summer-run chinook salmon as a threatened species under the Endangered Species Act has further constrained this fishery.

The fishery was managed for many years using coded-wire tag (CWT) recoveries. However, the expense of tagging adequate numbers of hatchery fish to provide enough tagged fish in samples from the fishery and the difficulty and expense of tagging wild stocks led to the application of GSI techniques in the late 1980s. For the past several years, decisions about whether to extend or terminate the fishery after the first week of fishing have been based solely on in-season GSI estimates of upper river (mid-Columbia and Snake rivers) stock contribution. Figure 3 illustrates estimated stock-group contributions to this fishery in three different time periods in one year (Fig. 3a) and in three different years (Fig. 3b). The substantial intra- and inter-annual variation of stock group contributions to this fishery makes annual in-season monitoring a necessity. Additionally, because the GSI technique has reasonable power to estimate the presence of Snake River spring chinook stocks (Shaklee 1991), the technique provides information

for evaluating harvest impacts on this ESA-protected stock. Without this information, continuation of the entire fishery could be in jeopardy. The relatively small cost of laboratory processing (approximately \$14.00/fish) and high precision of the stock-group contribution estimates makes GSI a cost-effective management tool for this fishery.

Similar in-season GSI fishery estimates are conducted to optimize the management of chum salmon fisheries in Puget Sound (Baker and Bishop 1993) and to manage fisheries in British Columbia for odd-year pink salmon (PSC 1990).

• **Selective fisheries and mass marking**

Most innovative methods used to manage mixed-stock fisheries are intended to protect weak stocks from over-exploitation by limiting harvest rate to that appropriate for the weakest stock in the co-mingled aggregation. However, it is not possible to utilize hatchery production fully using existing stock ID procedures such as GSI because the hatchery or natural origin of individual fish cannot be determined at the time and location of capture. Thus, despite weak stock management intent, natural stock production goals are often not achieved. Without changes to management, it is likely there will be a continued deterioration of both mixed-stock fisheries and resource status.

It would be highly desirable if the intended harvest of robust hatchery stocks could be separated from the inadvertent harvest impacts on weaker naturally spawning (and hatchery) stocks. Mass marking of hatchery stocks shows some promise for achieving this goal. Application of visible marks to all fish produced in hatcheries (mass-marking) and selective fisheries could be an effective

instrument for achieving increased protection of weak wild and hatchery stocks by reducing their harvest in mixed-stock fisheries.

Managers must also consider the genetic implications of the increased exploitation of target hatchery stocks. The benefits gained through improved harvest access must be viewed in the context of long term genetic stability of the hatchery-based resource component. For example, it has been postulated that mean size of chinook and coho stocks harvested in British Columbia fisheries has been reduced due to the selective pressures applied by the commercial fisheries (Ricker 1980; Ricker and Wickett 1980). Additionally, the negative effects of hooking and handling mortality on the fish from the protected, unmarked stocks that would be released in such selective fisheries must also be considered.

Mass marking proposals are being actively pursued in Washington as well as Idaho, Oregon and British Columbia. Many of the proposals are aimed toward avoiding the fishery constraints posed by weak stock management, but the tool can be viewed just as easily as a potential way to reduce overall exploitation of natural stocks in order to meet escapement goals consistently and increase production, thereby reducing the risk of extinction or loss of genetic diversity.

#### **Hatchery Operations — Selected Case Histories**

Although many of WDF's fisheries policies are specifically designed to use cultured hatchery stocks to augment harvest opportunities, several of the department's newer hatchery programs are intended to enhance or supplement local native stocks. In the

latter context, the hatchery operations should be designed and carried out in such a manner as to have minimal or no impact on the original genetic and biological character of the stock being cultured. Genetic evaluations are being conducted to determine whether or not the Department's hatchery operations are achieving this goal. Four specific examples of recent or ongoing studies illustrate how this is being done and what the results have been.

##### **• Skagit River summer chinook salmon**

The Skagit River is a major river system in northern Puget Sound (Fig. 1) that supports spring-, summer- and fall-run chinook stocks. The WDF Skagit Hatchery has, for many years, cultured all three races of chinook. The fall stock cultured at the hatchery actually originated in the Green River (in central Puget Sound) and is intended to augment fishery harvests. The spring stock in the hatchery was derived from chinook spawning in tributaries to the Skagit River and is, therefore, presumed to represent the native stock. The primary purpose of the hatchery was to increase the production of spring-run fish in the region. The summer chinook program at the hatchery was initiated to augment the numbers of fish produced naturally by the healthy wild stock in the upper river. Because the fish in this stock return as adults at a large size and in prime condition, they are highly regarded by both commercial and sport fishers. This was a major factor contributing to the initiation of the summer chinook program at the hatchery.

An ambitious and labor-intensive broodstock collecting program was conducted by WDF staff from 1975 through 1979 to obtain enough spawners to establish a hatchery

Table 2. Allele frequencies at ten informative loci in three chinook stocks propagated at the WDF Skagit River Hatchery. (year collected; N = number of fish collected). Locus and allele designations follow Shaklee et al. 1990a.

Locus & Allele	Upper Skagit River Wild Summer Chinook	Skagit Hatchery "Summer" Chinook	Skagit Hatchery Fall Chinook
	(1986; N =100)	(1986; N =102)	(1987; N =107)
<b>sAAT-3</b>			
*100	0.935	0.995	1.000
*90	0.065	0.005	0.000
<b>sAAT-4</b>			
*100	0.935	0.990	0.986
*63	0.065	0.010	0.005
*130	0.000	0.000	0.009
<b>ADA-1</b>			
*100	0.910	0.951	0.958
*83	0.090	0.049	0.042
<b>sAH</b>			
*100	0.825	0.911	0.906
*86	0.160	0.089	0.094
*116	0.015	0.000	0.000
<b>sMEP-1</b>			
*100	0.600	0.384	0.420
*92	0.380	0.611	0.547
*105	0.020	0.005	0.033
<b>PGK-2</b>			
*100	0.470	0.765	0.668
*90	0.530	0.235	0.332
<b>PEPA</b>			
*100	0.965	0.907	0.892
*90	0.035	0.093	0.108
<b>PEPB-1</b>			
*100	0.660	0.613	0.537
*130	0.340	0.387	0.463
<b>sSOD-1</b>			
*-100	0.730	0.623	0.570
*-260	0.255	0.328	0.388
*580	0.015	0.049	0.042
<b>TPI-4</b>			
*100	0.965	0.995	0.995
*104	0.035	0.005	0.000
*101	0.000	0.000	0.005

stock that would have the same (or very similar) genetic characteristics as the wild summer-run stock. The actual numbers of fish used to establish the hatchery stock totaled approximately 560 fish (ranging from 82 fish in 1975 to 142 in 1977). Since 1980, the hatchery has produced and reared large numbers of this presumed summer chinook stock. Indeed, the hatchery program was so successful that this hatchery stock was chosen as a CWT indicator stock to be used to represent the performance of wild summer chinook from northern Puget Sound in the Pacific Salmon Treaty process.

A genetic evaluation of this program was initiated in 1986 by comparing the characteristics of the summer chinook stock cultured in the hatchery, the wild upper Skagit River summer chinook stock and the fall chinook stock cultured in the hatchery. Horizontal starch-gel electrophoresis (Shaklee and Keenan 1986; Aebersold et al. 1987) was used to screen samples from each of the three groups for approximately 40 variable gene loci. The allele frequencies at several informative loci in each of these three groups of fish are shown in Table 2. Surprisingly, this analysis clearly indicated that the "summer" stock being cultured in the hatchery was significantly different ( $p \leq 0.001$ ) from its source (the wild summer stock in the upper Skagit River). Furthermore, the hatchery "summer" stock was similar to the introduced fall stock reared at the hatchery. This analysis was repeated two years later with a second collection of the "summer" stock at the hatchery with basically the same result.

Subsequent examination of hatchery spawning records suggested that there was likely substantial (albeit unintentional) interbreeding between the fall hatchery stock and the

wild summer fish brought into the hatchery to be the source for establishing a summer stock program. Because this direct genetic evaluation of the Skagit Hatchery summer chinook program showed it was not achieving its goal of propagating pure summer chinook, the hatchery stock was dropped as a CWT indicator stock for northern Puget Sound summer chinook in 1987 and the entire hatchery program for summer chinook at this hatchery is being phased out.

#### • Snake River fall chinook salmon

Legislation was passed in the mid-1970s for hatchery mitigation to compensate for fall chinook losses caused by four dams on the lower Snake River in Washington. A hatchery site was chosen at Lyons Ferry, above the lower two dams on the Snake River (Fig. 1). The fall chinook run was so low at that time, however, that a temporary hatchery operation, called an egg-bank program, was begun while the new hatchery was being built. Adult fall chinook were trapped in the Snake River, but to avoid dam passage mortalities, their progeny were reared and released at a downriver location.

The program began in 1976 and from 1977 onward adults were trapped at Ice Harbor Dam and spawned. The resulting juveniles were all marked (by fin-clipping) and were released from WDF's Kalama Falls Hatchery, which is on a Columbia River tributary below all mainstem dams (Fig. 1). Egg-bank fish began returning to Kalama Falls in 1980, and were used as broodstock along with fish trapped at Ice Harbor. A similar but much smaller operation was conducted by the U.S. Fish and Wildlife Service at two federal hatcheries in Idaho. The egg-bank program ended as the Lyons Ferry Hatchery became operational. Adults from Ice Harbor were

spawned at Lyons Ferry in 1984, and releases there began in 1985. Adults began returning to the Lyons Ferry Hatchery in 1987. Until 1990, when operations at the hatchery were changed in response to concerns raised by the petitioning and subsequent listing of Snake River fall chinook as threatened under the ESA, the Lyons Ferry broodstock consisted of adults trapped at Ice Harbor Dam and volunteers entering the hatchery itself.

Understandably, concerns were raised about the genetic impact of the egg bank program; specifically the effect of temporarily transplanting fish several hundred miles downriver. What effects the egg-bank program had on quantitative genetic variation in the stock will never be known, but a comparison using allele frequencies at thirty loci was made between adults returning to Kalama Falls ( $N = 100$ ) in 1986 and fish collected at Ice Harbor and Lyons Ferry ( $N = 100$ ) in 1986. Significant differences ( $p \leq 0.05$  by

G-test) were found at only two loci; overall the collections were not significantly different ( $p \leq 0.3$ ) (Seidel et al. 1988).

The intent of the Lyons Ferry Hatchery program has always been to culture the native Snake River fall chinook. However, genetic purity of the Lyons Ferry stock has been a central issue for several years, and there have been two concerns. The first was the questionable wisdom of collecting broodstock for the hatchery program at Ice Harbor Dam. Although the dam is far downstream of the remaining natural spawning grounds in the upper Snake River, fish were collected at this location because this site allowed access to more fish than any more upstream alternative due to dam passage mortalities. Nevertheless, because the dam is only about 16 kilometers above the Columbia River, there was also a possibility of trapping mid-Columbia "dip-ins" — Columbia River origin fish that had entered the Snake River, but actually would have dropped back to the Columbia River and spawned there. The second concern focused on strays in the broodstock. A low frequency of CTW strays from other hatch-

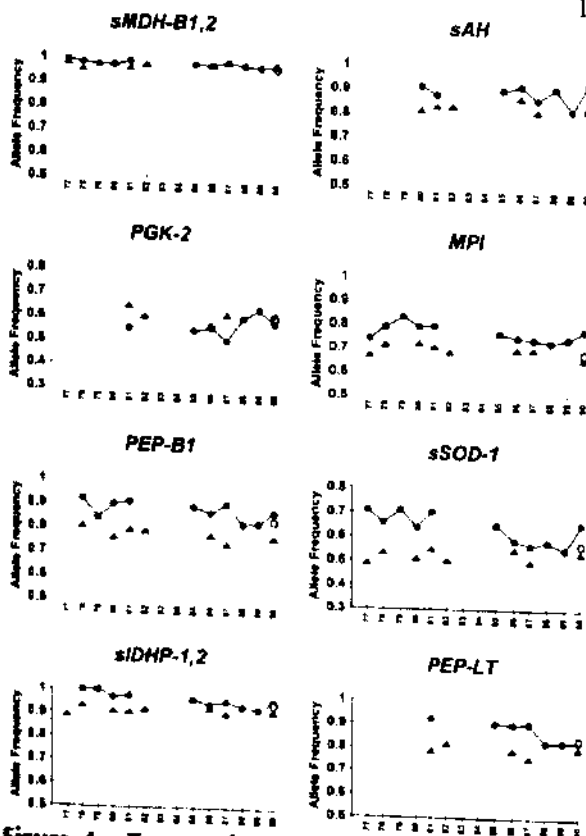


Figure 4. Temporal pattern of allele frequencies ( $N=100$ ) in mid-Columbia and Snake River fall chinook. Solid circles = Ice Harbor/Lyons Ferry Hatchery: pure Lyons Ferry stock. Open circle = "mixed" collection of untagged fish that returned to the Lyons Ferry Hatchery in 1990 and contained an unknown number of Umatilla Hatchery strays. Solid triangles = mid-Columbia River (Hanford Reach and Priest Rapids Hatchery stock). Collection sizes ranged from 65 to 300.

eries had always been noted at the hatchery. However, in 1989, strays from a single hatchery operation on the nearby Umatilla River in Oregon accounted for an estimated 30% of the Lyons Ferry broodstock. Native fall chinook had been extirpated from the Umatilla long ago; consequently, the stock used in this hatchery was derived from fish collected at Bonneville and Priest Rapids dams.

Unfortunately, there are no existing electrophoretic data characterizing unequivocally pure Snake River fall chinook. There are, however, electrophoretic data collected by NMFS and WDF dating back to 1977 from Ice Harbor Dam, Lyons Ferry Hatchery and the mid-Columbia. Figure 4 summarizes much of these data to display temporal trends in allele frequencies at eight genetic systems in Ice Harbor/Lyons Ferry fish and the mid-Columbia fish (including the Umatilla Hatchery fish). In years for which data from multiple collections are available, composite allele frequencies were calculated as the mean of the individual collection frequencies, with one exception: in 1990, two collections of samples were taken at Lyons Ferry, one of "known" Lyons Ferry stock (CWT-tagged fish) and one of untagged fish. Data from the untagged fish are plotted separately in Figure 4. Note that locus and allele designations throughout this report follow Shaklee et al. (1990a). Frequencies at *sMDH-B1,2\** (and at *LDH-B2\**; *LDH-C\**; and *PEPA\** — data not shown) are too similar between the two stocks to be informative. Although frequencies at *sAH\** and *PGK-2\** are too erratic to indicate trends, it is clear that the untagged 1990 Lyons Ferry fish are more similar to mid-Columbia fish at *sAH\** than the tagged fish are. The two series are nearly parallel for *MPI\** frequen-

cies, except that the 1990 untagged Lyons Ferry collection is again more similar to the mid-Columbia collections than to the true Lyons Ferry collections. The series of *PEPB-1\** frequencies appear approximately parallel, and in both the frequency of the *\*100* allele appears to be declining slightly. Lyons Ferry frequencies at *sSOD-1\**, *sIDHP-1,2\** and *PEP-LT\** exhibit definite trends in the direction of the mid-Columbia series, which for each locus remains relatively stable. The frequency of the *\*100* allele at *sSOD-1\** in the 1990 untagged Lyons Ferry collection is more similar to the 1990 mid-Columbia collection, than it is to the 1990 tagged Lyons Ferry collection.

Two time periods are of interest in examining these trends, before Umatilla straying (before 1984) and after. Four systems provide some insight into the question of whether the increasing similarity between Snake River and mid-Columbia stocks was coincident with the egg-bank program and collection of broodstock at Ice Harbor Dam or the Umatilla Hatchery straying. Three of these (*MPI\**, *PEPB-1\** and *sSOD-1\**) exhibit little convergence in allele frequency prior to 1984. The isolocus pair *sIDHP-1,2\** shows a slight convergence in 1980 and 1981. The existing data are too limited to draw strong inferences, but they provide little evidence that significant directional changes in allele frequency of the Lyons Ferry stock occurred before the time when substantial Umatilla Hatchery straying was first noted.

Although a genetic impact from mid-Columbia fish through straying and possible dip-in capture is evident, the genetic distinction between Snake and mid-Columbia fall chinook remains. A comparison of allele frequencies for the 1990 tagged Lyons Ferry and the 1990 mid-Columbia (Priest Rapids

Dam) collections by chi-square heterogeneity test is highly significant ( $p \leq 0.00002$ ). A similar comparison of the 1990 tagged Lyons Ferry collection and the 1986 Lyons Ferry collection is not significant ( $p \leq 0.71$ ), indicating the effect of heavy Umatilla straying in recent years could be diminished by restricting the broodstock to known Lyons Ferry fish.

In response to the high stray rate in 1989, WDF instituted two important hatchery management changes. One was to tag 100% of the 1989 Lyons Ferry brood (with CWTs) in order to exclude all of these fish from subsequent broods at the hatchery. The second was to modify broodstock collection operations for the Lyons Ferry Hatchery for 1990 and beyond. The normal broodstock collection procedure at Ice Harbor Dam and Lyons Ferry Hatchery was continued, but these fish were augmented by trapping approximately 50% of the tagged adults that reached Lower Granite Dam, the uppermost of the four dams on the Snake River and the last before the spawning grounds (Fig. 1). In addition to providing fish, this allowed monitoring of the adult run composition at the dam for the first time. The second change in management was a screening of spawners for stock origin. All CWTs were read as the fish were spawned, so that the fish could be spawned in three groups: only Lyons Ferry tagged fish, only foreign tagged fish, and all untagged fish. Progeny of untagged adults were to be used in the Lyons Ferry program only if the stray rate was deemed to be below an acceptable level. In 1990, stray levels were appreciable, so only the progeny of the Lyons Ferry tagged adults were retained for program use. Current broodstock procedures for Lyons Ferry involve use of only tagged Lyons Ferry fish in order to exclude

fish of unknown origin from the gene pool. To sustain this program, 100% of the Lyons Ferry releases are now tagged. While the flow of foreign genes into the hatchery stock has been stopped by this tagging and tag reading effort, untagged strays cannot be prevented from continuing upriver to the natural spawning grounds. The Lyons Ferry Hatchery stock may well turn out to be a better representation of the original Snake River fall chinook than the natural spawners now protected under the ESA. In this regard, the Lyons Ferry Hatchery fish have recently been determined by NMFS to be part of the Snake River fall chinook "ESU."

#### • Minter Creek chum salmon

Despite a stated intent to manage chum salmon fisheries in south Puget Sound on the basis of local wild stocks, chum production at the Minter Creek Hatchery (Fig. 1) has utilized a stock that was originally derived from the Hood Canal Hatchery. In 1986, the stock being propagated at the Minter Creek Hatchery was electrophoretically characterized and determined to have a genetic profile that was basically identical to that of the Hood Canal stock. Because GSI is the primary method for estimating stock contributions to chum salmon fisheries in Puget Sound, the high degree of genetic similarity between the fish produced at the Minter Creek facility and the large numbers of chum produced at the state, tribal and federal hatcheries in Hood Canal made it impossible to estimate contributions from all south Puget Sound sources (including Minter Creek) accurately. This, in turn, made effective harvest management of south Puget Sound chum extremely difficult. Furthermore, the propagation of Hood Canal type fish in south Puget Sound and their possible straying from the facility to spawn naturally

in adjacent south Puget Sound tributaries and the use of these fish for volunteer enhancement projects in south Puget Sound clearly violated the department's goal of maintaining among-stock genetic variability.

For the reasons outlined above, the Department of Fisheries and tribal co-managers implemented a program to replace the Hood Canal original chum stock at the Minter Creek Hatchery with a native south Puget Sound stock (Elson Creek). Each year, beginning in 1988, adults returning to the Minter Creek Hatchery (presumably from the Hood Canal type stock) were removed from the system by a wipe-out fishery outside the mouth of Minter Creek and their production was replaced at the hatchery with fertilized eggs from the Elson Creek stock obtained from the Squaxin tribal facility. The eggs from Elson were taken from females throughout the run and a total of approximately 1300 females and 1300 males were spawned to provide fertilized eggs for the Minter Creek Hatchery. These practices were followed in order to meet the production goals for Minter Creek and to assure that the recipient hatchery stock (Minter Creek) would be genetically representative of the donor stock (Elson). The program proceeded in this manner for four years — the average duration of the life cycle of the Hood Canal Hatchery stock. In the fifth year (1992), because only the small fraction of fish returning as five-year-olds were of the Hood Canal Hatchery type, we simply had to identify these fish (by scale reading at the hatchery) and remove them prior to spawning to achieve complete removal of all Hood Canal Hatchery type chum from the facility. Beginning in 1993, all broods at the Minter Creek Hatchery should be the native south Puget Sound (Elson) type.

This conversion of hatchery production to a native south Puget Sound stock would not have been successful without tribal participation to furnish the fertilized eggs necessary to replace production losses resulting from elimination of the Hood Canal origin spawners. Joint state/tribal alterations in harvest management regimes were also necessary to support the program. WDF salmon culture and research staff were responsible for accomplishing the conversion at the hatchery and for identifying the nature and extent of the problem and contributing to its solution by aging the large fish returning in the final year of conversion to allow identification and removal of five-year-olds.

The situation at a small volunteer chum salmon enhancement program at Donkey Creek (also in south Puget Sound) run by the Gig Harbor Fisherman's Civic Club, closely paralleled the Minter Creek Hatchery program. The Donkey Creek program was initiated 20 years ago using fertilized eggs (Hood Canal chum stock) originally obtained from the Minter Creek facility. Although this program had been successful in establishing a run of chum back to Donkey Creek, it was inconsistent with the department's intent to use local stocks because it was founded using a foreign gene pool. Using a similar approach to that employed at the Minter Creek Hatchery, the department and the co-op replaced the potential production from all adults returning to the Donkey Creek program over the course of the last five years with fertilized eggs from the Elson stock. This remedial action should have successfully replaced the Hood Canal origin population in Donkey Creek with the more appropriate Elson stock.

- **Dungeness River chinook captive broodstock program**

The Dungeness River once supported a large, productive chinook salmon population, but in recent years the number of adults returning to spawn has decreased to approximately 200 fish per year (C. Smith, WDF; unpublished data). The depressed run size of this population threatens its long term survival due to the increased risk of a genetic bottleneck or extinction from an environmental catastrophe. In response to the critical status of Dungeness chinook, state, tribal and federal fisheries biologists and concerned citizens have joined forces in a restoration effort. The long term goal of this recovery program is to increase the number of naturally spawning fish in the river while maintaining the genetic characteristics (diversity, pattern and amount of variation) of the existing stock. However, all parties involved agreed that the critically low numbers of returning adults place this stock in such jeopardy that priority be given to increasing population size as quickly as possible.

After considering several approaches for achieving an immediate increase in fish numbers, the group decided to implement a captive broodstock program. This relatively new approach — rearing normally anadromous salmon in captivity throughout their entire life cycle — has the potential to increase population numbers dramatically in a single generation because of the high fecundity of the species (approximately 3,500 eggs per female) and the low mortalities expected from hatchery propagation. Because the design of this program was driven by concern to minimize inbreeding and genetic drift (maintain the amount and pattern of genetic variation characteristic of the natural population), an effective number of breeders ( $N_b$ )

goal of 50 per year in each of four successive years was established, for an  $N_e$  of approximately 200 over the average four-year generation time of this stock.

Two concerns made achieving this goal via the traditional capture of pre-spawning adults seem unrealistic or undesirable. First, it was doubtful that the 25 pairs of adults needed for hatchery spawning to achieve the  $N_b$  goal could be obtained because of the small size, low density and protracted freshwater maturation schedule of this population. Second, there was a strong desire to retain a high level of natural production in the Dungeness River during the captive broodstock program. Removing 50 adults from the river for the captive broodstock would have removed approximately one-quarter of the natural production from the system, and would have yielded far more eggs than necessary for the program.

Because of these concerns, a novel experimental approach was devised for establishing the captive broodstock program based on the collection of fry rather than adults. The two-component approach involves the collection of pre-emergent fry by hydraulic sampling of redds (salmon nests in stream bed gravel) and the capture of post-emergent fry by electroshocking or seining in the river. The intent is to collect approximately 200 fry from each of 25 redds and up to 2500 fry from throughout the river. Redd sampling will yield representatives of a known number of essentially discrete family groups, yet will remove less than 10% of the production of each family from the river. Electroshocking/seining has the potential of capturing representatives from all families produced in the system, while also having only a small impact on the total production. These two approaches together should provide adequate

genetic representation of the natural population and yield enough fish to establish the captive broodstock program. The fish in each of the above lots will be tagged in such a way that specific crosses of individuals of known origin can be made when the fish mature.

The Dungeness chinook captive broodstock program was initiated in 1993. Fourteen family groups (N = 2,600 fish) were successfully sampled from redds and approximately 1300 post-emergent fry were obtained by electroshocking. All fish in the broodstock are presently being reared at the WDF Hurd Creek Hatchery in the lower Dungeness watershed.

Another notable feature of this captive broodstock program is that one-half of the fish will be reared to maturity in freshwater tanks (at the hatchery) and one-half in salt-water net pens (in the Strait of Juan de Fuca). This approach will allow evaluation of the relative merits of freshwater and marine captive rearing and will also minimize the risk of catastrophic failure of the program due to having all broodstock in a single facility.

The current plan calls for this captive broodstock program to be conducted for an eight-year period and monitoring and evaluation to continue for an additional four years. This will represent two generations of chinook production, will provide enough tagged fish to assess fishery impacts on the stock and should allow enough time for the limiting factor(s) responsible for the depressed status of this stock to be identified and corrective measures to be initiated. Restricting the program to two generations should also limit inadvertent domestication selection on the stock. While the captive broodstock program is expected to dramatically increase

fish numbers in the short term, the long term success of Dungeness chinook restoration is entirely dependent on identifying and overcoming habitat and/or harvest management impacts that have driven the stock to its current critical state.

#### **Hatchery Monitoring, Evaluation and Research Programs**

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- **Tucannon River spring chinook monitoring and evaluation**

The Tucannon River, in southeastern Washington, is a tributary of the lower Snake River. As part of the Lower Snake River Fish and Wildlife Compensation Plan, the wild spring chinook stock in this river was targeted for hatchery supplementation to provide compensation for salmon production lost because of hydroelectric development in the Snake River Basin. Because the Tucannon River spring chinook population represented one of the last wild chinook stocks in Washington with no history of significant exposure to hatchery origin fish, WDF recognized this as a unique opportunity to monitor and evaluate the effects of a new hatchery on the genetic and biological characteristics of the native stock. The Tucannon Hatchery operation was designed to incorporate the genetic principles and concerns recognized in the mid-1980s. Hatchery operations commenced in 1986, with an initial year's spawning of 48 females and 43 males, and continue (with similar numbers) to the present.

While the hatchery operations were beginning, genetic characterization of the native, pre-facility spring chinook population was initiated. In 1985, 100 outmigrating smolts from the 1983 brood were sampled from the river. In subsequent years, samples of naturally produced fish were obtained, both from

returning adults and from pre-smolts and smolts from the river. Each of these collections was electrophoretically analyzed at approximately 35 variable loci to provide a genetic characterization of the native Tucannon spring chinook stock.

Beginning in 1990, offspring from the hatchery program began returning to the system in significant numbers. Because all individuals produced in the hatchery were marked with CWTs, it was possible to separate the returning adults into either hatchery-produced or wild-origin fish. Electrophoretic analysis of returning adults and of pre-smolt/smolt collections each year has allowed monitoring of the genetic characteristics of the stock and comparison of the

genetic profiles of the stock before and after artificial production was initiated.

Figure 5 shows examples of the temporal patterns in allele frequency seen at four loci in this stock. Two important patterns were evident from this analysis. First, there was significant year-to-year variation in allele frequencies at many loci. Indeed, this variation was sufficient to make overall G-tests among pairs of annual collections statistically significant in many cases. The magnitude of the inter-annual variation in allele frequencies may be a consequence of the small effective population size of this stock. Second, despite the significant annual variability, there does not seem to be any clear directional shift in allele frequency, either at

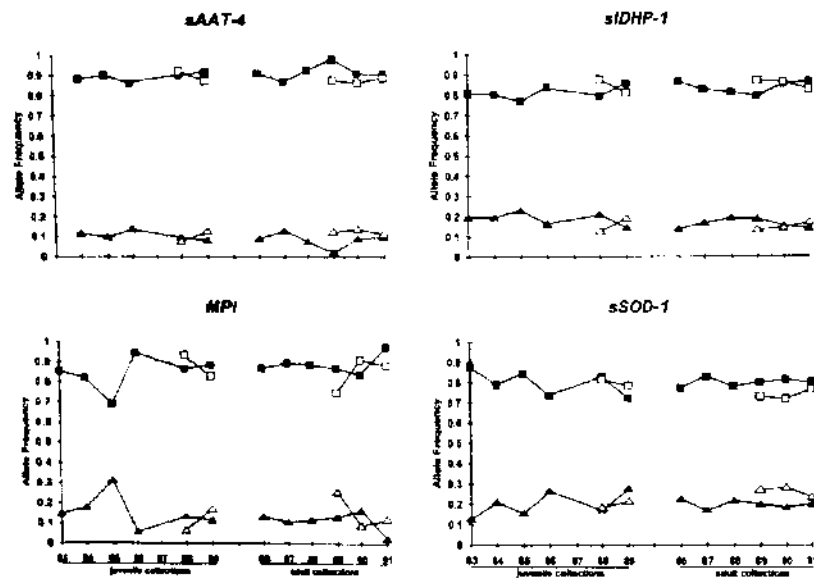


Figure 5. Allele frequency trajectories at four loci in juvenile and adult Tucannon River spring chinook before and after initiation of hatchery supplementation activities. Years shown along the x-axis at the bottom of the figure refer to the year the fish were produced (juvenile collections) or the year fish returned to spawn (adult collections). Solid symbols = frequencies for naturally produced fish; open symbols = frequencies for hatchery produced fish. Squares show the frequency of the most common allele ( $\times 100$ ) at each locus, triangles show the frequency of the second most abundant allele at each locus.  $N = 50 - 100$  per collection.

the four loci shown in Figure 5 or any of the 31 other variable loci being screened.

Because we have less than one complete cycle's worth of data for the stock after the hatchery operation began, it is premature to conclude that there have been no measurable changes at the loci monitored by electrophoresis. Although, as shown in Figure 5, there is no evidence of substantial directional changes. Furthermore, because electrophoresis only allows us to monitor a very small proportion of genes in the genome, there could well be substantial changes at other loci that we would never detect by the electrophoretic screening. Nevertheless, the electrophoretic monitoring represents an attempt to evaluate genetic effects of the hatchery operation. As such, this electrophoretic monitoring and evaluation is an important aspect of the supplementation effort because it has the potential to provide an early warning of genetic problems in the hatchery. However, because hatchery-produced fish are now being allowed to spawn naturally upstream (and their progeny are unmarked), our ability to distinguish between fish with and without past hatchery influence will end within the next three years and subsequent monitoring can only be done for the combined hatchery and naturally-spawning stock.

• **Hatchery conservation genetics research**

As mentioned above, there are numerous questions about conservation genetics that need to be answered for effective, rational programs to control genetic risk. Some questions can be answered experimentally and some by modelling. In cooperation with WDF's Salmon Culture Division, two small research programs at WDF hatcheries are

currently underway to address some of this uncertainty.

One study, at Tucannon, is designed to evaluate the genetic impact of a single generation of hatchery rearing on performance, an opportunity created by the fact that we are still in the first cycle of returns from the hatchery. The method used is to make *inter se* matings of known hatchery (HxH) and wild (WxW) returning adults, and evaluate their progeny. Family lots are reared individually until the families are combined in rearing ponds (= "ponded"), so early performance by family can be readily evaluated. Although family identity is lost when the fish are ponded, they are ponded by treatment group (HxH or WxW) and tagged by treatment group upon release for further evaluation of group performance. Started in 1990, this study has so far revealed striking differences between hatchery and wild females in prespawning survival of adults and early survival of progeny, but the cause is unclear. Hatchery females tend to be younger and smaller than wild females, and this may account for much of the performance difference between the two groups. The data are currently being analyzed to evaluate this effect.

At the Methow Hatchery Complex (on the mid-Columbia River) the relationship between census and effective population size is being studied. Typically hatchery broodstock guidelines assume that one fish equals one effective spawner, and that the most serious departures from this are due to unequal sex ratios. In reality, probably the most important determinant of effective size in Pacific salmon is variance of family size. At Methow, full-sib families are being individually reared and marked before release. Upon their return we will be able to calculate

the variance of family size. This study was initiated in 1992 with 21 families and will be replicated in future years.

- **Future monitoring and research at WDF hatcheries**

A major issue surrounding the increasingly pervasive use of hatcheries is to what extent they domesticate the fish, making them less fit in the wild. Questions about domestication selection need to be answered, but the type of monitoring conducted in the Tucan-

non operation to date is unlikely to provide the information needed. The issue of domestication selection is currently being studied, but monitoring programs should be developed to evaluate changes at quantitative loci and changes in demographic profiles. This is considerably more expensive, logistically demanding and difficult to design than an electrophoresis-based monitoring program, but needs to be done.

### Conclusions and Recommendations

The Washington Department of Fisheries has, like other agencies in the Pacific Northwest, conducted a number of programs and pursued policies that have almost certainly had negative impacts on the genetic integrity, productivity and survival of salmon stocks under its stewardship. Some of these effects are irreversible. However, if the department learns from past mistakes, if current practices and programs are evaluated and corrected aggressively and if enlightened policies and programs are developed and implemented in the future, it is reasonable to presume that the continuing erosion of biodiversity that threatens our fish and fishery resources can be halted or even reversed.

In conclusion, the following actions for fish management agencies are recommended:

- > Establish stock management policies based on sound genetic (and ecological) principles,

- > Recognize the strengths and limitations of hatchery production and ensure that it is used in appropriate situations only,
- > Develop a detailed inventory of the locations, characteristics and status of all stocks, both natural and cultured,
- > Implement adequate monitoring and evaluation programs for both native stocks and for hatchery programs,
- > Develop an aggressive program of public education that emphasizes genetic principles, the importance of native stocks and the critical role of habitat,
- > Recognize that, in the long run, there is no substitute for adequate habitat.

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## Literature Cited

- Aebersold, P.B., G.A. Winans, D.J. Teel, G.B. Milner and F.M. Utter. 1987. Manual for starch gel electrophoresis: a method for the detection of genetic variation. NOAA Technical Report. NMFS 61, 19pp.
- Allendorf, F.W. and N. Ryman. 1987. Genetic management of hatchery stocks. Pages 141-159 *In*: N. Ryman and F. Utter (eds.), *Population Genetics and Fishery Management*. Washington Sea Grant Program, Seattle. 420 pp.
- Baker, B.M. and S. Bishop. 1993. Genetic stock identification estimates of chum salmon stocks contributing to 1992 weekly test fisheries at Apple Cove Point, Washington - Areas 9 and 10. unpublished WDF and NWIFC report. Olympia, WA.
- Beacham, T.D., R.E. Withler and A.P. Gould. 1985a. Biochemical genetic stock identification of pink salmon (*Oncorhynchus gorbuscha*) in southern British Columbia and Puget Sound. *Can. J. Fish. Aquat. Sci.* 42: 1474-1483.
- Beacham, T.D., R.E. Withler and A.P. Gould. 1985b. Biochemical genetic stock identification of chum salmon (*Oncorhynchus keta*) in southern British Columbia. *Can. J. Fish. Aquat. Sci.* 42:437-448.
- Berst, A. H. and R. C. Simon, eds. 1981. Proceedings of the Stock Concept International Symposium (STOCS). *Can. J. Fish. Aquat. Sci.* 38:1457-1923.
- Busack, C.A. 1990. Yakima/Klickitat Production Project genetic risk assessment. *In*: Yakima/Klickitat Production Project Preliminary Design Report, Appendix A, Bonneville Power Administration Report DOE/BP-00245-2. 20pp.
- Currens, K.P. 1993. Genetic vulnerability of the Yakima Fishery Project: A risk assessment (draft). Washington Department of Fisheries, 83pp.
- Fournier, D.A., T.D. Beacham, B.E. Riddell and C.A. Busack. 1984. Estimating stock composition in mixed stock fisheries using morphometric, meristic, and electrophoretic characteristics. *Can. J. Fish. Aquat. Sci.* 41:400-408.
- Fraidenburg, M.E. and R. H. Lincoln. 1985. Wild chinook salmon management: An international conservation challenge. *N. Amer. J. Fish. Mgmt.* 5:311-329.
- Frankel, O.H. and M.E. Soule. 1981. *Conservation and Evolution*. Cambridge University Press, Cambridge.
- Franklin, I.R. 1980. Evolutionary change in small populations. pp.135-149. *In*: (M.E. Soule and B.A. Wilcox, eds.) *Conservation Biology: An Evolutionary-Ecological Perspective*. Sinauer Associates, Inc., Sunderland, MA.
- Hershberger, W.K. and R.N. Iwamoto. 1981. Genetics Manual and Guidelines for the Pacific Salmon Hatcheries of Washington. WDF, Olympia, WA. unpublished. 83pp.
- Hill, W.G. 1981. Estimation of effective population size from data on linkage disequilibrium. *Genet. Res.* (Cambridge) 38: 209-216.
- Holtby, L.B., R.K. Kadowaki and K.S. Simpson. 1992. Factors affecting the vulnerability of juvenile coho (*Oncorhynchus kisutch*) and chinook salmon (*O. tshawytscha*) in a saltwater sport fishery. *Can. J. Fish. Aquat. Sci.* 49:2164-2178.
- Hynes, J.D., E.H. Brown, Jr., J.H. Helle, N. Ryman and D.A. Webster. 1981. Guidelines for the culture of fish stocks for resource management. *Can. J. Fish. Aquat. Sci.* 38:1867-1876.
- Kapuscinski, A.R. and L.M. Miller. 1993. Genetic hatchery guidelines for the Yakima/Klickitat Fisheries Project (draft).

- Washington Department of Fisheries, 75pp.+ appendices.
- Lande, R. and G.F. Barrowclough. 1987. Effective population size, genetic variation, and their use in population management. pp.87-123. *In:* (M. Soule, ed.) *Viable Populations for Conservation*. Cambridge University Press, New York.
- Mace, G.M. and R. Lande. 1991. Assessing extinction threats: Toward a reevaluation of IUCN threatened species categories. *Conserv. Biol.* 5:148-157.
- Millar, R.B. 1987. Maximum likelihood estimation of mixed stock fishery composition. *Can. J. Fish. Aquat. Sci.* 44:583-590.
- Milner, G.B., D.J. Teel, F.M. Utter and G.A. Winans. 1985. A genetic method of stock identification in mixed populations of Pacific salmon, *Oncorhynchus* spp. *Mar. Fish. Rev.* 47(1):1-8.
- Nehlsen, W., J.E. Williams and J.A. Lichatowich. 1991. Pacific salmon at the crossroads: Stocks at risk from California, Oregon, Idaho, and Washington. *Fisheries* 16:4-21.
- Nelson, K. and M. Soule. 1987. Genetical conservation of exploited fishes. pp.345-368. *In:* (N. Ryman and F. Utter, eds.) *Population Genetics and Fishery Management*. Washington Sea Grant Program, Seattle, WA.
- PSC. 1990. Report of the Fraser River Panel to the Pacific Salmon Commission on the 1989 Fraser River sockeye and pink salmon fishing season. Pacific Salmon Commission. Vancouver, B.C. 51pp.
- Ricker, W.E. 1972. Hereditary and environmental factors affecting certain salmonid populations. pp.19-160. *In:* (R.C. Simon and P.A. Larkin, eds.) *The Stock Concept in Pacific Salmon*. University of British Columbia. Vancouver.
- Ricker, W.E. 1980a. Changes in age and size of chum salmon (*Oncorhynchus keta*). *Can. Tech. Rpt. Fish. Aquat. Sci.* No. 930. Pacific Biological Station, Nanaimo, B.C. 99pp.
- Ricker, W.E. 1980b. Causes of the decrease in age and size in chinook salmon (*Oncorhynchus tshawytscha*). *Can. Tech. Rpt. Fish. Aquat. Sci.* No. 944. Pacific Biological Station, Nanaimo, B.C. 25pp.
- Ricker, W.E. and W.P. Wickett. 1980. Causes of the decrease in size in coho salmon (*Oncorhynchus kisutch*). *Can. Tech. Rpt. Fish. Aquat. Sci.* No. 971. Pacific Biological Station, Nanaimo, B.C. 63pp.
- Rohlf, D.J. 1991. Six biological reasons why the Endangered Species Act doesn't work--and what to do about it. *Conserv. Biology* 5: 273-282.
- Ryman, N. 1991. Conservation genetics considerations in fishery management. *J. Fish. Biol.* 39(Supplement A): 211-224.
- Seeb, J.E., J.H.Helle, L.W. Seeb, R.L. Wilmot, A.J. Gharrett and W.W. Smoker. eds. *Proceedings of the International Symposium on the Genetics of Subarctic Fish and Shellfish*. *Can. J. Fish. Aquat. Sci.* (Supplement; in press).
- Seidel, P. 1983. *Spawning Guidelines for Washington Department of Fisheries Hatcheries*. WDF, unpublished. 15pp.
- Seidel, P., R. Bugert, P. LaRiviere, D. Marbach, S. Martin and L. Ross. 1988. Lower Snake River compensation plan Lyons Ferry evaluation program 1987 annual report. WDF unpublished, 106pp.
- Shaklee, J.B. 1991. Simulation and other analysis of the 1991 Columbia River spring chinook GSI baseline. *Wash. Dept. Fish. Tech. Rpt.* 115, 40pp.
- Shaklee, J.B. and C.P. Keenan. 1986. A practical laboratory guide to the techniques and methodology of electrophoresis and its application to fish fillet identification. *CSIRO Rpt. Aust.* 177:59pp.
- Shaklee, J.B., F.W. Allendorf, D.C. Morizot and G.S. Whitt. 1990a. Gene nomenclature for protein-coding loci in fish. *Trans. Amer. Fish. Soc.* 119:2-15.

- Shaklee, J.B., C. Busack, A. Marshall, M. Miller and S.R. Phelps. 1990b. The electrophoretic analysis of mixed-stock fisheries of Pacific salmon, p.235-265. *In: Z-I. Ogita and C.L. Markert (eds.) Isozymes: Structure, Function, and Use in Biology and Medicine Progress In Clinical and Biological Research. Vol. 344. Wiley-Liss, Inc. New York.*
- Shields, W.M. 1982. Philopatry, Inbreeding, and the Evolution of Sex. State Univ. of New York Press, Albany, N.Y.
- Simon, R.C. 1991. Management techniques to minimize the loss of genetic variability in hatchery fish populations. *Amer. Fish. Soc. Symp.* 10:487-494.
- Utter, F. and N. Ryman. 1993. Genetic markers and mixed stock fisheries. *Fisheries* 18(8):11-21.
- Utter, F., D. Teel, G. Milner and D. McIsaac. 1987. Genetic estimates of stock compositions of 1983 chinook salmon harvests off the Washington Coast and the Columbia River. *Fish. Bull.* 85:13-23.
- Wallace, B. 1991. Coadaptation revisited. *J. Hered.* 82:89-95.
- Waples, R.S. 1990. Conservation genetics of Pacific salmon. II. Effective population size and the rate of loss of genetic variability. *J. Hered.* 81:267-276.
- Waples, R.S. 1991. Definition of "species" under the Endangered Species Act: Application to Pacific salmon. U.S. Dept. Commerce, NOAA Tech. Memo. NMFS N/NWC-194, 29pp.
- Waples, R.S., G.A. Winans, F.M. Utter and C. Mahnken. 1990. Genetic approaches to the management of Pacific salmon. *Fisheries* 15(5):19-25.
- Washington Department of Fisheries, Washington Department of Wildlife, and Western Washington Treaty Tribes. 1993. 1992 Washington state salmon and steelhead stock inventory. Washington Department of Fisheries. Olympia, WA.