Use of molecular genetic marker data and pedigree inference to evaluate the efficacy of an adult-release stocking program on the Point Wolfe River, New Brunswick

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Abstract

Following recent declines in endangered inner Bay of Fundy (iBoF) Atlantic Salmon *(Salmo salar)*, a recovery program involving elements of captive rearing was initiated for the Point Wolfe River (PWR) of Fundy National Park, New Brunswick. In 2003 and 2004, 286 and 280, respectively, captive-reared adult Atlantic Salmon originally obtained from the Big Salmon River (BSR), were released into the PWR to spawn and potentially contribute to the next generation of this endangered population. In 2004 and 2005, fry (age 0+ juveniles) and parr (age 1+ juveniles), potential offspring of released adults, were collected and tissue sampled for subsequent analyses of molecular genetic variation. Exclusion- and likelihood-based parentage analyses were used to test the sampled offspring against all genotyped adults that were released into the PWR. First-order relatedness was also assessed in the group of PWR juveniles collected using kinship analyses, a method of pedigree reconstruction that can be performed in the absence of parental genotype information. Results from these analyses were combined and used to evaluate the efficacy of the adult-release stocking program currently in place for the PWR.

Results from parentage assignment analyses, testing offspring against pairs of adult releases, provide very strong evidence that at least 21 adults spawned in 2003. Results from parentage analyses where offspring were tested against parents singly, supported by simulation analyses and kinship reconstruction, further indicate that at least 29, and as many as 32, released adults likely contributed to the group of juveniles analyzed. Because the sample of juveniles was limited in size, and may not have been representative of the entire river basin population of Atlantic Salmon, these results should be considered minimum estimates of the number of adult releases that spawned in 2003. Kinship analyses also indicate contributions by multiple non-genotyped parents, likely mature male parr from the PWR. Estimates of the number of contributing parents and the mating structure in the PWR in 2003 indicate that the effective number of breeders that produced the entire collection of 2003 year-class juveniles sampled was approximately 28. Reductions in levels of genetic variation in the offspring (2003 year-class juveniles sampled from the PWR) relative to the putative parental group (adults released in 2003) were observed. Overall, pairs of genotyped male and female adult releases spawning together produced approximately 23 percent of the juveniles sampled, and single adult releases, for the most part spawning with, we suspect, mature male parr, produced a further 68 percent of the juveniles sampled.

In 2004, this same strategy, release of captive adults to spawn in natural river habitat, was less successful, as evidenced by both the reduced number of fry captured in 2005 and the observation that half of the 2004 year-class juveniles analyzed did not assign to any adult release. Possible reasons for the variable success include 1) reductions in the numbers of mature parr in the PWR in 2004, and 2) unknown environmental factors that may not have favoured complete maturation of BSR adults in 2004. Recommendations are made that will hopefully lead to increased, and more consistent, spawning success of released adults.

Résumé

Suite aux récents déclins du saumon atlantique *(Salmo salar)* de l'arrière-baie de Fundy, qui est en voie de disparition, un programme de rétablissement, comportant des apports de l'élevage en captivité, a été mis en œuvre dans la rivière Point Wolve, au sein du parc national Fundy, au Nouveau-Brunswick. En 2003 et 2004 on a lâché dans cette rivière, respectivement, 286 et 280 saumons atlantiques adultes élevés en captivité qui provenaient initialement de la rivière Big Salmon, pour qu'ils frayent et contribuent éventuellement à la prochaine génération de saumons de cette population en voie de disparition. En 2004 et 2005, on a prélevé des alevins (juvéniles d'âge 0 +) et des tacons (juvéniles d'âge 1 +), susceptibles de faire partie de la descendance des adultes lâchés dans la rivière, et procédé sur eux à un échantillonnage de tissus afin d'effectuer ensuite des analyses de la variation génétique moléculaire. Des analyses d'exclusion et de vraisemblance de parenté ont été utilisées pour comparer les descendants prélevés à tous les adultes de génotype connu qui avaient été lâchés dans la rivière. La parenté au premier degré a aussi été évaluée dans le groupe de juvéniles prélevé dans la rivière Point Wolfe, d'après des analyses de filiation, une méthode de reconstitution généalogique qui peut être utilisée en l'absence d'information sur le génotype parental. Une fois combinés, les résultats de ces analyses ont servi à évaluer l'efficacité du programme d'empoissonnement par lâcher de saumons adultes qui est actuellement en place dans la rivière Point Wolfe.

Les résultats des analyses de détermination de la parenté, comparant la descendance à des couples d'adultes lâchés dans la rivière, révèlent de façon très probante qu'au moins 21 saumons adultes ont frayé avec succès en 2003. Les résultats des analyses de parenté comparant la descendance à chacun des parents séparément, appuyés par des analyses de simulation et la reconstitution de la filiation, révèlent de plus qu'au moins 29 et jusqu'à 32 des adultes lâchés dans la rivière ont très probablement contribué au groupe de juvéniles analysé. Étant donné que l'échantillon de juvéniles obtenu était d'une ampleur limitée, et que donc il n'était peut-être pas représentatif de toute la population de saumons atlantiques du bassin versant de la rivière, ces chiffres devraient être considérés comme des estimations minimales du nombre d'adultes lâchés dans la rivière qui ont frayé en 2003. Les analyses de filiation dénotent aussi des contributions de multiples parents dont le génotype n'a pas été établi, vraisemblablement des tacons mâles à maturité provenant de la rivière Point Wolfe. Il ressort des estimations du nombre de parents ayant contribué au groupe de descendants et de la structure d'accouplement dans la rivière Point Wolfe en 2003 que le nombre réel de géniteurs ayant produit tous les juvéniles de la classe d'âge de 2003 échantillonnés était d'environ 28. On a observé des réductions du degré de variation génétique chez la descendance (juvéniles de la classe d'âge de 2003 provenant de la rivière Point Wolfe qui ont été échantillonnés) par rapport au groupe parental putatif (adultes lâchés dans la rivière en 2003). Dans l'ensemble, les mâles et femelles adultes de génotype connu lâchés en couples dans la rivière et qui y ont frayé ensemble ont produit 23 % des juvéniles échantillonnés, tandis que les adultes lâchés seuls dans la rivière et dont on pense qu'ils se sont accouplés pour la plupart avec des tacons mâles à maturité ont produit 68 % des juvéniles échantillonnés.

En 2004, cette même stratégie de lâcher d'adultes élevés en captivité pour qu'ils frayent dans l'habitat naturel de la rivière a remporté moins de succès, comme le montrent à la fois le plus petit nombre d'alevins capturés en 2005, et le fait que la moitié des juvéniles de la classe d'âge de 2004 analysés ne présentaient de lien de parenté avec aucun des adultes lâchés dans la rivière. La variabilité du succès de l'opération peut être due à : 1) des réductions dans le nombre de tacons à maturité présents dans la rivière Point Wolfe en 2004 et 2) des facteurs environnementaux inconnus qui n'ont peut-être pas été propices à une maturation complète des saumons provenant de la rivière Big Salmon en 2004. Le présent document contient des recommandations qui, espère-t-on, aboutiront à un succès de reproduction plus grand et plus constant chez les adultes lâchés dans la rivière.

Introduction

By greatly minimizing mortality at one or more life stages relative to that experienced in the wild, captive breeding and rearing has historically been used to provide additional salmon for fisheries, or to compensate for downstream mortality associated with the building of dams and other barriers to fish passage. However, traditional approaches often involved suboptimal management practices, such as the use of broodstock obtained from non-local sources, and the use of lineages maintained in captivity for multiple generations. These practices are suspected of possibly lowering the viability of populations in the wild (Brannon, 1993; Fleming and Petersson, 2001). Today, captive breeding and rearing is more commonly being used in a new role, termed 'supplementation', that aims to restore or augment declining populations while minimizing unnatural genetic changes (Cuenco *et al*., 1993; Kapuscinski, 1991; Miller and Kapuscinski, 2003). Typically, supplementation involves the capturing of broodstock from the wild, the artificial spawning of wild-origin adults, and the release of early- or late-stage juveniles back into rivers from which their parents were obtained. Although potentially less risky to wild populations than strategies involving multi-generation hatchery salmon or non-native salmon broodstock, there are still concerns over changes in the combined wild-hatchery populations relative to truly wild populations.

The artificial rearing environment, particularly during early embryological and juvenile development, may bring about direct behavioural, physiological, and neurological changes in released salmon relative to their counterparts growing up in the wild. For example, juvenile Steelhead Salmon *(Oncorhynchus mykiss)* reared in traditional smooth-bottom tanks have markedly smaller cerebellums relative to conspecifics that develop in the wild and relative to steelhead that develop in tanks with complex gravel-bottom substrates (Kihslinger and Nevitt, 2006). These changes may limit the effectiveness of supplementation programs by reducing the survival or breeding success of juveniles released into the wild.

Hatchery supplementation may also bring about a number of genetic changes, including the loss of genetic variation due to increased variance in family size and associated reductions in effective population size, in what has become known as the Ryman-Laikre effect (Ryman and Laikre, 1991). Other genetic modifications include changes in life history traits via unintentional selection associated with, for example, collection of broodstock (Miller and Kapuscinski, 2003), and the gradual accumulation of genetic adaptation to captive conditions in the combined hatchery-wild population even where broodstock are obtained from the wild each generation (see Reisenbichler *et al*., 2003). The absence of natural mate choice and associated benefits, such as the production of juveniles with 'compatible genes' and 'good genes' (Wedekind *et al*., 2008), may also have negative fitness consequences for salmonids produced through artificial spawning, as recently demonstrated by Pitcher and Neff (2007).

Recent research involving a range of vertebrate species is revealing another potentially important mechanism through which the early rearing environment may impact the phenotype of individuals and their offspring, which could be relevant to salmonid supplementation. It is now known that environmental variables such as tactile stimuli (Weaver *et al*., 2004), exposure to chemicals (Anway *et al*., 2005), and nutritional availability during early development (Heijmans *et al*., 2008) can result in modifications

to DNA (or associated histones) that can impact gene regulation without changes to the underlying sequence of the DNA itself. Surprisingly, these non-genetic or 'epigenetic' changes can be passed on to offspring through one or more generations (Anway *et al*., 2005).

Another strategy for potentially increasing salmon population size involves the release of adults into estuary or river environments for subsequent spawning and deposition of eggs into natural river habitat (reviewed in Berejikian *et al*., 2004). Under this approach, early salmonid embryological development could occur in natural river habitat, perhaps minimizing the scope for ontogenetic physiological and neurological change. The exposure of salmon to natural selection during early life history stages, when mortality is highest and natural selection most intense, may also minimize genetic adaptation to captive conditions and loss of fitness in the wild. Additionally, as opposed to traditional supplementation strategies, release of adults provides some opportunity for mate selection and breeding competition and associated fitness benefits to offspring.

There are, however, several potential drawbacks of adult-release recovery strategies relative to traditional supplementation approaches. First and foremost, released adults may exhibit little if any successful reproduction, as seen in Carr *et al*. (2004), resulting in a minimal demographic boost to the population of juveniles in the next generation. Second, considerable genetic variation may be lost in the production of the next generation of salmon, resulting from limited spawning success overall, reduced breeding success of hatchery-reared males and a resulting high ratio of female-to-male spawners, and increased variance in family size resulting from more variable fertilization success, poor egg survival due to poor redd site selection, etc. By failing to maintain levels of genetic variation in the founding population, these effects may also impact the future adaptability of the population to changing environmental conditions (Fraser, 2008), and lead to increased accumulation of inbreeding over time. Other less immediate but equally important concerns include whether or not offspring that are produced survive in freshwater and marine environments, whether they return to rivers of origin, and whether they spawn successfully. Reasons why offspring may not survive as well as offspring of truly wild salmon include 1) the impact of the adult rearing environment (food, exercise, etc.) on egg quality (egg membrane strength and integrity, egg size, quantity of lipid resources, egg composition, etc.), 2) poor spawning site selection and high early mortality, and 3) absence of benefits of natural *appropriate* mate choice; although released adults may have access to suboptimal and optimal mates, they may not exhibit normal behaviour that would result in the most favourable pairing of salmon in terms of maximizing offspring fitness. Clearly, both traditional supplementation and adult release programs are uncertain technologies, each with their own risks and potential benefits.

In the fall of 2003, biologists at Fundy National Park initiated a recovery program for the Point Wolfe River (PWR) population of endangered inner Bay of Fundy (iBoF) Atlantic Salmon (*Salmo salar*). The strategy involved the release of captive-reared adults into natural river habitat, as described above. Specifically, 286 captively bred and reared mature adult salmon, whose ancestors were obtained one or two generations previously from the nearby Big Salmon River (BSR) were released into the PWR; adults have been released into the river in subsequent years, though both the number and nature of adult releases have varied through time. In 2004 and every year thereafter, fry, parr and, in some years, smolts have been sampled from the PWR. Information has been recorded on

each individual collected, including length, site of capture, etc., and tissue samples taken and preserved for later genetic analyses, for the purpose of contributing information relevant to evaluating the success of the PWR adult-release spawning program.

Molecular genetic data, and subsequent parentage determination analyses, have been used elsewhere to monitor spawning and reproductive success of artificially produced salmonids in both semi-natural and natural river settings (Araki *et al*., 2007a,b; Berejikian *et al*., 2003). Briefly, offspring and potential candidate parents are tissue sampled and genotyped at 10 or more highly variable microsatellite molecular genetic markers. Multi-locus genotypes of offspring are then compared against all known candidate parents, using either exclusion or likelihood methods. Here, because of incomplete sampling of the possible candidate parents and the absence of gender information on the released adults, we use exclusion and likelihood methods, supported by the novel use of simulation and kinship analyses, to investigate potential offspring-parent relationships between captured juveniles and adults released into the PWR in 2003.

The primary objectives of this research are as follows: 1) to ascertain whether there was any effective reproduction by the adults released into the PWR, or whether juveniles observed in subsequent years were produced by wild returning adults, strays, and remaining mature male parr; 2) to estimate the number of adult releases that spawned and contributed to the group of juveniles sampled; 3) to infer the mating structure of the group of salmon that produced the sampled juveniles, including the relative contribution of genotyped adults and non-genotyped parents; 4) to estimate the effective number of breeders that produced the juvenile group sampled; and 5) to estimate levels of genetic diversity in the group of released BSR adults or candidate parents, the juvenile sample collection or putative offspring, and several other available reference groups. In the future, information contained within this report may help guide management decisions involving Atlantic Salmon conservation at Fundy National Park and elsewhere.

Methods

Study site: The PWR is located in New Brunswick, Canada, and empties into the Bay of Fundy (Figure 1) at 45°25'N, 65°01'W. Most of the watershed is contained within the boundaries of Fundy National Park, but northwest portions extend into largely undeveloped but recently logged areas. The river is approximately 15 to 20 kilometres in length and drains an area of approximately 14,000 hectares. Several smaller tributaries (brooks or creeks) flow into the PWR at various points along its length.

Release of adults or candidate parents: In 2003 and 2004, 286 and 280 adult salmon, respectively, were released into the PWR (see Tables 1, A1 and A2; Figure 1). Up to the point of release, all adults spent their life in captivity. The majority of individuals released in 2003 and 2004 were produced through the artificial spawning of adults captured as juveniles from the iBoF Big Salmon River a few years earlier. A smaller proportion of adults released in 2003 and 2004 (less than 10 percent) were offspring of salmon obtained from the Minto fish hatchery (see Tables A1 and A2). The grandparents of this latter group of released fish were collected from the BSR as juveniles, reared at the

Minto hatchery to maturity, then crossed to produce the next generation of salmon. A subsample of these families was then transferred to the Mactaquac fish hatchery and reared through to maturity. These fish were then crossed to produce this second group of adult releases. The lineage of BSR released adults descended from salmon obtained from the Minto fish hatchery (hereafter referred to as Minto BSR salmon) had been exposed to 2.5 generations of captive rearing and two cycles of captive breeding; the lineage of BSR released adults reared exclusively at Mactaquac (hereafter referred to as Mactaquac BSR salmon) had undergone 1.5 generations of captive rearing and one cycle of captive breeding. Of the 286 and 280 salmon released into the PWR in 2003 and 2004, 216 (75.5 percent) and 212 (75.7 percent), respectively, were genotyped at eight or more microsatellite loci and, in the vast majority of instances, at 10 or more loci (Table 1).

Collection of juveniles or candidate offspring: Juvenile salmon (fry and parr) were collected from the PWR from multiple sites (see Tables 2, A3 and A4; Figure 1) in 2004 and 2005. In addition to the taking and preserving of fin tissue for subsequent analyses, fork length, location of capture, date of capture, and other information were also recorded for each (Tables A3 and A4). Length and year of collection information were then used to determine the year class, or the year that an individual was produced via spawning in natural river habitat. Although we recognize that year class is typically used to refer to the year in which an individual was hatched, associating it with the year of production facilitated comparisons between juvenile groups (candidate offspring) and adult release groups (candidate parents).

Note that fry (age 0+ juveniles less than 70 millimetres in length) were produced one year previous to the collection year, but that parr (all juveniles sampled that were greater than 130 millimetres in length) may have been produced two or three years prior to the collection year. Parr collected in 2004 in excess of 130 millimetres were therefore not possible offspring of 2003 releases but instead were likely produced in 2002. These fish were not tested against 2003 releases. Fry collected in 2005 were likely produced in 2004 and were tested against salmon released in 2004 only. Parr collected in 2005 were produced either in 2002 or 2003 and were tested against parents released in 2003.

Molecular genetic laboratory analyses: All tissue samples (typically a caudal fin clip weighing between 0.1 and 25 milligrams) collected from live adults or juveniles were immediately stored in 1 to 2 ml of 95 to 99% ethanol in 1.5 ml screw-cap tubes. Tissue was then transferred to Qiagen's 96-well DNeasy plates, and DNA extracted and purified following the manufacturer's specifications. Polymerase Chain Reaction (PCR) amplifications were carried out in 10 µl volumes, containing between 1 and 100 nanograms of template DNA, 2mM of each dNTP, 0.5 µM labelled and unlabelled primers, 50mM KCl, 0.5 units of Taq DNA polymerase supplied by MBI Fermentis, and 2.0 mM $MgCl_2$. Thermal cycling conditions were as follows: (94°C for 3 min)X1, (94°C for 1 min, 58°C for 30 seconds, 72°C for 30 sec) X 5, and (90°C for 30 seconds, 58°C for 30 seconds, and 72°C for 30 seconds) X 30, followed by a 15- minute extension step at 72°C. Primer sequences for loci *Ssa*171, *Ssa*197 and *Ssa*202 are given in O'Reilly *et al*. (1996), SSsp2210, SSsp2215, SSsp2216, SSsp2201, SSsp1G7, and SSsp1605 are given in Paterson *et al*. (2004), and *Ssa*D144, *Ssa*D58, and *Ssa*D486 are given in King *et al*. (2005).

PCR products were combined, and salt, unincorporated dNTPs, and unincorporated labelled and non-labelled primers were removed using Qiagen's 96-well PCR Purification plates, as specified by the manufacturer. Fragments were size-fractionated and detected using either a Hitachi MJ Research Basestation automated fragment analyser/sequencer or an Applied Biosystems 3130 XL. Samples were cross-standardised between platforms and across batches of 96 samples by including two individuals with known genotypes in all batches of samples. One sample from each strip of eight tubes was duplicated within each set of 96 samples to identify sample placement errors, column inversions, and plate inversions. Duplication of samples also permitted quantification of rates of genotyping errors.

Exclusion analysis: Typically, offspring inherit a single autosomal (non-sex-linked) chromosome from each of their two true parents. In principle, candidate parents that do not share at least one allele at each locus surveyed with a given offspring can therefore be excluded as possible true parents. If both of the true parents are contained within the set of genotyped candidate parents, the two parents not removed following exclusion-based pairwise testing of each parent with a given offspring would be inferred to be the true parents. If the parents are not contained within the set of candidate parents genotyped, all candidate parents would fail to share an allele with a given offspring at all loci analysed, and would be removed as possible true parents, provided enough loci were analyzed to minimize the likelihood of chance sharing of alleles between candidate parents and offspring (discussed further below). If a single true parent is contained within the set of candidate parents analyzed, then the candidate parent sharing an allele with a given offspring across all loci would be identified as a likely true parent, and it would be inferred that the other parent was not contained within the set of parents analysed.

In practice, candidate parents may match a given offspring at all loci by chance alone and be incorrectly inferred to be the true parent. The frequency of occurrence of chance candidate parent-offspring compatibilities at a given number of loci, under the present conditions, was assessed using simulation analyses (explained further in Appendix III). Basically, if chance parent-offspring compatibilities across a specified number of loci are rare, given an appropriate number of analysis-wide parent-offspring pairwise comparisons, the finding of multi-locus compatibility between a candidate parent and an offspring can be taken as evidence for true parentage.

Conversely, a genotyping error (null alleles, replication slippage, or laboratory mistakes) or a mutation in either the offspring or candidate parent may result in a parent-offspring incompatibility and a false exclusion of a true parent. The potential impact of both genotyping errors and mutations on the ability to successfully and accurately assign offspring to true parents largely depends on the number of candidate parents offspring were tested against, the number of non-genotyped candidate parents, the number and variability of loci surveyed, and genotyping error rates. In this analysis, the impact of single-locus genotyping errors on parentage assignment results (in terms of excluding true parents) was minimized by initially allowing for single-locus incompatibilities, followed by an exploration of the details of the single-locus mismatch. Candidate parents exhibiting two or more incompatibilities when compared against a given offspring in single parent-offspring analyses, were generally excluded as possible true parents, but this was expected to have a minimal impact on excluding true parents. Given a

genotyping error rate of approximately 1% for these loci (see Herbinger *et al*., 2006), and an average number of 10 loci scored in both offspring and candidate parents, and given that a little less than half of all errors in both the parents and offspring will result in parent-offspring single-locus incompatibilities in single parent-offspring analyses, we expect as few as approximately 1 in 25 true parents to be excluded due to the occurrence of two genotyping errors.

When two or more BSR adults matched a given offspring at all or *L*-1 loci (where *L* is the total number of loci screened in both a given offspring and a candidate parent), the hypothesis of parentage was further tested by evaluating whether offspring inherited different alleles from the two candidate parents (the putative mother and father) at all of the loci tested at which the offspring was heterozygous; this will be referred to hereafter as the Inherit Different Alleles (IDA) test. Simulation analyses carried out on a collection of Atlantic Salmon candidate parents and offspring from the nearby Gold River, involving the same set of loci assayed here, indicate that offspring rarely (less than 1 percent of the time) inherit alleles from two unrelated parents that are singly compatible across all loci by chance alone. This would also be the case for situations where one candidate parent is the true parent of a given offspring, but the other is not, sharing alleles across all loci due to chance alone.

Likelihood analysis: Likelihood-based parentage assignment is based on allele frequency information and the probability of observing genotypes in the candidate parent and offspring given the hypothesis of parent-offspring relatedness versus that the two are unrelated. If several candidate parents both share an allele with a given offspring, but the first parent shares a rare allele with the offspring and the others a common allele, the first candidate parent will be considered a more likely true parent. Using this approach, it is possible to estimate true parentage when three or more candidate parents share a single allele with a given offspring at all loci. Also, by allowing for genotyping errors, candidate parents exhibiting one or even two mismatches with a given offspring can still be identified as the most likely parent by sharing rare alleles at the loci not exhibiting genotyping errors or mutations. The likelihood-based parentage analysis carried out here was performed using the program *CERVUS* 3.0.3 (Marshall *et al*., 1998) with recent modifications to maximum likelihood equations (Kalinowski *et al*., 2007). The program uses allele frequency information to calculate log-likelihood ratios or LOD scores for all parent-offspring pairs (the likelihood ratio is the likelihood of a given individual being the parent over the likelihood of parentage of an arbitrary individual (Marshall *et al*., (1998)). The higher the LOD score, the more likely the parent in a given parent-offspring set is the true parent.

In addition to testing offspring and single parents, *CERVUS* also evaluates offspring against maternal and paternal pairs of candidate parents (triad comparisons). We carried out both types of likelihood analyses for the following reasons. Testing of offspring against parental pairs makes use of likelihood information in the context of the two parents contributing opposite alleles, as discussed earlier for exclusion tests, which is considerably more powerful then tests of offspring against single parents. Analyses comparing offspring against single parents was done to accommodate instances where one parent was a genotyped BSR adult, and the other a non-genotyped individual. In both analyses, the error rate was set to 0.01 (as in Herbinger *et al*., 2006 for the same set

of loci), and we assumed that only 40 percent of the candidate parents were genotyped. The proportion of candidate parents genotyped is a value specified by the user when running the program *CERVUS*, that can have a marked impact on estimates of confidence levels (Marshall *et al*., 1998). The value used here was conservative, and was based on results from all three analyses that indicate that the vast majority of offspring appeared to have descended from at least one genotyped adult BSR salmon, and a number of other offspring from two genotyped adult BSR parents (indicating that at least half of all parents were probably genotyped). Although it could be argued that this reasoning is somewhat circular in that the proportion of candidate parents does affect confidence level estimates that do factor into levels of assignment certainty (discussed below), confidence levels were only used in assignment of offspring to pairs of parents, and most offspring were assigned based on single-parent analyses (likelihood or exclusion) only.

Kinship analysis: In recent reviews of pedigree reconstruction in natural populations, there has been a growing consensus that researchers ought to consider kinship analyses in investigations of wild populations in addition to standard parentage-based approaches (Wilson and Ferguson, 2002; Blouin, 2003). This type of analysis can be useful in the present study for the following reasons. First, kinship information can be used to estimate the number of contributing parents even when no other information (such as genotype information) on the parents exists. For example, if a group of offspring are partitioned into two full-sib families nested within a half-sib family, we know that three parents contributed to the pool of offspring sampled. Second, when full-sib group size exceeds three in number, kinship information and laws of Mendelian inheritance can be used to partially reconstruct the genotypes of the two parents. When two full-sib groups exist within a half-sib group, this information can be used to completely infer the parental configuration of alleles in each of the hypothesized parents and hence the actual parental genotypes. This information can be used to relate juveniles recovered from the Point Wolfe in 2004 and 2005 to non-genotyped BSR adult releases through grandparent analyses (Letcher and King, 2001), utilizing existing information on the parents of the group of adult releases. This is further explained in Appendix I in the context of a real example. Third, kinship information can be analyzed in the context of single-parent parentage results to further test (corroborate or refute) hypotheses of parentage based on exclusion or *CERVUS* analyses (discussed below).

Here, kinship was assessed using the program *COLONY* (Wang, 2004), a maximum likelihood-based method that partitions individuals into full- or half-sib groups while allowing for genotyping errors. This method clusters siblings together using information from both alleles from each offspring, without any information from the parents. The error rate used in this analysis was 0.01 for each of Class I (upper allele drop out) and Class II (stochastic) errors, for all loci.

Integration of results from parentage and kinship analyses: All information on parentage, kinship, site of release, age, etc., was compiled for each sampled juvenile. Juveniles were then sorted by half-sib group assignment, and then full-sib group assignment, so that individuals in the same full-sib group appeared next to each other, and then adjacent to half-siblings that were placed into a different full-sib grouping. Offspring assigning to the same full-sib group via kinship analyses should also assign to

1) the same two BSR adult releases, if descended from two genotyped BSR adult parents, 2) the same single BSR adult release, if descended from one genotyped BSR adult parent and one non-genotyped parent, or 3) no BSR adult release if descended from wild parr, strays, etc. Note that concordance between kinship and parentage analyses when two BSR adult candidate parents are identified will in itself yield little additional confidence in parentage assignment because offspring sharing a different allele with each of two parents across all loci due to chance alone are expected to also cluster into the same full-sib group. However, investigating whether multiple offspring that assign to a single known parent also fall into the same full-sib group does allow for a more rigorous testing of hypotheses of parentage. Were several (three or more) offspring to share a single allele with a given candidate parent due to chance alone, the other allele at each locus in each of these offspring would be free to vary. This would almost certainly result in the group of offspring failing to cluster into a single full-sib family via *COLONY*. In other words, groups of three or more offspring that cluster into the same full-sib family, and that share an allele with a single released candidate parent, are very likely both a) progeny of the single identified candidate parent, and b) progeny of a single other non-genotyped parent. Such a finding would increase the certainty of assignments of all offspring in the full-sib family to the single genotyped parent. Note, however, that it is possible for a group of juveniles to be the true offspring of a single released candidate parent and not group into the same full-sib family via kinship analyses. This would happen, for example, if the second parent of each juvenile assigning to the same first parent were different; these juveniles would be expected to group into the same half-sib family.

Estimating the type, gender, number of contributing parents, and the overall mating system that produced the group of PWR juveniles sampled in 2003: Results from parentage and kinship analyses presented here, and information from studies of declining inner Bay of Fundy salmonid mating systems from the published literature (e.g., Herbinger *et al*., 2006; de Mestral Bezanson *et al*., 2010), were used to estimate the number of parents, the gender of individual parents, and the type (wild parr versus released adults) that contributed to the sampled juveniles produced in the PWR in 2003. In this analysis, we assumed there were only three types or classes of contributing parents: mature wild male parr, released genotyped BSR adult males, and released genotyped BSR adult females. Contribution by a genotyped adult release was directly indicated by parentage analyses. If the existence of a parent was inferred through kinship analyses (as described in Herbinger *et al*., 2006), but no BSR adult was indicated via parentage analyses, we assumed that the parent was a wild mature male parr. However, we recognize that it is possible that the true parent was a non-genotyped BSR adult release, a returning wild PWR adult, a wild stray, or an aquaculture escape.

Additional inferences of parental gender were based on the following. For half-sib groups with full-sib groups nested within, the common (half-sib) parent, whether a genotyped adult release or a non-genotyped parent, was inferred to be female, as in Herbinger *et al*. (2006) and de Mestral Bezanson *et al*. (2010), and the parent specific to a particular full-sib group (the full-sib parent), was inferred to be male. For pure full-sib families, where both parents are identified as adult releases and where neither is hypothesized as contributing to another family, gender was assigned arbitrarily, as no

information was available to designate either as male or female, and because the specific assignment of gender will not impact gender-specific counts of the number of successfully spawning BSR adults, or estimates of mating structure, or estimates of effective numbers of breeders. For pure full-sib families, where one parent is identified as an adult release and the other an unknown non-genotyped parent, the adult release was designated to be female and the non-genotyped parent male. This inference was based on observations from elsewhere indicating that captive-reared females are much more likely to reproduce in the wild than are captive-reared males (Fleming and Petersson, 2001; McGinnity *et al*., 2003), and the fact that non-genotyped males (numerous male parr plus non-genotyped released males) likely greatly outnumbered non-genotyped released females, suggesting that the second unidentified parent was probably male.

A minimum estimate of the total number of genotyped BSR adults contributing to the group of juveniles sampled was made by summing the number of different BSR parents that were identified as the true parent of one or more PWR offspring. The number of contributing parr was estimated from kinship information. If, for example, a particular BSR release was implicated as the only genotyped parent of 15 juveniles from three full-sib groups that were assigned to a single half-sib family, it was inferred that three different mature parr were the alternate parents in each of the different full-sib groups.

It should be understood, however, that the mating system constructed in this study is an approximation of the actual mating system that gave rise to the juveniles produced in 2003, the accuracy of which will be dependent on 1) the accuracy of the original parentage and kinship analyses, 2) the number of non-genotyped adult fish (non-genotyped BSR releases, returning PWR salmon and strays) that did actually contribute to the pool of sampled juveniles, and 3) the robustness of above assumptions, such as the increased reproductive performance of captive-reared females relative to males, though often evaluations were based on several lines of evidence.

Estimating effective number of breeders (N_b): Estimates of effective number of breeders, accounting for the effects of different variables, were made using formulas from Chapter 10 of Frankham *et al*. (2002).

The effective number of breeders for a given cohort, accounting for departures from the idealized 1:1 sex ratio (N_{b1}), was approximated using:

$$N_{b1} \approx 4N_f N_m / (N_f + N_m)$$

where N_f is the number of breeding females and N_m is the number of breeding males.

Single-generation effective number of breeders for a given cohort, accounting for the influence of variance in family size (N_{b2}) was estimated using:

$$N_{b2} = (Nk - 1) / [k - 1 + (V_k / k)]$$

where N is the number of individuals, k is the average family size, and V_k is the variance in family size.

Single-generation effective number of breeders for a given cohort, accounting for departures from the idealized sex ratio and variance in family size (N_{b3}), was estimated by first calculating N_{b2} for females and males separately using:

$N_{b2f} = (N_f k - 1) / [k - 1 + (V_k / k)]$
$N_{b2m} = (N_m k - 1) / [k - 1 + (V_k / k)]$

where N_f is the number of females, N_m is the number of males, and k and V_k are mean and variance of family size for the respective sex group.

Next, N_{b3} was estimated by combining N_{b2f} and N_{b2m} as follows:

$N_{b3} = 4N_{b2f}N_{b2m} / (N_{b2f} + N_{b2m})$

Variance in family size was based on the family sizes observed in the PWR.

Estimating levels of molecular genetic variation: Gene diversity, which is approximately equivalent to the likelihood that two alleles drawn at random from a given sample are different, and allele richness, the number of alleles observed and standardized for differences in sample size (Hurlbert, 1971), were estimated using *FSTAT* 1.2 (Goudet, 2001). *FSTAT* was also used to enumerate the number of different alleles observed in the sample collection and to estimate F_{IS} values, an analog of Wright's inbreeding coefficient.

Assessing genotypic similarity amongst the BSR adult releases: The degree of genotypic similarity of BSR adult releases was determined by calculating the percent identity between pairs of adults. Percent identity was simply the percent of all single-locus genotypes that were identical in the set of loci common between two BSR adult releases, and was calculated using the program *Microsatellite* (Park, 2007). This value was calculated to address observations of some offspring being compatible with more than two parents at a large number of microsatellite loci.

Parentage and kinship analyses of released parents: Relatedness among the BSR adult candidate parents was assessed using kinship and exclusion-based parentage methods, involving genotype information from the parents of the adult releases themselves, as described above for PWR offspring. This analysis was also performed to investigate occasional occurrences of offspring assigning to two or more adult releases at a large number of loci, but not exhibiting IDA. Such occurrences, for example, may be due to an offspring exhibiting multiple compatibilities to a first candidate parent due to parent-offspring relatedness, and a second parent because of its high degree of genotypic similarity with its sibling, the true parent of the offspring.

Assessment of levels of inbreeding in the Point Wolfe juveniles: Levels of actual observed inbreeding resulting from consanguineous matings in 2003 only were determined for all PWR juveniles that could be assigned to two BSR adult releases.

Inbreeding resulting from matings between relatives in earlier generations, or due to relatedness among non-genotyped parents, was not considered. Instances where the maternal and paternal parents of a given PWR juvenile shared two parents in common resulted in an inbreeding coefficient of F=0.25, and instances where the maternal and paternal parents of a given PWR juvenile shared a single parent in common resulted in an inbreeding coefficient of F =0.125.

Results

Completion of genotype datasets: In total, 216 of the 286 adults released in 2003, and 212 of the 280 adults released in 2004, were tissue sampled and genotyped at 8 or more loci (Table 1). For the group of BSR adults from 2003, the failure to analyze approximately 70 samples was due to the degradation of DNA. DNA from these adults was extracted years earlier for other purposes and had undergone repeated freeze-thaw cycles which results in DNA degradation. For the group of BSR adults from 2004, data were not available for approximately 73 individuals because these fish had lost their Passive Integrated Transponder (PIT) tags, and so could not be linked to individual tissue samples and individual genotypes. DNA degradation was also a problem for the group of BSR adults released in 2004, which again were analyzed years earlier for other purposes. Of the 216 and 212 BSR adults released in 2003 and 2004, respectively, for which analyses were possible, genotype datasets were 92.4 and 89.4 percent complete, respectively. In total, 98 juveniles collected in 2004 and 2005 from the 2003 year class, and 10 juveniles collected in 2005 from the 2004 year class, were successfully analyzed.

A higher proportion of the Point Wolfe juveniles analyzed were successfully genotyped, 57 of the 61 juveniles collected in 2004, and 63 of the 64 juveniles collected in 2005 (Table 2), despite the fact that tissue weights were very low (often between 0.1 and 0.5 milligrams). In fact, genotype databases for these two groups were 95.5 and 98.4 percent complete, respectively. This increased genotyping success likely reflects the increased quality of DNA of the juveniles relative to the adults.

Summary statistics of microsatellite informativeness for likelihood analyses: Summary statistics of individual locus variability and their power to resolve parentage using likelihood based methods, as estimated using the program *CERVUS* for the present dataset, are given in Table 3. Note that all loci are variable, exhibiting multiple different alleles and expected heterozygosity values ranging from 0.636 to 0.939. In fact, the majority of loci are exceptionally variable compared to other data sets seen in the literature, approaching expected heterozygosity values of 0.90 or greater. When individual single-locus exclusion powers (the inverse of non-exclusion powers given in Table 3) are combined, this suite of markers should exclude 99.99961 percent of all non-true candidate parents in single parent-offspring analyses.

In most instances, the frequency of null alleles, alleles that failed to amplify sufficiently to yield enough product to permit detection, was low, 1.5 percent or smaller (Table 3). However, several loci exhibit moderately high null allele frequencies, in the range of 2 to 5 percent, which is also reflected in slight reductions in levels of observed heterozygosity relative to expected heterozygosity (Table 3).

Comparison of microsatellite allele variants observed in the Big Salmon River adult releases and juveniles recovered from the PWR: Multiple microsatellite alleles, ranging from 6 to 29 per locus, were observed in the combined BSR adult-PWR gene pool (Tables 4a and 4b). Generally speaking, there was considerable overlap in the distribution of alleles observed in the BSR adult and PWR juvenile groups; however, several different alleles (12) involving multiple (7) loci were observed in the PWR juvenile group that were absent in the BSR adult collection (Tables 4a and b). In several instances, the variant observed in the PWR collection only was found in multiple (up to 5) PWR juveniles. In total, 32 alleles were observed in PWR salmon that were absent in the group of genotyped BSR adult releases.

Detailed analyses of parentage and kinship results for Point Wolfe River juveniles produced in 2003 and 2004: Once information from all parentage and kinship analyses were tabulated, a final parentage conclusion was made based on all of the above information. In some instances, the strength of evidence that a given candidate parent was the true parent of a particular offspring was considerable. In other cases, however, the assignment was less certain, due, for the most part, to insufficient genotype information (relatively few loci in common between the candidate parent and offspring), but also to the existence of a single-locus parent-offspring mismatch, or non-concordant results between the different analyses performed. To accommodate this uncertainty, all assignments of offspring were designated as high, medium, or low confidence.

Assignment of offspring to two candidate parents at all of 11 or more loci and the observance of IDA was considered to be of high confidence, because simulation analyses indicate that the chance that an offspring will match a single candidate parent at 11 or more loci when that offspring is not a progeny of that parent is very low under present conditions (Figure AIII-1a) and, additionally, offspring are very unlikely to share different alleles with each of a given pair of candidate parents if they match one or both parents due to chance alone ($p < 0.01$, unpublished data involving the same set of loci and a nearby Atlantic Salmon population from Nova Scotia). In fact, because of the low likelihood of observing IDA, assignments of offspring matching to each of two parents at 11 of 12, 10 of 11, or 10 of 10 loci, where each offspring inherited a different allele from each parent at all or all less one locus, were considered to be of high confidence. Assignments of offspring to a single candidate parent at all of 11 or more loci was also considered to be of high confidence, because, once again, simulation analyses indicate that assignment of offspring to a single candidate parent at all loci by chance alone under the present conditions is rare (Figure AIII-1a). Offspring were also assigned with high confidence if there was reasonable evidence for assignment to a single parent (e.g., compatibility at 9 of 9 or 10 of 11 loci), two or more additional juveniles assigned to the same BSR adult via parentage analyses, and all clustered into the same full-sib group via *COLONY* (see methods section on *Kinship analyses* for discussion on why this specific scenario supports assignment of offspring to individual parents). The above conditions account for greater than 90 percent of all high confidence assignments. However, a few additional offspring were also assigned to a single parent with high confidence because of moderate support from multiple analyses (exclusion, likelihood and kinship), and because analyses involving other offspring implicated the parent as having spawned successfully

in 2003. Note, too, that for the vast majority of offspring, high confidence assignments were supported by multiple lines of evidence.

A few individuals were also assigned with moderate confidence. In such instances offspring typically assigned to a single parent at either a high number of loci but exhibited a single locus mismatch, or at a moderate number of loci but exhibited no mismatches. However, in all cases, assignments to an individual parent were consistent with kinship analyses and were associated with moderate support from likelihood analyses (modest to high LOD scores), and analyses involving other offspring implicated the candidate parent as having spawned successfully in 2003.

Several offspring were assigned to parents with low confidence. In these instances, one (and occasionally two) parent-offspring mismatches were observed, likelihood-based LOD scores were generally low, analyses involving other offspring had not implicated the parent as having spawned successfully in 2003, and results from different analyses were not concordant. These offspring-candidate parent pairs may still very well reflect true parent-offspring relatedness, or the chance sharing of alleles between offspring and unrelated adults (parent-offspring matches at all but one locus are not unexpected given the large number of analysis-wide pairwise comparisons; Figure AIII-1b). They are included here as possible instances of parentage because the evidence that a given candidate parent is not the true parent is weak. In contrast, several offspring exhibited multiple single-locus incompatibilities when compared against any genotyped candidate parent, and often no parent was identified as plausible in the likelihood analyses performed (all parent-offspring pairs exhibited negative LOD scores). Furthermore, nearly all clustered into the same half-sib group in kinship analyses. That nearly all of the siblings from this group also failed to assign to any genotyped parent indicates that one or two genotyping errors or mutations in a few offspring are probably not responsible for the absence of parent-offspring matches in this group. These juveniles are likely not the progeny of any genotyped adult release, and were designated as unassigned.

In some instances, for example, when estimating the *minimum* number of successfully spawning adults, when the consequences of a Type II error (accepting a given candidate parent when it was not the true parent) are greater than those of a Type I error (rejecting a given candidate parent when it was the true parent), we were conservative and only presented results based on high, and high + medium, confidence assignments. In other instances, the consequences of creating Type I and Type II errors were similar, for example, when assessing the relative contribution of BSR adult x BSR adult versus mature PWR male parr x BSR female crosses. BSR adult x putative male parr, Here, excluding a particular BSR adult male as a possible parent when it is the true parent underreports the contribution of the first type of parental cross, whereas identifying a BSR adult as a true parent when it is not underreports the contribution from the second type of parental cross. When consequences of a Type I or Type II error were similar, results were presented for high + medium and high + medium + low confidence assignments. The level of confidence of relevant parentage assignment results associated with a particular analysis is stated in the corresponding text.

Results from kinship, exclusion, and likelihood analyses, involving offspring collected from the Point Wolfe River in 2004 and 2005 but produced in 2003, are given in Table 5. Results from exclusion analyses, involving offspring collected from the Point

Wolfe River in 2005 but produced in 2004, are given in Table 6. Details on the assignment of juveniles to single parents or parental pairs, including reasons for designated levels of confidence for specific offspring produced in 2003 and 2004, are given in Appendix I.

Summary of parentage assignment results for the 2003 PWR year-class group: When considering high confidence assignments only, 11.6 percent of the 216 genotyped BSR adults released into the PWR in 2003 were found to have spawned successfully, producing one or more offspring that survived to the point of sampling as either fry in 2004 or parr in 2005 (Table 7). If medium confidence assignments are included, 13.4 percent of the genotyped BSR adults reproduced successfully, and if low confidence assignments are considered, 14.8 percent of BSR adults likely contributed to the 2003 year class of salmon sampled from the PWR in 2004 or 2005 (Table 7).

Instances where two BSR adult releases were identified as the parents of a given PWR juvenile provide clear evidence that, to some extent, both male and female adult releases spawned successfully, even without any gender information on the adult releases (Tables 5 and 8). Indeed, based on high and medium confidence assignments only, 15 different spawning events (the mating between a specific male and a specific female), involving only BSR adults, were observed, 16 if low confidence assignments are included (Tables 5 and 8). However, a greater number (20) of spawning events were observed involving one BSR adult and a putative PWR male parr (28 if low confidence assignments and kinship information are considered; Tables 5, 8 and A7). Moreover, this latter class of spawnings accounts for nearly three quarters of the juveniles produced (Table 8).

Female BSR adults may have been more likely to spawn than male BSR adults (Tables 5, 8, A7), and often appear to have mated with multiple males, including multiple male adult releases, but also multiple non-genotyped males, probably mature male parr, or both genotyped BSR adult males and mature male parr (half-sib families 1.X, 2.X, 3.X, 5.X, 6.X, 7.X and 9.X; Tables 5 and A7). Specifically, nine incidences of polyandry, the spawning of a female with multiple males, were observed in 2003, versus only three incidences of polygyny, the spawning of a male with multiple females (Tables 5, 8 and A7).

A large percentage of the PWR 2003 year-class juveniles sampled appear to be direct descendents of at least one genotyped BSR adult release (68.4 percent based on high confidence assignments, 73.5 percent based on high or medium confidence assignments, Table 7). Many of the offspring that assigned with low confidence may also be progeny of the BSR adult releases, so it is likely that somewhere between 73 and 92 percent of the offspring sampled are progeny of either one or two genotyped BSR adult releases.

Estimates of effective number of breeders contributing to 2003 year-class juveniles sampled from the PWR: The effective number of breeders (N_b) in the Point Wolfe River in 2003 was estimated for 1) the parental group that produced the entire 2003 year-class juveniles analyzed, and 2) the parental group that produced the subset of juveniles descended from pairs of BSR parents. The N_b of the parental group contributing to the entire collection of PWR juveniles produced in 2003 was 55.2, 28.0 and 28.04, when

accounting for unequal sex ratios, variance in family size, and both unequal sex ratios and variance in family size, respectively (Table 9). Corresponding values for the group of parents of offspring that were produced solely by pairs of male and female BSR adults were 22.9, 43.4 and 20.6, generally lower than those reported for the group of parents that produced the entire collection of 2003 year-class juveniles, except N_b accounting for variation in family size.

Estimates of neutral molecular genetic variation in the BSR candidate parents, PWR juveniles, and other reference populations: Several indicators of levels of within-population genetic variation, including gene diversity or effective heterozygosity, the observed number of alleles, and allele richness, were estimated for the BSR adults (candidate parents), PWR juveniles (putative offspring), and a number of reference populations. Specifically, the groups contrasted here were 1) the 216 successfully genotyped BSR adults released into the PWR in 2003 (BSR ADULT REL 2003), 2) the 98 PWR juveniles produced in 2003 that were successfully genotyped (PWR WILD 2004/2005), 3) the 25 PWR juveniles produced in 2003 that assigned to two BSR candidate parents with high, medium or low confidence (PWR WILD 04/05 PAIRS), 4) a previously analyzed group of 56 juveniles collected from the PWR river in 2001 (PWR WILD PARR 2001), 5) a previously analyzed group of 98 smolt collected from the PWR in 2004 (PWR WILD SMOLT 2004), 6) a previously analyzed group of wild parr collected from the nearby inner Bay of Fundy BSR in 2001 (BSR WILD PARR 2001), 7) a previously analyzed group of wild parr collected from the inner Bay of Fundy Stewiacke River in 2001 (STW WILD PARR 2001), and 8) a previously analyzed group of wild parr collected from the outer Bay of Fundy Saint John River in 2001 (SJR WILD PARR 2001). Of primary interest in this analysis were comparisons between the BSR ADULT REL 2003 group (the candidate parents) and the PWR WILD 2004/2005 group (the putative offspring). Also of particular interest are comparisons between the BSR ADULT REL 2003 and the PWR WILD 04/05 PAIRS groups, as the latter represent the group of offspring that were produced solely by BSR adults spawning with other BSR adults, without contributions by native wild male parr. This latter comparison will be important when considering the efficacy of the approach in the absence of native wild parr.

Gene diversity, the metric considered to be the least sensitive to population bottlenecks, declined noticeably between the BSR ADULT REL 2003 group and the PWR WILD 2004/2005 group, based on either the nine-locus dataset or the seven-locus dataset (Table 10). Allele richness, usually considered to be more sensitive to population bottlenecks, also declined between these two sample collections, in both nine- and seven-locus datasets, and when standardizing to large datasets (for more robust estimates of the statistic) or small datasets (allowing for inclusion of the PWR WILD 04/05 PAIRS sample collection). The observed number of alleles decreased the most steeply between the BSR ADULT REL 2003 group and the PWR WILD 2004/2005 group, in both the large and small datasets. Reductions between the parental and offspring groups were much more pronounced, however, when comparing the BSR ADULT REL 2003 and PWR WILD 04/05 PAIRS groups for all three measures of genetic variation, particularly in terms of the observed number of alleles, where we report a 33.6% decline based on the nine-locus dataset.

Although all measures of genetic variation were much reduced relative to the BSR ADULT REL 2003 group, the PWR WILD 2004/2005 sample collection was either as genetically variable as the other PWR reference groups or slightly more variable, with the exception of allele richness for the latter collection, which was slightly elevated. In fact, the PWR WILD 2004/2005 group exhibited higher levels of variation than the STW WILD PARR 2001 group, but slightly lower levels compared to the BSR WILD PARR 2001 sample collection. The PWR WILD 2004/2005 group did, however, exhibit moderate reductions in genetic variation compared to the SJR WILD PARR 2001 reference group, as did all other inner Bay reference populations, for all metrics estimated.

Genotypic similarity among the candidate parents: In order to help interpret patterns of assignments of PWR offspring to candidate parents, we assessed the genotypic similarity of the candidate parents. In Table A5, candidate parents with greater than 75% identity are listed. In total, 46 pairs of individuals exhibited greater than 75% identity, including two individuals that had identical genotypes across 10 loci. Note that the two individuals exhibiting identical genotypes had similar but not sequentially adjacent Carlin tag identifiers (F6533 and F6537) (Table A5). These samples were not located in wells physically adjacent in 96-well sample plates in which DNA was extracted in preparation for microsatellite amplification, but rather were separated by three other samples. Therefore, it is unlikely that this was a duplicated sample, i.e. the same fish sampled twice. Instead, two BSR parents with identical genotypes is not unexpected given the large number of pairwise parental comparisons (93,961), the occurrence of full-sibling relationships in the parents (see below), and the relatively small number of founders (24, Herbinger *et al*., 2006) from which the Minto BSR adult releases descended.

Kinship and parentage analysis of the BSR released adults: Kinship analysis of the genotyped BSR adults indicated considerable relatedness among the candidate parents (Table A6), with half-sib group size ranging from 2 to 15, with an average and variance of 6.22 and 7.97, respectively.

Relatedness amongst the candidate parents was also investigated through parentage analysis, testing each of the BSR adults against known parental crosses carried out in 2000 as part of the iBoF Live Gene Banking program (see O'Reilly and Doyle, 2007). Note that these results involve only BSR salmon released into the PWR in 2003, and are a subset of those involved in the kinship analysis. Here full-sib groupings ranged from one to nine, with an average and variance of 2.88 and 3.16, respectively. Concordance between parentage and kinship analyses was very high, with groups of offspring assigning to the same two parents by parentage analysis also grouping via *COLONY* into the same kin groups. Note that because the BSR adult releases were produced by paired spawnings, where nearly all females were mated once with a single male, half-sib groups identified by *COLONY* are almost always simple full-sib groups.

Discussion

To review, four groups of Atlantic Salmon were analyzed, BSR 2003 adult releases, BSR 2004 adult releases, 2003 year-class juveniles sampled from the PWR and 2004 year-class juveniles sampled from the PWR. The PWR 2003 year-class collection actually included 0+ fry (individuals less than 70 millimetres), and 1+ parr (individuals greater than 130 millimetres sampled in 2005), numbering 98 in total. The 2004 year-class collection contained only 0+ fry sampled in 2005, numbering only 10 in total. Because of the small sample size of the latter, most of the subsequent discussion will be based on comparisons of the BSR 2003 releases as the main candidate parent group, and the PWR 2003 year-class juveniles as the main potential offspring group.

Results from these analyses clearly indicate some successful spawning by BSR adults released into the PWR in 2003. This may appear to be self-evident by the observation of juveniles in the river in 2004 and 2005, but it should be noted that a modest number of juveniles were observed in the river in 2002 and 2003, prior to the release of any captive-reared adults or juveniles, and must have been produced by returning salmon, strays, or aquaculture escapes spawning in the PWR. These results also allow us to estimate the number of BSR adults that spawned successfully, by counting the number of different parents that contributed to the pool of PWR juveniles sampled in 2004 and 2005, produced in 2003. Assuming for a moment that all parentage assignments are accurate, it should be noted that this is indeed a minimum estimate for the following reasons: 1) the sample of juveniles collected is small, and the number of adults detected could grow with an increase in the number of juveniles sampled; 2) the sampling of the river is incomplete, and the numbers of adults detected could increase with a more representative sample of the entire drainage; 3) mortality could have occurred between fertilization and the time of sampling, so adults that released gametes that resulted in successful fertilization may not have been represented in the pool of surviving juveniles sampled; and 4) not all BSR adults were genotyped.

Between 25 (11.6 percent) and 32 (14.8 percent) of the BSR adults genotyped, depending on the level of confidence accepted (Table 7), appear to have spawned successfully. Furthermore, the relationship between the number of juveniles sampled and the number of adults detected (Figure 2) suggests that analyses of a larger number juveniles would indeed identify additional BSR adult spawners, though it should be noted that as the number of offspring analyzed increased, many fewer adults were being detected per additional juvenile sampled.

Parentage analysis results presented here also provide reasonable evidence that the genotyped BSR adults released in 2003 contributed to between 68.4 and 73.5 percent of the 2003 year-class juveniles sampled from the PWR. If a portion of the low confidence assignments represent true parent-offspring relationships, it is likely that somewhere between 70 and 90% of PWR 2003 year-class juveniles were produced by at least one genotyped BSR adult spawning in the PWR in 2003. Additionally, reconstruction of parental genotypes and subsequent grandparentage analyses as employed by Letcher and King (2001) suggest that many of the remaining unassigned juveniles may have been offspring of one non-genotyped BSR adult release, itself an offspring of BSR founders T52699 and T52698 (see Appendix II, and Tables A8a and A8b). Cleary, the BSR adult releases made an important demographic contribution to the

juveniles sampled here. However, our results also indicate the probable contribution by salmon other than the genotyped BSR adults, as we could only identify one of the two parents of most of the PWR juveniles analyzed.

The second parent of many of the offspring analyzed could be non-genotyped BSR adult releases, returning PWR adults, wild strays, or aquaculture escapes. Several lines of evidence suggest that non-genotyped BSR adults did not account for the majority of unidentified second parents. First, only approximately 25% of the BSR adults released in 2003 were not genotyped, yet approximately half of the 60 parents inferred through parentage and kinship analyses (Tables 7 and A7) were non-genotyped salmon. Second, captive-reared males appear to be less likely to spawn successfully in the wild relative to captive-reared females (Fleming and Petersson, 2001; McGinnity *et al*., 2003). Third, 32 alleles, involving over 30 offspring, were absent in the BSR adult gene pool, but present in the gene pools of PWR sample collections obtained in 2001 and 2004 (Tables 4a and 4b, and unpublished data). These non-genotyped parents may be wild PWR adult returns, wild or aquaculture strays, or PWR mature male parr.

The presence and prevalence of alleles observed in the juvenile sample collection that were also common in recent historical PWR reference populations surveyed suggest that strays (wild or aquaculture) may not be important contributors. Instead, the mating structure inferred for many kin groups in this study, and results reported above, suggest that residual populations of male parr (observed in the river at the time of release of the BSR adults in 2003) may have been important contributors to the 2003 year class of juveniles sampled. Specifically, we observed a high incidence of occurrences of a single parent of one sex spawning with multiple members of the opposite sex (see Tables 5, 8 and A7), similar to that reported in Herbinger *et al*. (2006), which they argued reflected the spawning of a handful of females with a larger number of mature male parr and the occasional returning adult male. This finding of polyandry (the mating of a single female with multiple males) in the recent wild-spawning group of BSR parents analyzed by Herbinger *et al*. (2006) has been corroborated by de Mestral Bezanson *et al*. (2010) using the sex-linked genetic marker *Ssa*202. Herbinger *et al*. (2006) and de Mestral Bezanson *et al*. (2010) both argue that the polyandrous mating system observed is likely, at least in part, a function of recent and sharp population declines and high marine mortality, resulting in a situation where a handful of returning adults (males and females) are left to spawn with still comparatively large populations of mature male parr. Although with the release of nearly 300 BSR salmon into the PWR the population of mature adult salmon in 2003 was likely somewhat larger than that observed in the BSR in recent years, results here indicate that only a small portion likely spawned successfully, creating a situation once again where reproductively competent adult salmon (consisting of males and females) were likely greatly out numbered by reproductive male parr. The overall importance of this putative group of parents is reflected by the fact that they contributed to the production of between 43 and 65 percent of juveniles sampled. Note, too, that contributions by native wild parr may also be important in 1) minimizing loss of local adaptation, 2) minimizing rates of domestication selection over time, and 3) reducing rates of loss of genetic variation (discussed below). Note, however, that it is unknown whether (and how many) male adult returns also contributed to the group of juveniles sampled (two wild adult returns were observed in the PWR in 2003).

One incidence of mating between related adult releases in 2003 was observed (Table A9). This particular cross produced only one sampled offspring, and resulted in a level of inbreeding, due to consanguity in the previous generation only, of F=0.25 (Table A9).

Whereas the vast majority of juveniles produced in 2003 appeared to be directly descended from one or two genotyped adult releases, 5 of the 10 juveniles from the 2004 year class were offspring of non-genotyped parents (non-genotyped adult releases, wild PWR mature parr, wild PWR adult returns, or strays). It is interesting to note many of the several alleles from this group of unassigned offspring were absent from the BSR adult gene pool, but were present in the Point Wolfe reference collections obtained in 2001-2004 (see O'Reilly and Cox, 2004; unpublished data). These results are consistent with one, and possibly two, parents of these offspring being of PWR in origin. When taken together, the recovery of many fewer 0+ fry in 2005 relative to 2004, the reduced smolt run in 2007 relative to 2006 (Corey Clarke, unpublished data), the failure of half of the juveniles sampled to assign to any adult release, the inference of spawnings between two non-genotyped BSR adults from a group of only 10 sampled juveniles, and the occurrence of multiple alleles observed in PWR reference populations but not the BSR adult gene pools analyzed suggests that although some BSR adults released in 2004 did spawn successfully, the overall spawning success of the released adults was markedly lower than in 2003. This lower efficacy may be due to the reported marked reduction in the number of male parr observed in the river in 2004 relative to 2003, and the importance of parr in directly contributing as parents and in possibly initiating spawning behaviour in the adults. Alternatively, the reduced spawning performance may be due to a greater mismatch between natural and artificial rearing conditions (temperature, photoperiod, etc.) in 2004 relative to 2003, and potentially reduced maturity of adult releases in 2004 compared to those released in 2003.

The effective number of breeders contributing to the 2003 year class of juveniles sampled from the PWR in 2004 and 2005, when accounting for both unequal sex ratios and variance in family size, was quite low, 28.04. Important factors contributing to this low value are the number of successfully reproducing parents and high variance in family size (see Table 5). The N_b of the parents of PWR juveniles produced solely by pairs of spawning BSR adults, again accounting for both variance in family size and unequal sex ratios, was even lower (20.6). In this case, variation in family size was less marked, and had a smaller impact on N_b. Here, low N_b values reflect mostly the smaller number of contributing parents. In either case, estimates are well below N_b = 100 recommended by Waples (1990) to minimize loss of genetic variation in salmonids. It should be noted, however, that estimates of N_b are partly dependent on the extent of sampling, and could increase slightly with both additional juveniles and more representative sample collections (e.g., samples obtained via rotary screw traps near the mouth of the river).

When effective population size is small, it is expected that some genetic variation will be lost in the production of offspring from the preceding parental generation due to genetic drift. Of concern here, however, is both the magnitude of the loss, approximately 10 percent reduction in allele richness between the BSR ADULT REL 2003 and the PWR WILD 2004/2005 groups, and the fact that reductions were observed in levels of gene diversity, a metric that is relatively insensitive to population bottlenecks, over a single generation. Indeed, gene diversity was not observed to decrease in offspring groups

relative to parental groups in any of the multiple comparisons made for captive Stewaicke populations recently evaluated (O'Reilly and Harvie, 2009) and is rarely seen to decline in other studies of genetic variation in salmonid captive breeding programs (recently reviewed in Fraser, 2008), when assessed over a single generation. There is, however, an important complicating factor associated with analyses of loss of genetic variation between parent and offspring in this study.

The PWR WILD 2004/2005 juveniles are not exclusively offspring of the BSR ADULT REL 2003 parental group, as multiple individuals, presumably mostly male parr, resident in the PWR river in 2003 also appear to have contributed to the offspring generation. Typically, both the number of different alleles and gene diversity would normally be expected to increase in a hybrid offspring group relative to the two parental groups, particularly when allele frequency distributions are different in the parental groups. There are circumstances, however, in which a hybrid group could exhibit lower levels of genetic variation than one of the two parental groups in the absence of significant amounts of loss of genetic variation due to the normal sources of genetic drift (for example, the failure of some individuals to spawn successfully, or the random failure of one of the two parental alleles to be passed on to the offspring in the next generation). If, for example, the PWR parental population was very genetically depauperate, exhibiting only a few alleles per locus, and these alleles were also the more common alleles observed in the BSR ADULT REL 2003 parental group, then the hybrid population could exhibit lower levels of gene diversity compared to the BSR ADULT REL 2003 parental group. However, the PWR reference groups did not exhibit markedly lower levels of genetic variation relative to the BSR ADULT REL 2003 parental group, and did exhibit slightly different allele frequency distributions as seen in Tables 4a and 4b and as reflected in the negative F_{IS} values observed at all loci in the PWR WILD 2004/2005 group (Table 10). Even if contributions by the PWR wild parr parents did not have a positive influence on levels of genetic variation in the PWR 2003 year-class juveniles, it is clear that much of the genetic variation present in the BSR ADULT REL 2003 parental group, including a number of unique alleles, was not being passed on to the offspring group. It would also appear that single-generation rates of decline, particularly in regards to gene diversity, were much greater than observed for similarly sized (N=216) captive populations where spawnings are managed (see O'Reilly and Harvie, 2009).

When comparing levels of genetic variation between the BSR ADULT REL 2003 sample collection and offspring produced solely by BSR adult releases (PWR WILD 04/05 PAIRS), declines in gene diversity, a metric relatively insensitive to differences in sample size, were even greater. Observed numbers of alleles were also much reduced relative to the BSR ADULT REL 2003 group, but this is in part an artefact of the sample size of the PWR WILD 04/05 PAIRS group. Note that levels of allele richness, though reduced relative to the BSR ADULT REL 2003 group, did not decline as much relative to the parental group, compared to the PWR WILD 2004/2005 offspring group. This was unexpected, and may reflect imprecision in estimates of allele richness in either the BSR ADULT REL 2003 or PWR WILD 04/05 PAIRS group, due to the small sample size standardized to in this particular comparison for this metric (N=25).

In summary, the release of captive BSR adults into the Point Wolfe River, which still harboured remnant populations of mature male parr, was successful in achieving the goal of contributing to, or increasing, the river's production of endangered inner Bay of

Fundy Atlantic salmon, at least in 2003. Exclusion-based and likelihood-based parentage analyses, associated simulation analyses and kinship analyses provide considerable evidence that some BSR adults did spawn successfully, and produced offspring that survived at least to the fry and 1+ parr stage. Indeed, in 2003, at least 29, and perhaps a few more, BSR adults appeared to have spawned successfully, with other BSR adults but likely also with mature male parr. In 2004, however, there is evidence of very few successful spawnings by BSR adults, and this includes the reduced number of fry electrofished in 2005, the markedly reduced smolt run in 2007 relative to 2006, and the observation that half of the 2004 year-class offspring did not assign to captive adult releases. Estimates of the effective number of breeders based on inferred mating structures, and analyses of neutral molecular genetic variation, indicate that under both the present management strategy of releasing captive reared adults into a river containing residual native mature wild parr, and a strategy involving the release of captive reared adults into a river lacking mature parr, genetic variation will not be maintained over the longer term, and probably not in the short term either (over two to three generations). Rather, it is likely that considerable genetic variation is being lost due to genetic drift, mostly a function of the small number of successfully reproducing parents and, to a lesser extent, sex ratio bias and variance in family size. However, it is possible that the group of offspring produced by this strategy, having developed in natural river habitat from the egg to the smolt stage and having been exposed to natural selection during the high juvenile mortality phase of their life cycle, may be more fit than offspring produced via artificial spawning, where no benefits of mate choice are possible and where early development occurs in the hatchery. Additional research is needed to determine whether this is indeed the case and, if so, to quantify fitness gains so that the relative merits of the two supplementation strategies, adult release versus artificial spawning and juvenile release, can be evaluated, given the likely tendency for the latter to minimize rates of loss of genetic variation.

Conclusions and Management Recommendations

Given variation between years in overall spawning success, the moderate number of successfully spawning adults during the more favourable year, the small effective number of breeders, and likely high rates of loss of genetic variation, improvements in this program would be beneficial. Our primary recommendation in this regard is to increase the number of effective spawners, by increasing the spawning efficiency of released adults. Suggestions that may increase spawning efficiency include the following:

1. Release of adults that have undergone fewer generations of captive breeding and rearing; the use of locally adapted broodstock for production of adults for release into the PWR; release of adults that have been reared through juvenile life history stages in more naturalized hatchery conditions (D. MacDonald and T. Goff, pers. comm.);
2. Release of adults that that have developed from egg to the smolt stage in native Point Wolfe River habitat;

3. Release of adults that have developed from the smolt to adult stage in more naturalized conditions, such as in net pens in the Bay of Fundy/Gulf of Maine area;
4. Release of adults that have developed from egg to smolt in native river habitat, and from smolt to adult stages in net pens in the Bay of Fundy/Gulf of Maine;
5. Release of genetically variable offspring as unfed fry one and two years previous to the release of adults, to hopefully increase genetic variation contributed by the male parr group of parents, and to possibly increase the likelihood of spawning by mature adults;
6. Control of temperature and photoperiod conditions, and possibly other environmental variables, to more closely match natural conditions. For example, Berejikian *et al*. (2005) found that current velocity in the hatchery can impact spawning success of released adult Steelhead.
7. Use of hormones to ensure maturation at the time of release; injection of spawning hormones has led to dramatic increases in the numbers of redds constructed by captive-reared Steelhead in the Hamma Hamma River, Washington (Berejikian *et al*., 2003). Although hormone injection may appear to be a departure from the general recommendation to increased naturalization of spawning conditions, it is difficult to argue that the benefits might not outweigh the costs if little to no spawning success is observed in one out of every two years that adults are released.

As the above recommendations are unproven, we also suggest that one variable be modified at a time, and that well designed research programmes be implemented to assess the effects of changes on spawning success, effective numbers of breeders, maintenance of genetic variation, offspring survival, offspring growth, and other proxies of fitness in the wild. Finally, we recommend that the PWR population also be maintained in captivity, using sound genetic practices and artificial spawning, to minimize loss of genetic variation, at least until the spawning success of adult releases is increased to the point where N_b is sufficient to minimize loss of genetic variation over time.

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Table 1. Summary information for Big Salmon River (BSR) adult salmon released into the Point Wolfe River in 2003 and 2004.

	Year 2003	Year 2004
Total number of BSR adults released	286	280
Total number of BSR adults missing tag information and for which parentage could not be tested	0	73
Total number of BSR adults for which analyses were possible	286	219
Total number of BSR adults successfully analyzed*	216 (187)	212 (192)
Overall completion of genotype database**	92.4%	89.4%

NOTE: 73 of the 280 BSR salmon released into the Point Wolfe River in 2004 lost their Carlin tags, so existing DNA information and tissue samples could not be associated with any fish (explained further in text).

* analyses were considered successful if an adult could be genotyped at eight or more loci (number analyzed at 10 or more loci given in parentheses)
** percent completion was based on the group of 216 2003 adults and 212 2004 adults for which analyses were possible

Table 2. Summary information of fry and parr collections obtained from the Point Wolfe River in 2004 and 2005.

	Number submitted	Number successfully analyzed**
PWR juveniles collected in 2004	61	57
PWR 2004 juveniles produced in 2003 (< 70 mm, 0+)	49	45
PWR 2004 juveniles produced in 2002 (> 70 mm, 1+)*	12	12
PWR juveniles collected in 2005	64	63
PWR 2005 juveniles produced in 2004 (< 70 mm, 0+)	10	10
PWR 2005 juveniles produced in 2003* (> 70 mm, 1+)	54	53
PWR juveniles collected in 2004 or 2005 produced in 2003	103	98

*a small portion of juveniles collected in 2005 that were greater than 70 mm in length may have been two years of age and would have been produced in 2002

**analyses were considered successful if an individual could be genotyped at eight or more loci

Table 3. Single-locus summary statistics for microsatellite markers for the 2003 BSR adult release group of candidate parents. See note for explanation of column headings.

Locus	N different alleles	Het. Obs.	Het. Exp.	PIC	Avg NEP (1st par.)	Avg NEP (par. pair)	HWE test	Est. Freq. null alleles
SSsp1605	9	0.714	0.726	0.699	0.656	0.262	NS	0.012
SSsp2201	25	0.835	0.918	0.91	0.287	0.045	NS	0.047
SSsp2210	6	0.726	0.717	0.67	0.697	0.339	NS	-0.0108
SSsp2215	13	0.892	0.853	0.834	0.46	0.128	NS	-0.023
SSsp2216	17	0.933	0.903	0.893	0.334	0.063	NS	-0.0184
SSsp1G7	17	0.933	0.906	0.896	0.327	0.061	ND	-0.0162
*Ssa*197	14	0.853	0.868	0.852	0.423	0.106	NS	0.0062
*Ssa*202	17	0.901	0.903	0.892	0.334	0.063	NS	-0.0005
*Ssa*486	9	0.647	0.636	0.601	0.759	0.378	NS	-0.0182
*Ssa*144	26	0.872	0.939	0.933	0.226	0.028	ND	0.0362
*Ssa*D71	28	0.846	0.914	0.905	0.294	0.045	NS	0.0333
*Ssa*171	23	0.852	0.894	0.883	0.354	0.071	NS	0.0235
*Ssa*58	28	0.892	0.935	0.928	0.24	0.032	ND	0.0219

Note:
N different alleles - Total number of different alleles observed
Het. Obs. - Heterozygosity Observed
Het. Exp. - Heterozygosity Expected
PIC - Polymorphic Information Content
Avg. NEP (1st par.) - Average non-exclusion power for 1st or single parent
Avg. NEP (par. pair) - Average non-exclusion power of parental pair
HWE test - Significance of test for departure from Hardy-Weinberg equilibrium
Est. Freq. null alleles - Estimated frequency of null alleles

Table 4a. Microsatellite allele frequencies for the Big Salmon River (BSR) adults released in 2003 and juveniles sampled from the Point Wolfe River (PWR) produced that same year (loci SSsp1605 - SSsp1G7).

1605 BSR ALLELE	1605 BSR COUNT	1605 PWR ALLELE	1605 PWR COUNT	2201 BSR ALLELE	2201 BSR COUNT	2201 PWR ALLELE	2201 PWR COUNT	2210 BSR ALLELE	2210 BSR COUNT	2210 PWR ALLELE	2210 PWR COUNT	2215 BSR ALLELE	2215 BSR COUNT	2215 PWR ALLELE	2215 PWR COUNT	2216 BSR ALLELE	2216 BSR COUNT	2216 PWR ALLELE	2216 PWR COUNT	1G7 BSR ALLELE	1G7 BSR COUNT	1G7 PWR ALLELE	1G7 PWR COUNT
220	**0**	**220**	**2**	267	3	267	11	112	176	112	105	**130**	**0**	**130**	**5**	**189**	**0**	**189**	**3**	126	11	126	7
224	**0**	**224**	**1**	275	8	275	3	120	21	120	10	**134**	**0**	**134**	**2**	197	1	197	0	**130**	**0**	**130**	**2**
228	58	228	45	279	35	279	6	124	35	124	29	142	2	142	0	201	19	201	24	142	2	142	0
232	63	232	30	283	1	283	0	132	84	132	24	146	2	146	0	205	50	205	12	166	10	166	45
236	213	236	104	287	54	287	6	136	108	136	70	150	53	150	29	209	30	209	27	170	7	170	0
240	**0**	**240**	**4**	291	17	291	10	152	6	152	4	154	58	154	29	217	5	217	2	174	27	174	25
244	5	244	0	295	21	295	13					158	112	158	74	221	3	221	2	178	88	178	26
248	31	248	20	299	24	299	26					162	63	162	54	225	18	225	5	182	61	182	35
252	5	252	6	303	61	303	19					166	42	166	7	229	6	229	2	186	29	186	31
256	17	256	10	307	8	307	9					170	35	170	14	233	18	233	3	190	57	190	28
260	28	260	16	311	10	311	5					174	29	174	4	237	5	237	17	194	48	194	21
276	8	276	0	315	20	315	22					178	14	178	2	241	37	241	15	198	52	198	10
				319	15	319	2					182	13	182	3	245	61	245	23	202	25	202	4
				323	8	323	15					186	16	186	16	249	99	249	56	206	28	206	4
				327	6	327	17					190	5	190	1	253	5	253	7	**210**	**0**	**210**	**2**
				331	16	331	16									257	21	257	7	218	1	218	0
				335	5	335	0									265	56	265	33				
				339	1	339	0									289	12	269	2				
				343	12	343	0																
				347	28	347	8																
				351	8	351	1																
				355	31	355	32																
				359	1	359	2																
				363	4	363	0																
				367	**0**	**367**	**1**																
				375	5	375	8																

Note: bolded values are alleles, and their respective number of occurrences, that were observed in candidate offspring (PWR juveniles sampled), but not in the group of genotyped BSR adults

Table 4b. Microsatellite allele frequencies for the Big Salmon River (BSR) adults released in 2003 and juveniles sampled from the Point Wolfe River (PWR) produced that same year (loci *Ssa*197 to *Ssa*171).

197 ALLELE	BSR COUNT	197 ALLELE	PWR COUNT	202 ALLELE	BSR COUNT	202 ALLELE	PWR COUNT	144 ALLELE	BSR COUNT	144 ALLELE	PWR COUNT	486 ALLELE	BSR COUNT	486 ALLELE	PWR COUNT	171 ALLELE	BSR COUNT	171 ALLELE	PWR COUNT
163	39	159	2	255	46	255	18	162	17	162	7	174	242	174	125	211	1	211	0
167	82	163	27	259	1	259	0	166	2	166	6	178	79	178	62	215	1	215	0
171	64	167	57	263	1	263	0	**170**	**0**	**170**	**4**	182	15	182	1	225	6	225	14
175	84	171	38	267	9	267	0	178	1	178	0	186	13	186	2	229	29	229	23
179	49	175	49	271	8	271	0	182	43	182	25	190	25	190	29	231	63	231	37
183	54	179	15	275	32	275	9	186	8	186	2	194	23	194	6	233	49	233	32
187	14	183	25	279	18	279	16	190	29	190	36	198	27	198	9	235	18	235	16
191	13	187	7	283	25	283	20	194	8	194	6	202	2	202	0	237	11	237	28
195	7	191	3	287	8	287	9	198	10	198	3	206	1	206	0	239	41	239	11
199	20	195	1	291	45	291	29	202	9	202	21	210	1	210	4	241	18	241	6
203	13	199	14	295	39	295	60	206	11	206	9					**243**	**0**	**243**	**5**
211	4	203	1	299	87	299	34	210	6	210	1					245	13	245	13
223	3	223	1	303	26	303	17	214	22	214	5					249	17	249	2
				307	32	307	6	218	19	218	4					251	7	251	9
				311	32	311	11	222	32	222	17					253	7	253	6
				315	3	315	10	226	8	226	13					255	6	255	0
				319	4	319	0	230	28	230	21					257	12	257	7
				323	2	323	0	234	8	234	9					261	5	261	5
				327	6	327	1	238	14	238	18					263	3	263	0
								242	4	242	3					269	3	269	0
								246	5	246	0								
								250	15	250	5								
								254	20	254	19								
								258	7	258	2								
								262	7	262	0								
								266	**0**	**266**	**1**								
								270	6	270	0								
								274	8	274	4								
								278	3	278	1								

Note: bolded values are alleles, and their respective number of occurrences, that were observed in PWR but not genotyped BSR adults

Table 5. Summary of kinship and parentage results for PWR juveniles collected in 2004 and 2005 and produced in 2003.

		KIN-SHIP ANAL.	EXCLUSION ANALYSIS				LIKELIHOOD ANALYSIS						
Offspring ID	Site Info	Half-sib group ID	Parent ID	Total # loci	# mismatches	IDA TEST +	Parent ID	Pair LOD score	Trio LOD score	Trio conf.	Analysis Summary	Assign conf.	Foot-note
PWF010904HO22	PWR-003	1.1	F8108	12	0		F8108	7.94			12of12, concord. across 3 analyses	HIGH	
PWF020805HOS07PB2130M	PB2	1.1	F8108	11	0		F8108	11.79			11of11, concord. across 3 analyses	HIGH	
PWF250805HOS07P05126M	005	1.1	F8108	11	0		F8108	22.05			11of11, concord. across 3 analyses	HIGH	
PWF220805HOS08P04122M	004	1.1					F8108	6.45			F8108 in full-sib group of 4	HIGH	1
PWF220805HOS04P04130M	004	1.2	F8108	11	0		F8108	12.42			11of11, concord. across 3 analyses	HIGH	
PWF150604HO004AS06	PWR-004	1.3	C115	11	0	Y	C115	13.97	29.73	<80%	MATCH TO PAIR+concord all 3	HIGH	
PWF150604HO004AS06		1.3	F8108	12	0	Y	F8108	12.13	29.73	<80%	MATCH TO PAIR+concord all 3	HIGH	
PWF220805HOS06P04121M	004	1.3	F8108	11	0	Y	F8108	11.49	23.21	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF220805HOS06P04121M		1.3	C115	11	1	Y	C115	8.55	23.21	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF250805HOS01P05125M	005	1.3	F8108	11	0	Y	F8108	11.08	21.68	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF250805HOS01P05125M		1.3	C115	11	1	Y	C115	6.36	21.68	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF250805HOS02P05117M	005	1.3	C115	11	0	Y	C115	18.60	26.90	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF250805HOS02P05117M		1.3	F8108	11	0	Y	F8108	11.02	26.90	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF150604HO004AS19	PWR-004	1.4	F8108	12	1		F8108	9.09			11of12,1add locus+highLOD+concord 3	HIGH	
PWF150805HOS06P01136M	001	2.1	C653	10	0	Y	C653	10.73	32.47	95%	MATCH TO PAIR+95%	HIGH	2
PWF150805HOS06P01136M		2.1	C819	11	0	Y	C819	15.95	32.47	95%	MATCH TO PAIR+95%	HIGH	
PWF010904HO8	PWR-001	2.2	C056	10	0	Y	C056	9.34	23.75	95%	MATCH TO PAIR+95%	HIGH	
PWF010904HO8		2.2	C819	10	0	Y	C819	12.31	23.75	95%	MATCH TO PAIR+95%	HIGH	
PWF170805HOS03P02127M	002	2.2	C056	11	0	P	C056	17.09	21.00	80%	11of11,very high LOD,concord (single)	HIGH	
PWF170805HOS03P02127M		2.2	C797	11	1	P	C797	4.13	21.00	80%	conflict, PROB C819	LOW	3
PWF170805HOS11P02102M	002	2.2	C056	11	0	P	C056	12.99	30.98	80%	MATCH TO PAIR+80%+concord	HIGH	
PWF170805HOS11P02102M		2.2				P	C819	14.92	30.98	80%	MATCH TO PAIR+80%+concord	HIGH	
PWF010904HO9	PWR-001	2.3	C056	11	0		C056	10.71			11of11+condord+high LOD	HIGH	
PWF170805HOS05P02126M	002	2.3	C056	11	0		C056	11.84			11of11+condord+high LOD	HIGH	
PWF170805HOS10P02120M	002	2.4	C056	11	0	Y	C056	13.38	28.24	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF170805HOS10P02120M	002	2.4	C137	11	0	Y	C137	10.65	28.24	95%	MATCH TO PAIR+concord all 3,95%	HIGH	

		KIN-SHIP ANAL.	EXCLUSION ANALYSIS				LIKELIHOOD ANALYSIS						
Offspring ID	Site Info	Half-sib group ID	Parent ID	Total # loci	# mismatches	IDA TEST +	Parent ID	Pair LOD score	Trio LOD score	Trio conf.	Analysis Summary	Assign conf.	Foot-note
PWF010904HO14	PWR-002	2.5	C056	11	0	Y	C056	10.18	31.46	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF010904HO14		2.5	F8052	11	0	Y	F8052	16.22	31.46	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF010904HO7	PWR-001	2.6	C056	10	0	Y	C056	8.91	22.71	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF010904HO7		2.6	C327	10	0	Y	C327	7.58	22.71	95%	MATCH TO PAIR+concord all 3,95%	HIGH	
PWF010904HO15	PWR-002	3.1	C842	12	1		C842	6.65			concordance across 3 analyses	HIGH	
PWF150805HOS08P01128M	001	3.1	C842	11	1		C842	4.15			concordance across 3 analyses	HIGH	
PWF010904HO4	PWR-001	3.2	C842	12	2	P	C842	-0.06	2.00	<80%	MATCH TO PAIR, concord 2, 2errors	HIGH	
PWF010904HO4		3.2	C819	12	0	P	C819	7.33	2.00	<80%	MATCH TO PAIR, concord 2, 2errors	HIGH	
PWF010904HO6	PWR-001	3.2	C819	12	0	P	C819	15.05	20.16	80%	MATCH TO PAIR, concord 2, 2errors	HIGH	
PWF010904HO6		3.2				P	C842	0.34	20.16	80%	MATCH TO PAIR, concord 2, 2errors	HIGH	
PWF020805HOS08PB4119M	PB4	4.1	C100	9	0		C100	7.30			few loci, concordance, mod LOD	LOW	
PWF190805HOS02P03197M	003	4.2	C100	9	1		C100	1.77			few loci, concordance, low LOD	LOW	
PWF010904HO18	PWR-002	5.1	C499	10	1		C499	4.82			Possible assign to relative C499 etc	LOW	4
PWF010904HO23	PWR-003	5.1	C083	10	1		C083	1.25			Possible assign to relative C499 etc	LOW	4
PWF150805HOS05P01137M	001	5.1	C499	10	1						Possible assign to relative C499 etc	LOW	4
PWF150805HOS07P01129M	001	5.1	C312	10	1		C020	1.55			Possible assign to relative C499 etc	LOW	4
PWF170805HOS04P02127M	002	5.1	C354	11	1		C354	6.60			Possible assign to relative C499 etc	LOW	4
PWF170805HOS12P02122M	002	5.1	C499	10	1		C499	7.48			Possible assign to relative C499 etc	LOW	4
PWF170805HOS14P02138M	002	5.1	C120	11	1		C499	7.75			Possible assign to relative C499 etc	LOW	4
PWF220805HOS01P01114M	001	5.1	C083	10	1		C083	1.37			Possible assign to relative C499 etc	LOW	4
PWF170805HOS09P02134M	002	5.1									5.Xuncertain+no close match	UNAS	4
PWF170805HOS13P02124M	002	5.1					C083	0.49			5.Xuncertain+no close match	UNAS	4
PWF010904HO12	PWR-001	5.1									5.Xuncertain+no close match	UNAS	4
PWF220805HOS02P01116M	001	5.1									5.Xuncertain+no close match	UNAS	4
PWF170805HOS02P02116M	002	5.2	C623	11	1		C623	9.26			Possible assign to relative C499 etc	LOW	4
PWF010904HO17	PWR-002	5.3	C499	11	1		C499	7.30			Possible assign to relative C499 etc	LOW	4
PWF150604HOFOSTER79MM	B. foster	5.3	C499	11	1		C499	6.73			Possible assign to relative C499 etc	LOW	4
PWF280705HOS08PF3131M	PF3	5.3	C033	7	1						Possible assign to relative C499 etc	LOW	4

		KIN-SHIP ANAL.	EXCLUSION ANALYSIS				LIKELIHOOD ANALYSIS						
Offspring ID	Site Info	Half-sib group ID	Parent ID	Total # loci	# mismatches	IDA TEST +	Parent ID	Pair LOD score	Trio LOD score	Trio conf.	Analysis Summary	Assign conf.	Foot-note
PWF170805HOS08P02122M	002	5.3					C623	1.48			5.Xuncertain+no close match	UNAS	4
PWF010904HO10	PWR-001	5.3									5.Xuncertain+no close match	UNAS	4
PWF010904HO11	PWR-001	5.3	C361	11	1		C361	4.22			10of11but5.Xuncertain+C361not seen	UNAS	4a
PWF280705HOS07PF2124M	PF2	5.3									5.Xuncertain+no close match	UNAS	4
PWF020805HOS02PB1124M	PB1	6.1	C918	11	0		C918	8.58			11of11+concord-C918 full-sib parent	HIGH	
PWF020805HOS03PB1140M	PB1	6.1	C918	11	0		C918	11.61			11of11+concord-C918 full-sib parent	HIGH	
PWF020805HOS05PB1124M	PB1	6.1	C918	11	0		C918	10.37			11of11+concord-C918full-sib parent	HIGH	
PWF150604HO004AS04	PWR-004	6.1	C918	11	0		C918	11.81			11of11+concord-C918full-sib parent	HIGH	
PWF150604HO004AS07	PWR-004	6.1	C918	12	0		C918	12.67			12of12+concord-C918full-sib parent	HIGH	
PWF150604HO004AS13	PWR-004	6.1	C918	11	0		C918	8.28			11of11+concord-C918full-sib parent	HIGH	
PWF150604HO004AS14	PWR-004	6.1	C918	12	0		C918	9.00			12of12+concord-C918full-sib parent	HIGH	
PWF220805HOS02P04127M	004	6.1	C918	11	0		C918	9.00			11of11+concord-C918full-sib parent	HIGH	
PWF220805HOS03P04127M	004	6.1	C918	10	0		C918	8.98			10of10+concord-C918full-sib parent	HIGH	
PWF220805HOS07P04129M	004	6.1	C918	10	0		C918	9.66			10of10+concord-C918full-sib parent	HIGH	
PWF220805HOS01P04113M	004	6.2	C033	7	0	Y	C033	4.57	17.84	80%	MATCH TO PAIR+concord+80%	HIGH	
PWF220805HOS01P04113M		6.2	C918	11	0	Y	C918	11.17	17.84	80%	MATCH TO PAIR+concord+80%	HIGH	
PWF150604HO004AS02	PWR-004	6.3	C918	12	0		C918	8.82			12of12+concord	HIGH	
PWF150604HO004AS03	PWR-004	6.4	C918	10	0		C918	11.55			10of10+concord	HIGH	
PWF150604HO004AS16	PWR-004	6.4	C918	11	0	P	C918	8.57	19.15	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF150604HO004AS16		6.4	C115	10	1	P	C115	7.87	19.15	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF150604HO004AS05	PWR-004	6.5	C918	11	0	P	C918	10.19	5.99	<80	11 of 11+concord	HIGH	
PWF150604HO004AS05		6.5	C033	12	2	P	C033	-2.92	5.99	<80	2 mismat,low LOD, 2 errors?	LOW	5
PWF150604HO004AS09	PWR-004	6.5	C918	10	0		C918	7.81			10of10+concord,mod high LOD	HIGH	
PWF150604HO004AS11	PWR-004	6.5	C918	11	0		C918	8.50			10of11+concord,mod high LOD	HIGH	
PWF150604HO004AS12	PWR-004	6.6	C918	11	0		C918	11.31			11of11+concord,highLOD	HIGH	
PWF190805HOS03P03136M	003	7.1	C775	11	0	P	C775	14.47	11.58	<80%	11of11+very high LOD	HIGH	
PWF190805HOS03P03136M		7.1				P	C779	-5.11	11.58	<80%	Several mismatch, errors?	LOW	6
PWF280705HOS06PF1124M	PF1	7.2	C779	10	0	P	C779	11.10		<80%	MATCH TO PAIR, concord	HIGH	

		KIN-SHIP ANAL.	EXCLUSION ANALYSIS				LIKELIHOOD ANALYSIS						
Offspring ID	Site Info	Half-sib group ID	Parent ID	Total # loci	# mismatches	IDA TEST +	Parent ID	Pair LOD score	Trio LOD score	Trio conf.	Analysis Summary	Assign conf.	Foot-note
PWF280705HOS06PF1124M		7.2	C775	10	1	P	C775	6.49		<80%	MATCH TO PAIR, concord	HIGH	
PWF010904HO21	PWR-003	7.3	C775	12	1		C775	10.17			11of12,extra locus, high LOD+concord	HIGH	
PWF010904HO24	PWR-003	7.3	C775	12	0		C775	16.92			12of12	HIGH	
PWF010904HO16	PWR-002	8.1	F8093	12	0		F8093	13.27			12of12,concord,F8093 full-sib grp	HIGH	
PWF010904HO29	Oxbow	8.1	F8093	11	0		F8093	14.04	10.15		11of11,concord,F8093 full-sib grp	HIGH	
PWF010904HO30	Oxbow	8.1	F8093	12	0		F8093	10.24			12of12,concord,F8093 full-sib grp	HIGH	
PWF010904HO32	Oxbow	8.1	F8093	12	1		F8093	9.85			11of12, + F8093 full-sib grp	HIGH	
PWF170805HOS07P02116M	002	8.1	F8093	11	0		F8093	7.45			11of11,concord,F8093 full-sib grp	HIGH	
PWF180805HOS02P06117M	006	8.1	F8093	9	1		F8093	7.33			8 of 9,F8093 full-sib grp	HIGH	
PWF190805HOS01P03135M	003	8.1	F8093	11	0		F8093	9.38			11of11,concord,F8093 full-sib grp	HIGH	
PWF190805HOS06P03117M	003	8.1	F8093	11	0		F8093	14.29	8.80		11of11,concord,F8093 full-sib grp	HIGH	
PWF220805HOS04P01116M	001	8.1	F8093	11	0		F8093	13.46			11of11,concord,F8093 full-sib grp	HIGH	
PWF280705HOS09PF3120M	PF3	8.1	F8093	11	1		F8093	7.81	0.54		10of11, + F8093 full-sib grp	HIGH	
PWF280705HOS10PF4123M	PF4	8.1	F8093	11	0		F8093	8.96			11of11,concord,F8093 full-sib grp	HIGH	
PWF190805HOS04P03133M	003	9.1	C761	11	0		C761	11.72			11of11+highLOD,no concord	MED	7
PWF010904HO13	PWR-002	9.3	C059	10	0	Y	C059	9.94	23.62	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF010904HO13		9.3	C797	12	0	Y	C797	8.62	23.62	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF010904HO5	PWR-001	9.4	C059	10	0	Y	C059	8.16	28.67	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF010904HO5		9.4	C797	12	0	Y	C797	14.41	28.67	95%	MATCH TO PAIR+concord+95%	HIGH	
PWF150604HO004AS08	PWR-004	9.5	C299	10	1		C299	3.84			no concordance, 9of10	LOW	
PWF250805HOS03P05128M	005	10.1	C730	11	0		C730	14.37			11of11,very high LOD,concord	HIGH	
PWF010904HO31	Oxbow	10.2	C100	8	0	P	C100	5.13	7.32	<80%	8of8,MATCH TO PAIR MOSTLY	MED	8
PWF010904HO31		10.2	C730	10	1	P	C842	0.00	7.32	<80%	9of10 and c730 and c100 sibs	MED	9
PWF190805HOS05P03126M	003	11.1	C700	10	0		C700	14.46			10 of 10 and high LOD	HIGH	
PWF010904HO20	PWR-003	12.1	C348	11	0		C348	15.55			11 of 11 and high LOD	HIGH	
PWF010904HO19	PWR-002	13.1	C900	11	1		C900	4.62			10 of 11 and mod LOD	LOW	
PWF170805HOS01P02127M	002	14.1	C653	10	0		C653	12.88			10 of 10 and high LOD	HIGH	

		KIN-SHIP ANAL.	EXCLUSION ANALYSIS				LIKELIHOOD ANALYSIS						
Offspring ID	Site Info	Half-sib group ID	Parent ID	Total # loci	# mismatches	IDA TEST +	Parent ID	Pair LOD score	Trio LOD score	Trio conf.	Analysis Summary	Assign conf.	Foot-note
PWF010904HO26	A. upper rel	14.2	C609	12	1		C609	5.12			11of12,xtra locus, mod LOD	MED	
PWF010904HO3	A foster	14.3	C031	8	0	P	C031	3.26	6.09	<80%	MATCH TO PAIR,some concord	HIGH	
PWF010904HO3		14.3	C653	8	0	P	C622	1.32	6.09	<80%	MATCH TO PAIR,some concord	HIGH	
PWF010904HO25	A. upper rel	15.1	C301	10	1	P	C301	1.79	14.49	95%	MATCH TO PAIR+ 95%	HIGH	
PWF010904HO25		15.1	C203	11	1	P	C203	8.19	14.49	95%	MATCH TO PAIR+ 95%	HIGH	
PWF010904HO27	upper rel	16.1	C400	10	1		C400	5.81			9of10but concord+mod LOD	MED	
PWF010904HO28	upper rel	16.2	C400	10	1		C400	8.01			9of10but concord+mod LOD	MED	
PWF180805HOS01P06115M	006	17.1					C023	4.35			Several mismatches but C023 concord	LOW	
PWF280705HOS05PF1107M	PF1	17.2	C033	7	0	P	C762	4.00	12.87	<80%	MATCH TO PAIR, C023 concord	MED	
PWF280705HOS05PF1107M		17.2	C023	11	0	P	C023	11.94	12.87	<80%	11of11+MATCH TO PAIR,C023	HIGH	
PWF170805HOS06P02130M	002	18.1	C618	10	0		C618	10.80			10of10+high LOD	HIGH	
PWF020805HOS04PB1123M	PB1	18.1	C853	8	0		C853	12.24			8of8, though high LOD	LOW	
PWF020805HOS06PB2112M	PB2	19.1	F8104	11	0	P	F8104	14.40	19.32	95%	11of11,MATCH TO PAIR,95%	HIGH	
PWF020805HOS06PB2112M		19.1	C116			P	C116	1.60	19.32	95%	Multiple mismatch+low single LOD	LOW	10

mismatches - Number of mismatching loci, or loci incompatible between candidate parent and offspring
IDA test + (Y) - Offspring inherit different alleles from the maternal and parental parent at all or all less one loci
IDA test + (P) - Offspring exhibit Partial IDA, inheriting different alleles at most loci (exceptions usually involve 2 or 3 loci).
Trio conf. - Confidence level assigned to parental pair and offspring (triad) by *CERVUS* (percent)
Assign conf. - Assignment confidence estimated for individual offspring based on exclusion, likelihood and kinship analyses
UNAS - Unassigned, likely progeny of non-genotyped adult releases, returning adults, strays or aquaculture escapes

Footnotes:

1 PWF220805HOS08P04122M and F8108 incompatible at 2 or more loci, but F8108 identified as most likely by *CERVUS*, and in a full-sib group of 4 where all offspring have F8108 as the common parent
2 PWF150805HOS06P01136M may have clustered with the rest of this half-sib group due to the parent C819
3 2nd parent may be C979 (a unique parental pair) or C819 (encountered previously); assignment confidence is low
4 Common parent of half-sib group 5.X may be a non-genotyped relative of C499, C033 or C623, etc.
4a C361 not seen in kin group and not from cross 75
5 LOD for PWF150604HO004AS05-C033 grouping low but C033 observed in same kin group; low LOD may be due to 2 errors

6 LOD for PWF190805HOS03P03136M-C779 grouping low but C779 observed in same kin group
7 Common parent to kin group either C797 or close relative
8 Few loci and low LOD, but 80% conf. and C100 observed above
9 C730 common parent and observed at 11 of 11 loci above
10 PWF020805HOS06PB2112M and C116 exhibit multiple single-locus mismatches and the pair LOD scores are low; however, the trio exhibit high LOD scores and 95% confidence levels

Table 6. Parentage analysis results for the 0+ fry sampled from the Point Wolfe River in 2005, produced in 2004.

Offspring ID	Number of loci	Number of mismatches	Parent ID	IDA test*	Conclusion	Confidence	Footnotes
PWF020805HOS01PB1064M	13	1	F8095		probable single parent	high	1
PWF220805HOS05P04063M	13	0	F6632	P	probable match to pair	high	2
PWF220805HOS05P04063M	13	2	F6797	P	probable match to pair	high	
PWF220805HOS09P04068M	8	1	C013	N	possible single match	low	3
PWF220805HOS09P04068M	11	2	F6828	N	possible single match	low	4
PWF250805HOS04P05064M	12	0	C474	Y	probable match to pair	high	5
PWF250805HOS04P05064M	13	0	F6632	Y	probable match to pair	high	
PWF250805HOS05P05062M	12	0	C474		probable single parent	high	6

Note: Either C013 or F6828 is a possible parent of PWF220805HOS09P04068M, but not both (fails IDA test at multiple loci)
Note: The remaining 5 of 10 0+ fry collected in 2005, and produced in 2004, exhibited multiple (three or greater) single-locus mismatches when compared to the 215 BSR adults released into the PWR in 2004, indicating that they were indeed not offspring of BSR adults released in 2004.
* IDA test: The **I**nherit **D**ifferent **A**lleles (**IDA**) test was used to further assess hypotheses of parentage, when two candidate parents were identified. (Y=yes, Inherit Different Alleles at all loci tested; P=probably, Inherit Different alleles at all but one or two loci tested; N=No, Inherit same allele from both parents at multiple loci)
Footnotes:
1 – Candidate parent homozygous at mismatching locus, pattern likely due to a segregating null allele
2 – The two loci that do not follow Mendelian inheritance are also the loci that exhibit the single-locus mismatch with parent F6797
3 – Compatibility at 7 of 8 loci not unlikely to occur by chance, but very small dataset
4 – Compatibility at 9 of 11 loci not unlikely to occur by chance, but very small dataset

Table 7. Summary of parentage assignment results for the Point Wolfe River 2003 year-class group of juveniles tested.

Group	Number	Percent of total
PWR 2003 year-class juveniles assigning to one or two BSR candidate parents with high confidence	67	68.4
PWR 2003 year-class juveniles assigning to one or two BSR candidate parents with medium confidence	5	5.1
PWR 2003 year-class juveniles assigning to one or two BSR candidate parents with low confidence	18	18.4
PWR 2003 year-class juveniles that failed to assign to any BSR candidate parent	8	8.2
Total	98	100.0
Number of putative female BSR candidate parents that produced one or more offspring (high confidence)*	15	13.8
Number of putative male BSR candidate parents that produced one or more offspring (high confidence) *	10	9.3
Total number of putative BSR candidate parents that produced one or more offspring (high confidence)	25	11.6
Number of putative female BSR candidate parents that produced one or more offspring (medium confidence) *	4	3.7
Number of putative male BSR candidate parents that produced one or more offspring (medium confidence) *	0	0.0
Total number of putative BSR candidate parents that produced one or more offspring (medium confidence)	4	1.9
Number of putative female BSR candidate parents that produced one or more offspring (low confidence) *	3	2.8
Number of putative male BSR candidate parents that produced one or more offspring (low confidence) *	0	0.0
Total number of putative BSR candidate parents that produced one or more offspring (low confidence)	3	1.4
Number of putative female BSR candidate parents that produced one or more offspring (high or medium confidence) *	19	17.6
Number of putative male BSR candidate parents that produced one or more offspring (high or medium confidence) *	10	9.2
Total number of putative BSR candidate parents that produced one or more offspring (high or medium confidence)	29	13.4
Number of putative female BSR candidate parents that produced one or more offspring (high or medium or low confidence) *	22	20.4
Number of putative male BSR candidate parents that produced one or more offspring (high or medium or low confidence) *	10	9.2
Total number of putative BSR candidate parents that produced one or more offspring (high or medium or low confidence)	32	14.8

Note: Year class as used here refers to the year an individual was conceived, and not the hatch year.
*assumes a 1:1 ratio of males to females in the group of released BSR salmon

Table 8. Number of occurrences of spawnings of different types and associated production of juveniles in the PWR in 2003.

Spawning event	Number of occurrences detected	Number of juveniles produced
BSR adult x BSR adult	15 (16)*	25
BSR adult x PWR mature parr	20 (28)**	43 (65)**
All of spawning events	35 (44)**	68 (90)**
Number of polyandrous spawning events	9	n/a
Number of polygynous spawning events+	3	n/a
Number of monogamous spawning events	5	n/a

Note: with the exception of the BSR adult x BSR adult spawning type, all results are based on inferences of gender and mating structure, the rationale for which is given in the accompanying text.

*number outside of parentheses reflects uncertainty with one assignment to a parental pair (offspring PWF170805HOS03P02127M, assigned with low confidence, parental pair could be unique)
** numbers outside of parentheses are based on both kinship and parentage assignment results, numbers inside parentheses include additional hypothesized parents inferred from kinship analyses only
+ Incidents of polygyny inferred from the appearance of the same male parent in different half-sib groups

Table 9. Estimates of the effective number of breeders (N_b) contributing to the 2003 year class of juveniles sampled from the Point Wolfe River.

Group	N_b accounting for unequal sex ratio	N_b accounting for variation in family size	N_b accounting for unequal sex ratio and variation in family size
All parents contributing to the PWR sample collection produced in 2003 (BSR adults and PWR mature parr)	55.2	28.0	28.04
Parents contributing to the group of offspring obtained in the PWR produced in 2003, by pairs of BSR spawners only	22.9	43.3	20.61

Table 10. Estimates of neutral molecular genetic variation in the Big Salmon River (BSR) candidate parents released in 2003, parr collected in the Point Wolfe River (PWR) in 2004 and 2005, and various other reference populations. Values above the forward slash in individual cells are based on nine loci and those below the diagonals on seven loci (9 loci / 7 loci).

	BSR ADULT REL 2003	PWR WILD 2004/2005*	PWR WILD 04/05 PAIRS**	PWR WILD PARR 2001	PWR WILD SMOLT 2004	BSR WILD PARR 2001	STW WIL D PARR 2001	SJR WILD PARR 2001
Sample size	216	98	25	56	98	98	98	98
Gene diversity	0.824/0.834	0.806/0.813	0.792/0.802	NA/0.789	0.774/0.785	0.819/0.836	0.782/0.783	0.837/0.849
Variance	0.012/0.007	0.009/0.005	0.009/0.004	NA/0.018	0.013/0.009	0.013/0.007	0.007/0.004	0.009/0.005
Observed # alleles	14.222/13	12.222/11.143	9.444/8.857	NA/10.143	10.444/10	12.556/11.857	12.333/11.429	14.778/14.143
Variance	38.694/19.667	30.194/7.143	11.528/3.476	NA/8.143	16.278/8.667	22.528/11.143	31.25/7.286	31.694/18.81
Allele Richness (standardized to 25 individuals)	10.856/10.127	9.376/8.798	9.444/8.857	NA/9.012	8.292/8.197	10.04/9.726	8.879/8.355	11.353/10.928
Allele Richness (standardized to 95 individuals)	13.381/ 11.138	12.095 / 9.691	NA/NA	NA / 9.866	10.352/ 9.028	12.472 / 10.680	12.151 / 9.467	14.678/ 12.292
Variance AR (25 individuals)	18.36/7.941	12.463/4.335	11.528/3.476	NA/5.427	8.832/4.441	13.276/7.47	11.212/2.873	16.232/8.884
Variance AR (95 individuals)	35.332 / 10.677	29.077/ 5.434	NA/NA	NA / 7.224	15.729/ 5.944	22.309 / 9.006	30.215/ 4.070	30.707/ 12.786
F_{IS}	-0.006/-0.008	-0.03/-0.025	-0.049/-0.04	NA/-0.064	-0.073/-0.069	-0.042/-0.055	-0.069/-0.057	-0.011/-0.022

Note: One existing reference dataset, (PWR WILD PARR 2001), exhibited only 7 loci in common with all others; therefore, results for this group are given for 7 loci only.
* Group includes all 98 wild parr collected from the Point Wolfe River in 2004 and 2005, and produced in 2003 (potential offspring of adult releases)
** Group includes only wild parr collected from the Point Wolfe River, produced in 2003 exclusively by pairs of Big Salmon River adults identified with high, medium or low confidence via parentage analyses
F_{IS} = Wright's coefficient of inbreeding (additional detail in report)
STW=Stewiacke River, NS; SJR= Saint John River, NB

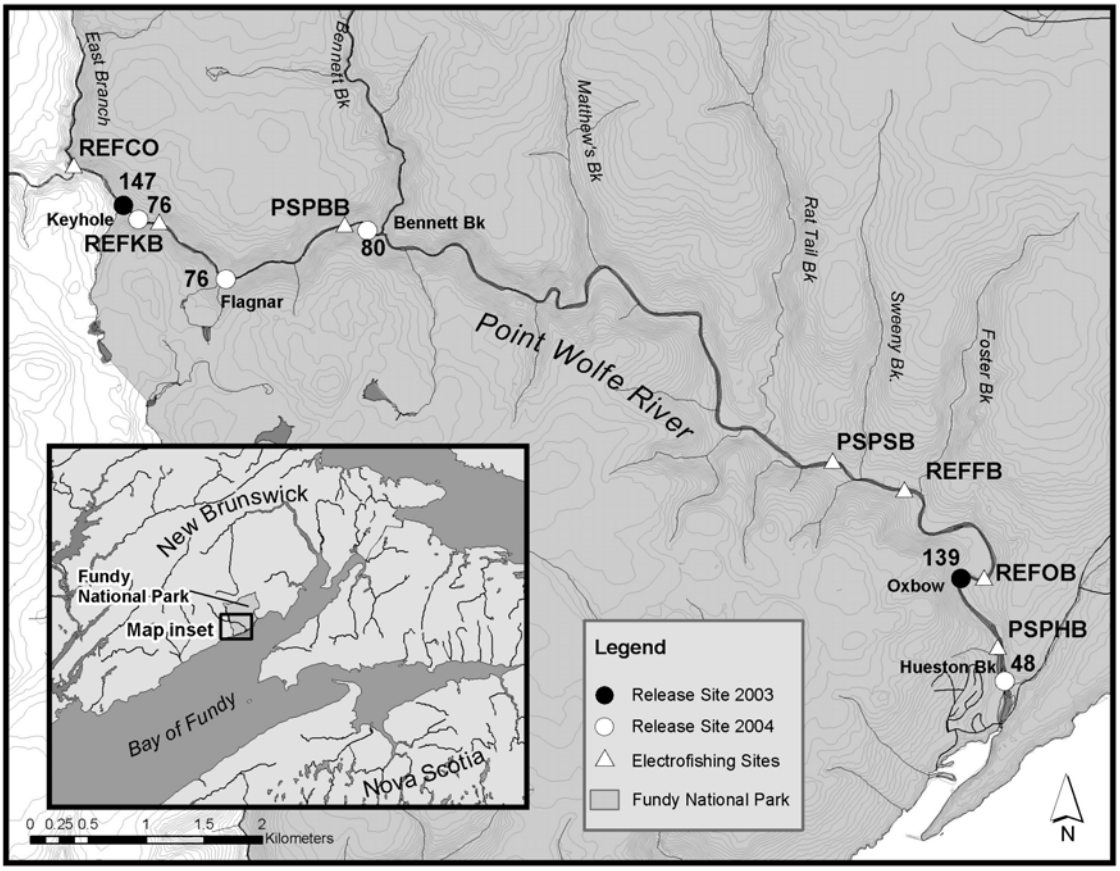

Figure 1. Locations of sites where captive-reared adults were released (circles) and juveniles collected (triangles) on the Point Wolfe River, NB. Numbers of adults released are given next to release sites. Detailed information on which individuals were collected or released at particular sites can be found in Tables A1 to A4. The location of the Point Wolfe River basin in the broader context of the Bay of Fundy and the provinces of New Brunswick and Nova Scotia is shown in the inset map.
REFCO=Random Electrofishing Confluence; REFKB=Random Electrofishing Keyhole; PSPBB=Permanent Electrofishing Plot Bennet Brook; PSPSB= Permanent Electrofishing Plot Sweeny Brook (labelled as Permanent Electrofishing plot Foster Brook in Parks records); REFFB= Random Electrofishing Foster Brook; REFOB=Random Electrofishing OxBow

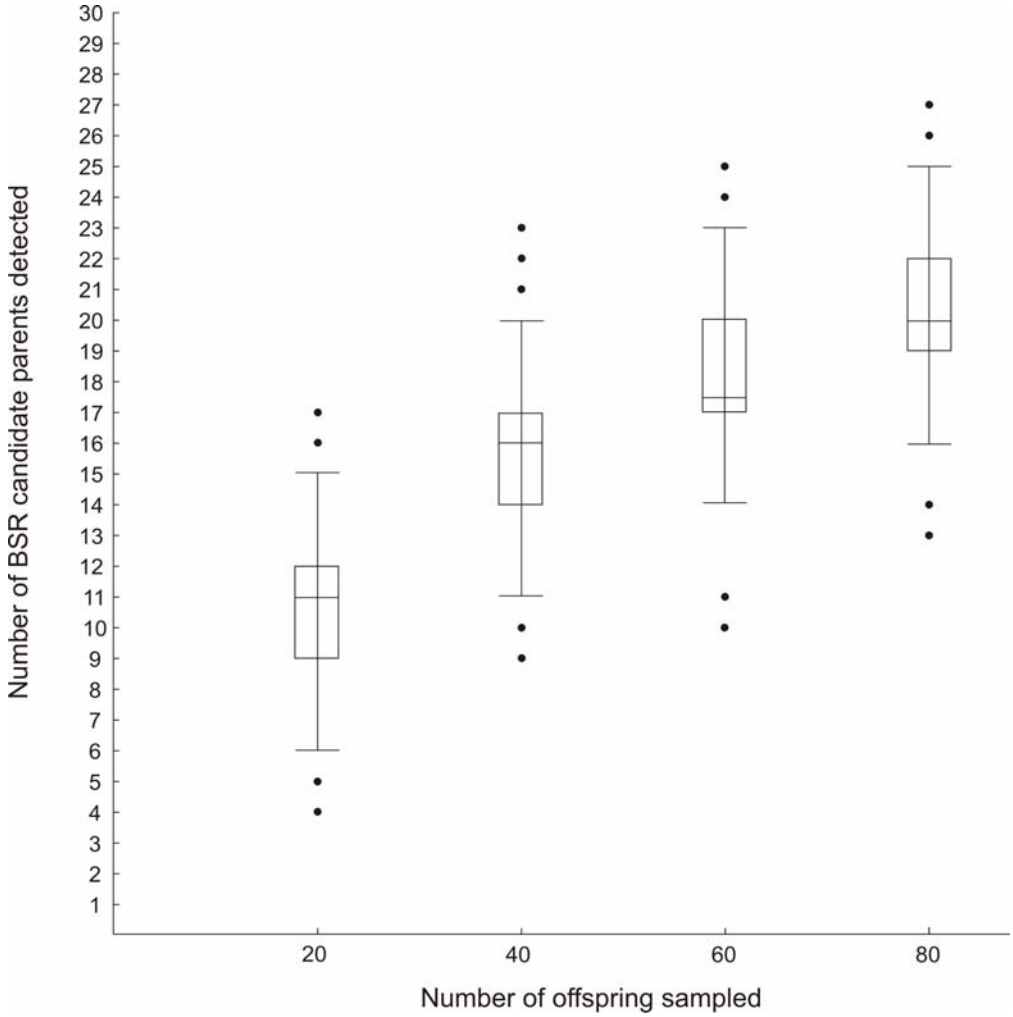

Figure 2. Detection of Big Salmon River candidate parents in 1,000 samples of 20, 40, 60 and 80 Point Wolfe River juveniles drawn randomly from the total collection of 98 individuals produced in 2003. Boxes denote quartiles, single bands within the boxes median values, and whiskers the 2.5 and 97.5 percentiles. Individual dots represent values lying beyond the percentiles plotted.

Appendix I. Details of parentage analyses of PWR juveniles

Several offspring were compatible with each of two parents at 10 of 10, 11 of 11, or 12 of 12 loci, inherited different alleles from the putative maternal and paternal BSR parents, and are considered to be assigned with high confidence. Many other offspring were compatible with a single BSR parent at 11 of 11 or 12 of 12 loci, and are also considered to be assigned with high confidence. Note that these parents are also almost always identified in likelihood analyses as the most probable parent for a given offspring, and that when two parents are identified, *CERVUS* often assigns the pair with a level of confidence. Overall, the results of the two parentage analysis methods were very concordant, and combined results were also remarkably consistent with results of the kinship analyses performed.

The 98 PWR juveniles produced in 2003 that were successfully analyzed were clustered into 19 half-sib groups by the program *COLONY* (Table 5). In the majority of instances, a single BSR adult release candidate parent was common to all (or almost all) members of a given half-sib group, particularly when family groups were moderately large (see half-sib groups 1.X, 2.X, 3.X, 4.X, 6.X, 7.X, 8.X, 10.X, 16.X, and 17.X, where the number preceding the decimal point represents the half-sib group, and the number following the decimal point the full-sib group nested within; see Table 5), and often two adult releases were common to identified full-sib groups (see full-sib groups 1.3, 2.2, and 3.2). Occasionally, two offspring in a particular half-sib group shared two parents in common but were placed into different full-sib groups, but this is not unexpected when full-sib size is below four because of the reduced power of kinship analyses to identify full siblings. Half-sib groups 11.X, 12.X, 13.X, 15.X and 19.X consisted of single individuals and, as expected, offspring within each assigned uniquely to one or two BSR adult candidate parents.

In many instances, a single mismatch was observed between putative BSR candidate parents and a given offspring (e.g., Table 5, half-sib group 8), and yet offspring were assigned with high confidence, despite the fact that simulation analyses indicate that parent-offspring matches under these conditions are expected to occur fairly frequently (Figure AIII-1b). Note that all 11 PWR juveniles in this group also cluster into a single full-sib family (8.1). Were even a single juvenile in full-sib group 8.1 not the offspring of BSR adult F8093, sharing a single allele with this parent across all loci by chance alone, the other allele would have been free to vary, and would very likely have expelled the offspring from full-sib group 8.1. In this instance, and several others, the concordance between kinship and parentage analyses allowed us to assign offspring to a BSR adult release with a high level of confidence.

High correspondence between kinship and parentage analyses, however, was not observed in half-sib groups 5.X, 14.X and 18.X. Half-sib group 5.X, in particular, is quite large (involving 20 individuals), and contains two large full-sib groups (12 and 7 individuals), so kinship estimates would have been expected to have been fairly precise. Since half-sib group 5.X represents most of the PWR offspring either not assigning to any parent or assigning with low confidence, we analyzed this group further using grandparentage analyses. In other words, we evaluated whether the individuals in group 5.X may have been the offspring of a BSR adult release for which genotype information was not available, by reconstructing the genotypes of the full and half-sib parents of group 5.X, and comparing these to the parents of the BSR adult releases showing high

levels of compatibility with offspring in half-sib group 5.X (BSR wild founders, putative grandparents T52699 and T52698, Tables A8a and A8b). Indeed, the deduced common parent of half-sib group 5.X may be the offspring of T52699 and T52698. The nature of the mismatch at locus *Ssa*202 is consistent with the segregation of a null allele at this locus in parent T52698. Note that although several single-locus mismatches were observed, several hundred alleles were involved in this analysis, and would not be unexpected given a genotyping error rate of 1-1.5 percent. In other words, it is quite possible that the half-sib group 5.X was produced by a non-genotyped BSR adult related to C499, C354 and C623. However, it is also possible that the half-sib parent was another adult release that was genotypically similar to C499 by chance alone. High levels of genotypic similarity between random pairs of adults is, however, quite rare, with as few as 30 of the 93,961 possible pairs of genotyped BSR adults exhibiting greater than 75% identity (see Table A5).

Half-sib family 14.X is quite small, so good correspondence between kinship and parentage analyses is not expected due to reduced sampling of the parental alleles in the kinship analyses. However, a single parent (C653) was identified in two of the three individuals assigned to this group. The two individuals assigned to half-sib group 18.X and, indeed, full-sib group 18.1 assigned to different BSR candidate parents. Again, this likely reflects the low certainty of kinship assignments when group size is small and more weight is given to results of parentage analyses.

Several other juveniles are compatible across all of nine or fewer loci with a given candidate parent, are associated with little or no other supporting evidence, and are therefore assigned with low confidence. Individuals compatible with a given BSR adult at 10 of 11 or 11 of 12 loci (exhibiting a single-locus mismatch), and that are associated with no other supporting evidence, are also assigned with low confidence.

Five of the 10 juveniles produced in 2004 exhibited 3 or more mismatches with any adult released into the PWR that year, and were not considered further as plausible offspring of any genotyped BSR adult released in 2004 (Table 6). Two of the remaining five offspring, PWF220805HOS05P04063M and PWF250805HOS04P05064M, were compatible with two BSR adults at 12 of 12, 13 of 13, or 11 of 13 loci, and either inherited a different allele across all loci, or at 11 of 13 loci tested. Both assignments are considered to be of high confidence. The juvenile PWF250805HOS05P05062M was compatible with the parent C474 at 12 of 12 loci and is considered to be assigned with high confidence. A fourth individual, PWF020805HOS01PB1064M, was compatible with the BSR parent F8095 at 12 of 13 loci. This assignment was considered to be of high confidence because of the very limited number of total pairwise comparisons involved in the 2004 analyses (2,120: 10 offspring X 212 parents), where many fewer chance matches at 12 of 13 loci would be expected compared to conditions used in the simulation analyses (Figure AIII-1b, 21,168 pairwise comparisons). Finally, PWF220805HOS09P04068M was compatible with C013 and F6828 at 7 of 8 and 9 of 11 loci, respectively, but did not inherit different alleles across the loci analyzed. This assignment was considered to be of low confidence.

Appendix II. Additional tables providing information on specific BSR adult releases, PWR juveniles, and analyses in support of parentage assignments

Table A1. Available information for the Big Salmon River adults released into the Point Wolfe River in 2003.

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
1	C007	Mactaquac, F1			Keyhole	16-Oct-03	
2	C011	Mactaquac, F1			Keyhole	16-Oct-03	
3	C020	Mactaquac, F1			Keyhole	16-Oct-03	
4	C023	Mactaquac, F1			Keyhole	16-Oct-03	
5	C036	Mactaquac, F1			Keyhole	16-Oct-03	
6	C037	Mactaquac, F1			Keyhole	16-Oct-03	
7	C041	Mactaquac, F1			Keyhole	16-Oct-03	
8	C042	Mactaquac, F1			Keyhole	16-Oct-03	
9	C049	Mactaquac, F1			Keyhole	16-Oct-03	
10	C062	Mactaquac, F1			Keyhole	16-Oct-03	
11	C065	Mactaquac, F1			Keyhole	16-Oct-03	
12	C068	Mactaquac, F1			Keyhole	16-Oct-03	
13	C074	Mactaquac, F1			Keyhole	16-Oct-03	
14	C075	Mactaquac, F1			Keyhole	16-Oct-03	
15	C076	Mactaquac, F1			Keyhole	16-Oct-03	
16	C078	Mactaquac, F1			Keyhole	16-Oct-03	
17	C083	Mactaquac, F1			Keyhole	16-Oct-03	
18	C095	Mactaquac, F1			Keyhole	16-Oct-03	
19	C100	Mactaquac, F1			Keyhole	16-Oct-03	
20	C115	Mactaquac, F1			Keyhole	16-Oct-03	
21	C120	Mactaquac, F1			Keyhole	16-Oct-03	
22	C127	Mactaquac, F1			Keyhole	16-Oct-03	
23	C131	Mactaquac, F1			Keyhole	16-Oct-03	
24	C136	Mactaquac, F1			Keyhole	16-Oct-03	
25	C140	Mactaquac, F1			Keyhole	16-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
26	C145	Mactaquac, F1			Keyhole	16-Oct-03	
27	C157	Mactaquac, F1			Keyhole	16-Oct-03	
28	C161	Mactaquac, F1			Keyhole	16-Oct-03	
29	C164	Mactaquac, F1			Keyhole	16-Oct-03	
30	C167	Mactaquac, F1			Keyhole	16-Oct-03	
31	C168	Mactaquac, F1			Keyhole	16-Oct-03	
32	C177	Mactaquac, F1	59.3	M	Keyhole	16-Oct-03	
33	C179	Mactaquac, F1			Keyhole	16-Oct-03	
34	C180	Mactaquac, F1			Keyhole	16-Oct-03	
35	C181	Mactaquac, F1			Keyhole	16-Oct-03	
36	C189	Mactaquac, F1			Keyhole	16-Oct-03	
37	C194	Mactaquac, F1	49	F	Keyhole	16-Oct-03	
38	C203	Mactaquac, F1			Keyhole	16-Oct-03	
39	C204	Mactaquac, F1			Keyhole	16-Oct-03	
40	C212	Mactaquac, F1			Keyhole	16-Oct-03	
41	C213	Mactaquac, F1			Keyhole	16-Oct-03	
42	C222	Mactaquac, F1			Keyhole	16-Oct-03	
43	C227	Mactaquac, F1			Keyhole	16-Oct-03	
44	C232	Mactaquac, F1			Keyhole	16-Oct-03	
45	C237	Mactaquac, F1			Keyhole	16-Oct-03	
46	C242	Mactaquac, F1			Keyhole	16-Oct-03	
47	C243	Mactaquac, F1			Keyhole	16-Oct-03	
48	C244	Mactaquac, F1			Keyhole	16-Oct-03	
49	C245	Mactaquac, F1			Keyhole	16-Oct-03	
50	C248	Mactaquac, F1			Keyhole	16-Oct-03	
51	C251	Mactaquac, F1			Keyhole	16-Oct-03	
52	C257	Mactaquac, F1			Keyhole	16-Oct-03	
53	C265	Mactaquac, F1			Keyhole	16-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
54	C276	Mactaquac, F1			Keyhole	16-Oct-03	
55	C277	Mactaquac, F1			Keyhole	16-Oct-03	
56	C299	Mactaquac, F1			Keyhole	16-Oct-03	
57	C302	Mactaquac, F1			Keyhole	16-Oct-03	
58	C312	Mactaquac, F1			Keyhole	16-Oct-03	
59	C322	Mactaquac, F1			Keyhole	16-Oct-03	
60	C335	Mactaquac, F1			Keyhole	16-Oct-03	
61	C340	Mactaquac, F1			Keyhole	16-Oct-03	
62	C345	Mactaquac, F1			Keyhole	16-Oct-03	
63	C348	Mactaquac, F1			Keyhole	16-Oct-03	
64	C352	Mactaquac, F1			Keyhole	16-Oct-03	
65	C354	Mactaquac, F1			Keyhole	16-Oct-03	
66	C361	Mactaquac, F1	49	F	Keyhole	16-Oct-03	
67	C362	Mactaquac, F1			Keyhole	16-Oct-03	
68	C364	Mactaquac, F1			Keyhole	16-Oct-03	
69	C365	Mactaquac, F1			Keyhole	16-Oct-03	
70	C372	Mactaquac, F1			Keyhole	16-Oct-03	
71	C375	Mactaquac, F1			Keyhole	16-Oct-03	
72	C376	Mactaquac, F1			Keyhole	16-Oct-03	
73	C386	Mactaquac, F1			Keyhole	16-Oct-03	
74	C387	Mactaquac, F1			Keyhole	16-Oct-03	
75	C399	Mactaquac, F1	44.7	I	Keyhole	16-Oct-03	
76	C400	Mactaquac, F1	56.4	F	Keyhole	16-Oct-03	
77	C413	Mactaquac, F1			Keyhole	16-Oct-03	
78	C419	Mactaquac, F1			Keyhole	16-Oct-03	
79	C456	Mactaquac, F1	61.9	M	Keyhole	16-Oct-03	
80	C457	Mactaquac, F1			Keyhole	16-Oct-03	
81	C465	Mactaquac, F1			Keyhole	16-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
82	C470	Mactaquac, F1			Keyhole	16-Oct-03	
83	C482	Mactaquac, F1			Keyhole	16-Oct-03	
84	C497	Mactaquac, F1			Keyhole	16-Oct-03	
85	C520	Mactaquac, F1			Keyhole	16-Oct-03	
86	C526	Mactaquac, F1			Keyhole	16-Oct-03	
87	C533	Mactaquac, F1			Keyhole	16-Oct-03	
88	C538	Mactaquac, F1			Keyhole	16-Oct-03	
89	C545	Mactaquac, F1			Keyhole	16-Oct-03	
90	C554	Mactaquac, F1	56	I	Keyhole	16-Oct-03	
91	C567	Mactaquac, F1			Keyhole	16-Oct-03	
92	C589	Mactaquac, F1	54.6	F	Keyhole	16-Oct-03	
93	C590	Mactaquac, F1			Keyhole	16-Oct-03	
94	C593	Mactaquac, F1			Keyhole	16-Oct-03	
95	C601	Mactaquac, F1			Keyhole	16-Oct-03	
96	C607	Mactaquac, F1			Keyhole	16-Oct-03	
97	C608	Mactaquac, F1			Keyhole	16-Oct-03	
98	C609	Mactaquac, F1			Keyhole	16-Oct-03	
99	C612	Mactaquac, F1			Keyhole	16-Oct-03	
100	C617	Mactaquac, F1			Keyhole	16-Oct-03	
101	C621	Mactaquac, F1			Keyhole	16-Oct-03	
102	C624	Mactaquac, F1			Keyhole	16-Oct-03	
103	C628	Mactaquac, F1			Keyhole	16-Oct-03	
104	C632	Mactaquac, F1			Keyhole	16-Oct-03	
105	C645	Mactaquac, F1			Keyhole	16-Oct-03	
106	C682	Mactaquac, F1			Keyhole	16-Oct-03	
107	C685	Mactaquac, F1			Keyhole	16-Oct-03	
108	C688	Mactaquac, F1			Keyhole	16-Oct-03	
109	C699	Mactaquac, F1	57.5	M	Keyhole	16-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
110	C700	Mactaquac, F1			Keyhole	16-Oct-03	
111	C713	Mactaquac, F1			Keyhole	16-Oct-03	
112	C714	Mactaquac, F1			Keyhole	16-Oct-03	
113	C716	Mactaquac, F1			Keyhole	16-Oct-03	
114	C730	Mactaquac, F1			Keyhole	16-Oct-03	
115	C747	Mactaquac, F1			Keyhole	16-Oct-03	
116	C750	Mactaquac, F1			Keyhole	16-Oct-03	
117	C758	Mactaquac, F1			Keyhole	16-Oct-03	
118	C762	Mactaquac, F1			Keyhole	16-Oct-03	
119	C780	Mactaquac, F1			Keyhole	16-Oct-03	
120	C787	Mactaquac, F1			Keyhole	16-Oct-03	
121	C803	Mactaquac, F1			Keyhole	16-Oct-03	
122	C805	Mactaquac, F1			Keyhole	16-Oct-03	
123	C810	Mactaquac, F1			Keyhole	16-Oct-03	
124	C819	Mactaquac, F1			Keyhole	16-Oct-03	
125	C826	Mactaquac, F1			Keyhole	16-Oct-03	
126	C831	Mactaquac, F1			Keyhole	16-Oct-03	
127	C833	Mactaquac, F1			Keyhole	16-Oct-03	
128	C842	Mactaquac, F1			Keyhole	16-Oct-03	
129	C843	Mactaquac, F1	57	M	Keyhole	16-Oct-03	
130	C846	Mactaquac, F1			Keyhole	16-Oct-03	
131	C848	Mactaquac, F1			Keyhole	16-Oct-03	
132	C854	Mactaquac, F1			Keyhole	16-Oct-03	
133	C865	Mactaquac, F1			Keyhole	16-Oct-03	
134	C874	Mactaquac, F1			Keyhole	16-Oct-03	
135	C876	Mactaquac, F1			Keyhole	16-Oct-03	
136	C887	Mactaquac, F1			Keyhole	16-Oct-03	
137	C898	Mactaquac, F1			Keyhole	16-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
138	C901	Mactaquac, F1			Keyhole	16-Oct-03	
139	C905	Mactaquac, F1	52.9	F	Keyhole	16-Oct-03	
140	C917	Mactaquac, F1			Keyhole	16-Oct-03	
141	C918	Mactaquac, F1			Keyhole	16-Oct-03	
142	C921	Mactaquac, F1			Keyhole	16-Oct-03	
143	C929	Mactaquac, F1			Keyhole	16-Oct-03	
144	C942	Mactaquac, F1			Keyhole	16-Oct-03	
145	C949	Mactaquac, F1			Keyhole	16-Oct-03	
146	C960	Mactaquac, F1			Keyhole	16-Oct-03	
147	F8116	Minto, F2	52.8	F	Keyhole	16-Oct-03	
148	C021	Mactaquac, F1			Oxbow	17-Oct-03	
149	C027	Mactaquac, F1	49.4	I	Oxbow	17-Oct-03	
150	C031	Mactaquac, F1			Oxbow	17-Oct-03	
151	C033	Mactaquac, F1			Oxbow	17-Oct-03	
152	C048	Mactaquac, F1			Oxbow	17-Oct-03	
153	C056	Mactaquac, F1			Oxbow	17-Oct-03	
154	C059	Mactaquac, F1			Oxbow	17-Oct-03	
155	C088	Mactaquac, F1			Oxbow	17-Oct-03	
156	C099	Mactaquac, F1			Oxbow	17-Oct-03	
157	C106	Mactaquac, F1			Oxbow	17-Oct-03	
158	C110	Mactaquac, F1			Oxbow	17-Oct-03	
159	C112	Mactaquac, F1			Oxbow	17-Oct-03	
160	C116	Mactaquac, F1			Oxbow	17-Oct-03	
161	C117	Mactaquac, F1			Oxbow	17-Oct-03	
162	C125	Mactaquac, F1			Oxbow	17-Oct-03	
163	C128	Mactaquac, F1			Oxbow	17-Oct-03	
164	C135	Mactaquac, F1			Oxbow	17-Oct-03	
165	C137	Mactaquac, F1			Oxbow	17-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
166	C216	Mactaquac, F1			Oxbow	17-Oct-03	
167	C217	Mactaquac, F1			Oxbow	17-Oct-03	
168	C228	Mactaquac, F1			Oxbow	17-Oct-03	
169	C229	Mactaquac, F1			Oxbow	17-Oct-03	
170	C233	Mactaquac, F1			Oxbow	17-Oct-03	
171	C264	Mactaquac, F1	56	F	Oxbow	17-Oct-03	
172	C266	Mactaquac, F1			Oxbow	17-Oct-03	
173	C301	Mactaquac, F1	53.5	F	Oxbow	17-Oct-03	
174	C318	Mactaquac, F1			Oxbow	17-Oct-03	
175	C327	Mactaquac, F1			Oxbow	17-Oct-03	
176	C330	Mactaquac, F1			Oxbow	17-Oct-03	
177	C341	Mactaquac, F1			Oxbow	17-Oct-03	
178	C349	Mactaquac, F1			Oxbow	17-Oct-03	
179	C353	Mactaquac, F1			Oxbow	17-Oct-03	
180	C357	Mactaquac, F1			Oxbow	17-Oct-03	
181	C371	Mactaquac, F1	49.8	M	Oxbow	17-Oct-03	
182	C379	Mactaquac, F1			Oxbow	17-Oct-03	
183	C382	Mactaquac, F1			Oxbow	17-Oct-03	
184	C384	Mactaquac, F1			Oxbow	17-Oct-03	
185	C388	Mactaquac, F1			Oxbow	17-Oct-03	
186	C394	Mactaquac, F1			Oxbow	17-Oct-03	
187	C397	Mactaquac, F1			Oxbow	17-Oct-03	
188	C420	Mactaquac, F1			Oxbow	17-Oct-03	
189	C421	Mactaquac, F1			Oxbow	17-Oct-03	
190	C426	Mactaquac, F1			Oxbow	17-Oct-03	
191	C439	Mactaquac, F1			Oxbow	17-Oct-03	
192	C450	Mactaquac, F1			Oxbow	17-Oct-03	
193	C461	Mactaquac, F1			Oxbow	17-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
194	C462	Mactaquac, F1			Oxbow	17-Oct-03	
195	C473	Mactaquac, F1			Oxbow	17-Oct-03	
196	C476	Mactaquac, F1	50.4	F	Oxbow	17-Oct-03	
197	C488	Mactaquac, F1			Oxbow	17-Oct-03	
198	C491	Mactaquac, F1			Oxbow	17-Oct-03	
199	C499	Mactaquac, F1			Oxbow	17-Oct-03	
200	C505	Mactaquac, F1			Oxbow	17-Oct-03	
201	C514	Mactaquac, F1			Oxbow	17-Oct-03	
202	C521	Mactaquac, F1			Oxbow	17-Oct-03	
203	C541	Mactaquac, F1			Oxbow	17-Oct-03	
204	C542	Mactaquac, F1			Oxbow	17-Oct-03	
205	C556	Mactaquac, F1			Oxbow	17-Oct-03	
206	C572	Mactaquac, F1			Oxbow	17-Oct-03	
207	C574	Mactaquac, F1			Oxbow	17-Oct-03	
208	C587	Mactaquac, F1			Oxbow	17-Oct-03	
209	C594	Mactaquac, F1			Oxbow	17-Oct-03	
210	C614	Mactaquac, F1			Oxbow	17-Oct-03	
211	C618	Mactaquac, F1			Oxbow	17-Oct-03	
212	C622	Mactaquac, F1	58.7	F	Oxbow	17-Oct-03	
213	C623	Mactaquac, F1			Oxbow	17-Oct-03	
214	C625	Mactaquac, F1			Oxbow	17-Oct-03	
215	C633	Mactaquac, F1			Oxbow	17-Oct-03	
216	C637	Mactaquac, F1			Oxbow	17-Oct-03	
217	C653	Mactaquac, F1			Oxbow	17-Oct-03	
218	C662	Mactaquac, F1			Oxbow	17-Oct-03	
219	C668	Mactaquac, F1			Oxbow	17-Oct-03	
220	C671	Mactaquac, F1			Oxbow	17-Oct-03	
221	C674	Mactaquac, F1			Oxbow	17-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
222	C698	Mactaquac, F1			Oxbow	17-Oct-03	
223	C707	Mactaquac, F1			Oxbow	17-Oct-03	
224	C708	Mactaquac, F1			Oxbow	17-Oct-03	
225	C717	Mactaquac, F1			Oxbow	17-Oct-03	
226	C725	Mactaquac, F1			Oxbow	17-Oct-03	
227	C731	Mactaquac, F1			Oxbow	17-Oct-03	
228	C733	Mactaquac, F1			Oxbow	17-Oct-03	
229	C735	Mactaquac, F1			Oxbow	17-Oct-03	
230	C736	Mactaquac, F1			Oxbow	17-Oct-03	
231	C745	Mactaquac, F1			Oxbow	17-Oct-03	
232	C749	Mactaquac, F1			Oxbow	17-Oct-03	
233	C760	Mactaquac, F1			Oxbow	17-Oct-03	
234	C761	Mactaquac, F1			Oxbow	17-Oct-03	
235	C763	Mactaquac, F1			Oxbow	17-Oct-03	
236	C774	Mactaquac, F1			Oxbow	17-Oct-03	
237	C775	Mactaquac, F1			Oxbow	17-Oct-03	
238	C779	Mactaquac, F1			Oxbow	17-Oct-03	
239	C783	Mactaquac, F1			Oxbow	17-Oct-03	
240	C789	Mactaquac, F1			Oxbow	17-Oct-03	
241	C790	Mactaquac, F1			Oxbow	17-Oct-03	
242	C791	Mactaquac, F1			Oxbow	17-Oct-03	
243	C793	Mactaquac, F1			Oxbow	17-Oct-03	
244	C796	Mactaquac, F1	52.9	F	Oxbow	17-Oct-03	
245	C797	Mactaquac, F1			Oxbow	17-Oct-03	
246	C802	Mactaquac, F1			Oxbow	17-Oct-03	
247	C807	Mactaquac, F1			Oxbow	17-Oct-03	
248	C812	Mactaquac, F1			Oxbow	17-Oct-03	
249	C814	Mactaquac, F1			Oxbow	17-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
250	C820	Mactaquac, F1	51.9	M	Oxbow	17-Oct-03	
251	C823	Mactaquac, F1	54	F	Oxbow	17-Oct-03	
252	C824	Mactaquac, F1			Oxbow	17-Oct-03	
253	C825	Mactaquac, F1	45.5	I	Oxbow	17-Oct-03	
254	C832	Mactaquac, F1			Oxbow	17-Oct-03	
255	C853	Mactaquac, F1			Oxbow	17-Oct-03	
256	C859	Mactaquac, F1			Oxbow	17-Oct-03	
257	C866	Mactaquac, F1			Oxbow	17-Oct-03	
258	C873	Mactaquac, F1			Oxbow	17-Oct-03	
259	C892	Mactaquac, F1			Oxbow	17-Oct-03	
260	C894	Mactaquac, F1			Oxbow	17-Oct-03	
261	C896	Mactaquac, F1			Oxbow	17-Oct-03	
262	C900	Mactaquac, F1			Oxbow	17-Oct-03	
263	C904	Mactaquac, F1			Oxbow	17-Oct-03	
264	C909	Mactaquac, F1			Oxbow	17-Oct-03	
265	C924	Mactaquac, F1			Oxbow	17-Oct-03	
266	C928	Mactaquac, F1	54.1	M	Oxbow	17-Oct-03	
267	C950	Mactaquac, F1			Oxbow	17-Oct-03	
268	C953	Mactaquac, F1			Oxbow	17-Oct-03	
269	F8052	Minto, F2			Oxbow	17-Oct-03	
270	F8055	Minto, F2			Oxbow	17-Oct-03	
271	F8070	Minto, F2			Oxbow	17-Oct-03	
272	F8086	Minto, F2			Oxbow	17-Oct-03	
273	F8093	Minto, F2			Oxbow	17-Oct-03	
274	F8094	Minto, F2			Oxbow	17-Oct-03	
275	F8102	Minto, F2	58.9	M	Oxbow	17-Oct-03	
276	F8104	Minto, F2			Oxbow	17-Oct-03	
277	F8108	Minto, F2			Oxbow	17-Oct-03	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
278	F8111	Minto, F2			Oxbow	17-Oct-03	
279	F8117	Minto, F2			Oxbow	17-Oct-03	
280	F8125	Minto, F2			Oxbow	17-Oct-03	
281	F8131	Minto, F2			Oxbow	17-Oct-03	
282	F8134	Minto, F2			Oxbow	17-Oct-03	
283	F8137	Minto, F2			Oxbow	17-Oct-03	
284	F8140	Minto, F2			Oxbow	17-Oct-03	
285	F8142	Minto, F2			Oxbow	17-Oct-03	
286	F8145	Minto, F2			Oxbow	17-Oct-03	

* Captive history: Mactaquac, F1 = Salmon produced through the artificial spawning of parents obtained from the Big Salmon River as juveniles and that therefore have accumulated approximately 1.5 generations of domestication selection.
Minto, F2 = Salmon produced through the artificial spawning of parents obtained from the Minto Fish Hatchery. Minto hatchery fish were themselves produced through the artificial spawning of parents obtained from the Big Salmon River as juveniles. These adult releases have therefore accumulated approximately 2.5 generations of domestication selection.
** Sex: M=male, F=female, I=immature
***Release location information (locations as specified in Figure 1)

Table A2. Available information for the Big Salmon River adults released into the Point Wolfe River in 2004.

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
1	F6731	Mactaquac, F1		I	Keyhole	8-Oct-04	
2	F6669	Mactaquac, F1		M	Flagnar	8-Oct-04	
3	F6717	Mactaquac, F1		F	Flagnar	8-Oct-04	
4	F6866	Mactaquac, F1		I		8-Oct-04	not released
5	F6868	Mactaquac, F1		I		8-Oct-04	not released
6	F6502	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
7	F6678	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
8	F6702	Mactaquac, F1	52	M	Bennett Bk	8-OCT-04	
9	F6824	Mactaquac, F1		M	Flagnar	8-OCT-04	
10	F6881	Mactaquac, F1		F	Keyhole	8-OCT-04	
11	F6810	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
12	F6812	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
13	F6531	Mactaquac, F1		M	Keyhole	8-OCT-04	
14	F6839	Mactaquac, F1		I	Keyhole	8-OCT-04	
15	F6825	Mactaquac, F1		F	flagnar	8-OCT-04	
16	F6713	Mactaquac, F1		F	Keyhole	8-OCT-04	
17	F6884	Mactaquac, F1		F	Keyhole	8-OCT-04	
18	F6670	Mactaquac, F1	32	I	Bennett Bk	8-OCT-04	
19	F6816	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
20	F6828	Mactaquac, F1		M	Flagnar	8-OCT-04	
21	F6861	Mactaquac, F1		M	Keyhole	8-OCT-04	
22	F6711	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
23	F6714	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
24	F6771	Mactaquac, F1		F	Keyhole	8-OCT-04	
25	F6836	Mactaquac, F1		M	Keyhole	8-OCT-04	
26	F6842	Mactaquac, F1		M	Flagnar	8-OCT-04	
27	F6844	Mactaquac, F1		F	Flagnar	8-OCT-04	
28	F6811	Mactaquac, F1		I	Flagnar	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
29	F6823	Mactaquac, F1		I	Bennett Bk	8-OCT-04	
30	F6876	Mactaquac, F1		I	Keyhole	8-OCT-04	
31	F6583	Mactaquac, F1		F	flagnar	8-OCT-04	
32	F6802	Mactaquac, F1		F	Keyhole	8-OCT-04	
33	F6745	Mactaquac, F1		I	Bennett Bk	8-OCT-04	
34	F6750	Mactaquac, F1		F	Flagnar	8-OCT-04	
35	F6758	Mactaquac, F1		F	Flagnar	8-OCT-04	
36	F6559	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
37	F6790	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
38	F6785	Mactaquac, F1		F	Keyhole	8-OCT-04	
39	F6801	Mactaquac, F1		F	Flagnar	8-OCT-04	
40	F6722	Mactaquac, F1		F	Keyhole	8-OCT-04	
41	F6853	Mactaquac, F1	49	F	Hueston Bk	8-OCT-04	
42	F6689	Mactaquac, F1		I	Keyhole	8-OCT-04	
43	F6736	Mactaquac, F1	52	F	Bennett Bk	8-OCT-04	
44	F6743	Mactaquac, F1		M	Flagnar	8-OCT-04	
45	F6795	Mactaquac, F1		M	Hueston Bk	8-OCT-04	
46	F6507	Mactaquac, F1	50	F	Hueston Bk	8-OCT-04	
47	F6535	Mactaquac, F1		M	Flagnar	8-OCT-04	
48	F6582	Mactaquac, F1		M	Keyhole	8-OCT-04	
49	F6674	Mactaquac, F1		F	Keyhole	8-OCT-04	
50	F6732	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
51	F6544	Mactaquac, F1		F		8-OCT-04	not released
52	F6571	Mactaquac, F1	51	M	Hueston Bk	8-OCT-04	
53	F6581	Mactaquac, F1		M	Keyhole	8-OCT-04	
54	F6568	Mactaquac, F1		F	Keyhole	8-OCT-04	
55	F6768	Mactaquac, F1		F	keyhole	8-OCT-04	
56	F6764	Mactaquac, F1		I	Keyhole	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
57	F6826	Mactaquac, F1		I	Keyhole	8-OCT-04	
58	F6840	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
59	F6882	Mactaquac, F1		I	Keyhole	8-OCT-04	
60	D9800	Mactaquac, F1	57	M	Bennett Bk	8-OCT-04	
61	F6503	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
62	F6504	Mactaquac, F1	52	M	Hueston Bk	8-OCT-04	
63	F6516	Mactaquac, F1		M	Flagnar	8-OCT-04	
64	F6519	Mactaquac, F1		M	Hueston Bk	8-OCT-04	
65	F6526	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
66	F6528	Mactaquac, F1	43	F	Hueston Bk	8-OCT-04	
67	F6532	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
68	F6533	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
69	F6536	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
70	F6537	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
71	F6540	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
72	F6551	Mactaquac, F1		M	Flagnar	8-OCT-04	
73	F6552	Mactaquac, F1		F	Keyhole	8-OCT-04	
74	F6557	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
75	F6558	Mactaquac, F1		M	Flagnar	8-OCT-04	
76	F6563	Mactaquac, F1		F	Keyhole	8-OCT-04	
77	F6565	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
78	F6567	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
79	F6570	Mactaquac, F1	46	F	Bennett Bk	8-OCT-04	
80	F6573	Mactaquac, F1		M	Hueston Bk	8-OCT-04	
81	F6574	Mactaquac, F1		F	Keyhole	8-OCT-04	
82	F6580	Mactaquac, F1		F	Bennett Bk	8-OCT-04	Mortality post release, Oct 13
83	F6584	Mactaquac, F1	48	F	Bennett Bk	8-OCT-04	
84	F6586	Mactaquac, F1		M	Hueston Bk	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
85	F6587	Mactaquac, F1	49	F	Bennett Bk	8-OCT-04	
86	F6588	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
87	F6589	Mactaquac, F1	54	F	Hueston Bk	8-OCT-04	
88	F6590	Mactaquac, F1		F	Flagnar	8-OCT-04	
89	F6591	Mactaquac, F1		F	Keyhole	8-OCT-04	
90	F6592	Mactaquac, F1		F	Keyhole	8-OCT-04	
91	F6593	Mactaquac, F1		I	Keyhole	8-OCT-04	
92	F6594	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
93	F6595	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
94	F6596	Mactaquac, F1		F	Keyhole	8-OCT-04	
95	F6597	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
96	F6598	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
97	F6599	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
98	F6601	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
99	F6602	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
100	F6603	Mactaquac, F1		F	flagnar	8-OCT-04	
101	F6604	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
102	F6605	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
103	F6606	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
104	F6607	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
105	F6608	Mactaquac, F1	46	M	Flagnar	8-OCT-04	
106	F6609	Mactaquac, F1	48	M	Bennett Bk	8-OCT-04	
107	F6610	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
108	F6611	Mactaquac, F1		F		8-OCT-04	not released
109	F6612	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
110	F6614	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
111	F6616	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
112	F6617	Mactaquac, F1		M	Hueston Bk	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
113	F6618	Mactaquac, F1	44	M	Bennett Bk	8-OCT-04	
114	F6619	Mactaquac, F1	49	F	Hueston Bk	8-OCT-04	
115	F6620	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
116	F6621	Mactaquac, F1	53	M	Bennett Bk	8-OCT-04	
117	F6623	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
118	F6624	Mactaquac, F1		I	Bennett Bk	8-OCT-04	
119	F6625	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
120	F6626	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
121	F6627	Mactaquac, F1		M	Keyhole	8-OCT-04	
122	F6628	Mactaquac, F1	53	F	Bennett Bk	8-OCT-04	
123	F6629	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
124	F6630	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
125	F6632	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
126	F6633	Mactaquac, F1	53	M	Hueston Bk	8-OCT-04	
127	F6634	Mactaquac, F1		F	Flagnar	8-OCT-04	
128	F6635	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
129	F6636	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
130	F6637	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
131	F6638	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
132	F6640	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
133	F6641	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
134	F6642	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
135	F6643	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
136	F6644	Mactaquac, F1		F	flagnar	8-OCT-04	
137	F6645	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
138	F6646	Mactaquac, F1	44	F	Hueston Bk	8-OCT-04	
139	F6647	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
140	F6648	Mactaquac, F1		M	Bennett Bk	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
141	F6649	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
142	F6650	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
143	F6651	Mactaquac, F1		I	Hueston Bk	8-OCT-04	
144	F6652	Mactaquac, F1		I	Hueston Bk	8-OCT-04	
145	F6653	Mactaquac, F1		I	Keyhole	8-OCT-04	
146	F6654	Mactaquac, F1	49	M	Hueston Bk	8-OCT-04	
147	F6655	Mactaquac, F1		F	Flagnar	8-OCT-04	
148	F6656	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
149	F6657	Mactaquac, F1	41	M	Bennett Bk	8-OCT-04	
150	F6659	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
151	F6660	Mactaquac, F1	55	M	Bennett Bk	8-OCT-04	
152	F6661	Mactaquac, F1		F	Flagnar	8-OCT-04	
153	F6662	Mactaquac, F1	48	M	Bennett Bk	8-OCT-04	
154	F6663	Mactaquac, F1		M	Hueston Bk	8-OCT-04	
155	F6664	Mactaquac, F1		I	Keyhole	8-OCT-04	
156	f6665	Mactaquac, F1		M	Keyhole	8-OCT-04	
157	F6666	Mactaquac, F1	52	F	flagnar	8-OCT-04	
158	F6727	Mactaquac, F1	37	F	flagnar	8-OCT-04	
159	F6728	Mactaquac, F1	37	I	Bennett Bk	8-OCT-04	
160	F6729	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
161	F6740	Mactaquac, F1		F	Keyhole	8-OCT-04	
162	F6746	Mactaquac, F1		F	Keyhole	8-OCT-04	
163	F6751	Mactaquac, F1		F	Keyhole	8-OCT-04	
164	F6753	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
165	F6754	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
166	F6765	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
167	F6775	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
168	F6792	Mactaquac, F1		I	Keyhole	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
169	F6796	Mactaquac, F1		M	Keyhole	8-OCT-04	
170	F6797	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
171	F6799	Mactaquac, F1		I	Flagnar	8-OCT-04	
172	F6804	Mactaquac, F1	52	F	Hueston Bk	8-OCT-04	
173	F6817	Mactaquac, F1		M	Hueston Bk	8-OCT-04	
174	F6820	Mactaquac, F1		M	flagnar	8-OCT-04	
175	F6821	Mactaquac, F1	52	M	Bennett Bk	8-OCT-04	
176	F6829	Mactaquac, F1		I	Bennett Bk	8-OCT-04	
177	F6833	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
178	F6835	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
179	F6838	Mactaquac, F1		F	keyhole	8-OCT-04	
180	F6841	Mactaquac, F1		F	Hueston Bk	8-OCT-04	
181	F6846	Mactaquac, F1		M	keyhole	8-OCT-04	
182	F6849	Mactaquac, F1		M	Bennett Bk	8-OCT-04	
183	F6862	Mactaquac, F1		F	Bennett Bk	8-OCT-04	
184	no tag	Unknown		i	Flagnar	8-OCT-04	
185	no tag	Unknown		F	Flagnar	8-OCT-04	
186	no tag	Unknown		I	Flagnar	8-OCT-04	
187	no tag	Unknown		I	Flagnar	8-OCT-04	
188	no tag	Unknown		I	Flagnar	8-OCT-04	
189	no tag	Unknown		F	Flagnar	8-OCT-04	
190	no tag	Unknown		I	Flagnar	8-OCT-04	
191	no tag	Unknown		I	Flagnar	8-OCT-04	
192	no tag	Unknown		I	Flagnar	8-OCT-04	
193	no tag	Unknown		I	Flagnar	8-OCT-04	
194	no tag	Unknown		F	Flagnar	8-OCT-04	
195	no tag	Unknown		F	Hueston Bk	8-OCT-04	
196	no tag	Unknown		I	Hueston Bk	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
197	no tag	Unknown		I	Hueston Bk	8-OCT-04	
198	no tag	Unknown		F	Hueston Bk	8-OCT-04	
199	no tag	Unknown		I	Hueston Bk	8-OCT-04	
200	no tag	Unknown		I	Hueston Bk	8-OCT-04	
201	no tag	Unknown		F	Hueston Bk	8-OCT-04	
202	no tag	Unknown		I	Hueston Bk	8-OCT-04	
203	no tag	Unknown		I	Hueston Bk	8-OCT-04	
204	no tag	Unknown		I	Keyhole	8-OCT-04	
205	no tag	Unknown		F	Flagnar	8-OCT-04	
206	no tag	Unknown		I	Keyhole	8-OCT-04	
207	no tag	Unknown		I	Keyhole	8-OCT-04	
208	no tag	Unknown		I	Keyhole	8-OCT-04	
209	no tag	Unknown		I	Keyhole	8-OCT-04	
210	no tag	Unknown		F	Flagnar	8-OCT-04	
211	no tag	Unknown		I	Keyhole	8-OCT-04	
212	no tag	Unknown		F	Flagnar	8-OCT-04	
213	no tag	Unknown		I	Keyhole	8-OCT-04	
214	no tag	Unknown		I	Keyhole	8-OCT-04	
215	no tag	Unknown		I	Keyhole	8-OCT-04	
216	no tag	Unknown		I	Keyhole	8-OCT-04	
217	no tag	Unknown		I	Keyhole	8-OCT-04	
218	no tag	Unknown		I	Keyhole	8-OCT-04	
219	no tag	Unknown		I	Keyhole	8-OCT-04	
220	no tag	Unknown		I	Keyhole	8-OCT-04	
221	no tag	Unknown		I	Keyhole	8-OCT-04	
222	no tag	Unknown		I	Keyhole	8-OCT-04	
223	no tag	Unknown		F	Flagnar	8-OCT-04	
224	no tag	Unknown		I	Keyhole	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
225	no tag	Unknown		I	Keyhole	8-OCT-04	
226	no tag	Unknown		I	Flagnar	8-OCT-04	
227	no tag	Unknown		F	Flagnar	8-OCT-04	
228	no tag	Unknown		I	Flagnar	8-OCT-04	
229	no tag	Unknown		I	Flagnar	8-OCT-04	
230	no tag	Unknown		I	Flagnar	8-OCT-04	
231	no tag	Unknown		F	Flagnar	8-OCT-04	
232	no tag	Unknown		I	Flagnar	8-OCT-04	
233	no tag	Unknown		I	Flagnar	8-OCT-04	
234	no tag	Unknown		F	Flagnar	8-OCT-04	
235	no tag	Unknown		I	Flagnar	8-OCT-04	
236	no tag	Unknown		I		8-OCT-04	not released
237	no tag	Unknown		I	Flagnar	8-OCT-04	
238	no tag	Unknown		I	Flagnar	8-OCT-04	
239	no tag	Unknown		M	Flagnar	8-OCT-04	
240	no tag	Unknown		F		8-OCT-04	not released
241	no tag	Unknown		M	Flagnar	8-OCT-04	
242	no tag	Unknown		M	Flagnar	8-OCT-04	
243	no tag	Unknown		M	Flagnar	8-OCT-04	
244	no tag	Unknown		F		8-OCT-04	not released
245	no tag	Unknown		I	Flagnar	8-OCT-04	
246	no tag	Unknown		I		8-OCT-04	not released
247	no tag	Unknown		I	Bennett Bk	8-OCT-04	
248	no tag	Unknown		I	Bennett Bk	8-OCT-04	
249	no tag	Unknown		F	Bennett Bk	8-OCT-04	
250	no tag	Unknown		f	Keyhole	8-OCT-04	
251	no tag	Unknown		f	Keyhole	8-OCT-04	
252	no tag	Unknown		F	Bennett Bk	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
253	no tag	Unknown		F	Bennett Bk	8-OCT-04	
254	no tag	Unknown		I	Bennett Bk	8-OCT-04	
255	no tag	Unknown		I	Bennett Bk	8-OCT-04	
256	no tag	Unknown		m	Bennett Bk	8-OCT-04	
257	C458	Mactaquac, F1	51	F	Keyhole	8-OCT-04	
258	F8057	Minto, F2	62	F	Flagnar	8-OCT-04	
259	C573	Mactaquac, F1	58	F	Flagnar	8-OCT-04	
260	C523	Mactaquac, F1	51	F	Keyhole	8-OCT-04	
261	C529	Mactaquac, F1	53	F	Flagnar	8-OCT-04	
262	C540	Mactaquac, F1	52	F	Keyhole	8-OCT-04	
263	C474	Mactaquac, F1	66	F	Keyhole	8-OCT-04	
264	C077	Minto, F2	60	F	Flagnar	8-OCT-04	
265	C047	Minto, F2	67	F	Flagnar	8-OCT-04	
266	C030	Mactaquac, F1	54	F	Keyhole	8-OCT-04	
267	C002	Mactaquac, F1	61	F	Keyhole	8-OCT-04	
268	C502	Mactaquac, F1	64	F	Keyhole	8-OCT-04	
269	F8105	Minto, F2	67	F	Flagnar	8-OCT-04	
270	C004	Mactaquac, F1	58	M	Flagnar	8-OCT-04	
271	C221	Mactaquac, F1	58	F		8-OCT-04	mortality prior to release
272	C055	Minto, F2	68	F	Flagnar	8-OCT-04	
273	F8056	Minto, F2	68	F	Flagnar	8-OCT-04	
274	C535	Mactaquac, F1	64	F	Flagnar	8-OCT-04	
275	C175	Mactaquac, F1	53	M	Keyhole	8-OCT-04	
276	C013	Mactaquac, F1	61	F	Keyhole	8-OCT-04	
277	C202	Mactaquac, F1	62	F	Keyhole	8-OCT-04	
278	C234	Mactaquac, F1	46	F	Flagnar	8-OCT-04	
279	C433	Mactaquac, F1	65	F	Keyhole	8-OCT-04	
280	C239	Mactaquac, F1	68	F	Flagnar	8-OCT-04	

Cumulative count	Carlin tag	Captive history*	Fork Length (cm)	Sex **	Release Location***	Release date	Comments
281	C208	Mactaquac, F1	59	M		8-OCT-04	mortality prior to release
282	C007	Mactaquac, F1	64	M	Flagnar	8-OCT-04	
283	F8095	Minto, F2	64	F	Keyhole	8-OCT-04	
284	F8083	Minto, F2	60	F	Flagnar	8-OCT-04	
285	F8067	Minto, F2	65	F		8-OCT-04	mortality prior to release
286	C477	Mactaquac, F1	50	F	Keyhole	8-OCT-04	
287	C569	Mactaquac, F1	55	M	Keyhole	8-OCT-04	
288	C512	Mactaquac, F1	64	M	Flagnar	8-OCT-04	
289	C240	Mactaquac, F1	54	F	Keyhole	8-OCT-04	
290	C187	Mactaquac, F1	60	M		XX-OCT-04	mortality prior to release
291	C201	Mactaquac, F1	63	F	Keyhole	XX-OCT-04	
292	C231	Mactaquac, F1	64	M	Flagnar	XX-OCT-04	

* Captive history: Mactaquac, F1 = Salmon produced through the artificial spawning of parents obtained from the Big Salmon River as juveniles and that therefore have accumulated approximately 1.5 generations of domestication selection; Minto, F2 = Salmon produced through the artificial spawning of parents obtained from the Minto Fish Hatchery. Minto hatchery fish were themselves produced through the artificial spawning of parents obtained from the Big Salmon River as juveniles. These adult releases have therefore accumulated approximately 2.5 generations of domestication selection.
** Sex: M=male, F=female, I=immature
***Release location information (locations as specified in Figure 1)

Table A3. Sample information for fry and parr collected from the Point Wolfe River in 2004.

Cumulative count	Laboratory ID	Site*	Field ID	Length (mm)	Weight (g)	Date collected	Collector	Analysis Summary**	Year class***
1	PWF010904HO1	REFFB		58	2.38	July 27,04	MC	failed	2003
2	PWF010904HO2	REFFB		62	2.63	July27,04	MC	failed	2003
3	PWF010904HO3	REFFB		55	1.82	July 27,04	MC	succ.	2003
4	PWF010904HO4	PSPHB	AS01	66		Aug 17,04	AC	succ.	2003
5	PWF010904HO5	PSPHB	AS02	72	5	Aug 17,04	AC	succ.	2003
6	PWF010904HO6	PSPHB	AS 03	59	1.8	Aug 17,04	AC	succ.	2003
7	PWF010904HO7	PSPHB	AS 04	60	2.5	Aug 17,04	AC	succ.	2003
8	PWF010904HO8	PSPHB	AS 05	60	1.8	Aug 17,04	AC	succ.	2003
9	PWF010904HO9	PSPHB	AS 06	61		Aug 17,04	AC	succ.	2003
10	PWF010904HO10	PSPHB	AS 07	72		Aug 17,04	AC	succ.	2003
11	PWF010904HO11	PSPHB	AS 08	67		Aug 17,04	AC	succ.	2003
12	PWF010904HO12	PSPHB	AS 09	66		Aug 17,04	AC	succ.	2003
13	PWF010904HO13	PSPHB	AS 01	75	3.5	Aug 18,04	AC	succ.	2003
14	PWF010904HO14	PSPHB	AS 02	61	2.7	Aug 18,04	AC	succ.	2003
15	PWF010904HO15	PSPHB	AS 03	62	2.7	Aug 18,04	AC	succ.	2003
16	PWF010904HO16	PSPHB	AS 04	64	3	Aug 18,04	AC	succ.	2003
17	PWF010904HO17	PSPHB	AS 05	71	3.6	Aug 18,04	AC	succ.	2003
18	PWF010904HO18	PSPHB	AS 06	62	2.7	Aug 18,04	AC	succ.	2003
19	PWF010904HO19	PSPHB	AS 07	63	3.6	Aug 18,04	AC	succ.	2003
20	PWF010904HO20	PSPSB	AS 02	67		Aug 26,04	AC	succ.	2003
21	PWF010904HO21	PSPSB	AS 03	80		Aug 26,04	AC	succ.	2003
22	PWF010904HO22	PSPSB	AS 04	64		Aug 26,04	AC	succ.	2003
23	PWF010904HO23	PSPSB	AS 05	79		Aug 26,04	AC	succ.	2003
24	PWF010904HO24	PSPSB	AS 06	74		Aug 26,04	AC	succ.	2003
25	PWF010904HO25	REFCO	AS 07			Aug 18,04	TR	succ.	2003
26	PWF010904HO26	REFCO	AS 08			Aug 18,04	TR	succ.	2003
27	PWF010904HO27	REFCO	AS 09			Aug 18,04	TR	succ.	2003
28	PWF010904HO28	REFCO	AS 10			Aug 18,04	TR	succ.	2003
29	PWF010904HO29	REFOB	AS 01	67		Aug 26, 04	TR	succ.	2003
30	PWF010904HO30	REFOB	AS 02	68		Aug 26, 04	TR	succ.	2003

Cumulative count	Laboratory ID	Site*	Field ID	Length (mm)	Weight (g)	Date collected	Collector	Analysis Summary**	Year class***
31	PWF010904HO31	REFOB	AS 03	65		Aug 26, 04	TR	succ.	2003
32	PWF010904HO32	REFOB	AS 04	68		Aug 26, 04	TR	succ.	2003
33	PWF150604HO003AS01	PSPSB	AS 01	164		Aug 26, 04	AC	succ.	2002
34	PWF150604HO004AS01	PSPBB	AS 01	170		Sep 7,04	AC	succ.	2002
35	PWF150604HO004AS02	PSPBB	AS 02	83		Sep 7,04	AC	succ.	2003
36	PWF150604HO004AS03	PSPBB	AS 03	78		Sep 7,04	AC	succ.	2003
37	PWF150604HO004AS04	PSPBB	AS 04	78		Sep 7,04	AC	succ.	2003
38	PWF150604HO004AS05	PSPBB	AS 05	77		Sep 7,04	AC	succ.	2003
39	PWF150604HO004AS06	PSPBB	AS 06	71		Sep 7,04	AC	succ.	2003
40	PWF150604HO004AS07	PSPBB	AS 07	79		Sep 7,04	AC	succ.	2003
41	PWF150604HO004AS08	PSPBB	AS 08	70		Sep 7,04	AC	succ.	2003
42	PWF150604HO004AS09	PSPBB	AS 09	81		Sep 7,04	AC	succ.	2003
43	PWF150604HO004AS10	PSPBB	AS 10	167		Sep 7,04	AC	succ.	2002
44	PWF150604HO004AS11	PSPBB	AS 11	73		Sep 7,04	AC	succ.	2003
45	PWF150604HO004AS12	PSPBB	AS 12	80		Sep 7,04	AC	succ.	2003
46	PWF150604HO004AS13	PSPBB	AS 13	79		Sep 7,04	AC	succ.	2003
47	PWF150604HO004AS14	PSPBB	AS 14	74		Sep 7,04	AC	succ.	2003
48	PWF150604HO004AS15	PSPBB	AS 15	165		Sep 7,04	AC	succ.	2002
49	PWF150604HO004AS16	PSPBB	AS 16	77		Sep 7,04	AC	succ.	2003
50	PWF150604HO004AS17	PSPBB	AS 17	165		Sep 7,04	AC	succ.	2002
51	PWF150604HO004AS18	PSPBB	AS 18	177		Sep 7,04	AC	succ.	2002
52	PWF150604HO004AS19	PSPBB	AS 19	73		Sep 7,04	AC	succ.	2003
53	PWF150604HOCONFIVAS01	REFCO	AS 01	180		Aug 18, 04	TR	succ.	2002
54	PWF150604HOCONFIVAS02	REFCO	AS 02	175		Aug 18, 04	TR	succ.	2002
55	PWF150604HOCONFIVAS03	REFCO	AS 03	135		Aug 18, 04	TR	succ.	2002
56	PWF150604HOABOVURAS04	REFKB	AS 04	210		Aug 18, 04	TR	succ.	2002
57	PWF150604HOABOVURAS05	REFKB	AS 05	162		Aug 18, 04	TR	succ.	2002
58	PWF150604HOABOVURAS06	REFKB	AS 06	174		Aug 18, 04	TR	succ.	2002
59	PWF150604HODEAD	PSPHB	Dead*			Sep 30,04	AC	failed	2003
60	PWF150604HOFOSTER70MM	REFFB		70	4.13	Sep ,04	MC ?	failed	2003
61	PWF150604HOFOSTER79MM	REFFB		79	7.28	Sep ,04	MC ?	succ.	2003

*Site = specific location on the Point Wolfe River where samples were collected, and corresponds to locations specified in Figure 1.

** Analysis summary denotes whether laboratory analyses associated with a particular sample succeeded (succ.) or failed.
***Year class denotes the year a given juvenile was produced, or the year of conception.
REFCO=Random Electrofishing Confluence; REFKB=Random Electrofishing Keyhole;
PSPBB=Permanent Electrofishing Plot Bennet Brook; PSPSB= Permanent Electrofishing Plot Sweeny Brook (labelled as Permanent Electrofishing plot Foster Brook in parks records);
REFFB=Random Electrofishing Foster Brook; REFOB=Random Electrofishing OxBow

Table A4. Sample information for fry and parr collected from the Point Wolfe River in 2005.

Cumulative count	Laboratory ID	Site*	Field ID	Length (mm)	Weight (g)	Date collected	Collector	Analysis Summary**	Year class***
1	PWF220805HOS01P01114M	PSPHB	1	114	16.6	August 15 2005	AC	succ.	2003
2	PWF220805HOS02P01116M	PSPHB	2	116	20.1	August 15 2005	AC	succ.	2003
3	PWF150805HOS03P01122M	PSPHB	3	122	20.8	August 15 2005	AC	Partial	2003
4	PWF220805HOS04P01116M	PSPHB	4	116	16.2	August 15 2005	AC	succ.	2003
5	PWF150805HOS05P01137M	PSPHB	5	137	28.5	August 15 2005	AC	succ.	2003
6	PWF150805HOS06P01136M	PSPHB	6	136	30.0	August 15 2005	AC	succ.	2003
7	PWF150805HOS07P01129M	PSPHB	7	129	27.5	August 15 2005	AC	succ.	2003
8	PWF150805HOS08P01128M	PSPHB	8	128	26.3	August 15 2005	AC	succ.	2003
9	PWF170805HOS01P02127M	PSPHB	1	127	26.6	August 17 2005	AC	succ.	2003
10	PWF170805HOS02P02116M	PSPHB	2	116	17.4	August 17 2005	AC	succ.	2003
11	PWF170805HOS03P02127M	PSPHB	3	127	23.2	August 17 2005	AC	succ.	2003
12	PWF170805HOS04P02127M	PSPHB	4	127	28.2	August 17 2005	AC	succ.	2003
13	PWF170805HOS05P02126M	PSPHB	5	126	25.8	August 17 2005	AC	succ.	2003
14	PWF170805HOS06P02130M	PSPHB	6	130	29.3	August 17 2005	AC	succ.	2003
15	PWF170805HOS07P02116M	PSPHB	7	116	18.9	August 17 2005	AC	succ.	2003
16	PWF170805HOS08P02122M	PSPHB	8	122	23.1	August 17 2005	AC	succ.	2003
17	PWF170805HOS09P02134M	PSPHB	9	134	32.7	August 17 2005	AC	succ.	2003
18	PWF170805HOS10P02120M	PSPHB	10	120	20.5	August 17 2005	AC	succ.	2003
19	PWF170805HOS11P02102M	PSPHB	11	102	11.7	August 17 2005	AC	succ.	2003
20	PWF170805HOS12P02122M	PSPHB	12	122	22.2	August 17 2005	AC	succ.	2003
21	PWF170805HOS13P02124M	PSPHB	13	124	24.4	August 17 2005	AC	succ.	2003
22	PWF170805HOS14P02138M	PSPHB	14	138	30.2	August 17 2005	AC	succ.	2003
23	PWF190805HOS01P03135M	PSPSB	1	135		August 19 2005	AC	succ.	2003
24	PWF190805HOS02P03197M	PSPSB	2	197		August 19 2005	AC	succ.	2003
25	PWF190805HOS03P03136M	PSPSB	3	136		August 19 2005	AC	succ.	2003
26	PWF190805HOS04P03133M	PSPSB	4	133		August 19 2005	AC	succ.	2003
27	PWF190805HOS05P03126M	PSPSB	5	126		August 19 2005	AC	succ.	2003
28	PWF190805HOS06P03117M	PSPSB	6	117		August 19 2005	AC	succ.	2003
29	PWF220805HOS01P04113M	PSPBB	1	113	16.4	August 22 2005	AC	succ.	2003
30	PWF220805HOS02P04127M	PSPBB	2	127	24.3	August 22 2005	AC	succ.	2003
31	PWF220805HOS03P04127M	PSPBB	3	127	26.6	August 22 2005	AC	succ.	2003
32	PWF220805HOS04P04130M	PSPBB	4	130	27.0	August 22 2005	AC	succ.	2003

Cumulative count	Laboratory ID	Site*	Field ID	Length (mm)	Weight (g)	Date collected	Collector	Analysis Summary**	Year class***
33	PWF220805HOS05P04063M	PSPBB	5	63	3.2	August 22 2005	AC	succ.	2004
34	PWF220805HOS06P04121M	PSPBB	6	121	20.8	August 22 2005	AC	succ.	2003
35	PWF220805HOS07P04129M	PSPBB	7	129	24.1	August 22 2005	AC	succ.	2003
36	PWF220805HOS08P04122M	PSPBB	8	122	24.1	August 22 2005	AC	succ.	2003
37	PWF220805HOS09P04068M	PSPBB	9	68	3.3	August 22 2005	AC	succ.	2004
38	PWF250805HOS01P05125M	PSPBB	1	125	20.0	August 25 2005	AC	succ.	2003
39	PWF250805HOS02P05117M	PSPBB	2	117	8.0	August 25 2005	AC	succ.	2003
40	PWF250805HOS03P05128M	PSPBB	3	128	23.0	August 25 2005	AC	succ.	2003
41	PWF250805HOS04P05064M	PSPBB	4	64	3.0	August 25 2005	AC	succ.	2004
42	PWF250805HOS05P05062M	PSPBB	5	62	3.0	August 25 2005	AC	succ.	2004
43	PWF250805HOS06P05062M	PSPBB	6	62	3.0	August 25 2005	AC	succ.	2004
44	PWF250805HOS07P05126M	PSPBB	7	126	23.0	August 25 2005	AC	succ.	2003
45	PWF180805HOS01P06115M	PSPSB	1	115	23.2	August 18 2005	AC	succ.	2003
46	PWF180805HOS02P06117M	PSPSB	2	117	19.8	August 18 2005	AC	succ.	2003
47	PWF260705HOS01PK1163M	REFKB	001	163		July 26 2005	TR	succ.	2004
48	PWF260705HOS02PK1051M	REFKB	002	51		July 26 2005	TR	succ.	2004
49	PWF260705HOS03PK1055M	REFKB	003	55		July 26 2005	TR	succ.	2004
50	PWF260705HOS04PK1055M	REFKB	004	55		July 26 2005	TR	succ.	2004
51	PWF280705HOS05PF1107M	REFFB	005	107		July 28 2005	TR	succ.	2003
52	PWF280705HOS06PF1124M	REFFB	006	124		July 28 2005	TR	succ.	2003
53	PWF280705HOS07PF2124M	REFFB	007	124		July 28 2005	TR	succ.	2003
54	PWF280705HOS08PF3131M	REFFB	008	131		July 28 2005	TR	succ.	2003
55	PWF280705HOS09PF3120M	REFFB	009	120		July 28 2005	TR	succ.	2003
56	PWF280705HOS10PF4123M	REFFB	010	123		July 28 2005	TR	succ.	2003
57	PWF020805HOS01PB1064M	PSPBB	001	64		August 02 2005	TR	succ.	2004
58	PWF020805HOS02PB1124M	PSPBB	002	124		August 02 2005	TR	succ.	2003
59	PWF020805HOS03PB1140M	PSPBB	003	140		August 02 2005	TR	succ.	2003
60	PWF020805HOS04PB1123M	PSPBB	004	123		August 02 2005	TR	succ.	2003
61	PWF020805HOS05PB1124M	PSPBB	005	124		August 02 2005	TR	succ.	2003
62	PWF020805HOS06PB2112M	PSPBB	006	112		August 02 2005	TR	succ.	2003
63	PWF020805HOS07PB2130M	PSPBB	007	130		August 02 2005	TR	succ.	2003
64	PWF020805HOS08PB4119M	PSPBB	008	119		August 02 2005	TR	succ.	2003

*Site = specific location on the Point Wolfe River where samples were collected, and corresponds to locations specified in Figure 1.
** Analysis summary denotes whether laboratory analyses associated with a particular sample succeeded (succ.) or failed.
***Year class denotes the year a given juvenile was produced, or the year of conception.
REFCO=Random Electrofishing Confluence; REFKB=Random Electrofishing Keyhole; PSPBB=Permanent Electrofishing Plot Bennet Brook;
PSPSB= Permanent Electrofishing Plot; Sweeny Brook (labelled as Permanent Electrofishing plot Foster Brook in parks records);
REFFB=Random Electrofishing Foster Brook; REFOB=Random Electrofishing OxBow

Table A5. Genotypic similarity of Big Salmon River salmon released into the Point Wolfe River in 2003 and 2004.

BSR release 1	BSR release 2	Number of alleles evaluated	Number of alleles matching	Percent identity	Related (first gen. only)
BSR151101QCF6533	BSR151101QCF6537	20	20	100.00%	yes
BSR151100QCC157	BSR151100QCC397	14	13	92.86%	yes
BSR151101QCF6717	BSR151101QCF6866	24	22	91.67%	yes
BSR151100QCC662	BSR151100QCC477	16	14	87.50%	no
BSR151100QCC750	BSR151100QCC853	16	14	87.50%	yes
BSR151100QCC065	BSR151101QCF6650	14	12	85.71%	no
BSR151100QCC318	BSR151100QCC554	20	17	85.00%	yes
BSR151100QCC074	BSR151100QCC100	18	15	83.33%	yes
BSR151100QCC127	BSR151100QCC854	18	15	83.33%	yes
BSR151101QCF6557	BSR151101QCF6751	18	15	83.33%	yes
BSR151101QCF6616	BSR151101QCF6661	18	15	83.33%	yes
BSR151101QCF6711	BSR151101QCF6714	18	15	83.33%	yes
BSR151100QCC439	BSR151100QCC662	16	13	81.25%	yes
BSR151100QCC628	BSR151100QCC234	16	13	81.25%	yes
BSR151101QCF6745	BSR151101QCF6758	16	13	81.25%	yes
BSR151100QCC264	BSR151100QCC221	20	16	80.00%	yes
BSR151100QCC352	BSR151100QCC609	20	16	80.00%	no
BSR151100QCC357	BSR151101QCF6833	20	16	80.00%	yes
BSR151101QCF6636	BSR151101QCF6801	20	16	80.00%	yes
BSR151101QCF6531	BSR151101QCF6536	10	8	80.00%	yes
BSR151100QCC031	BSR151100QCC497	14	11	78.57%	yes
BSR151100QCC382	BSR151100QCC234	14	11	78.57%	yes
BSR151100QCC397	BSR151100QCC832	14	11	78.57%	yes
BSR151100QCC716	BSR151100QCC949	18	14	77.78%	yes
BSR151101QCF6640	BSR151101QCF6771	18	14	77.78%	yes
BSR151100QCC007	BSR151100QCC671	22	17	77.27%	yes
BSR151100QCC115	BSR151100QCC775	22	17	77.27%	yes
BSR151100QCC354	BSR151100QCC713	22	17	77.27%	yes
BSR151100QCC717	BSR151100QCC747	22	17	77.27%	yes
BSR151101QCF6764	BSR151101QCF6826	22	17	77.27%	yes
BSR151101QCF6604	BSR151101QCF6612	24	18	75.00%	yes
BSR151101QCF6669	BSR151101QCF6866	24	18	75.00%	no
BSR151100QCC049	BSR151100QCC059	20	15	75.00%	yes
BSR151100QCC167	BSR151100QCC632	20	15	75.00%	yes
BSR151100QCC276	BSR151100QCC340	20	15	75.00%	yes
BSR151100QCC348	BSR151100QCC609	20	15	75.00%	yes
BSR151100QCC668	BSR151100QCC894	20	15	75.00%	yes
BSR151100QCC011	BSR151100QCC876	16	12	75.00%	yes
BSR151100QCC127	BSR151100QCC458	16	12	75.00%	yes
BSR151100QCC181	BSR151100QCC462	16	12	75.00%	yes
BSR151100QCC386	BSR151100QCC399	16	12	75.00%	yes
BSR151100QCC456	BSR151100QCC202	16	12	75.00%	yes
BSR151101QCF6588	BSR151101QCF6647	16	12	75.00%	yes
BSR151100QCC074	BSR151101QCF6616	12	9	75.00%	no
BSR151100QCC628	BSR151101QCF6616	12	9	75.00%	no
BSR151101QCF6531	BSR151101QCF6588	12	9	75.00%	yes

Related (first gen. only) = related or not, based on estimates of first-order relatedness

Table A6. Parentage assignment and kinship results for Big Salmon River adults released into the Point Wolfe River in 2003 and 2004.

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC749	C749	1	T52454	T52428	8	8	0	37
BSR151100QCC928	C928	1	T52454	T52428	8	8	0	37
BSR151100QCC462	C462	2	T52626	T52431	7	6	1	60
BSR151100QCC736	C736	2	T52626	T52431	3	2	1	#N/A
BSR151100QCC181	C181	2	T52626	T52431	8	7	1	60
BSR151100QCC645	C645	4	T52495	T52437	8	8	0	21
BSR151100QCC814	C814	9	T52580	T52460	8	8	0	14
BSR151100QCC824	C824	9	T52580	T52460	8	8	0	14
BSR151100QCC896	C896	9	T52580	T52460	8	8	0	14
BSR151100QCC621	C621	10	T52566	T52473	8	8	0	59
BSR151100QCC413	C413	10	T52566	T52473	8	7	1	59
BSR151100QCC632	C632	12	T52471	T52478	8	8	0	56
BSR151100QCC033	C033	12	T52471	T52478	6	5	1	56
BSR151100QCC036	C036	12	T52471	T52478	8	8	0	56
BSR151100QCC140	C140	12	T52471	T52478	8	7	1	56
BSR151100QCC167	C167	12	T52471	T52478	8	8	0	56
BSR151100QCC708	C708	14	T52628	T52484	8	7	1	42
BSR151100QCC078	C078	14	T52628	T52484	8	7	1	42
BSR151100QCC783	C783	15	T52570	T52485	6	6	0	64
BSR151100QCC887	C887	15	T52570	T52485	6	6	0	64
BSR151100QCC942	C942	15	T52570	T52485	7	7	0	64
BSR151100QCC125	C125	15	T52570	T52485	7	7	0	64
BSR151100QCC674	C674	16	T52629	T52487	8	8	0	63
BSR151100QCC257	C257	16	T52629	T52487	8	7	1	63
BSR151100QCC618	C618	17	T52521	T52488	8	8	0	65
BSR151100QCC075	C075	17	T52521	T52488	8	8	0	65
BSR151100QCC365	C365	17	T52521	T52488	8	8	0	65
BSR151100QCC762	C762	18	T52707	T52489	8	8	0	30
BSR151100QCC780	C780	18	T52707	T52489	8	8	0	30

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC796	C796	18	T52707	T52489	8	8	0	30
BSR151100QCC825	C825	19	T52468	T52492	8	8	0	54
BSR151100QCC376	C376	19	T52468	T52492	3	3	0	#N/A
BSR151100QCC457	C457	20	T52568	T52494	7	6	1	51
BSR151100QCC797	C797	20	T52568	T52494	8	7	1	51
BSR151100QCC450	C450	20	T52568	T52494	8	7	1	51
BSR151100QCC761	C761	21	T52674	T52496	8	8	0	32
BSR151100QCC353	C353	21	T52674	T52496	7	7	0	32
BSR151100QCC521	C521	24	T52493	T52505	7	6	1	58
BSR151100QCC730	C730	24	T52493	T52505	7	6	1	58
BSR151100QCC100	C100	24	T52493	T52505	7	6	1	58
BSR151100QCC204	C204	24	T52493	T52505	7	6	1	58
BSR151100QCC341	C341	24	T52493	T52505	7	6	1	58
BSR151100QCC810	C810	25	T52560	T52506	8	8	0	35
BSR151100QCC062	C062	25	T52560	T52506	7	7	0	35
BSR151100QCC116	C116	25	T52560	T52506	7	7	0	35
BSR151100QCC322	C322	25	T52560	T52506	8	8	0	35
BSR151100QCC387	C387	25	T52560	T52506	8	7	1	35
BSR151100QCC135	C135	27	T52678	T52525	8	8	0	42
BSR151100QCC593	C593	28	T52515	T52527	8	7	1	1
BSR151100QCC335	C335	28	T52515	T52527	8	8	0	1
BSR151100QCC854	C854	29	T52439	T52533	8	8	0	8
BSR151100QCC127	C127	29	T52439	T52533	8	8	0	8
BSR151100QCC299	C299	29	T52439	T52533	8	8	0	8
BSR151100QCC832	C832	30	T52524	T52542	8	8	0	33
BSR151100QCC020	C020	30	T52524	T52542	7	7	0	33
BSR151100QCC065	C065	30	T52524	T52542	8	8	0	33
BSR151100QCC157	C157	30	T52524	T52542	8	8	0	33
BSR151100QCC397	C397	30	T52524	T52542	6	6	0	33
BSR151100QCC601	C601	32	T52658	T52545	7	6	1	68
BSR151100QCC617	C617	33	T52510	T52548	7	7	0	23

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC960	C960	33	T52510	T52548	8	8	0	23
BSR151100QCC266	C266	33	T52510	T52548	8	8	0	23
BSR151100QCC386	C386	33	T52510	T52548	7	7	0	23
BSR151100QCC399	C399	33	T52510	T52548	8	7	1	23
BSR151100QCC662	C662	34	T52470	T52550	8	8	0	57
BSR151100QCC042	C042	34	T52470	T52550	8	8	0	57
BSR151100QCC439	C439	34	T52470	T52550	7	7	0	57
BSR151100QCC117	C117	35	T52643	T52554	8	8	0	33
BSR151100QCC168	C168	35	T52643	T52554	8	8	0	33
BSR151100QCC929	C929	36	T52657	T52567	8	8	0	40
BSR151100QCC265	C265	36	T52657	T52567	8	8	0	12
BSR151100QCC491	C491	37	T52443	T52571	7	6	1	61
BSR151100QCC921	C921	37	T52443	T52571	8	7	1	61
BSR151100QCC068	C068	37	T52443	T52571	7	7	0	61
BSR151100QCC357	C357	37	T52443	T52571	8	8	0	61
BSR151100QCC362	C362	37	T52443	T52571	8	8	0	61
BSR151100QCC364	C364	37	T52443	T52571	8	8	0	61
BSR151100QCC622	C622	38	T52637	T52573	8	8	0	44
BSR151100QCC633	C633	38	T52637	T52573	8	8	0	44
BSR151100QCC049	C049	39	T52680	T52584	8	7	1	55
BSR151100QCC059	C059	39	T52680	T52584	7	6	1	55
BSR151100QCC637	C637	40	T52433	T52587	8	7	1	11
BSR151100QCC470	C470	43	T52480	T52592	7	6	1	13
BSR151100QCC473	C473	43	T52480	T52592	6	6	0	13
BSR151100QCC833	C833	43	T52480	T52592	6	6	0	13
BSR151100QCC873	C873	43	T52480	T52592	7	7	0	13
BSR151100QCC131	C131	43	T52480	T52592	7	7	0	13
BSR151100QCC716	C716	44	T52640	T52595	8	8	0	40
BSR151100QCC775	C775	44	T52640	T52595	8	7	1	40
BSR151100QCC787	C787	44	T52640	T52595	8	8	0	40
BSR151100QCC846	C846	44	T52640	T52595	8	7	1	40

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC924	C924	44	T52640	T52595	8	8	0	40
BSR151100QCC949	C949	44	T52640	T52595	7	7	0	40
BSR151100QCC115	C115	44	T52640	T52595	8	7	1	40
BSR151100QCC609	C609	45	T52435	T52598	8	8	0	7
BSR151100QCC717	C717	45	T52435	T52598	8	8	0	7
BSR151100QCC747	C747	45	T52435	T52598	8	8	0	7
BSR151100QCC203	C203	45	T52435	T52598	8	7	1	7
BSR151100QCC348	C348	45	T52435	T52598	8	8	0	7
BSR151100QCC352	C352	45	T52435	T52598	8	8	0	7
BSR151100QCC668	C668	46	T52652	T52606	7	7	0	29
BSR151100QCC758	C758	46	T52652	T52606	7	7	0	29
BSR151100QCC750	C750	47	T52552	T52608	8	8	0	22
BSR151100QCC812	C812	47	T52552	T52608	8	8	0	22
BSR151100QCC826	C826	47	T52552	T52608	8	8	0	22
BSR151100QCC853	C853	47	T52552	T52608	7	7	0	22
BSR151100QCC874	C874	47	T52552	T52608	8	8	0	22
BSR151100QCC876	C876	47	T52552	T52608	7	7	0	22
BSR151100QCC898	C898	47	T52552	T52608	8	7	1	22
BSR151100QCC011	C011	47	T52552	T52608	7	7	0	22
BSR151100QCC421	C421	47	T52552	T52608	7	6	1	22
BSR151100QCC021	C021	48	T52534	T52611	8	7	1	69
BSR151100QCC076	C076	48	T52534	T52611	8	8	0	69
BSR151100QCC379	C379	48	T52534	T52611	5	4	1	#N/A
BSR151100QCC688	C688	49	T52682	T52618	8	7	1	15
BSR151100QCC048	C048	49	T52682	T52618	8	8	0	15
BSR151100QCC276	C276	49	T52682	T52618	8	7	1	15
BSR151100QCC340	C340	49	T52682	T52618	8	8	0	15
BSR151100QCC476	C476	50	T52467	T52622	8	7	1	19
BSR151100QCC843	C843	50	T52467	T52622	7	7	0	19
BSR151100QCC700	C700	51	T52500	T52627	8	8	0	50
BSR151100QCC950	C950	52	T52700	T52630	8	8	0	31

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC905	C905	54	T52458	T52632	8	8	0	27
BSR151100QCC095	C095	54	T52458	T52632	8	8	0	27
BSR151100QCC400	C400	54	T52458	T52632	8	7	1	27
BSR151100QCC625	C625	55	T52450	T52633	8	7	1	16
BSR151100QCC628	C628	55	T52450	T52633	7	7	0	16
BSR151100QCC735	C735	55	T52450	T52633	7	7	0	#N/A
BSR151100QCC128	C128	55	T52450	T52633	8	7	1	16
BSR151100QCC866	C866	56	T52577	T52639	8	7	1	28
BSR151100QCC037	C037	56	T52577	T52639	8	7	1	28
BSR151100QCC264	C264	56	T52577	T52639	8	7	1	28
BSR151100QCC465	C465	57	T52538	T52644	8	8	0	5
BSR151100QCC714	C714	57	T52538	T52644	8	8	0	5
BSR151100QCC194	C194	57	T52538	T52644	8	8	0	5
BSR151100QCC312	C312	57	T52538	T52644	8	8	0	5
BSR151100QCC372	C372	57	T52538	T52644	8	7	1	5
BSR151100QCC375	C375	57	T52538	T52644	8	8	0	5
BSR151100QCC420	C420	57	T52538	T52644	8	7	1	5
BSR151100QCC497	C497	60	T52620	T52651	7	7	0	49
BSR151100QCC831	C831	60	T52620	T52651	7	7	0	49
BSR151100QCC031	C031	60	T52620	T52651	7	7	0	49
BSR151100QCC145	C145	60	T52620	T52651	8	8	0	49
BSR151100QCC388	C388	60	T52620	T52651	8	7	1	49
BSR151100QCC699	C699	61	T52464	T52654	8	7	1	24
BSR151100QCC589	C589	62	T52615	T52659	8	8	0	53
BSR151100QCC779	C779	62	T52615	T52659	8	8	0	53
BSR151100QCC419	C419	62	T52615	T52659	8	7	1	53
BSR151100QCC461	C461	65	T52709	T52679	6	6	0	2
BSR151100QCC607	C607	65	T52709	T52679	8	7	1	2
BSR151100QCC041	C041	65	T52709	T52679	8	7	1	2
BSR151100QCC112	C112	65	T52709	T52679	8	8	0	2
BSR151100QCC918	C918	66	T52549	T52681	8	8	0	21

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC371	C371	66	T52549	T52681	8	8	0	21
BSR151100QCC685	C685	67	T52459	T52683	8	8	0	26
BSR151100QCC707	C707	67	T52459	T52683	8	7	1	26
BSR151100QCC819	C819	67	T52459	T52683	8	7	1	26
BSR151100QCC859	C859	67	T52459	T52683	8	8	0	26
BSR151100QCC056	C056	67	T52459	T52683	8	8	0	26
BSR151100QCC653	C653	68	T52650	T52684	8	8	0	20
BSR151100QCC865	C865	68	T52650	T52684	8	8	0	20
BSR151100QCC904	C904	68	T52650	T52684	7	7	0	20
BSR151100QCC823	C823	71	T52432	T52693	8	7	1	62
BSR151100QCC892	C892	71	T52432	T52693	6	6	0	62
BSR151100QCC164	C164	71	T52432	T52693	8	7	1	62
BSR151100QCC349	C349	71	T52432	T52693	8	8	0	62
BSR151100QCC456	C456	72	T52597	T52695	8	7	1	58
BSR151100QCC909	C909	72	T52597	T52695	8	8	0	58
BSR151100QCC671	C671	74	T52582	T52697	8	8	0	52
BSR151100QCC007	C007	74	T52582	T52697	8	8	0	52
BSR151100QCC110	C110	74	T52582	T52697	8	8	0	52
BSR151100QCC177	C177	74	T52582	T52697	8	8	0	52
BSR151100QCC482	C482	75	T52699	T52698	7	6	1	10
BSR151100QCC623	C623	75	T52699	T52698	8	7	1	10
BSR151100QCC713	C713	75	T52699	T52698	8	7	1	10
BSR151100QCC842	C842	75	T52699	T52698	8	7	1	10
BSR151100QCC354	C354	75	T52699	T52698	8	7	1	10
BSR151100QCC554	C554	76	T52441	T52702	8	7	1	58
BSR151100QCC106	C106	76	T52441	T52702	7	7	0	28
BSR151100QCC318	C318	76	T52441	T52702	8	7	1	58
BSR151100QCC802	C802	79	T52586	WP1	8	8	0	38
BSR151100QCC023	C023	79	T52586	WP1	8	8	0	38
BSR151100QCC301	C301	79	T52586	WP1	8	8	0	38
BSR151100QCC302	C302	79	T52586	WP1	8	8	0	38

ID of the Big Salmon River adult released in 2003	Carlin tag	Cross #	Female parent	Male parent	Num. loci	Num. matches	Mis-match	Kin group #
BSR151100QCC330	C330	109	NAR04221	NAO03221	8	7	1	3
BSR151100QCC848	C848	115	NAR04227	NAO03227	8	8	0	41
BSR151100QCC137	C137	117	NAR04229	NAO03229	8	8	0	3
BSR151100MCF8086	F8086	121	NAR04233	NAO03233	8	8	0	4
BSR151100MCF8094	F8094	141	NAR04253	NAO03253	8	8	0	3
BSR151100MCF8111	F8111	142	NAR04254	NAO03254	8	8	0	3
BSR151100QCC572	C572	152	NAR04264	NAO03264	7	6	1	9
BSR151100MCF8055	F8055	154	NAR04266	NAO03266	8	8	0	4
BSR151100QCC594	C594	157	NAR04270	NAO03270	8	8	0	9
BSR151100QCC790	C790	157	NAR04270	NAO03270	8	7	1	9
BSR151100QCC917	C917	157	NAR04270	NAO03270	7	7	0	9
BSR151100QCC088	C088	160	NAR04273	NAO03273	8	8	0	6
BSR151100QCC361	C361	161	NAR04274	NAO03274	8	7	1	62
BSR151100QCC624	C624	164	NAR04277	NAO03277	8	8	0	18
BSR151100MCF8104	F8104	167	NAR04280	NAO03280	8	8	0	11
BSR151100MCF8093	F8093	187	NAR04300	NAO03011	8	7	1	56
BSR151100QCC900	C900	199	NAR04312	NAO03023	8	8	0	62
BSR151100MCF8108	F8108	199	NAR04312	NAO03023	8	8	0	41
BSR151100MCF8052	F8052	210	NAR04323	NAO03035	8	8	0	9
BSR151100MCF8102	F8102	210	NAR04323	NAO03035	8	8	0	69
BSR151100QCC327	C327	219	NAR04332	NAO03045	8	7	1	18

Cross # = cross number, involving female and male parents in columns immediately to the right, carried out in 2000 as part of the iBoF Live Gene Banking program.
Num. loci = the number of loci common between the parent and offspring, and therefore the number of loci upon which the test is based.
Num. matches = the number of loci at which the candidate parent and offspring share a single allele.
Mismatch refers to the number of loci at which the offspring does not share one allele with each parent.
Kin group # = the kin group number to which an adult release was assigned

Table A7. Counts of the number of successfully spawning Big Salmon River adult females, Big Salmon River adult males, and Point Wolfe River mature parr inferred from parentage and kinship analysis.

					Counts			Cumulative counts			
Offspring ID	Family ID	Parent ID	Assign conf.	Common female parent	BSR FEMALE	BSR MALE	Wild parr or adult	BSR FEMALE	BSR MALE	Wild parr or adult	Footnote
PWF010904HO22	1.1	F8108	HIGH	F8108	1		1	1		1	
PWF020805HOS07PB2130M	1.1	F8108	HIGH	F8108	1		1				
PWF250805HOS07P05126M	1.1	F8108	HIGH	F8108	1		1				
PWF220805HOS08P04122M	1.1		HIGH	F8108	1		1				
PWF220805HOS04P04130M	1.2	F8108	HIGH	F8108	1		1			2	
PWF150604HO004AS06	1.3	C115	HIGH	F8108		1			1		
PWF150604HO004AS06	1.3	F8108	HIGH	F8108	1						
PWF220805HOS06P04121M	1.3	F8108	HIGH	F8108	1						
PWF220805HOS06P04121M	1.3	C115	HIGH	F8108		1					
PWF250805HOS01P05125M	1.3	F8108	HIGH	F8108	1						
PWF250805HOS01P05125M	1.3	C115	HIGH	F8108		1					
PWF250805HOS02P05117M	1.3	C115	HIGH	F8108		1					
PWF250805HOS02P05117M	1.3	F8108	HIGH	F8108	1						
PWF150604HO004AS19	1.4	F8108	HIGH	F8108	1		1			3	
PWF150805HOS06P01136M	2.1	C653	HIGH	C056	1			2			1
PWF150805HOS06P01136M	2.1	C819	HIGH	C056		1			2		
PWF010904HO8	2.2	C056	HIGH	C056	1			3			
PWF010904HO8	2.2	C819	HIGH	C056		1					
PWF170805HOS03P02127M	2.2	C056	HIGH	C056	1						
PWF170805HOS03P02127M***	2.2	C797	LOW	C056							
PWF170805HOS11P02102M	2.2	C056	HIGH	C056	1						
PWF170805HOS11P02102M	2.2	**C819**	HIGH	C056		1					
PWF010904HO9	2.3	C056	HIGH	C056	1		1			4	
PWF170805HOS05P02126M	2.3	C056	HIGH	C056	1		1				
PWF170805HOS10P02120M	2.4	C056	HIGH	C056	1						

					Counts			Cumulative counts			
Offspring ID	Family ID	Parent ID	Assign conf.	Common female parent	BSR FEMALE	BSR MALE	Wild parr or adult	BSR FEMALE	BSR MALE	Wild parr or adult	Footnote
PWF170805HOS10P02120M	2.4	C137	HIGH	C056		1			3		
PWF010904HO14	2.5	C056	HIGH	C056	1						
PWF010904HO14	2.5	F8052	HIGH	C056		1			4		
PWF010904HO7	2.6	C056	HIGH	C056	1						
PWF010904HO7	2.6	C327	HIGH	C056		1			5		
PWF010904HO15	3.1	C842	HIGH	C842	1		1	4		5	
PWF150805HOS08P01128M	3.1	C842	HIGH	C842	1		1				
PWF010904HO4	3.2	C842	HIGH	C842	1						
PWF010904HO4	3.2	C819	HIGH	C842		1			MOA		
PWF010904HO6	3.2	C819	HIGH	C842		1			MOA		
PWF010904HO6	3.2		HIGH	C842	1						
PWF020805HOS08PB4119M	4.1	C100	LOW	C100	1X		1Y			+1Y	2
PWF190805HOS02P03197M	4.2	C100	LOW	C100			1Y			+1Y	
PWF010904HO18	5.1	C499	LOW	C499?	1X		1Y			+1Y	3
PWF010904HO23	5.1	C083	LOW	C499?			1Y				
PWF150805HOS05P01137M	5.1	C499	LOW	C499?			1Y				
PWF150805HOS07P01129M	5.1	C312	LOW	C499?			1Y				
PWF170805HOS04P02127M	5.1	C354	LOW	C499?			1Y				
PWF170805HOS12P02122M	5.1	C499	LOW	C499?			1Y				
PWF170805HOS14P02138M	5.1	C120	LOW	C499?			1Y				
PWF220805HOS01P01114M	5.1	C083	LOW	C499?			1Y				
PWF170805HOS09P02134M	5.1		UNASS	C499?			1Y				
PWF170805HOS13P02124M	5.1		UNASS	C499?			1Y				
PWF010904HO12	5.1		UNASS	C499?			1Y				
PWF220805HOS02P01116M	5.1		UNASS	C499?			1Y				
PWF170805HOS02P02116M	5.2	C623	LOW	C499?			1Y			+1Y	
PWF010904HO17	5.3	C499	LOW	C499?			1Y				
PWF150604HOFOSTER79MM	5.3	C499	LOW	C499?			1Y				
PWF280705HOS08PF3131M	5.3	C033	LOW	C499?			1Y				

					Counts			Cumulative counts			
Offspring ID	Family ID	Parent ID	Assign conf.	Common female parent	BSR FEMALE	BSR MALE	Wild parr or adult	BSR FEMALE	BSR MALE	Wild parr or adult	Footnote
PWF170805HOS08P02122M	5.3		UNASS	C499?			1Y			+1Y	
PWF010904HO10	5.3		UNASS	C499?			1Y				
PWF010904HO11	5.3	C361	UNASS	C499?			1Y				
PWF280705HOS07PF2124M	5.3		UNASS	C499?			1Y				
PWF020805HOS02PB1124M	6.1	C918	HIGH	C918	1		1	5		6	
PWF020805HOS03PB1140M	6.1	C918	HIGH	C918	1		1				
PWF020805HOS05PB1124M	6.1	C918	HIGH	C918	1		1				
PWF150604HO004AS04	6.1	C918	HIGH	C918	1		1				
PWF150604HO004AS07	6.1	C918	HIGH	C918	1		1				
PWF150604HO004AS13	6.1	C918	HIGH	C918	1		1				
PWF150604HO004AS14	6.1	C918	HIGH	C918	1		1				
PWF220805HOS02P04127M	6.1	C918	HIGH	C918	1		1				
PWF220805HOS03P04127M	6.1	C918	HIGH	C918	1		1				
PWF220805HOS07P04129M	6.1	C918	HIGH	C918	1		1				
PWF220805HOS01P04113M	6.2	C033	HIGH	C918		1			6		
PWF220805HOS01P04113M	6.2	C918	HIGH	C918	1						
PWF150604HO004AS02	6.3	C918	HIGH	C918	1		1			7	
PWF150604HO004AS03	6.4	C918	HIGH	C918	1		1			8	
PWF150604HO004AS16	6.4	C918	HIGH	C918	1						
PWF150604HO004AS16	6.4	C115	HIGH	C918		1			MOA		
PWF150604HO004AS05	6.5	C918	HIGH	C918	1						
PWF150604HO004AS05	6.5	*C033*	LOW	C918							
PWF150604HO004AS09	6.5	C918	HIGH	C918	1		1			9	
PWF150604HO004AS11	6.5	C918	HIGH	C918	1		1				
PWF150604HO004AS12	6.6	C918	HIGH	C918	1		1				
PWF190805HOS03P03136M	7.1	C775	HIGH	C775	1			6			
PWF190805HOS03P03136M	7.1	C779	LOW	C775							
PWF280705HOS06PF1124M	7.2	C779	HIGH	C775		1			7		

					Counts			Cumulative counts			
Offspring ID	Family ID	Parent ID	Assign conf.	Common female parent	BSR FEMALE	BSR MALE	Wild parr or adult	BSR FEMALE	BSR MALE	Wild parr or adult	Footnote
PWF280705HOS06PF1124M	7.2	C775	HIGH	C775	1						
PWF010904HO21	7.3	C775	HIGH	C775	1		1			10	
PWF010904HO24	7.3	C775	HIGH	C775	1		1				
PWF010904HO16	8.1	F8093	HIGH	F8093	1		1	7		11	
PWF010904HO29	8.1	F8093	HIGH	F8093	1		1				
PWF010904HO30	8.1	F8093	HIGH	F8093	1		1				
PWF010904HO32	8.1	F8093	HIGH	F8093	1		1				
PWF170805HOS07P02116M	8.1	F8093	HIGH	F8093	1		1				
PWF180805HOS02P06117M	8.1	F8093	HIGH	F8093	1		1				
PWF190805HOS01P03135M	8.1	F8093	HIGH	F8093	1		1				
PWF190805HOS06P03117M	8.1	F8093	HIGH	F8093	1		1				
PWF220805HOS04P01116M	8.1	F8093	HIGH	F8093	1		1				
PWF280705HOS09PF3120M	8.1	F8093	HIGH	F8093	1		1				
PWF280705HOS10PF4123M	8.1	F8093	HIGH	F8093	1		1				
PWF190805HOS04P03133M	9.1	C761	MED	C797	1		1	8		12	4
PWF010904HO13	9.3	C059	HIGH	C797		1					
PWF010904HO13	9.3	C797	HIGH	C797	1			9	MOA		
PWF010904HO5	9.4	C059	HIGH	C797		1					
PWF010904HO5	9.4	C797	HIGH	C797	1						
PWF150604HO004AS08	9.5	C299	LOW	C797			1Y			+1Y	
PWF250805HOS03P05128M	10.1	C730	HIGH	C730	1		1	10		13	
PWF010904HO31	10.2	C100	MED	C730		1			8		
PWF010904HO31	10.2	C730	MED	C730	1						
PWF190805HOS05P03126M	11.1	C700	HIGH	C700	1		1	11		14	
PWF010904HO20	12.1	C348	HIGH	C348	1		1	12		15	
PWF010904HO19	13.1	C900	LOW	C900			1Y			+1Y	5
PWF170805HOS01P02127M	14.1	C653	HIGH	C653	1		1	13		16	6
PWF010904HO26	14.2	C609	MED	C653	1		1	14		17	
PWF010904HO3	14.3	C031	HIGH	C653		1			9		

					Counts			Cumulative counts			
Offspring ID	Family ID	Parent ID	Assign conf.	Common female parent	BSR FEMALE	BSR MALE	Wild parr or adult	BSR FEMALE	BSR MALE	Wild parr or adult	Footnote
PWF010904HO3	14.3	C653	HIGH	C653	1						
PWF010904HO25	15.1	C301	HIGH	C301	1			15			
PWF010904HO25	15.1	C203	HIGH	C301		1			10		
PWF010904HO27	16.1	C400	MED	C400	1		1	16		18	
PWF010904HO28	16.2	C400	MED	C400	1		1			19	
PWF180805HOS01P06115M	17.1		LOW	C023	1X		1Y			+1Y	
PWF280705HOS05PF1107M	17.2	C033	MED	C023		1			MOA		
PWF280705HOS05PF1107M	17.2	C023	HIGH	C023	1			17			
PWF170805HOS06P02130M	18.1	C618	HIGH	C618	1		1	18		20	
PWF020805HOS04PB1123M	18.1	C853	LOW	C618							
PWF020805HOS06PB2112M	19.1	F8104	HIGH	F8104	1			19			
PWF020805HOS06PB2112M	19.1	C116	LOW	F8104							
					Cumulative totals			19 (22X)	10	20(28X)	

MOA = Male Occurs Above, so not included again in cumulative summation; note that such occurrences represent split kin groups
1X = possible contribution of female BSR adult inferred from LOW confidence assignment
1Y= possible contribution by male parr, involves LOW confidence assignment of one parent, and is based on kinship analyses
+1Y = instances where possible inferred male parr, associated with LOW confidence assignment, are added to cumulative sum given in parentheses
Note: cumulative sums outside of parentheses are based on HIGH and MED confidence assignments only or HIGH and MED confidence assignments and kinship information
Note: cumulative sums inside parentheses are based on LOW confidence assignments, or LOW confidence assignments and kinship analyses
Note: the possible existence of more females than half-sib groups reflects the possible presence of two females in some half-sib groups, as inferred from parentage analyses. Often this lack of concordance occurs where kin group size is less than 5 and confidence in half-sib assignments is low

Footnotes
1 Two female parents identified in half-sib family; count based on parentage because assignment at 10 of 10 loci
2 Female C100 not included in tally because of low confidence of assignment
3 Female C499 not included in tally because of low confidence of assignment
4 C761 is the probable parent (assigned at 11 of 11 loci); kin grouping small (N=4) so low confidence
5 Female C900 not included in tally because of low confidence of assignment
6 Two female parents identified in half-sib family; count based on parentage because assignment at 10 of 10 loci

Table A8a. Deduction of parental genotypes for Point Wolfe River kin group 5.0 and comparison with kin and parents of C499.

Offspring and deduced parental genotypes.

Fish ID	kin group	1605	1605	2201	2201	2210	2210	2215	2215	2216	2216	1G7	1G7	197	197	202	202	144	144	486	486	171	171
Parent 1		228	248	**303**	**303**	**136**	**136**	150	158	**249**	**265**	**166**	**182**	**183**	**171**	279	295	190	206	**174**	**174**	**237**	**233**
Parent 2		**236**	**248**	327	307	120	124	**154**	**158**	253	249	178	174	199	167	**295**	**295**	**202**	**166**	190	178	245	229
PWF150805HOS05P01137M	5.1	228	236	303	327	124	136	150	154	249	253	166	178	183	199	279	295	190	202	174	190	237	245
PWF150805HOS07P01129M	5.1	228	248	303	327	124	136	158	158	253	265	178	182	171	199	279	295	166	190	174	190	229	233
PWF170805HOS04P02127M	5.1	236	248	303	307	**120**	124	150	154	249	249	178	182	183	199	295	295	190	202	174	178	229	233
PWF170805HOS09P02134M	5.1	228	248	303	327	136	136	154	158	249	253	178	182	171	199	295	295	190	202	174	190	229	233
PWF170805HOS12P02122M	5.1	228	236	303	307	**120**	136	150	154	249	253	166	178	167	183	279	295	190	202	174	178	237	245
PWF170805HOS13P02124M	5.1	228	248	303	307	**120**	124	158	158	249	265	166	178	171	199	279	295	190	202	174	178	229	233
PWF170805HOS14P02138M	5.1	236	248	303	307	**120**	136	154	158	249	253	166	178	167	171	279	295	166	190	174	190	229	237
PWF220805HOS01P01114M	5.1	236	248	303	307	124	136	150	154	253	265	178	182	183	199	279	295	202	206	174	178	237	245
PWF220805HOS02P01116M	5.1	228	248	303	327	124	136	150	158	249	265	178	182	167	183	279	295	190	202	174	178	0	0
PWF010904HO12	5.1	228	248	303	327	124	136	150	154	249	249	166	**210**	183	199	295	295	166	206	174	178	229	233
PWF010904HO18	5.1	0	0	303	307	136	136	150	154	249	249	166	**210**	167	183	279	295	202	206	174	178	237	245
PWF010904HO23	5.1	228	236	303	307	136	136	150	154	249	253	174	182	167	171	279	295	190	202	174	190	233	245
Parent 1		236	232	**303**	**303**	136	112	**154**	**158**	237	245	166	178	167	163	295	295	190	238	**174**	**174**	229	245
Parent 2		**248**	**236**	291	299	**136**	**136**	154	162	**265**	**249**	**182**	**166**	**183**	**171**	**295**	**295**	**202**	**166**	178	174	**233**	**237**
PWF170805HOS08P02122M	5.3	236	248	303	291	136	136	158	162	237	265	166	182	167	183	295	295	190	202	174	178	229	233
PWF280705HOS07PF2124M	5.3	232	236	303	299	112	136	158	162	245	265	166	166	167	171	295	295	202	238	174	174	229	237
PWF280705HOS08PF3131M	5.3	236	248	303	**303**	112	136	158	162	245	265	166	178	167	171	295	295	202	238	174	174	229	237
PWF010904HO10	5.3	236	236	303	291	112	136	154	158	237	265	166	178	163	171	295	295	166	190	174	174	229	237
PWF010904HO11	5.3	232	248	303	**303**	136	136	158	162	245	265	166	178	167	183	295	295	202	238	174	174	233	245
PWF010904HO17	5.3	236	236	303	299	112	136	154	162	245	249	166	166	163	183	295	295	166	238	174	178	229	233
PWF150604HOFOSTER79MM	5.3	236	232	303	**327**	136	136	154	162	249	245	182	166	171	167	295	295	190	166	178	174	229	233

Underlined alleles represent single-locus incompatibilities and are either mutations or scoring errors.

Table A8b. Deduction of parental genotypes for Point Wolfe River kin group 5.0 and comparison with kin and parents of C499.

Parental genotypes with correct configuration of alleles at all loci

Fish ID	1605	1605	2201	2201	2210	2210	2215	2215	2216	2216	1G7	1G7	197	197	202	202	144	144	486	486	171	171
Common parent (CFA)	**236**	**248**	**303**	**303**	**136**	**136**	**154**	**158**	**249**	**265**	**166**	**182**	**171**	**183**	**295**	**295**	**166**	**202**	**174**	**174**	**233**	**237**
Other parent Group 5.1	228	248	327	307	120	124	150	158	253	249	178	174	199	167	279	295	190	206	190	178	245	229
Other parent Group 5.3	236	232	291	299	136	112	154	162	237	245	166	178	167	163	295	295	190	238	178	174	229	245

CFA = correct configuration of alleles

Comparison of deduced common parent of PWR juveniles from kin group 5.0 (from above) with the BSR LGB cross 75 (parents of C499 and siblings).

Parent Fish ID	1605	1605	2201	2201	2210	2210	2215	2215	2216	2216	1G7	1G7	197	197	202	202
T52699	**236**	248	**303**	307			**154**	174	245	**249**	**166**	190	175	**183**	**295**	299
T52698	**248**	256	267	279			**158**	174	225	**265**	**182**	202	167	**171**	*291*	*291*
Common parent (deduced)	**236**	**248**	**303**	**303**	**136**	**136**	**154**	**158**	**249**	**265**	**166**	**182**	**171**	**183**	**295**	**295**

Note: underlined alleles are genotyping errors, mutations, or indications that the suggested parentage is incorrect

Comparison of C499 with two other BSR adults released into the PWR in 2003, that also share multiple alleles with offspring from kin group 5.X.

Parent Fish ID	**Carlin**	**1605**	**1605**	**2201**	**2201**	**2210**	**2210**	**2215**	**2215**	**2216**	**2216**	**1G7**	**1G7**	**197**	**197**	**202**	**202**
BSR151100QCC499	C499	0	0	**267**	307	120	136	150	178	**225**	**249**	**166**	**202**	**167**	**183**	**295**	**299**
BSR151100QCC354	C354	236	248	267	303	120	152	154	174	249	265	182	190	167	183	291	299
BSR151100QCC623	C623	248	256	267	307	120	136	154	174	249	265	190	202	167	175	291	295

Table A9. Incidence of inbreeding among Big Salmon River salmon released into the Point Wolfe River in 2003.

BSR adult release	Parental pair number*	Parent 1	Parent 2	Increased level of inbreeding in the next generation
C115	1	T52640	T52595	0
F8108	1	NAR04312	NAO03023	0
C653	2	T52650	T52684	0
C819	2	T52459	T52683	0
C056	3	T52459	T52683	0.25
C819	3	T52459	T52683	0.25
C056	4	T52459	T52683	0
C137	4	NAR04229	NAO03229	0
C056	5	T52459	T52683	0
F8052	5	NAR04323	NAO03035	0
C056	6	T52459	T52683	0
C327	6	NAR04332	NAO03045	0
C842	7	T52699	T52698	0
C819	7	T52459	T52683	0
C918	8	T52549	T52681	0
C115	8	T52640	T52595	0
C779	9	T52615	T52659	0
C775	9	T52640	T52595	0
F8093	10	NAR04300	NAO03011	0
C420	10	T52538	T52644	0
F8093	11	Kin grp 56	Kin grp 56	0
C083	11	Kin grp 10	Kin grp	0
C059	12	T52680	T52584	0
C797	12	T52568	T52494	0
C031	13	T52620	T52651	0
C653	13	T52650	T52684	0
C301	14	T52586	WP1	0
C203	14	T52435	T52598	0
C033	15	T52471	T52478	0
C023	15	T52586	WP1	0
F8104	16	NAR04280	NAO03280	0
C116	16	T52560	T52506	0
F6632	17	Kin grp 45	Kin grp 45	0
F6797	17	Kin grp 35	Kin grp 35	0
C474	18	Kin grp 47	Kin grp 47	0
F6632	18	Kin grp 45	Kin grp 45	0

*information provided only for those pairs for which parentage/kinship information is available.

Appendix III. Details of simulation analyses carried out in support of parentage assignments

To investigate whether chance matches between parents and offspring under the present conditions were likely, we created 100 sets of 98 multi-locus genotypes by randomly sampling, with replacement, from the BSR adult gene pool. Simulated 11-locus genotypes could be considered equivalent to offspring unrelated to the 216 BSR candidate parents. Each group of 98 unrelated offspring were then tested against the 216 candidate parents using exclusion methods. The numbers of chance offspring-parent matches at either all 11 loci (allowing for zero parent-offspring mismatches, Figure AIII-1a) or nearly all 11 loci (allowing for one parent-offspring mismatch, Figure AIII-1b) were plotted for all of the 100 simulation runs. In most of the simulation runs, only 1 or 2 chance parent-offspring matches at all 11 loci were observed, though instances of 0, 3 or 4 chance matches were not uncommon. Instances of 5 or more chance parent-offspring matches were rare (< 5%). However, many more chance parent-offspring matches were observed when allowing for a single parent-offspring mismatch (Figure AIII-1b); at least 25 chance parent-offspring matches were observed per simulation run, with most simulation runs exhibiting between 33 and 47 chance parent-offspring matches.

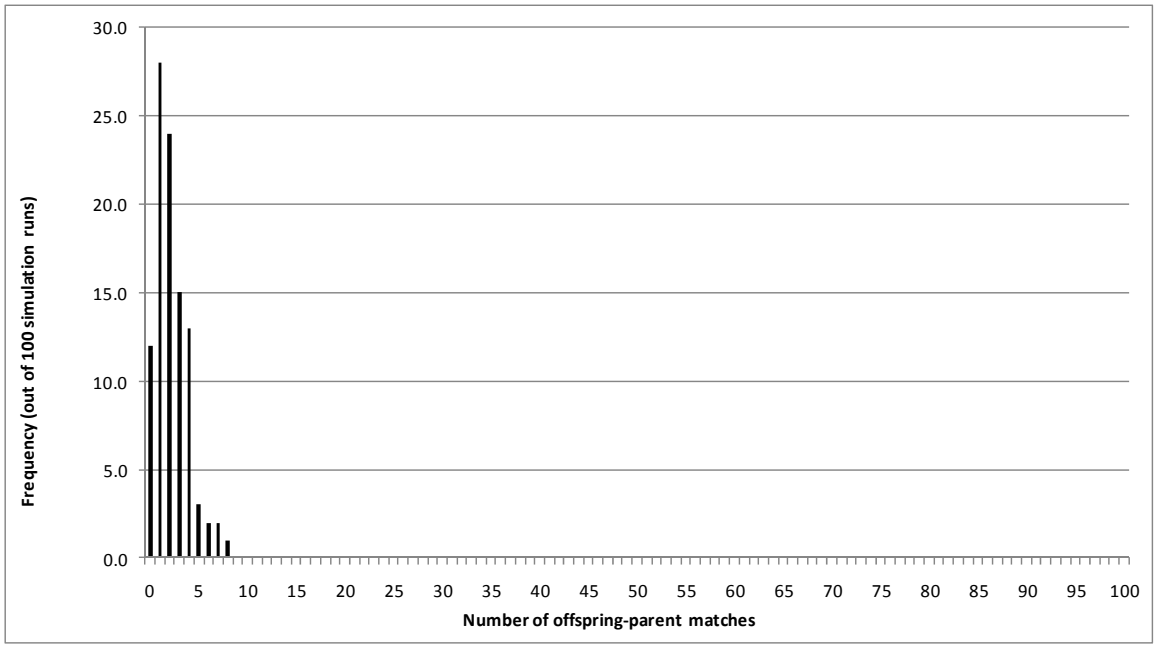

Figure AIII-1a. Results of simulation analyses, testing 100 sets of 98 randomly sampled genotypes against the 216 BSR candidate parents released in 2003, allowing for zero single-locus (single-allele) parent-offspring mismatches.

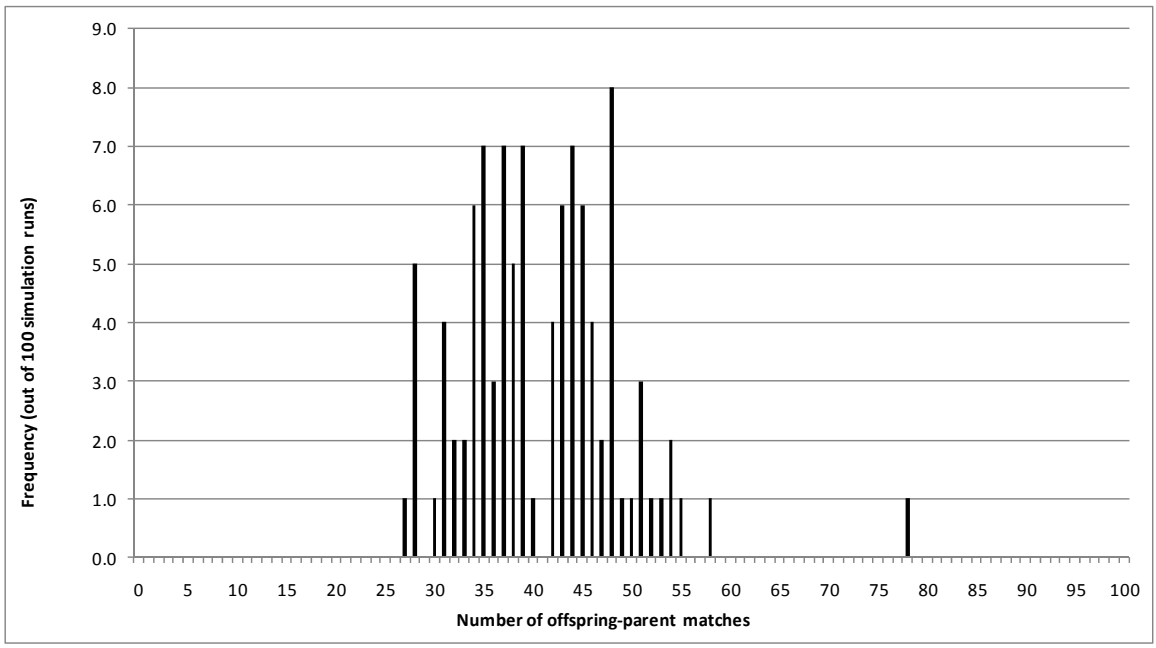

Figure AIII-1b. Results of simulation analyses, testing 100 sets of 98 randomly sampled genotypes against the 216 BSR candidate parents released in 2003, allowing for one single-locus (single-allele) parent-offspring mismatch.