Supporting Information

Materials and Methods

Sample collection and genotyping

To examine the reproductive success of the various life history strategies, we used a 16-year data set of 12,579 winter-run steelhead collected from the Hood River, Oregon between 1991 and 2006. Results are presented for only 13 run-years because the overlapping generations meant that the last 4 run years included fish that could only be identified as offspring. All steelhead returning to spawning grounds in the Hood River were passed over the Powerdale dam. Every fish passed over the dam was individually handled, and samples of scales and fin tissue were collected for aging and genetic analysis by staff of the Oregon Department of Fish and Wildlife. Also recorded were the length, weight, sex, and run-timing of every fish. Steelhead were easily categorized as hatchery or wild origin because all hatchery fish had, at minimum, their adipose fin clipped before being released as juveniles. All wild fish and an approximately equal number of hatchery fish were passed over the dam each year.

Samples were collected from the Hood River, Oregon, where winter-run steelhead are listed as threatened under the Endangered Species Act. Winter-run steelhead begin returning to their natal rivers in early December, the year of which designates the run-year, and do not spawn until spring of the next year. Thus, a steelhead that spawns in May of 2000 will belong to run-year 1999 (even if it returned in March of 2000) and its offspring will belong to brood-year 2000. Because of the accelerated growth-rate in hatcheries (i.e., decreased time to smoltification), most hatchery-born steelhead return to spawn at 2.5 years of age, whereas most wild-born steelhead return at 3.5 years (Fig. 1). Adult fish returning in a single run-year come from multiple brood-years. Extensive details on this study system, management practices, steelhead life-history and

reproductive success can be found elsewhere (1-4). All samples were genotyped at 8 highly polymorphic microsatellite loci (Omy 1001, Omy 1011, Omy 1191, Omy77, One108, One2, Ssa407, and Str2), which average 36 alleles per locus. Details about the genetic markers, laboratory methods, and genotyping can be found elsewhere (1, 2, 5).

Identification of repeat spawners

To identify repeat spawning fish, we first examined the scale reading data collected by ODFW on all fish. When steelhead spawn in freshwater a distinct mark known as a "spawning check" is laid down in a scale (6, 7), such that repeat spawners can be identified if growth continues past this mark. For example, if a steelhead spawned after spending two years in the ocean, and then returned one year later to spawn again it would be designated as a "2S.3", where the S indicates the spawning check. Because all fish were also genotyped at a minimum of eight highly polymorphic microsatellite loci (8, 9), we used these joint data to confirm the identification of repeat spawners. Repeat spawners, being the same individual, are expected to share both codominant alleles across all loci in the absence of genotyping errors and missing data. Given the high polymorphism associated with these markers, we had ample power to detect repeat spawners; a permutation procedure illustrated that two randomly selected individuals were unlikely to share both alleles at more than 3 loci (Fig. S4). However, to err on the conservative side, we required that all repeat spawners must share both alleles at a minimum of 5 loci. Even with this conservative threshold, the majority of identified repeats spawners (91%) shared both alleles at 7 or more loci.

The age of all returning individuals was also determined using their scale data, as was the year in which every individual was born (brood-year). The vast majority of identified repeat

spawners had the same brood-year (i.e., scales were read each year a fish returned to the spawning grounds) and we calculated an error rate in scale aging of 1.3%. However, to allow for some error in scale reading, we only removed candidate repeat spawners if their brood-years did not match by two or more years (n= 5 individuals removed). As a last check, we examined the FLOY tag numbers of repeat spawners. A number of repeat spawners lost their FLOY tags (and were given new ones), but of those individuals that had the same FLOY tag number in two distinct run-years (n = 165), all had been already identified as repeat spawners with the above procedure. We next split the files into males and females to be analyzed separately. A small portion of repeat spawners (n = 17) were phenotypically sexed as being of one sex (male or female) in their first spawning attempt, but as different sex in their second spawning attempt. Furthermore, there were very few male repeat spawners identified (n=30). Therefore, we used PCR of a sex-specific marker (10, 11) to genotypically sex all male repeat spawners and all repeat spawners that were originally assigned, by visual observation, to two separate sexes. We found that 14 of 17 repeat spawners phenotyped as two separate sexes were genotypically female, where the most common pattern was that small first time spawners were incorrectly phenotyped as males. All repeat spawners phenotyped as male in both run years were genotypically confirmed to be male.

Parentage analysis

We calculated the lifetime reproductive success (adult to adult) for all repeat spawning fish and all single-spawning fish. We performed all analyses by run-year, and for each run-year we included all wild adults as parents. We further added any hatchery fish identified as repeat spawners to the set of candidate parents. We next identified all candidate offspring as wild individuals assigned to appropriate brood-year. The hatchery-born adults spawned in the wild

such that all their offspring were also wild-born individuals. We performed parentage analysis in two ways. First, we identified all candidate offspring as having to share at least one allele at all 8 loci. Using these criteria, less than 5% of offspring were assigned to more than one parent. Second, to allow for genotyping errors and account for the frequencies of shared alleles, we also performed Bayesian parentage analysis using scripts from SOLOMON (12-14) updated according to Anderson (15) to make full use of the data. These analyses identified an additional portion of pairs that mismatched at one locus to be identified as parent-offspring pairs, and no offspring were assigned to more than one parent. The differences between the two sets of parentage analyses were qualitatively similar and here we present the results from SOLOMON because it is likely that genotyping and scoring errors sometimes led to at least one mismatch (2).

Number of hatchery vs. wild repeat spawners

We categorized identified repeat spawners as being born in the wild or born in the hatchery (see (1, 16) for details regarding hatchery practices). Not all hatchery fish were passed over the dam *en route* to the spawning grounds (ODFW did not pass more than one hatchery fish over per every returning wild fish), however, records were kept on how many unique hatchery fish showed up at the dam. Because a hatchery fish that was a repeat spawner may have not been passed over the dam (and hence genotyped) on its first or second spawning attempts, we may have underestimated the total number of hatchery repeat spawners. However, we account for this possibility by a random sampling exercise where we first created a set of hatchery fish equal to the total number of hatchery fish that arrived at the dam each year and identified 4% as being repeat spawners (the percent identified as repeat spawners had no bearing on results). We next conservatively estimating the percentage of hatchery fish that were passed above the dam (47%; (17)) and use this percentage to randomly sample the set of hatchery fish without replacement.

We repeated these steps 1000 times and calculated how many additional hatchery repeat spawners could have been present in the data set. We find that, at most, there could have been 2.81 times more hatchery repeat spawners and that, on average, there would be 2.13 times more hatchery repeat spawners. Using the most extreme estimate (2.81), this result means that there could have been a maximum of 115 hatchery repeat spawners. Using the average estimate (2.5x) reveals that there would have been 87 hatchery repeat spawners. Both of these estimates are substantially less than the 258 wild-origin repeat spawners identified (exact test: $p < 0.001$). It is important to note that the practice of not passing all hatchery fish over the dam in no way influence our estimates of lifetime reproductive success because all hatchery fish produced wild-born offspring, all of which were passed over the dam (and included in this study).

Mathematical and agent-based modeling

When is semelparity or iteroparity an evolutionarily stable strategy?

Consider the following payoff matrix that describes the fitness of three scenarios: a pure population of semelparous fish (top left corner), a pure population of iteroparous fish (bottom right corner) and mixed populations (remaining corners):

Table S1: Payoff matrix for semelparous and iteroparous fish. Fitness is assumed to be equal to fecundity (f) minus mortality (m).

	Semelparous	Iteroparous
Semelparous	$af - m$	$f - m$
Iteroparous	$2.5f - dm$	$2.5bf - dm$

The observed populations are mixed strategy populations, and the payoff matrix is tuned to match observed fecundity. Therefore, f is the fecundity of an average semelparous fish, and m is the mortality rate of an average semelparous fish. Iteroparous fish in this population are observed to have 2.5 times the fecundity of semelparous fish, and a mortality rate that is dm. The pure populations do not occur in nature, but we assume mortality in the open ocean would not change relative to the mixed populations, but fecundity in shared spawning grounds might according to the constants a, and b.

There are four possible solutions to this payoff matrix: 1) Semelparous fish are a pure ESS; 2) iteroparous fish are a pure ESS; 3) alternative stable states through positive frequency dependent selection, and; 4) coexistence through negative frequency dependent selection. Since these fish are observed to coexist, we focus only on situations that result in the fourth solution. We don't discuss the other options, though it should be noted that any modifications to the model can result in any of the four ESSs.

Coexistence of the two strategies occurs when each type of fish has higher fitness in the mixed population than in a pure population. This occurs when:

$$2.5f - dm > af - m \quad \text{and,} \quad 2.5bf - dm < f - m. \qquad \text{Condition S1}$$

Conditions S1 can be rearranged to plot in parameter space:

$$f > \frac{d-1}{2.5-a}m \quad \text{and,} \quad f < \frac{d-1}{2.5b-1}m. \qquad \text{Condition S2}$$

Condition 2 demarcates regions of parameter space where coexistence is possible. It should be clear that these conditions require $d>1$ otherwise the higher fecundity of iteroparous fish would

drive the semelparous fish to extinction. For any given values of a, b and d we can determine the fecundity and mortality required for coexistence (Fig 2E).

We can also determine the equilibrium frequency of each strategy when they coexist in a mixed strategy ESS. Let p represent the frequency of semelparous fish in the population, and thus, the frequency of iteroparous fish is (1-p). The average fitness will simply be determined by the frequency with which they interact with each other strategy given by:

$$w_S(p) = p(af - m) + (1 - p)(f - m),$$ Equation S1

and,

$$w_I(p) = p(2.5f - dm) + (1 - p)(2.5bf - dm)$$ Equation S2

For semelparous and iteroparous fish respectively. When these fish coexist via fitness tradeoffs in fecundity and mortality, average fitness must be equal otherwise one strategy would go to fixation, therefore we can solve for the equilibrium frequency, p^*, that satisfies $w_S(p^*) = w_I(p^*)$, given by:

$$p^* = \frac{f(2.5b-1) - m(d-1)}{f(a - 3.5 + 2.5b)}.$$ Equation S3

From the example shown in Fig 2E, we can pick any point (m,f) inside the region of coexistence, and determine the fitness landscape (Fig 2F). When coexistence is possible, we can plot the fitness landscape (eqns 1 and 2) showing the stable equilibrium frequencies and stable coexistence.

When are multiple life history strategies evolutionarily stable?

Continuous evolutionary game theory provides one mathematical tool for exploring negative frequency dependent selection of evolutionarily stable traits, combined with the ecological coexistence of genotypes exhibiting those evolutionarily stable traits (18, 19). We used a well-known, pre-existing evolutionary game theoretic model which incorporates continuous evolutionary dynamics and ecological dynamics, and has been extensively analysed previously (18, 20, 21). Consider a population with x true breeding life history traits. The different life history traits present in the population can be represented by a vector, $\mathbf{u} = (u_1, u_2 \dots u_x)$, where there are x different life history strategies. Similarly, the population can be represented by a vector of the population sizes of each genotype, $\mathbf{N} = (N_1, N_2 \dots N_x)$, such that the total population of all genotypes is $\sum_i^x N_i$. Negative frequency dependent selection conceptually implies that fitness, G, is a function of the life history strategies in the population ($\mathbf{u}$), and the abundances of each strategy ($\mathbf{N}$). We therefore model the per-capita population growth rate according to the following fitness function:

$$G(v, \mathbf{u}, \mathbf{N}) = r\left(1 - \frac{\sum_{j=1}^{S} a(v,u_j)N_j}{K(v)}\right)\bigg|_{v=u_i}, \qquad \text{Equation S4}$$

where, r is the intrinsic rate of increase, and; v is a virtual variable where we can generate the fitness of any possible mutant that might arise by evaluating the model at $v = u_i$. Readers should recognize this as Lotka-Volterra competition, with two important differences: notice that within equation 1, the life history strategy also shapes the competition coefficient, $a(v, u_j)$, and the carrying capacity, $K(v)$, which introduces evolutionary dynamics as described below.

Competition is assumed to follow the theory of limiting similarity (20, 22). We assume that competition is the most intense among individuals with the similar life-history strategy, and

becomes weaker among individuals with different life history strategies and that the width of this

competitive interaction relative to trait variation within a population can be described by a

Gaussian distribution. However, we also assume that older, larger fish have an asymmetric

competitive advantage over younger fish. Thus, competition of one strategy, v, relative any

another strategy, u_j, follows a Gaussian distribution (Fig S9A) according to:

$$a\big(v, u_j\big) = 1 + e^{\frac{-\big(v-u_j+\beta\big)^2}{2\sigma_a^2}} - e^{\frac{-\beta^2}{2\sigma_a^2}}. \qquad\qquad \text{Equation S5}$$

Where, β describes the level of asymmetry in competition such that older and larger fish have a

more negative competitive effect on younger smaller fish than younger fish have on older fish

(19), and; σ_a is the variance around the mean population trait, which determines the width of this

Gaussian distribution, and has been interpreted the width of the competitive niche. Intuitively,

the width of the competition niche determines how much alternative strategies interact. When the

competitive niche is narrow, species can be relatively similar and interact only weakly, and when

the competitive niche is wide species can be relatively dissimilar and interact strongly (equation

S5).

    We also assume that the environment constrains the life history strategies which are

possible based on the fit of form and function to the available niches. For example, it might be

advantageous for a fish to wait 50 years to reproduce, but the environment might be such that

this genotype has a carrying capacity of zero. Thus, the carrying capacity of each life history

strategy is influenced by the life history strategy, v, again following a Gaussian distribution (Fig

S9B) according to:

$$K(v) = K_{max} e^{\frac{(v-\gamma)^2}{2\sigma_K^2}}, \qquad\qquad \text{Equation S6}$$

where K_{max} is the maximum number of fish that can spawn in the river; γ centres the strategy

with highest fit of form and function and therefore the highest fecundity (based on these data we

set $\gamma = 3$ because age 3 fish had the highest fecundity; Fig 3B), and; σ_K is the variance around

the population mean, which determines the width of the Gaussian distribution around γ and has

been interpreted as the resource niche. Intuitively, the width of the resource niche determines the

carrying capacity of the population. When the resource niche is narrow, deviation from the

central tendency results in rapid declines in survival and reproduction and therefore smaller

carrying capacity (Fig S9. When the resource niche is wide, there is more capacity for deviations

in trait value to have minimal impact on survival and reproduction.

In the game theoretic literature, it is well known that when the competitive niche is wider

than the resource niche (i.e. $\sigma_a < \sigma_K$) there will only be one species due to competitive exclusion

and limiting similarity. Similarly, when the competitive niche is narrower than the resource niche

there can be multiple species due to frequency dependent selection. We simply make use of this

understanding here, and we would direct interested readers to the literature that is dedicated to

exploring this phenomenon in detail (23-26).

The fitness function in equation 1, determines the ecological population dynamics and the

dynamics describing the evolution of life history traits. Using a discretised version of the

continuous time model (18), populations change according to:

$$N_{i,t+1} = N_{i,t} e^{G(v,\mathbf{u},\mathbf{N})}|_{v=u_i}, for\ all\ i = 1, 2, \dots x. \qquad \text{Equation S7}$$

Strategies evolve through time according to:

$$u_{i,t+1} = u_{i,t} + s \frac{\partial G(v,\mathbf{u},\mathbf{N})}{\partial t}|_{v=u_i}, for\ all\ i = 1, 2, \dots x. \qquad \text{Equation S8}$$

Where s is analogous to the heritability of the trait. Typically, it is assumed that evolutionary dynamics are slower than ecological dynamics, and therefore $1 > s > 0$, though this doesn't influence the final solution, only the time taken to get to equilibrium. Smaller values of s will result in very slow evolution towards fixation due to low heritability.

An evolutionarily stable strategy (ESS) requires the life history strategies to be at an evolutionary equilibrium, $\mathbf{u}^*$, and the population sizes to be at an ecological equilibrium, $\mathbf{N}^*$, with a finite number, x, of life history strategy types, $u_1^*, u_2^* \dots u_x^*$, and positive population sizes $N_1^*, N_2^* \dots N_x^*$ such that $G(u_i^*, \mathbf{u}^*, \mathbf{N}^*) = 0$ for all $i = 1,2, \dots, x$. Furthermore, the ESS requires the eco-evolutionary equilibrium $(\mathbf{u}^*, \mathbf{N}^*)$, to be a convergent stable maxima on the fitness landscape such that $\frac{\partial G(u_i^*, \mathbf{u}^*, \mathbf{N}^*)}{\partial u_i} = 0$, and $\frac{\partial^2 G(u_i^*, \mathbf{u}^*, \mathbf{N}^*)}{\partial u_i^2} < 0$ for all $i = 1,2, \dots, x$. Convergent stable minima are possible (27) where $\frac{\partial G(u_i^*, \mathbf{u}^*, \mathbf{N}^*)}{\partial u_i} = 0$, and $\frac{\partial^2 G(u_i^*, \mathbf{u}^*, \mathbf{N}^*)}{\partial u_i^2} > 0$ for any $i = 1,2, \dots, x$. As we describe below, we treat these as evolutionary branching points where multiple strategies can arise via frequency dependent selection.

To find the ESS, which might be one life history strategy, or x life history strategies coexisting via negative frequency dependence, we developed a numerical simulation in the R statistical environment (version 3.4.3). The population began with 2 individuals with a strategy of $u_i = 1$, and the ecological and evolutionary dynamics were allowed to unfold according to equations (4) and (5). When the strategy reached a minimum on the evolutionary landscape, which has been called an evolutionary branch point (18), we allowed it to branch into two unique strategies, where the second strategy was phenotypically near to the original strategy according to, $u_j = u_i - 0.02$, and the population of the second genotype was 2 individuals. The rare new

strategy could either go extinct or increase according to negative frequency dependent selection. This continued until an ESS was found as described above.

It has been previously shown that if $\sigma_k \leq \sigma_a$ then negative frequency dependent selection will produce only one life history strategy, $u_1 = \gamma$ (21). Similarly, when $\sigma_k > \sigma_a$, then negative frequency dependent selection will produce some number of strategies, x, where $x > 1$. Here, we analyzed two different scenarios: $\sigma_k = 1.0$ and $\sigma_k = 1.9$ to highlight how negative frequency dependent selection can sometimes eliminate and sometimes maintain diversity respectively, depending on both the ecological and evolutionary relationships.

Agent-based model:

The strength of the above continuous evolutionary game is that it uses our estimates of relative fitness (Fig. 3) and demonstrates that four age-at-spawning life histories. The game theory model makes no assumptions about how many strategies there are or what the age-at-spawning is or should be. Indeed, our simulation began with just one strategy reproducing at age 1, which than evolved into four distinct coexisting strategies over 14000 generations (Fig 4D). However, we also wanted to examine whether our empirical estimates of NFD, provided by the slopes of the regressions between frequency and RRS (Fig. 3C), could also maintain coexistence. To examine whether these slopes could result in coexistence in greater detail we created a simple, forward-time, age and stage structured individual-based model (IBM). Unlike the above mathematical model, the IBM assumes that there are 4 age-at-spawning life histories initially represented in equal proportions within the population. These strategies might be lost due to extinction, but the strategies cannot evolve, and no new strategies can arise. Each individual was assigned a sex, a current age, and an age at reproduction (a heritable trait; (28)). The model begins with reproduction, where only individuals whose current age matches their age at spawning are

allowed to reproduce. We next calculate the relative frequency of each age group and use our empirical estimates of NFD provided by the slopes of the regression between frequency and RRS (Fig. 3C) to calculate the RRS for each age group present on the spawning ground. Where NFD was not detected in our empirical data, we assume a slope of 0. Each individual then reproduces with equal fecundity (here $f = 100$) that is subsequently adjusted by the RRS value for the age class in that particular spawning year. Note that as the relative frequencies of age-at spawning fluctuate from year to year in the IBM so to do the RRS values and subsequent per capita number of offspring produced by each age class. Here we set carrying capacity (k) to 1000 individuals (near the mean Hood River population size, see (9) for details), assume weak compensatory population dynamics, and introduce density independence by setting k each year as a random deviate drawn from a normal distribution with a mean of 1000 and a standard deviation of 20. Decreasing heritability increases variance but does not alter mean frequencies for each age-at-spawning strategy. After reproduction, all individuals that reproduced are removed from the model (assumed to all be semelparous) and mortality occurs by randomly removing individuals from the remaining population until carrying capacity is reached. Lastly, we increment each surviving individuals age by one year. We implemented this model for females in two ways: first, assuming that there was no NFD present (slopes of all age classes = 0; Fig. 4C) and, second, using our empirical slope estimates (Fig. 4F). We also ran the model for males assuming no NFD, but using the empirical RRS values for each age-at-spawning life history strategy (Fig. S10).

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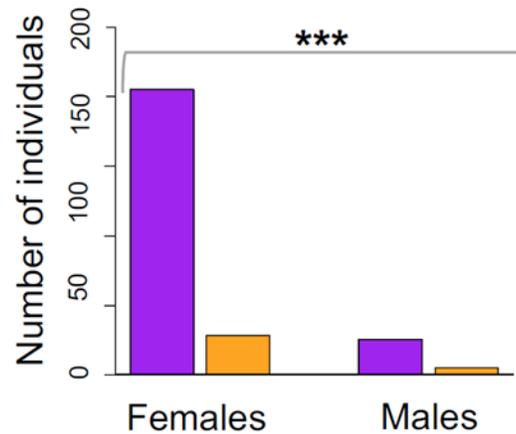
Fig. S1. There were fewer male than female repeat spawners, and fewer hatchery than wild repeat spawners. A ratio of 8:1 female to male repeat spawners was identified, which deviated substantially from equality (randomization test: $p < 0.001$; see details of test in above Supporting Methods) and is typical of steelhead populations, in which males are more likely to adopt the freshwater-resident life history strategy than females. There were also more wild-origin repeat spawners than hatchery-origin repeat spawners, both as a proportion and in absolute numbers ($p < 0.01$).
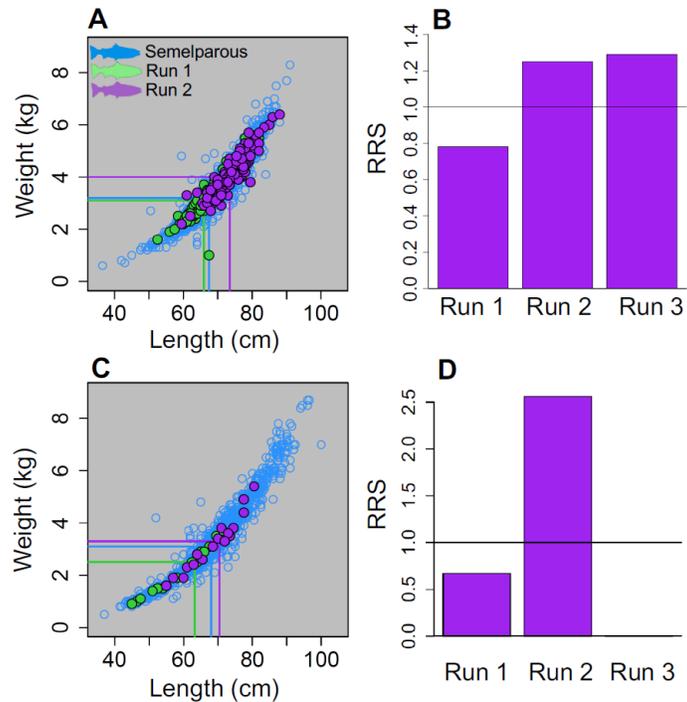
Fig. S2. Repeat spawning females were only slightly smaller than the average single spawning females of the same age the first time that they spawned, but substantially larger than the average single spawning female the second time that they spawned (A). Females also had lower reproductive success relative to single spawners of the same age the first time they spawned (i.e., run 1), but higher relative reproductive success the second and third times they spawned (i.e., run 2) (B). Repeat spawning males were substantially smaller than the average single spawning male of the same age the first time that they spawned, and were only slightly larger than single spawning males the second time they spawned (C). However, males also had substantially lower reproductive success relative to single spawners of the same age the first year that they spawned (i.e., run 1), but substantially higher reproductive success the second time that they spawned (i.e., run 2) (D).
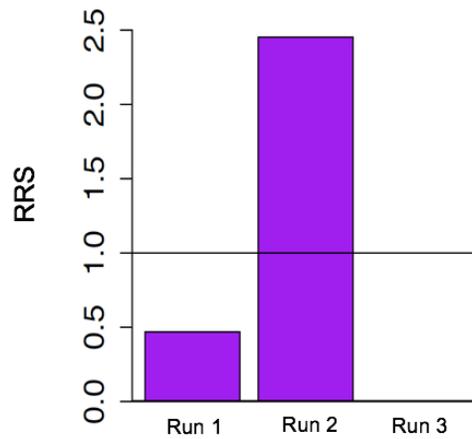
Fig. S3. Male repeat spawners had substantially lower reproductive success relative to single spawners the first run-year that they spawned, but substantially higher reproductive success in the second run-year that they spawned. Here, RRS was calculated relative to 5-year-old single-spawning males (the age class with highest fitness) as opposed to 3-year-old males (the most numerically abundant age class, *cf.* Fig.3D).
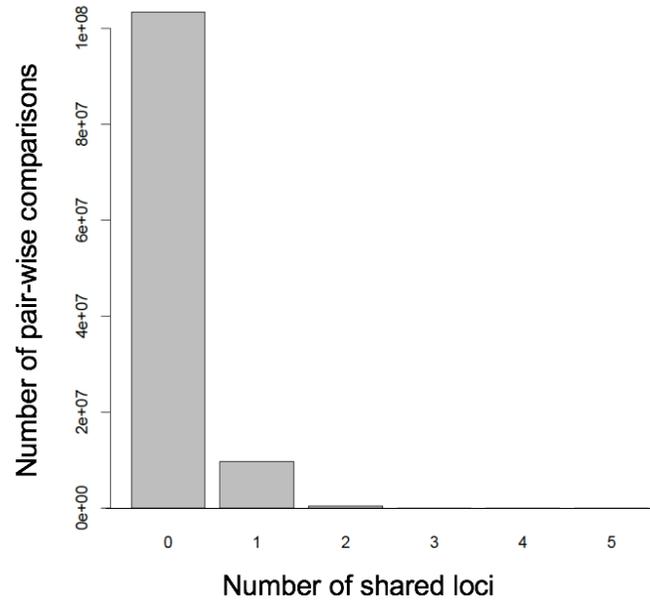
Fig. S4. To determine the probability of two individuals sharing the same genotype at all 8 microsatellite loci by chance alone (as opposed to being repeat spawners) we constructed two multilocus genotypes by randomly selecting two genotypes at each locus and creating two multilocus individuals. We then calculated the number of loci that shared both alleles for that particular pair-wise comparison, repeated the process millions of times, and counted the results. No pairwise comparisons shared the same multilocus genotype at more than 3 loci. To be conservative, we required that all identified repeat spawners shared alleles at a minimum of 5 loci and repeat spawners were further confirmed with scale analyses (see Methods for details).
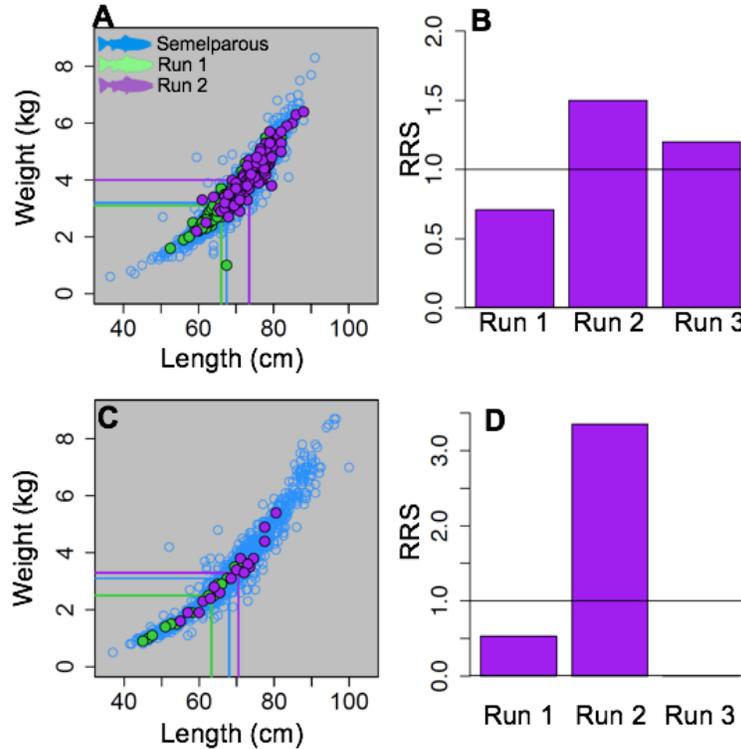
Fig. S5. Repeat spawning females were only slightly smaller than the average single spawning females of the same age the first time that they spawned, but substantially larger than the average single spawning female the second time that they spawned (A). Females also had lower relative reproductive success relative to single spawners of the same age the first time they spawned, but higher relative reproductive success the second and third times they spawned (B). Repeat spawning males were substantially smaller than the average single spawning male of the same age the first time that they spawned, and were only slightly larger than single spawning males the second time they spawned (C). However, repeat spawning males also had substantially lower reproductive success relative to single spawners of the same age the first year that they spawned, but substantially higher reproductive success the second time that they spawned (D). Here, RRS was calculated relative to the weighted average reproductive success of single spawning fish (where we weighted the mean fitness values of single-spawning fish by the proportion of repeat spawners present in each run-year, *cf.* Fig. 3, where we simply compared the average fitness of repeat spawners to the fitness of single spawning fish in the first year in which repeat spawners spawned).
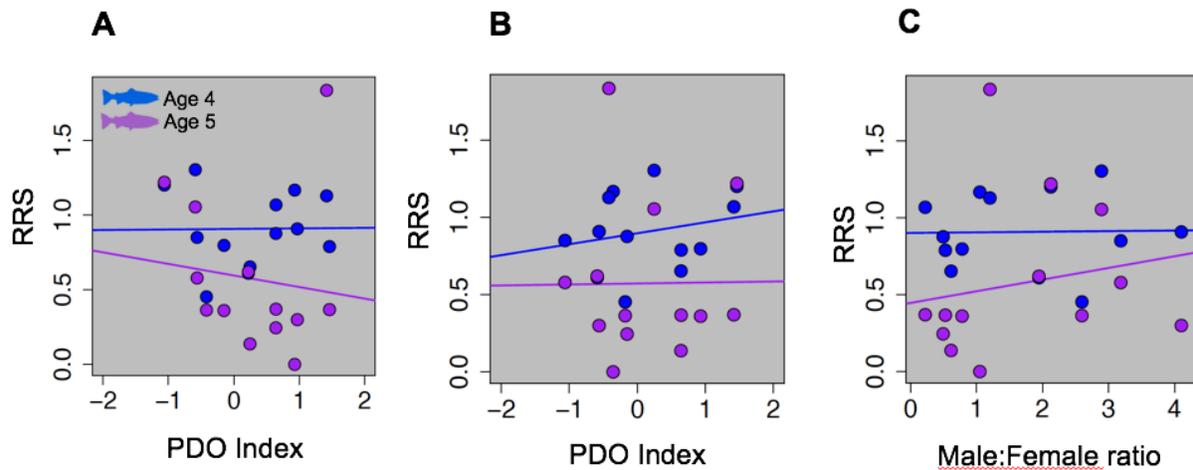
Fig. S6. While the Pacific Decadal Oscillation (PDO) can explain absolute abundance of steelhead on Hood River spawning grounds, it could not account for the observed patterns of frequency dependence. A) There was no relationship between female relative reproductive success (relative to three-year-old fish, see Fig. 4) and the PDO index the year that females returned to spawn. B) There was also no relationship between female relative reproductive success and the PDO index two years prior to the year in which females returned to spawn (i.e., when the fish would be growing in the ocean). C) The observed patterns of frequency dependence in females could also not be explained by the proportion of males on the spawning grounds.
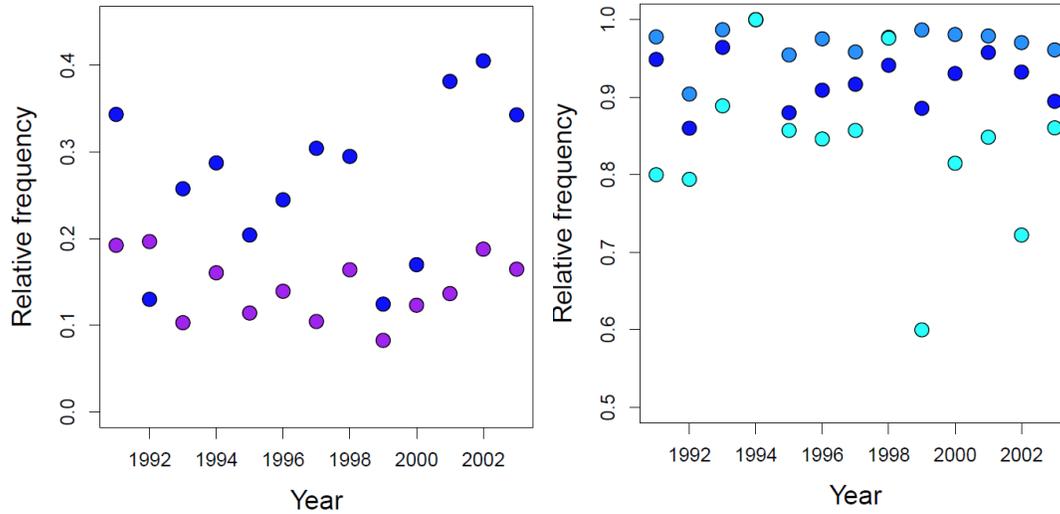
Fig. S7. The relative frequency of age classes through time. A.) The relative frequency of 4-year-old fish (blue circles) and 5-year-old fish (purple circles) did not change through time and cannot explain the negative relationship between frequency and reproductive success illustrated in Figure 4C, B.) Although no such pattern of negative frequency dependent selection was found in males (see Figure 4F), we also saw no substantial changes to the relative frequency of 2-year-old (cyan circles), 3-year-old (light blue circles), or 4-year-old fish (dark blue circles) on the spawning grounds through time. Fitting a linear regression to all age classes independently resulted in p-values greater than 0.1 for parameters associated with slope.
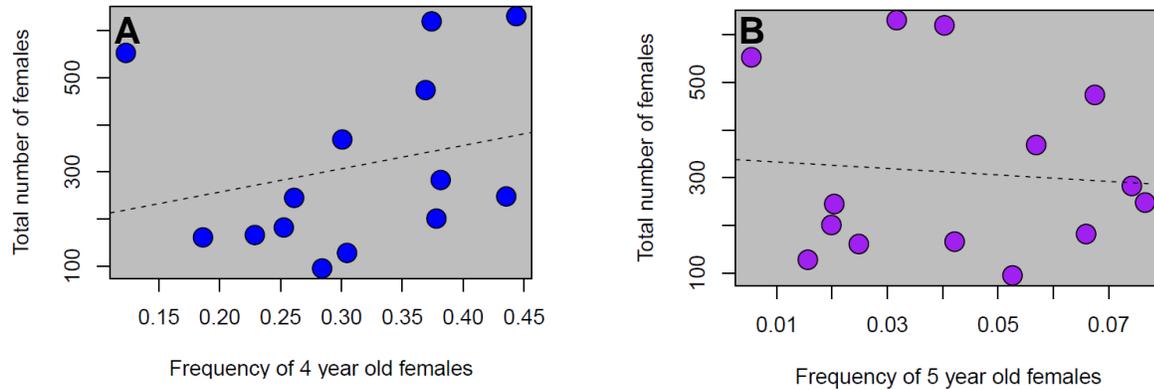
Fig. S8. The relative frequency of female age classes through time verses the total number of females present on the spawning grounds. A.) As four-year-old fish increase in frequency, there is a slight increase in the total number of fish on the spawning grounds, though this relationship was not significant ($p < 0.389$) and the correlation was low ($R^2 = 0.06245$). Nevertheless, this relationship, if real, posits a possible mechanism for the NFD; increased competition among the offspring of 4-year-old fish could occur in years when 4-year-old fish occur at high frequency due to more total fish spawning in the population. B.) There is no apparent relationship between the frequency of five-year-old fish and the total number of fish on the spawning grounds ($p < 0.769$, $R^2 = 0.0074$) likely because this age class is substantially less abundant (Fig. 1).
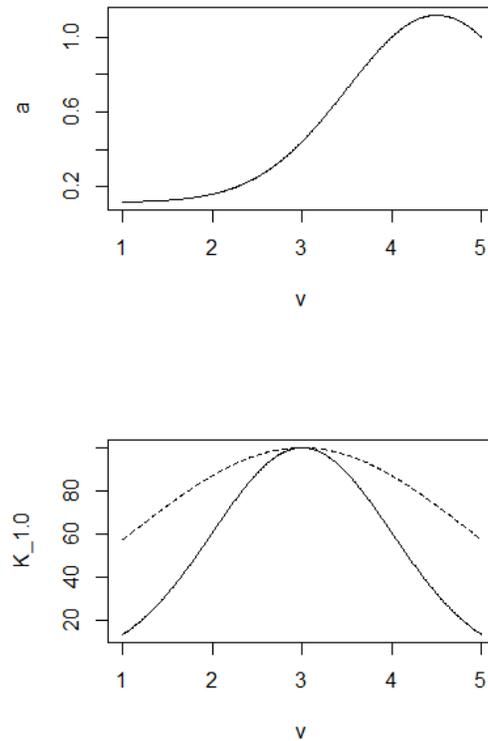
Fig S9: The assumed relationships between life history traits, v, and either (a) competition coefficients, or (b) carrying capacity. For the competition coefficient, $\sigma_a = 1$, and $\beta = 0.5$ throughout. Competition for age 5 fish is shown to highlight the asymmetric competitive ability. For carrying capacity, $K_m = 100$, and $\gamma = 3$ throughout. This causes fish in the model to have the highest fit of form and function at age 3. Two different simulations were performed that varied only in the value of σ_k. A narrow niche width with only one life history strategy was represented by $\sigma_k = 1.0$ (b, solid), and a wide niche width with multiple life history strategies was represented by $\sigma_k = 1.9$ (b, dashed).
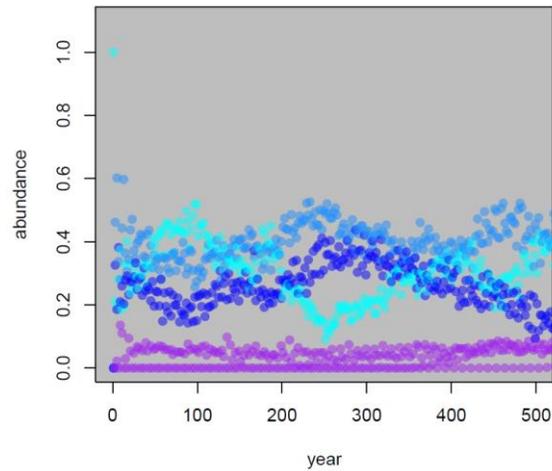
Fig S10: Results from IBM using the RRS data for males (Fig 3E) and assuming no NFD. Coexistence can occur for these fitness values (but not for females) in the absence of NFD because of trade-offs between mortality and reproduction (age classes with higher RRS values also have higher probability of mortality by staying in the ocean for a longer period of time). Colors correspond to age-at-spawning life histories associated with other figures where cyan equals age-2 fish, dodger blue equals age-3 fish, dark blue equals age-4 fish, and purple represents age-5 fish.