

Abstract. – To test the hypothesis that year-class strength in marine fishes is determined in the early-larval stages, and that these stages can be used to predict recruitment, I modeled the recruitment process using a modified form of key-factor analysis. Using data compiled from the fish literature, I found a significant relationship (R^2 0.90, $P \ll 0.001$, n 97) between the mean and interannual variance of stage-specific mortality rates that provided variance estimates for the model. The R^2 values for the true correlation between abundances of small larvae and subsequent recruitment for four example species of marine fish were predicted to lie between 0.10 and 0.57, depending on the assumptions of the model. I therefore suggest that recruitment levels are fixed after the early-larval period. However, the precision of sample correlations are too low (10-yr data series) to empirically test whether abundances or mortality rates of early larvae are in reality strongly or poorly correlated with recruitment. After metamorphosis, the strength of the true relationship and the precision of sample correlations increase sufficiently to permit precise forecasting of recruitment. Recruitment is a complex process in which variation in all life stages contributes substantially to the variability in final abundance; therefore, researchers should recognize the importance of the later prerecruit stages and the interactions among all stages.

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Precision of recruitment predictions from early life stages of marine fishes

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A major problem in the management of marine fisheries is the unpredictable fluctuations in stock size resulting from variable recruitment. Hjort (1913) first recognized this recruitment variability and proposed a number of hypotheses that linked the survival of small first-feeding larvae and subsequent year-class strength (reviewed by Wooster and Bailey 1989). These hypotheses have formed the basis of much research on the early life history of fishes, research which has been largely focused on the 'critical period' during the transition from endogenous to exogenous modes of feeding. While much has been learned about the biology of larval fish, the evidence for a critical period of increased mortality and a link between the larval stage and recruitment remains equivocal (May 1974, Ware and Lambert 1985, Peterman et al. 1988, Campana et al. 1989). Explanations for this failure have ranged from sampling and technical difficulties, such as inappropriate scales of sampling (Leggett 1986, Taggart and Leggett 1987, McGurk 1989), to the suggestion that no such critical period exists, and that all prerecruit stages contribute to some degree to variability in year-class strength (Sissenwine 1984, Anderson 1988, Peterman et al. 1988).

There have been few attempts to model the recruitment process to assess the likelihood that early-larval mortality is a dominant feature of year-class variability. Manipulations

of life tables have shown that small changes in larval mortality have the potential to cause great variation in recruitment (Smith 1985, Houde 1987 and 1989, Pepin and Myers 1991); however, the influence of the larval stages in a fully dynamic model incorporating variability in all stages has not been investigated. In particular, the role of postlarval mortality in causing recruitment variability is unclear and has been the cause of some controversy (Sissenwine 1984, Peterman et al. 1988, Taggart and Frank 1990, Wooster and Bailey 1989).

An often-stated justification for research on the early life history of fish is to provide short-term forecasts of recruitment, thereby allowing managers to adjust fishing regulations in response to changes in stock size (Gulland 1989). While it is obvious that the stages very close to recruitment will give the most accurate predictions, sampling these stages is often difficult and expensive (Smith 1985), unless they are caught incidentally in other fisheries. Rather, efforts have usually been concentrated on finding a predictive relationship between recruitment and the abundance or some measure of survival of larvae and recruits, on the working assumption that Hjort's hypothesis of year-class determination at this early stage is valid (Peterman et al. 1988, Cushing 1990).

The utility of short-term (i.e., annual) predictors of recruitment in the

management of fish stocks has recently been challenged by Walters and Collie (1988) and Walters (1989). In simulated management examples, Walters (1989) finds that only extremely accurate forecasts of recruitment can offer significant improvements over using the long-term mean recruitment in stock assessment models. Thus, while studies of the early stages of marine fish may reveal insights into their ecology, it is unclear whether sufficiently accurate forecasts of recruitment will ever be possible from these early stages.

In this paper I first pose the question, "How strong are the correlations between abundances or mortality rates of the early life stages and recruitment likely to be?" I develop a simple analytical model based on key-factor analysis (Varley and Gradwell 1960, Manly 1977). I use parameter estimates compiled from a literature survey to calculate the expected correlations between life stages for the prediction of fish recruitment. I suggest that the assertion that year-class strength is fixed in the early-larval stages is not general, and, furthermore, under likely field conditions it will be difficult to quantitatively test this hypothesis.

The model

I developed a simple model to simulate the variability in population numbers and the strength of correlations between life stages. In brief, the model generated annual abundances and mortality rates over a specified number of years from which correlations between early-life-history stages and recruitment were calculated. This process was repeated in a Monte Carlo fashion to estimate the sampling distribution of the correlation coefficients.

I divided the egg-recruit period into four intervals: (1) egg-yolksac larvae, (2) early-feeding larvae, (3) late-feeding larvae, and (4) juveniles from metamorphosis to age 1, which I assumed to be the age of recruitment. I assumed that populations would be sampled at five distinct times that divide the egg-recruit period into four intervals. Sampling points were: eggs spawned (N_e), first-feeding larvae (N_f), young larvae (N_l), metamorphs (N_m), and recruits (N_r). First-feeding larvae were operationally defined as larvae that have just begun to feed, while young larvae were defined as having an age of 10 days after the onset of feeding.

In any year, the number of recruits is the product of the number of eggs spawned and the survival rates of the prerecruit stages:

$$\text{Recruitment} = \text{Eggs} \cdot S_{ys} \cdot S_{el} \cdot S_{ll} \cdot S_j,$$

where the subscripts refer to the egg-yolksac, early-

larval, late-larval, and juvenile periods outlined above. Expressing survival rates as instantaneous mortalities, $M = -\ln(S)$, and taking logs of the abundances give the usual equation of key-factor analysis (Varley and Gradwell 1960):

$$N_r = N_e - M_{ys} - M_{el} - M_{ll} - M_j, \quad (1)$$

where N_r and N_e are log abundances of recruits and eggs of a particular cohort, and the M_i values are interval-specific instantaneous mortalities for four intervals defined above. I assume, following Hennemuth et al. (1980) and Peterman (1981), that log abundances and instantaneous mortality rates are normally distributed with stage-specific variances described below. This multiplicative process results in lognormally distributed recruitment, consistent with empirical results (Hennemuth et al. 1980). All subsequent references to abundance made in this paper are to log-transformed values.

Since I am interested in short-term forecasting, I assumed that stock size and, therefore, mean egg production are stationary in time and that variation in egg production is independent of recruitment. Thus, in the absence of density-dependent processes, recruitment is linearly related to egg production.

To introduce stochastic variation in the model, the abundance of eggs, N_e , and the interval-specific mortality rates were simulated as normal random variables. As the time-series of egg production was stationary and my interest is in correlations rather than abundances, the abundance of eggs and the mortality rates all had a mean of 0.

To start the sequence of calculations in a given model year, the initial abundance of eggs was randomly chosen. In the simplest version of the model, which assumes mortality in each interval is independent of the others and is density-independent, the following equation was then used to calculate the numbers of each subsequent stage:

$$N_{k+1} = N_k - m_k, \quad (1)$$

where N_k is the abundance of stage k , and m is a normal random deviate that simulates random interannual variability in mortality of interval k .

The complete independence of mortality of one stage with that of a subsequent stage is probably an unrealistic assumption because, for example, years which are good for yolksac larval survival may also be good for the survival of older larvae. This can be modeled by introducing covariances between the interval-specific mortality rates (Gerrodette et al. 1984). Covariation between interval-specific mortality rates was modeled by assuming that there was a positive corre-

lation between the mortality rate of adjacent intervals across years. The mortality of a given interval in any model year then depends partially on the mortality of the previous period in that same year. With ρ equal to the correlation between adjacent interval-specific mortality rates, I used the following equation to calculate the mortality rate of successive intervals:

$$M_{k+1} = \rho \left\{ \frac{SD(M_{k+1})}{SD(M_k)} \right\} M_k + (1 - \rho^2)^{1/2} M_{k+1}.$$

In this equation, the actual mortality for stage $k+1$ is a linear combination of the random variables simulating the variability in stages k and $k+1$. The correlation coefficient determines how much mortality in stage $k+1$ is similar to that of stage k . The ratio of standard deviations in the first term scales the contribution of the mortality of the previous interval to the appropriate variance. To simplify, I assumed throughout this paper that there was no covariance between the number of eggs spawned and mortality in subsequent intervals.

Finally, density-dependent mortality was incorporated in some versions of the model. Density-dependent mortality was added to the juvenile period, following suggestions of Houde (1987) and Smith (1985) that this is the most likely interval for density effects. While a number of formulations are possible, I chose a power function (Peterman 1982):

$$Y = aX^b,$$

where in this case X and Y are the abundances of juveniles and recruits, respectively. For density-independent mortality, $b = 1$; b is < 1 for density-dependent cases. The parameter a is thus the density-independent survival rate. After taking logs, the log of the abundance of recruits is now a function of the log of the number of metamorphs, N_m , and the density-independent mortality, M_j :

$$N_r = bN_m - M_j. \quad (2)$$

In the stochastic simulations, this equation was used to calculate recruitment with a random normal deviate substituted for M_j .

The full model was run for 1000 10-yr trials in SAS (1987), and a matrix of abundances and mortality rates for each stage was built up. For each 10-yr trial, correlation coefficients were calculated between the various predictors of recruitment (i.e., abundances and mortality rates of each of the prerecruit stages), and the numbers of recruits and summary statistics of the distributions of correlation coefficients were derived.

Table 1

Daily mortality rates (M) and interval durations (t , in days) for four species used as examples in the analysis. Egg mortality includes the yolk sac period up to first feeding; larval periods explained in text. Values were adapted from Houde (1987; cod *Gadus morhua*, and herring *Clupea harengus*), Smith (1985; anchovy *Engraulis mordax*), and Zijlstra and Witte (1985; plaice *Pleuronectes platessa*).

Species	Egg		Early larvae		Late larvae		Juveniles	
	M	t	M	t	M	t	M	t
Cod	0.061	18	0.160	10	0.063	46	0.010	291
Herring	0.050	21	0.080	10	0.034	70	0.015	264
Anchovy	0.250	7	0.160	10	0.050	79	0.012	269
Plaice	0.068	38	0.104	10	0.045	77	0.008	245

Model parameters

To generalize the results, I used four fish species as examples (Table 1). These were not chosen to be representative of a specific stock or situation, but rather to indicate the effect of different life histories on our ability to forecast recruitment. To parameterize the model for a specific species, the interannual variance of the number of eggs laid and the mortality of each prerecruit stage was required.

I obtained estimates of the variance in the number of eggs spawned from published reconstructions of stock abundances (Table 2). Except for cod, I used the residuals of linear regressions of $\log(\text{eggs})$ on time to estimate the variance, since time trends existed for some stocks.

Estimates of the variability in mortality rates for all prerecruit stages are unavailable; I therefore sought a predictive relationship between interannual variance and the mean of daily mortality rates. This allowed estimation of the variances of mortality rates of the early life stages from mean daily rates. I surveyed the literature for papers containing 2 or more years of estimates of age- or stage-specific mortality for the same population or stock. All stages from egg to adult were used, for marine, freshwater, and anadromous fish species. No screening of the data was done except for estimates from adult fish, where only estimates using methods independent of catch-data analysis were used (i.e., tagging). Most adult estimates were from lightly or unfished stocks. In some cases I estimated mortality from annual estimates of abundance or from regressions of \log abundance on time. All estimates were converted to daily values using annual estimates of stage duration if available, or the long-term average stage duration. Daily mortalities were then averaged

over the number of years of data available, and the variance calculated. Both variates were log-transformed, and a least-squares regression was fitted to the data.

I used the variance-mean relationship to calculate the interannual variance in mortality from mean daily mortality rates extracted from published life tables (Table 1). I split the larval period and defined the first 10 days of feeding as the early stage. This period corresponds to the usual definition of the 'critical period' for first-feeding larvae (Leggett 1986): few marine larvae can survive more than 10 days without feeding (Miller et al. 1988). Except for anchovy, where values were taken directly from Smith (1985), the daily mortality rate for the early period was set at twice the average rate for the whole larval period. Mortality rates for the late period were adjusted so that the mortality for the total larval period matched the published life tables. The result of these calculations was that the daily mortality rates of the early-larval interval were about 2.5 times those for the late-larval period. It is difficult to assess whether this decline is realistic, because there is considerable variability in the decline in mortality over time in empirical studies; in many cases mortality has been found to be nearly constant over much of the larval period (Dahlberg 1979), while there are other cases where significant declines have been observed (i.e., Savoy and Crecco 1988). Declines in mortality with larval age may be accentuated by a possible bias due to sampling interval (Taggart and Frank 1990). The variance in mortality over the duration of a particular interval was then calculated as the product of the square of the interval's duration (in days), and the variance of the daily mortality rate predicted from the variance-mean relationship.

Covariation in mortality rates

Two scenarios were developed concerning the effects of covariation between mortality rates. In the independent case, all mortality rates were varied independently of one another, while for the 'covariance' version, mortality rates of adjacent stages were assumed to be correlated across years. Few data are available to estimate the strength of these correlations, so I assumed ρ values for the correlations between adjacent M_k based on the likelihood of common agents of mortality. I assigned a relatively low ρ value of 0.25 for the correlation between the egg/yolk sac period and the early-larval mortality because early-larval mortality is thought to be strongly affected by feeding success, which does not affect egg survival. Nonetheless, predation pressures are probably similar for both stages, causing some covariation in mortality rates. A ρ value of 0.5 was used between the early- and late-

Table 2

Interannual variability in log-transformed egg production and recruitment, compiled from literature values. All egg estimates are residuals from linear regressions of log abundance on time, except for cod where an intermediate value between herring and plaice was used.

Species	Var(N_e)	Var(N_r)
Cod	0.075	0.40
Herring	0.081	1.92
Anchovy	0.282	1.91
Plaice	0.055	0.14

Data sources

Cod: mean of 5 northwest Atlantic stocks in Koslow et al. (1987).

Herring: mean of 7 northwest Atlantic stocks in Winters and Wheeler (1987).

Anchovy: eggs—Peterman et al. (1988), recruitment—Methot (1989).

Plaice: Bannister (1978).

larval intervals because of the similarity of habitat between these two periods. For the pelagic species, anchovy and herring, $\rho = 0.25$ was used for the correlation between the late-larval and juvenile intervals, while for the demersal species, cod and plaice, I set $\rho = 0$, reflecting the major habitat shifts associated with metamorphosis.

Density-dependence

To explore the effects of density-dependence on correlations, I ran the model with $b = 1.0$, the density-independent case, or $b = 0.7$, simulating moderately strong density-dependent mortality. The variance of juvenile mortality predicted from Figure 1 is in fact the sum of both the density-independent and density-dependent sources of mortality. To estimate the density-independent component of mortality (M_j) required for Eq. (2), I had to remove the density-dependent mortality from the total juvenile mortality predicted by Figure 1. Rearranging Eq. (2) and solving for the total juvenile mortality (M_{jtot}) yields

$$M_{jtot} = N_m - N_r = (1 - b)N_m + M_j.$$

In the models without covariances between mortality rates, and in the covariance model for cod and plaice where there is no covariation in mortality across metamorphosis, taking variances yields

$$\text{Var}(M_j) = \text{Var}(M_{jtot}) - (1 - b)^2 \text{Var}(N_m).$$

In these cases, to find $\text{Var}(M_j)$ I ran the stochastic

model up to the metamorph stage and calculated the median $\text{Var}(N_m)$. $\text{Var}(M_j)$ was then found by subtraction using $\text{Var}(M_{j\text{tot}})$ predicted from Figure 1 (Table 3). For herring and anchovy in the covariance model, the equation above should include a term for the covariance between $M_{j\text{tot}}$ and N_m . In these cases, $\text{Var}(M_j)$ was found by trial by running the model with different values of $\text{Var}(M_j)$ and matching the median $M_{j\text{tot}}$ with the value predicted from the regression equation of Figure 1.

To provide objective criteria for evaluating recruitment hypotheses, I defined two performance criteria for the correlations with recruitment. Recruitment research is commonly cast as a search for the stage when “year-class strength is determined” or “recruitment is fixed.” I define such a stage as having an $R^2 > 0.50$ with recruitment, i.e., being able to account for at least half of the variability in year-class strength. A more rigorous standard of $R^2 > 0.80$ was set for correlations to be used for management purposes (Walters 1989).

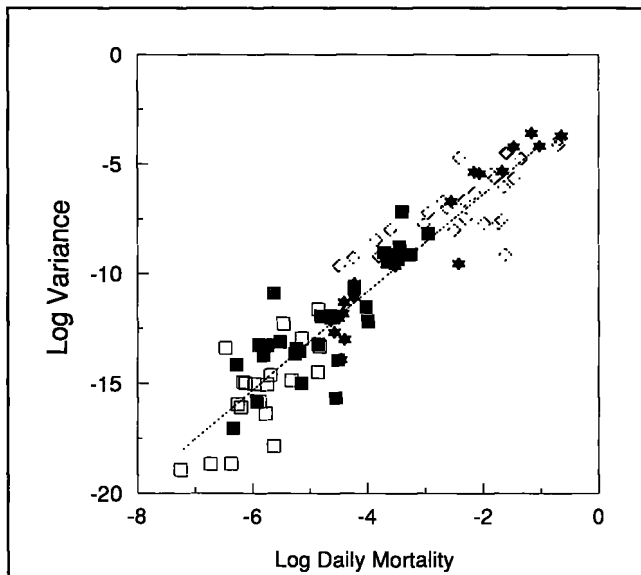


Figure 1

Relationship between interannual variance in daily mortality rates and mean daily mortality from published values. Symbols indicate eggs (*), larvae (◇), juveniles (■), and adults (□). Equation of the line: $\ln\{\text{Var}(M)\} = 2.231 \ln(M) - 1.893$ ($R^2 = 0.90$, $P < 0.0001$). Regression uses the square root of number of years comprising each data point as weights.

Results

Variance-mean relationship

There was a highly significant relationship ($R^2 = 0.90$, $P < 0.0001$, $n = 97$) between the log of mean daily stage-specific mortality and the log of the interannual variance in the daily mortality rate (Fig. 1). The variance in mortality rate was independent of the number of years of data comprising each point (multiple regression with mean mortality, $P = 0.81$ for sample size). The square root of sample size was used as a weight in all analyses. There was no significant effect of life history (freshwater, marine, or anadromous) on the variance-mean relationship (ANCOVAR; for slopes and adjusted means, all $P > 0.20$). There was no difference in the relationship between the variance and mean of mortality among the egg, juvenile, and adult stages ($P > 0.5$), but the slope for the larval stage was significantly different from the other three stages (intercept $P = 0.10$, slope $P = 0.010$). Because there were a number of studies on the same species, I also averaged the data across both species and stage to decrease the non-independence of the data due to common phylogeny. The variance-mean regression for this averaged dataset was almost identical to the full set ($R^2 = 0.92$, $P < 0.0001$, $n = 53$); the regression parameters differed by $< 2\%$. In this case, the regression for the larvae was not different than for the other three stages (intercept $P = 0.28$, slope $P = 0.11$), suggesting the significant effect found for the full dataset may have been due to the overrepresentation of some species. I therefore used the overall regression (Fig. 1) to predict the variance of mortality of all stages, rather than using a separate regression for larvae. This is a conservative procedure for rejecting Hjort’s hypothesis, because the single regression predicts a more variable mortality for the early-larval stage than does the separate larval regression; the single regression produces stronger correlations between abundance of

Table 3

Variances of juvenile mortality rates $V(M_j)$ used in the four versions of the model and the variance of log recruitment, $V(N_r)$, generated by the model. Model versions include density-dependent (DD) or independent (DI) juvenile mortality and, in some cases, covariance between stage-specific mortality rates (COV). Variances for M_j in the DD models are for the density-independent component only, and were found by simulation.

Species	DI		DI-COV		DD		DD-COV	
	$V(M_j)$	$V(N_r)$	$V(M_j)$	$V(N_r)$	$V(M_j)$	$V(N_r)$	$V(M_j)$	$V(N_r)$
Cod	0.45	1.49	0.45	2.04	0.35	0.87	0.34	1.15
Herring	0.91	1.49	0.91	2.08	0.85	1.14	0.92	1.59
Anchovy	0.58	2.54	0.58	3.91	0.40	1.36	0.45	2.16
Plaice	0.22	1.64	0.22	2.46	0.09	0.79	0.09	1.04

stronger correlations between abundance of

early larvae and recruitment than the separate larval regression.

Correlations between early life history and recruitment

Correlations between abundances at early life stages and recruitment increased in strength as the interval between the two stages decreased (Figs. 2, 3). Overall, covariances in mortality rates across stages increased R^2 values between early abundances and recruitment by 0.01–0.25, while density-dependent juvenile mortality had only a small and usually negative effect on R^2 values.

Correlations between egg or first-feeding larvae and recruitment were weak; the average R^2 over all species and models was 0.05 for eggs and 0.20 for first-feeding larvae. None of the values exceeded 0.50, indicating that these early stages have little predictive

capability. At the end of the early-larval stage, R^2 values increased; and in 4 of 16 cases in Figures 2 and 3 the R^2 values exceeded 0.50. However, no values exceeded 0.80, the suggested requirement for recruitment forecasting to be beneficial for management (Walters 1989).

In nearly all cases, the majority ($R^2 > 0.50$) of recruitment variation was predictable at the age of metamorphosis. The exception was the herring example, which gave low correlations because of high variability in the juvenile mortality rate. Half the correlations met the forecasting requirement of $R^2 > 0.80$ by the age of metamorphosis; these cases occurred in species with the lowest juvenile mortality rates.

The success of larval mortality rates in predicting recruitment was lower than for larval abundance estimates. The correlation between the mortality rate of the early-larval period and recruitment was strongly affected by the presence of covariation between stage-specific mortality rates; without these covariances the average R^2 was 0.12; the largest value was 0.18. When the covariances were incorporated, these correlations are increased, although none exceed 0.5 (Fig. 4). Ten of 16 R^2 values exceeded 0.50 for the much

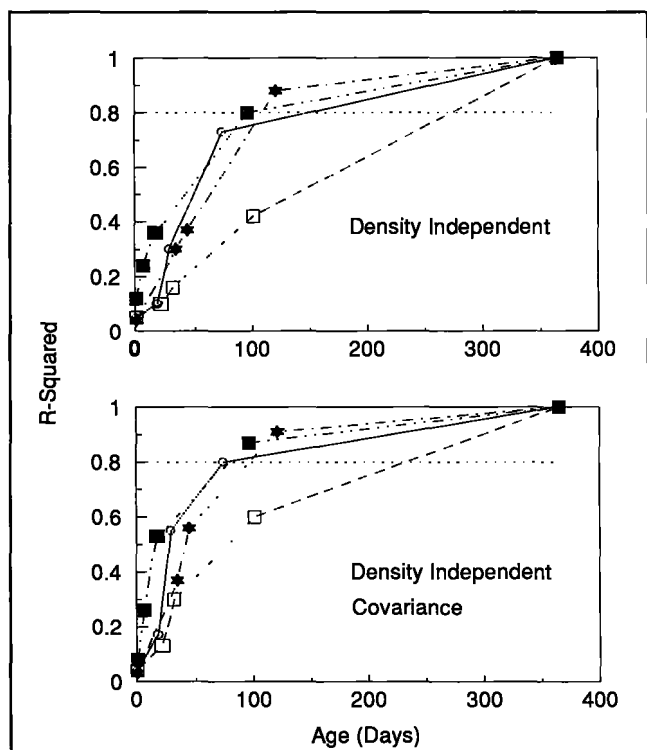


Figure 2

Predicted R^2 values for correlations between recruitment and early life stages for cod (O), anchovy (■), plaice (+), and herring (□). For each species, symbols represent, from left to right: abundance of eggs (at $t = 0$), first-feeding larvae, 10-d larvae, and metamorphs. Dotted line indicates the strength of correlations required for recruitment prediction (Walters 1989). Both examples include density-independent juvenile mortality; lower panel also incorporates covariance between interval-specific mortality rates.

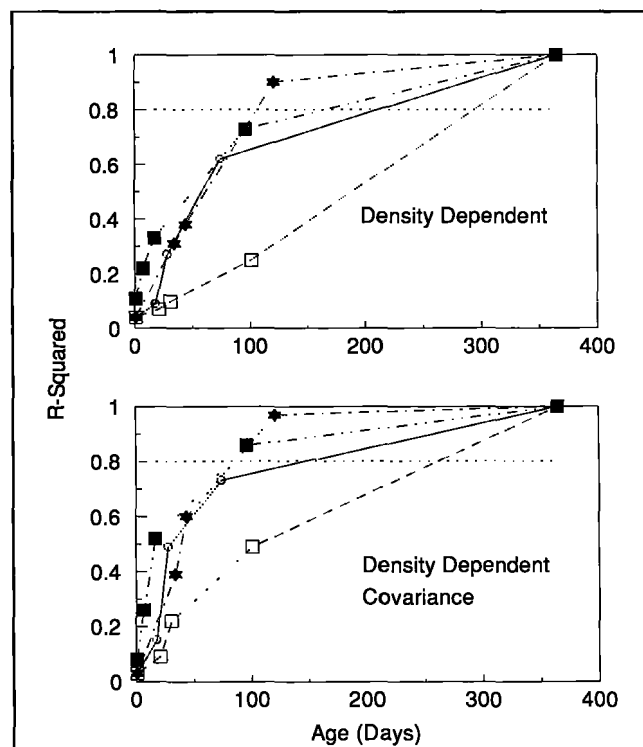


Figure 3

As in Figure 2, except both versions include density-dependent juvenile mortality; lower panel also incorporates mortality covariances.

longer late-larval period. The recruitment-forecasting threshold of 0.8 was never reached for correlations between recruitment and any larval mortality rate.

A wide range of R^2 values can result from a short time-series. For example, the 95% range of R^2 values for the correlation of early cod larvae with recruitment (10-yr time-series) in the density-independent model that includes covariance in mortality rates extended from 0.07 to 0.86 (Fig. 5). The 95% range decreases if the true relationship between the variables is stronger; for cod metamorphs the conclusion that this stage can be used to describe the majority of recruitment variation will nearly always be reached (Fig. 5).

Sensitivity analysis

Two sensitivity analyses were conducted to assess dependence of the results on input parameters. First, stage-specific variances in mortality were recalculated with the slope of the variance-mean regression set at

its 95% confidence limits; the intercept was derived by constraining the line through the mean of both variables. For the cod-DI model, increasing the slope to the upper confidence limit increased the R^2 for the correlations between the abundance of recruits and early larvae or metamorphs by about 0.05; decreasing the slope lowered R^2 values by similar amounts. There was little effect on correlations involving the egg or first-feeding stages. I also recalculated the correlations with the intercept of the variance-mean regression at its 95% confidence limits. With the intercept at its lower limit, R^2 values increased by 0.01–0.04, and at the upper limit the correlations decreased by a similar amount. Thus, the overall results are not particularly sensitive to the sampling error associated with the data in Figure 1.

I also varied the length of the early-larval period. In the life tables (Table 2), I fixed the early-larval period at 10 days and set the daily mortality rate at twice the average for the whole larval period. In sensitivity runs I varied this period from 5 to 15 days; duration and mortality rate of the late-larval period were recalculated to keep the total mortality for the larval period constant. The duration of this period of high larval mortality had a strong effect on the strength of the correlation between abundance of larvae sampled at the end of the early period and recruitment. When the early-larval period was increased by 5 days, the R^2 in the cod-DI model increased by 0.21 (Fig. 6).

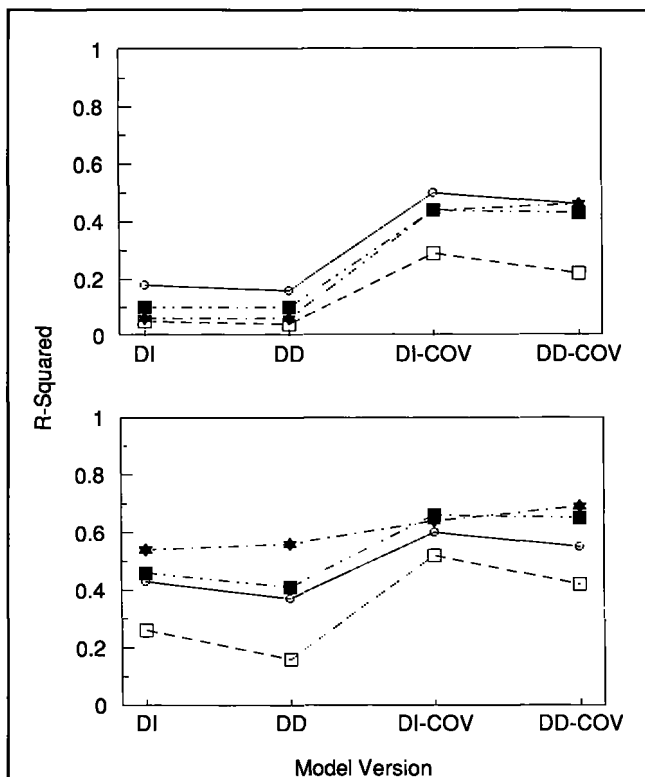


Figure 4

Predicted R^2 values for correlations between recruitment and early- and late-larval mortality rates for cod (O), anchovy (■), plaice (*), and herring (□). Axis labels refer to four versions of the model, incorporating density-independent (DI) or -dependent (DD) juvenile mortality and covariances between mortalities (COV).

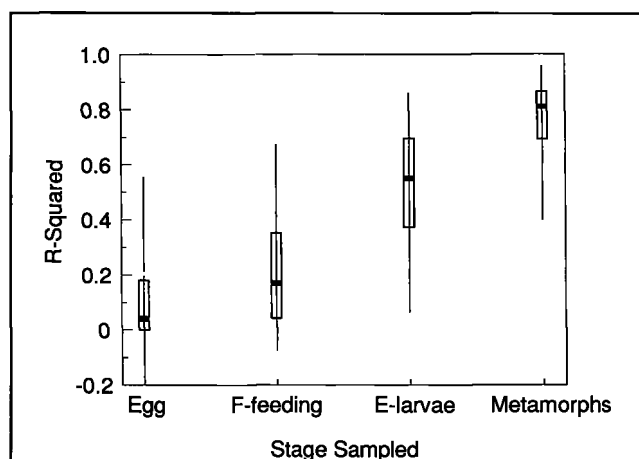
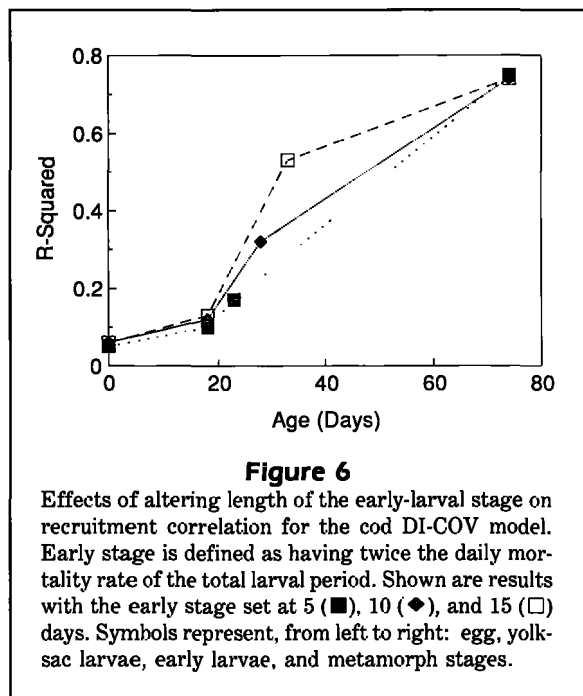


Figure 5

Variability in sample R^2 values (10-yr series) for the correlation between recruitment and abundances of early stages for cod in the model, with density-independent juvenile mortality and mortality covariances. Shown are the median (bar), interquartile (rectangle), and 95% ranges (line). Data are from 1000 runs; note that the criterion for significance ($R^2 > 0$, $\alpha 0.05$) is 0.40.



Discussion

My results indicate that only predictions of recruitment based on abundances of postmetamorphic fish are likely to be useful for the management of marine fishes. The contribution to recruitment variation made by egg number (and, therefore, stock biomass) is very small, a prediction confirmed by most stock-recruit data (Parish 1973). Correlations involving the abundance of early larvae are stronger, but are still too weak for forecasting. The model R^2 values for correlations involving early larvae are similar to the range, extending from 0.01 to 0.66, for published values compiled by Peterman et al. (1988). Accurate recruitment forecasting may be possible by sampling during the late-larval period (Graham and Sherman 1987). However, this is highly dependent on parameters and the dynamics of the particular species; only for cases with low variability in juvenile mortality or with mortality rates correlated across stages are the abundances of late larvae likely to be useful for recruitment forecasting.

Research on recruitment variability has been oriented to the early-larval stages largely as the result of Hjort's (1913) hypotheses and the observation that most of the individuals of a year-class die during the first few weeks of life (Wooster and Bailey 1989). In my four example species, the average cumulative mortality on the cohort to the 10-d larval stage is 93% (Table 1), yet the variation in abundance of these larvae explains more than 50% of recruitment variability

in less than half of the cases. Variability in the late-larval and juvenile stages is still large enough to influence the strength of correlations of recruitment with larval abundances. My results suggest that the stage 'when year-class strength is determined' (defined here as $R^2 > 0.5$) occurs after this early critical period. However, the sensitivity analysis indicates that the strength of the correlation between the abundance of larvae and recruitment will depend strongly on the rate at which mortality declines during the larval period, and at what age the larvae are being sampled.

Strong linkages in mortality rates across intervals also render the definition of a 'critical period' less concise. Correlations between early life stages and recruitment were stronger when there were linkages, because survival to the age of sampling will be correlated to survival in the future. An estimate of mortality or abundance in one stage will be an index of mortality in all early life stages. This may be especially true for the early-larval stages (the classical 'critical period') because small larvae are probably subjected to a similar source of mortality as older larvae, especially if spawning occurs over a protracted period, mixing larvae of different ages together in the same body of water. In addition, environmental conditions during an early stage may affect survival of the cohort in the future. Poor feeding conditions of early larvae, for example, may have a long-term effect on growth and survival (Frank and McRuer 1989). In these cases, recruitment will be somewhat predictable from the early-larval stages, but this is not support for a strict interpretation of Hjort's hypothesis that an early critical period determines recruitment because mortality is correlated across all prerecruit stages.

The difficulty and expense of obtaining accurate estimates of abundances of eggs and larval fish have led to increased interest in finding indirect estimates of mortality rates that may be simpler to collect and could provide an index of year-class strength. Such measures include estimates of growth (Houde 1987), condition, lipid content (Theilacker 1986), and RNA/DNA ratios (Buckley and Lough 1987) as well as oceanographic variables such as upwelling and wind events (Peterman and Bradford 1987). My results show that such mortality estimates made on small larvae are not likely to be strongly correlated with recruitment (Fig. 4). Mortality estimates on older larvae will have stronger correlations, potentially closer to a value of 0.50. Note that the correlations in Figure 4 are for direct estimates of mortality, indirect indices will be more poorly related to recruitment. A combination of larval abundances and mortality rate estimates may allow more precise prediction of recruitment (Graham and Sherman 1987, Frank and McRuer 1989); if estimates are accurate and are based on older larvae,

correlations nearly as strong as those predicted for metamorphs might be possible.

The correlations will be weaker if sampling errors are included in the estimates of abundance. Preliminary simulations with random sampling errors with a coefficient of variation of 50% (untransformed abundances) decreased R^2 values in Figures 2 and 3 by 0.10–0.15 (Bradford unpubl.). Biased estimates, e.g., due to gear avoidance (Lo et al. 1989), will not affect correlations between an early stage and recruitment, unless the magnitude of the bias is correlated with the estimate. Precision, through the use of consistent technique across years, is more important for the purposes of forecasting. Large-scale surveys of abundance of late larvae or juveniles may be sufficiently accurate for the forecasting of recruitment (Lo et al. 1989) if the stage sampled is likely to be strongly correlated with recruitment (Fig. 5).

An implicit, though infrequently stated, assumption of research on early-life-history influences on recruitment is that the mean and the interannual variance of mortality rates are correlated. High mortality alone will not cause recruitment variation; it must also be coupled with high interannual variability. The data compiled in Figure 1 provide evidence that this is generally true, and that the interannual variability in the larval period is proportionately no greater than that found for other stages. In addition, my sensitivity analysis suggests that the general conclusions of this paper are robust to the sampling variability of this relationship. However, detailed investigation of the recruitment dynamics of an individual species will require estimation of the variance of stage-specific mortality rates, because the predictive power of Figure 1 is still relatively low for any particular case, and the biology of an individual species may not result in rates that follow the overall average pattern. Examples are provided by species which spawn during periods of extreme climatic events such as wind storms (e.g., capelin *Mallotus villosus* or red drum *Sciaenops ocellatus*, reviewed by Taggart and Frank 1990). In these cases, interannual variability in the mortality of the earliest stages is probably larger than predicted by the regression of Figure 1, and the correlation between the early stages and recruitment is likely to be stronger than I have predicted. In contrast, for the North Sea plaice a relationship (R^2 0.7) was found between egg abundance and recruitment (Zijlstra and Witte 1985), which is higher than my model predicts for this species (although just within the 95% range). This species has relatively low recruitment variation, suggesting that larval and juvenile survival rates are not as variable as predicted by Figure 1, or that density-dependent mortality might be important in regulating recruitment (Zijlstra and Witte 1985).

The recruitment variances generated by various versions of the model tend to be higher than published values (Tables 2, 3). These literature estimates will likely be underestimates of the true variability in recruitment, because errors in catch sampling and ageing can greatly reduce recruitment variability estimated from sequential population analysis (Rivard 1989, Bradford 1991). Alternatively, my recruitment variances could be too high because I have either overestimated the variances of mortality rates or underestimated the severity of density-dependent mortality. Since the data in Figure 1 include sampling error, all of the variances in Tables 2 and 3 will be somewhat inflated. If sampling error is proportional to the rate of mortality, the sensitivity analysis suggests that removing sampling error (i.e., lowering the intercept of Fig. 1) will have only a slight effect on recruitment correlations.

One additional source of variability not explicitly considered in my analysis is the effect of varying stage duration, due to interannual variability in growth rates. Houde (1987, 1989) has demonstrated through life-table manipulation that small variations in larval growth may have large effects on the number of metamorphs produced. The effect on recruitment will be buffered somewhat as shortening the larval period will increase the length and, therefore, the total mortality of the juvenile stage. However, if the variation in growth rates is due to temperature, Pepin (1991) suggests that the offsetting effects of temperature on development and mortality will result in no net effect of temperature variation on cumulative mortality over the egg and larval stages. In this case, by not including variation in growth rates I will have overestimated the variability in larval mortality. However, to some extent the effects of growth-rate variation are already included in my model because many of the estimates in Figure 1 are based on total stage length and will, therefore, include the effects of varying stage duration caused by variation in growth rates in the calculation of the average daily mortality rate.

The sampling variability of correlations from short datasets makes it difficult to draw inferences about the causes of recruitment variability. This low precision suggests that confidence limits around the sample estimates, r or R^2 , should always be supplied, much in the same way that standard errors are given for sample means. A population correlation from Figures 2 and 3 is a value that would be obtained from a very long time-series of data, and is a true measure (in the context of the model) of the contribution of an early life stage to recruitment variation. However, there is a good chance (e.g., >30% for early larvae in Fig. 5) that a sample correlation between the abundance of an early stage and recruitment may not be significantly different from 0. Even if the correlation is significant,

statements about whether the relationship is, in reality, weak or strong cannot be made because the 95% confidence limits around the sample correlation are wide (Fig. 5). Published correlations between early life stages and recruitment vary greatly in strength (e.g., Peterman et al. 1988, Stevenson et al. 1989, Cushing 1990); unfortunately with short data series, true differences in the biology of these species cannot be distinguished from sampling error. The correlations between early larval abundances and recruitment compiled by Peterman et al. (1988) also illustrate this point: in only 1 of 7 cases do the 95% confidence limits around R^2 not include both 0.2 and 0.8. This problem of low precision is less serious when the true correlation is likely to be fairly high (Fig. 5, metamorphs).

The precision of correlations is also relevant to analyses involving oceanographic or climatic variables and recruitment. These studies usually invoke hypotheses that the environmental variables are agents of larval mortality, either through transport or their effects on the production or concentration of larval food (Shepherd et al. 1984, Hollowed and Bailey 1989); therefore, their true correlations with recruitment can be no stronger than the correlations for mortality rates directly (Fig. 4). Yet the sampling variability of R^2 for a short series of data suggests that there will be a good chance of finding at least one strong sample correlation among a group of 4–5 predictors that may be, in reality, only weakly related to recruitment. Adding more data will result in the sample correlation declining towards ρ ; this frequently results in the sample correlation becoming nonsignificant (Koslow et al. 1987, Walters and Collie 1988, Prager and Hoenig 1989). My model results suggest environmental variables will be strongly correlated with recruitment only if the environmental factor is related to mortality across all prerecruit stages (e.g., Fig. 4; covariance models).

In summary, my analysis indicates that it is unlikely that estimates of abundance of survival rates of the egg and early-larval stages of marine fish will lead to useful predictions of recruitment. Although mortality in the earliest life stages is a major source of recruitment variability, the late-larval and juvenile periods are also important. Peterman et al. (1988), Fritz et al. (1990), and Pepin and Myers (1991) argue for the need for coordinated research on all prerecruit stages, rather than focusing only on the early stages, and my results support this view. The modeling approach I have developed here can be easily modified for any particular species to estimate *a priori* the likelihood of success of proposed recruitment research and to suggest particularly fruitful avenues of investigation.

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Appendix

Daily mortality rates and interannual variances plotted in Figure 1. Stage refers to egg (E), larval (L), juvenile (J), or adult (A) periods. For anadromous salmon, fry-smolt and smolt-adult mortality were classified as juvenile and adult mortality, respectively. *N* is the number of years of data in each study.

Species	Stage	M	var(M)	N	Study
<i>Alosa pseudoharengus</i>	L	0.0490	4.31E-04	9	Mansfield and Jude 1986
	L	0.1980	1.07E-04	8	Walton 1987
<i>A. sapidissima</i>	L	0.0524	2.96E-04	8	Savoy and Crecco 1988
	L	0.0978	1.28E-03	8	
	L	0.2290	3.50E-03	8	
	J	0.0027	1.30E-07	8	
	J	0.0185	5.08E-06	8	
<i>Clupea harengus</i>	E	0.3135	2.80E-02	2	Dragesund and Nakken 1973
	L	0.2060	1.10E-02	2	
	L	0.0275	3.38E-04	11	Graham and Sherman 1987
	L	0.1168	1.83E-03	4	Johannessen 1986
<i>Cololabis saira</i>	L	0.0900	8.98E-03	2	McGurk 1989
	L	0.0726	9.19E-04	14	Watanabe and Lo 1989
	L	0.5000	1.63E-02	2	Hatch and Underhill 1988
<i>Coregonus artedii</i>	L	0.5000	1.63E-02	2	Hatch and Underhill 1988
<i>C. clupeaformis</i>	E	0.0299	6.40E-05	2	Taylor et al. 1987
	L	0.0143	9.30E-05	2	
	L	0.0216	2.10E-04	2	Freeberg et al. 1990
<i>Engraulis encrasicolus</i>	L	0.2000	1.11E-02	3	Palomera and Leonart 1989
<i>E. mordax</i>	E	0.3600	1.53E-02	13	Peterman et al. 1988
	L	0.1860	5.52E-04	13	
	J	0.0180	9.77E-06	13	
<i>Esox lucius</i>	L	0.1650	3.60E-03	3	Franklin and Smith 1963
<i>Gadus morhua</i>	E	0.1890	4.84E-03	3	Campana et al. 1989
	L	0.1940	2.37E-03	3	
	E	0.2304	1.48E-02	7	Heessen and Rijnsdorp 1989
	L	0.1010	5.63E-04	8	Sunby et al. 1989
	J	0.0312	8.90E-05	7	
<i>Melanogrammus aeglefinus</i>	E	0.1270	4.43E-03	3	Campana et al. 1989
	L	0.2630	8.56E-03	3	
<i>Micropterus dolomieu</i>	E	0.0890	7.12E-05	3	Clady 1975
	L	0.0310	7.74E-05	3	
	A	0.0007	6.00E-09	2	Van Woert 1980
<i>M. salmoides</i>	L	0.0224	9.90E-05	3	Kramer and Smith 1962
	J	0.0078	1.80E-06	4	
<i>Morone saxatilis</i>	L	0.1770	4.50E-04	2	Dey 1981
	J	0.0040	2.00E-06	2	
	L	0.1550	4.30E-03	6	
	J	0.0530	2.80E-04	10	
<i>Oncorhynchus gorbuscha</i>	E	0.0097	5.32E-06	6	Pritchard 1948
	J	0.0260	7.80E-05	3	Parker 1968
	A	0.0080	1.65E-06	3	
<i>O. kisutch</i>	A	0.0028	1.37E-07	8	Mathews 1984
	A	0.0078	5.15E-07	17	Mathews and Olson 1980
	A	0.0049	3.51E-07	22	Nickelson 1986
<i>O. mykiss</i>	J	0.0036	1.85E-05	3	Seelbach 1987
	A	0.0020	1.02E-07	4	Allen 1977
	A	0.0022	3.08E-07	7	Ward and Slaney 1988

Appendix (continued)					
Species	Stage	M	var(M)	N	Study
<i>Oncorhynchus nerka</i>					
Sixmile Creek	E	0.0108	3.15E-06	2	Foerster 1968
Scully Creek	E	0.0116	8.82E-07	6	
Williams Creek	E	0.0111	5.91E-06	3	
Chilko Creek	E	0.0123	2.24E-06	7	
Tally Creek	E	0.0146	1.53E-05	11	
Port John Lake	E	0.0123	1.20E-05	9	
Karymai Spring	E	0.0120	7.23E-06	8	
Chilko Lake	J	0.0018	3.96E-08	7	
Karymai Spring	J	0.0056	1.31E-06	8	
Cultus Lake	J	0.0053	1.47E-06	10	
Port John Lake	J	0.0028	1.77E-06	8	
Babine Lake	J	0.0052	1.17E-06	10	
	J	0.0032	1.72E-06	14	McDonald and Hume 1984
	A	0.0026	2.98E-07	7	Foerster 1968
	A	0.0021	3.26E-07	24	Peterman 1982
Karluik River	A	0.0017	7.86E-09	6	Barnaby 1944
Summit Lake	A	0.0036	1.73E-08	3	Roberson and Holder 1987
Ten Mile Lake	A	0.0032	2.88E-07	6	
Gulkana Hatchery	A	0.0031	7.65E-08	9	
Lake Washington	A	0.0034	4.42E-07	11	Thorne and Ames 1987
<i>Oncorhynchus</i> spp.	E	0.0147	2.90E-05	23	McNeil 1969
<i>Pagrus pagrus</i>	A	0.0012	7.76E-09	3	Manooch and Huntsman 1977
<i>Perca flavescans</i>	J	0.0146	2.36E-05	6	Forney 1971
	J	0.0320	1.53E-04	8	
	A	0.0079	8.90E-06	12	Nielson 1980
<i>Plecoglossus altivelis</i>	J	0.0097	6.70E-06	3	Kawanabe 1969
<i>Pleuronectes platessa</i>	E	0.0783	1.24E-03	11	Harding et al. 1978
	E	0.1165	4.70E-03	2	Heessen and Rijnsdorp 1989
	L	0.0525	7.24E-04	4	Bannister et al. 1974
	L	0.0112	6.46E-05	7	Zijlstra et al. 1982
	J	0.0336	7.69E-04	2	Al-Hossaini et al. 1989
Firemore	J	0.0303	1.07E-04	4	Lockwood 1980
Filey Bay	J	0.0245	1.18E-04	4	
	J	0.0030	1.08E-06	5	Zijlstra et al. 1982
<i>Pseudopleuronectes americanus</i>	J	0.0389	1.09E-04	3	Howe et al. 1976
	J	0.0058	3.04E-07	2	Pearcy 1962
	A	0.0019	1.18E-07	5	Poole 1969
<i>Salmo salar</i>	J	0.0019	7.07E-07	7	Chadwick 1982
	J	0.0027	1.38E-07	10	Chadwick 1987
	A	0.0058	2.36E-06	9	
<i>Salvelinus alpinus</i>	A	0.0015	1.53E-06	2	Jonsson et al. 1988
<i>S. frontinalis</i>	J	0.0082	6.47E-06	6	Shetter 1961
	J	0.0110	8.76E-07	9	
	J	0.0106	1.55E-07	3	
<i>S. salvelinus</i>	A	0.0042	4.59E-06	5	Alexander and Shetter 1969
<i>Sardinops caerulea</i>	L	0.0831	3.32E-04	2	Ahlstrom 1954
<i>Scomber scomber</i>	E	0.5260	2.50E-02	4	Ware and Lambert 1985
	L	0.5110	2.12E-02	3	
<i>Sebastes</i> spp.	L	0.0680	1.25E-03	2	Anderson 1984
<i>Trachurus symmetricus</i>	L	0.1387	4.62E-04	3	Farris 1960