SEDAR7-RW 7

ALTERNATE FISHERY INDEPENDENT LARVAL INDICES OF ABUNDANCE FOR RED SNAPPER

David S. Hanisko, Joanne Lyczkowski-Shultz
and Walter Ingram

August, 2004

National Marine Fisheries Service
Southeast Fisheries Science Center
Pascagoula Laboratory
3209 Frederic Street
Pascagoula MS,

This document describes the steps and procedures taken to develop several alternate larval indices for red snapper. The primary goal of the alternate indices were to (1) account for duplicate and/or multiple sampling at each grid station (bnumber); (2) account for inconsistent spatial coverage of the SEAMAP sampling grid from year to year during the summer groundfish and fall plankton surveys; and (3) account for "missing" observations resulting from the variable coverage from year to year; and (4) development of a size-corrected abundance index for red snapper larvae.

Accounting for Multiple Sampling

The SEAMAP sampling design calls for a single bongo and neuston net sample to be taken at each station (bnumber) in a systematic grid. Occasionally during surveys, samples are taken at nonstandard locations or stations are moved to avoid navigational hazards. In addition, more than one sample may have been taken at a bnumber. Duplicate and/or multiple sampling at grid stations may impose bias in the base estimates, since much of the multiple and/or duplicate sampling was taken at the same bnumbers from year to year. The base indices developed for the Snapper SEDAR (April, 2004) included both non-standard stations and duplicate and/or multiple samples per bnumber. The following steps were taken to create a new dataset that approximates the intended sample design:

1. Non-Standard grid stations were deleted from the dataset.

2. The data set was then filtered to allow for only a single bongo and/or nueston sample for each standard grid station (bnumber) for a survey. The following criteria was used to determine which sample was chosen in a multi-sample situation:

   (a) If a bnumber was sampled by both a NMFS and a State vessel, priority was given to the NMFS vessel. This decision was based on the fact that NMFS vessels conduct a majority of the survey in a given year, and therefore are the most consistent in temporal and spatial coverage.

   (b) If multiple samples were then taken at a bnumber station by a NMFS vessels during the same survey, then the sample closest in distance to the central location of the systematic grid station was chosen.

   (c) If multiple samples were then taken at a bnumber by more than one state vessel during the same survey, then the sample closest in distance to the central location of the systematic grid station was chosen.

The final filtering resulted in a single sample per bnumber for each year and survey (summer groundfish or fall plankton and gear (bongo or neuston).

Larval indices were then generated for each combination of gear, survey (summer groundfish, fall plankton, summer groundfish/fall plankton combined) and area (East or West; demarcation line is 89.25 west longitude).

Accounting for Variable Spatial Coverage of the SEAMAP Systematic Sampling Grid

Although the goal of each survey is to completely sample the same grid stations each year, many factors (i.e, weather, vessel breakdowns, plankton sampling dropped due to time constraints (plankton sampling not the primary objective of the survey), the addition or reduction of stations to expand or limit coverage, and samples taken utilizing only one gear or the other). The result is inconsistent coverage of individual bnumbers from year to year, and therefore inconsistent spatial converage.

In order to address the inconsistent coverage of the individual bnumbers, i.e., standardization of the systematic sampling grid, another SAS routine was utilized to determine which of the bnumbers in the grid were sampled at least 75% of the time during the summer groundfish and fall plankton surveys. The input dataset for this routine is the 1 sample per bnumber dataset generated to account for duplicate and/or multiple sampling. The 75% cutoff was determined separately for each survey and gear (bongo or neuston). In addition, only years in which the majority systematic grid was adequately sampled were included in the time series. Table 1 indicates the years includes in the data set for the summer groundfish and fall plankton surveys. Two output datasets were generated. The first included samples making the 75% cutoff. The second, uses the first to generate a unique list of the bnumbers sampled respectively for summer groundfish and fall plankton surveys, and then generates a matrix that includes a data point for each unique bnumber and year. The resulting dataset then has data points for each bnumber and year, with the dataset containing missing values for bnumbers not sampled in that particular year.

Table 1. Years included in the alternative red snapper larval indices utilizing 1 sample per bnumber with 75% consistent coverage.

Summer Groundfish

Bongo Net1

1982-1997 = 16 years
1999-2002 = 4 years
Total 20 years

Neuston Net1
1982 - 1989 = 8 years
1991 - 1997 = 7 years
1999 - 2002 = 4 years
Total 19 years

Fall Plankton

Bongo Net1
1986-1997 = 12 years
1999-2002 = 4 years
Total 16 years

Neuston Net1
1986 - 1997 = 12 years
1999 - 2002 = 4 years
Total 16 years

From this point, catch estimates were made for stations with missing values using a negative binomial regression (GENMOD) procedure in SAS with year and bnumber as variables. Data sets for both bongo and neuston catches were developed in this manner. In order to cope with unrealistic fill-in values provided by the negative binomial regression, the lowest possible CPUE values for both bongo and neuston tows were calculated. This corresponded to the CPUE value of a single specimen being captured in a bongo or neuston at a single station, and was used as a threshold for fill-in values. If a fill-in value was not equal to or greater than the threshold, it was changed to a zero before missing in the missing data.

Larval indices were then generated for each output dataset and each combination of gear, survey (summer groundfish, fall plankton, summer groundfish/fall plankton combined) and area (East or West; demarcation line is 89.25 west longitude).

Size Adjusted Indices

Inter-annual differences in the size (age) composition of sampled red snapper larvae could contribute to a large amount of variation in estimates of mean annual abundance because of the exponential decline in numbers of larvae with size (age). In an attempt to reduce the variation associated with the mean annual abundance or red snapper larvae, size adjusted indices were developed utilizing the 1 sample per bnumber and 1 sample per bnumber 75% consistent coverage datasets. For each dataset, survey estimates of total larval abundance for each size class (catch curves) were developed for red snapper by summing the abundance estimate of each size class under 10 m^2 for bongo samples, or per 10 min tow for neuston samples. The abundance estimates for each size bin used data pooled from both the summer groundfish and fall plankton surveys over their entire time series. Size classes of .5 mm were utilized, with the midpoint of each size representing larvae lengths ±.25 mm. Estimates of larval red snapper mortality were then estimated from catch curve analysis. The instantaneous mortality rate (Z) was estimated by the slope of the exponential function relating larval abundance and size (Ricker, 1975):

$$N_b = N_0 \exp(-Zb)$$

where N_b = total abundance of larvae in length frequency bin b;

N_0 = total abundance of individuals in length frequency bin 0;

Z = instantaneous mortality rate: and

b = number of length frequency bin from bin 0;

Only, larvae fully recruited to each gear were used to develop the catch curves. Fully recruited larvae ranged from 4.0 mm to 8.0 mm for the bongo gears, and from 4.0 mm to 6 mm for the neuston nets. The lower limit (4.0 mm) was determined by the ability to identify red snapper at smaller sizes. At the 4.0 mm (±.25 mm) length range, all captured larvae were able to be positively identified as red snapper or not. However, below this level there is variable success in identification based on the development of individual larvae. The upper limits were determined by examining plots of abundance by size class for consistent captures at those lengths over the time series. The estimated instantaneous mortality rate for each data set and gear combination are shown in Table 2.

Table 2. Size based catch curve estimated instantaneous mortality rates for bongo and neuston nets utilizing the pooled summer groundfish and fall plankton surveys over all years for the 1 sample per bnumber and 1 sample per bnumber 75% cutoff datasets.

---

1 Sample Per Bnumber

Bongo $Z = 0.7548 \pm 0.0901$ ($r^2 = 0.9092$)
Neuston $Z = 1.6897 \pm 0.2348$ ($r^2 = 0.9453$)

1 Sample Per Bnumber 75% Cutoff

Bongo $Z = 0.7045 \pm 0.0947$ ($r^2 = 0.8857$)
Neuston $Z = 1.6662 \pm 0.2721$ ($r^2 = 0.9259$)

The abundance of each sample in the respective datasets was then adjusted to the abundance of a single size class (4.0 mm) to account for variable larvae size composition. Only larvae size classes fully recruited to each gear were used to estimate sample abundance. Larval abundance in each sample was back-calculated by summing their numbers from larger size classes using the estimates of instantaneous mortality rate. The abundance (A) of 4.0 mm size class larvae in each sample was estimated as

$$A_s = \sum_{b=0}^{k} N_{s,b} \exp^{(Zb)}$$

where A_s = then number of 4.0 mm size class larvae under 10 m^2 of sea surface (bongo) or larvae/10 min (neuston) (s = sample) and;

$N_{s,b}$ = the number of larvae under 10 m^2 of sea surface (bongo) or larvae/10 min (neuston) for each fully recruited size class represented in the sample (b = size class, with b = 0 equivalent to the 4.0 mm size class)

Larval indices were then generated for each combination of gear, survey (summer groundfish, fall plankton, summer groundfish/fall plankton combined) and area (East or West; demarcation line is 89.25 west longitude) for the 1 sample per bnumber, 1 sample per bnumber 75% cutoff, and filled 1 sample per bnumber 75% cutoff datasets utilizing the size adjusted abundances.

The final Lo-Method indices were submitted to the assessment group as excel data files, and are based on the size-adjusted, filled missing values, 1 sample per bnumber, 75% cutoff dataset.