A Generalized Model For Estimating Mortality In Field-Released Queen Conch (*Strombus gigas* L.): An Overview

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ABSTRACT

The estimation of mortality in a stock-rehabilitation program is critical to the evaluation of the efficacy of that program. We present here an overview of a generalized model for estimating mortality rates of the benthic marine gastropod *Strombus gigas* based upon movements of individuals within an x:y array. The model assumes linear movements of individuals in random directions. We used this model to estimate mortality in field-released hatchery conch. Individually tagged conch were distributed uniformly within a 20 m x 20 m array. Subsequent surveys determined x:y coordinates of individuals within the grid, and individual movements were derived from these data. The negative binomial distribution best represented movements of the population and was used to estimate the probability of emigration of individuals from the grid. A probability matrix was developed that consisted of values which represented the probability of emigration of individuals located within specific cells in the array. Missing individuals were assigned a value representing the probability of emigration. Natural mortality was calculated by subtracting the estimated emigrants from the total missing conch. To the best of our knowledge, this model presents a new approach for estimating mortality for slow-moving, benthic marine species.

KEY WORDS: Emigration, mortality, queen conch, *Strombus gigas*, surveys, tag-recapture

INTRODUCTION

The estimation of mortality is a critical component in fisheries models and has been used to evaluate the biological benefits of stock-enhancement programs (Stoner and Glazer, in review). However, loss as defined in most models consists of emigration *plus* mortality and separating these two components is difficult and complex. In most cases where conch survival has been evaluated, open models were used (Jolly-Seber model) that incorporate emigration into mortality (Appeldoorn, 1987; Glazer and Berg, 1992). In mobile species, emigration may contribute disproportionately to the overall loss estimates. As a result, isolating emigration from mortality is critical for the accurate estimation of population parameters.

Jackson (1935) originally proposed a model for estimating emigration in butterflies using a 'box-in-box' design. Removal of emigrants from the loss model yielded mortality. Schwarz *et al.* (1993) extended the model to include herrings. Manly (1985) tested Jackson's method and found it to be robust and a good estimator of mortality. We present here a generalized adaptation of this model for estimating mortality rates of the benthic marine gastropod *Strombus gigas*.

MATERIALS AND METHODS

The generalized mortality model is based upon movements of tagged individuals within an x:y array. Overall mortality is derived from these estimates based on a six-step process: 1) determination of movements within the grid per unit time based upon distance traveled by each individual; 2) development of a probability distribution composed of movement frequencies of the population; 3) assignment of probabilities for emigration $p_{e(x,y)}$ from each cell in the grid for a given time interval based upon the expected values of the function derived from the probability distribution; 4) assignment of emigration probabilities ($p_{e(I)}$) to each missing individual found at t_0 but not at t_1 using the emigration probabilities derived in 3; 5) calculate mortality for each individual as $m_i = 1 - p_{e(i)}$; and 6) calculate population mortality as $M = (N - N_t) * \sum m_i / n$ where N = the number of individuals at time t_0, N_t = the number of individuals at time t_1, m_i = the mortality probability of a missing individual, and n = the total number of missing individuals.

We used this method to estimate mortality in a population of hatchery-reared queen conch outplants released in the spring of 1995. Eighty individually tagged conch were distributed uniformly within each of two 20m x 20m plots. Subsequent weekly surveys over a three-month interval determined x:y coordinates of individuals within each plot, and individual movements were derived from these data. These data were used to develop a probability distribution function that described the movements of individuals within the population (negative binomial). The population parameters and expected frequencies that best described the distribution function were then calculated using the methods of Ludwig and Reynolds (1988). Movement probabilities for a given time interval were determined using the expected frequencies from the probability distribution. Emigration probabilities were determined for each cell within the grid (Figure 1). Each missing individual was assigned a value that represented the emigration probability based upon the previous location of that individual in the x:y grid and its distance from the perimeter of the grid.

y \ x	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
19	0.24																			
18	0.17																			
17	0.12																			
16	0.12																			
15	.																			
14	.																			
13	.																			
12	.																			
11	.																			
10	.																			
9	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
8	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
7	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
6	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
5	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
4	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
3	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
2	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00										
1	0.17	0.09	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05										
0	0.24	0.17	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	.	.	.	.	.	0.12	0.12	0.12	0.17	0.24

Figure 1. The probability matrix derived from movement data of individual conch within a 20 x 20 m grid. The values represent the probability of emigration from the corresponding location within the grid over a one week interval. The x and y axes values represent the location within the grid for the cell. The emigration probability matrix is symmetrical for each of four quadrants. For example, the lower left hand value represents the probability of emigration in one week from a missing individual previously located in cell *0,0*. A missing individual previously located in cells *0,19*, *19,19* and *19,0* has an identical emigration probability. An individual located in cell 2,17 had a 0 probability of emigrating from that cell within one week.

RESULTS AND DISCUSSION

A total of 220 individual observations on movements within the grid were used to derive the probability distribution. After approximately 3 months, 9 conch were recaptured which represented a 5.6% recovery. Emigration was estimated to be 10.2%. Natural mortality, calculated by subtracting the estimated emigrants from the total missing conch, was estimated to be 84.2%.

The model is being evaluated using empirical data and simulation modeling to determine its power. To the best of our knowledge this model presents a new approach for estimating mortality for slow-moving, benthic marine species.

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