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A hierarchical Bayesian approach for estimating freshwater mussel growth based on tag-recapture data

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ABSTRACT

In fisheries stock assessment and management, the von Bertalanffy growth model is commonly used to describe individual growth of many species by fitting age-at-length data. However, it is difficult or impossible to determine accurate individual ages in some cases. Mark-recapture survey becomes an alternative choice to collect individual growth information. In mark-recapture studies, some tagged animals can be recaptured more than one time and ignorance of the autocorrelations for each individual may result in substantial biases in estimations of growth parameters. To investigate the existence of individual and sex variability in growth, we designed an experiment to collect mark-recapture data for one endangered freshwater mussel species (*Epioblasma capsaeformis*) and one common, non-imperiled species (*Actinonaias pectorosa*) by using a passive integrated transponder (PIT) technique. Models with individual and sex variability (M1), sex-related differences (M2), individual variability (M3) and nonhierarchy (M4) were developed to estimate growth of *E. capsaeformis* and *A. pectorosa*. Deviance information criterion (DIC) was used to measure the performance of these models. For *E. capsaeformis*, female mussels tended to have higher means of asymptotic length (44.96 mm) and growth rate coefficient (0.283/year) than males (42.18 mm and 0.213/year). The model M3 yielded the lowest DIC value for both species, indicating individual differences should be considered in parameter estimation. Thus, we suggest that a hierarchical approach be used to consider individual variability for modeling growth of mussels with mark-recapture data, especially when there is a high percentage of multiple recaptures.

1. Introduction

Freshwater mussels are major components of freshwater biodiversity in North America. However, they have experienced severe declines during the last several decades (Williams et al., 1993; Neves et al., 1997; Neves, 1999; Lydeard et al., 2004). To successfully implement conservation actions for freshwater mussels, managers must understand and estimate their life history parameters, such as individual growth rates (Dennis et al., 1991). Knowledge of growth is a critical consideration in assessing population dynamics and population sustainability (Alo's et al., 2010). The von Bertalanffy growth model is commonly used in fisheries science and management to describe individual growth of many species and populations (Hilborn and Walters, 1992; Quinn and Deriso, 1999; Haddon, 2010). Generally, non-linear regression is used to estimate key parameters: L_∞ (asymptotic length), K (growth rate coefficient), and t_0 (the age when length was zero) (von Bertalanffy, 1938). In most cases, the parameters in the von Bertalanffy model are considered as parameters of a population, and they are assumed to represent all individuals from the same population. However, this assumption can be unrealistic, as growth rate from that population can be influenced by many factors, such as temperature, food availability, latitude, and population density (Krohn et al., 1997; Swain et al., 2003; Kimura, 2008; Jiao et al., 2010). Individual growth can differ due to different responses to these factors among individuals. It is more biologically realistic to assume each individual has its unique growth pattern even in a population (Sainsbury, 1980; James, 1991; Smith et al., 1997).

In growth estimation, von Bertalanffy models are usually fit to age-at-length data. However, for some species, it is difficult or impossible to determine accurate individual ages. For example, there are two commonly used methods to determine the age of freshwater mussels, growth ring counts on the outside of the shell and thin section counts of the internal shell growth annuli, with detailed descriptions of each method provided by Clark (1980) and Neves and Moyer (1988). However, these methods may lack accuracy or are inappropriate for a large number of mussels due to cost and time (Neves and Moyer, 1988). In these cases, a tag-recapture

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survey may be a better alternative for collecting individual growth information for freshwater mussels. To conduct such a survey, a number of mussels must be collected, tagged and then released to a site. The tagged mussels can be recaptured and measured for lengths after a period of time. The von Bertalanffy model can be reformulated to fit tag-recapture data to include the lengths and times at initial tagging and each recapture (Fabens, 1965; Quinn and Deriso, 1999).

The main problem in implementing a mark-recapture survey is that of monitoring tagged individuals effectively so that continuous data can be used in growth analyses. In this study, we used a passive integrated transponder (PIT) technology to monitor *Epioblasma capsaeformis* and *Actinonaias pectorosa* in the Clinch River in southwestern Virginia. The PIT tag is a small-sized tag, virtually eliminating negative impacts on animals and has little or no influence on growth-rate, behavior, health, or predator susceptibility (Elbin and Burger, 1994). The PIT tag has no battery and therefore its longevity appears indefinite (Gibbons and Andrews, 2004; Kurth et al., 2007). The PIT tag is activated by a fixed or portable reader, which transmits its unique code to the reader to identify the individual animal. While PIT technology was first used to monitoring fish movement, its use has expanded to include mammals, reptiles, amphibians, birds, and invertebrates (Prentice et al., 1990; Gibbons and Andrews, 2004). In recent years, PIT tags have been increasingly applied to freshwater mussels. Compared with traditional mussel mark-recapture methods, which largely depend on glue-on shellfish tags and visual encounters to locate mussels, PIT tags enhance the recapture rate, especially in muddy water conditions (Kurth et al., 2007).

In a conventional approach, individual growth is ignored when fitting the von Bertalanffy growth model, as it does not incorporate individual growth characteristics when modeling growth, which can introduce bias in stock assessment (Watson and Pauly, 2001; Lewin et al., 2006). Furthermore, in mark-recapture studies, some tagged animals can be recaptured more than one time. Individual lengths, which are measured at every recapture, provide growth data over the period. However, the mark-recapture length data contain autocorrelations for each individual and ignoring the autocorrelations may result in substantial biases in estimations of growth parameters (Maller and deBoer, 1988; Wang et al., 1995; Eveson et al., 2007; Zhang et al., 2009).

Two species were selected as example freshwater mussel species for this study. The oyster mussel (*E. capsaeformis*) is one of the few remaining extant species of the genus *Epioblasma*, which represents the most endangered group of freshwater mussels in North America (Jones et al., 2006), and it was selected as a representative endangered mussel species. It was historically distributed throughout the Tennessee and Cumberland River systems in Virginia, North Carolina, Georgia, Tennessee, Kentucky and Northern Alabama (Johnson, 1978). However, it has suffered great declines during the last 100 years and was listed as an endangered species in 1996 (Cummings and Cordeiro, 2012). On the other hand, the pheasantshell (*A. pectorosa*) was selected to represent a non-imperiled species. It is distributed throughout the Tennessee and Cumberland River systems. The species exhibits a different life history than *E. capsaeformis* in that it is typically longer-lived and more abundant (Scott, 1994). Both species have been selected as augmentation species for restoration of freshwater mussels in the Upper Tennessee River Basin by the Virginia Department of Game and Inland Fisheries (VDGIF, 2010). In previous studies, the von Bertalanffy model was used to estimate the “average” growth parameters of *E. capsaeformis* and *A. pectorosa* (Scott, 1994; Jones and Neves, 2011). However, neither study considered variation in growth among individuals.

In recent years, hierarchical Bayesian methods have been widely used in fisheries science because they provide a reliable tool to estimate vital parameters and quantify uncertainty by incorporating stochastic factors in modeling population dynamics (Punt and Hilborn, 1997; Helser and Lai, 2004; Forrest et al., 2010). These statistical methods are ideally suited for analyses of fish growth using the von Bertalanffy growth model (Pilling et al., 2002; Zhang et al., 2009). In acknowledging the existence of individual variance in a population, a hierarchical approach can effectively address the question of describing variation in growth of individuals. Individual growth rate is connected to population growth due to various biological and environmental factors, which can be represented by multilevel priors in a hierarchical model (Zhang et al., 2009). The multilevel priors are assumed to follow underlying distributions in a hierarchical growth model (Gelman et al., 2004; Jiao et al., 2009, 2010). Thus, the hierarchical Bayesian approach enables us to conveniently integrate uncertainty at both the individual and population level.

The aim of this paper is to investigate the existence of individual and sex variability in growth of mussels. Specifically, we first designed a field study to collect mark-recapture data for *E. capsaeformis* and *A. pectorosa* using PIT tag technology and then secondly, we developed Bayesian hierarchical models to incorporate individual growth variability to fit our mark-recapture data. We further extended the study to estimate growth variability between males and females, as *E. capsaeformis* exhibits pronounced sexual dimorphism (male and female shells differ in form). Analyses of individual and sex variability in growth rate estimation will be useful in evaluating population restoration activities and provide insights for conservation and management of mussels.

2. Materials and methods

2.1. Study sites

Cleveland Islands is located near the town of Cleveland in Russell Co., Virginia at Clinch River Mile (CRM) 270.8 (Fig. 1). A Norfolk Southern Railroad runs parallel to the stream along the right ascending bank and the site contains three mature islands that create four braided channels (Eckert et al., 2008). This site has been selected as an augmentation reach to implement components of the Virginia Freshwater Mussel Restoration Plan (Eckert et al., 2008). Cleveland Islands represents a biologically significant section in the upper Clinch River, has stable habitat for mussels to survive and grow, and has been regularly surveyed since 2002 to monitor freshwater mussel abundance and diversity (Eckert et al., 2008). However, growth of mussel species has not been estimated quantitatively and will be useful in evaluating population restoration activities at the site.

2.2. Mark-recapture experiment and data collection

A Bio-mark PIT tag kit, which include the FS2001F-ISO reader, portable BP antenna and bulk PIT tags (TX1411SST), was used for monitoring released *E. capsaeformis* and *A. pectorosa*. We placed external PIT tags on 30 male (length: 22–40 mm) and 30 female (length: 28–44 mm) *E. capsaeformis* and 60 *A. pectorosa* (length: 51–109 mm) collected from Kyles Ford (CRM 189) in the Clinch River in July, 2011. We affixed the PIT tag to the mussel's right shell using super glue and encapsulated it in dental cement to increase tag retention, a technique developed by D. Hua at the Freshwater Mollusk Conservation Center, Blacksburg, VA (Hua, D., personal communication). During the tagging process, mussels were kept in water at all times except when tagging them to minimize handling stress. The shell length of each mussel was measured to the nearest millimeter using a caliper. After tagging, the mussels were placed at Cleveland Islands. A Global Positioning System (GPS) was used to