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Development of a growth model for penaeid shrimp

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Abstract

An individual growth model for penaeid shrimp is presented. The main physiological processes simulated were: ingestion, assimilation, faeces production, respiration and female reproduction. The model was used to quantify the most important physiological processes involved in growth and also to examine the effect of food availability and water temperature on shrimp final weight.

The simulation reproduces the typical pattern of growth of penaeid shrimp, characterised by a rapid weight gain during the early life stages and by the achievement of asymptotic length in adults.

The ingestion and respiration rates increased as the animal grew but the weight-specific rates decreased with an increase of shrimp weight.

A sensitivity analysis showed that the model does not produce differences at a 10% change in juvenile food availability. On the other hand, a change of water temperature of the same magnitude had an effect on shrimp final weight.

The model was developed in the visual simulation software Powersim™.

The individual growth model presented in this paper may be integrated into population dynamics models in order to simulate the biomass and density throughout the stages of the shrimp life cycle; such models may be usefully applied both to penaeid aquaculture and to management of wild fisheries.

Keywords: Penaeid; Individual model; Pond culture; Mangroves; Aquaculture; Visual simulation

1. Introduction

Shrimp growth is a discontinuous process regulated by the moult cycle, which is made up of short moult periods of rapid growth and of longer intermoult periods when no growth occurs. The duration of the moult cycle depends on species and size, and it influences the morphology, physiology and behaviour of these animals (Bureau et al., 2000; Vega-Villasante et al., 2000). Growth depends on sex, stage and environmental factors such as food quantity and quality, water temperature and salinity (Dall et al., 1990).

Due to the economic importance of penaeid shrimp worldwide, particularly in aquaculture, a great effort to understand the growth biology of *Penaeus* spp. has been made in recent years. This includes studies on the influence of environmental factors such as temperature (Wyban et al., 1995; Miao and Tu, 1996; Ye et al., 2003; López-Martínez et al., 2003), salinity (Lemos et al., 2001) and lunar cycles (Griffith and Wigglesworth, 1993) on shrimp growth.

The valuable information presented in those studies may be synthesised and integrated into general models

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in order to simulate the growth of *Penaeus* individuals. These models provide more detailed information concerning physiological processes and their quantification in terms of bioenergetics. The simulation of individual growth can also be used to study the population dynamics through the development of population models that predict population growth and biomass in a given ecosystem. These models are useful for aquaculture planning and management as they provide estimates of growth conditioned by different factors and allow the selection of the conditions that provide a better growth potential.

Despite the great economic importance of these animals and their suitability to aquaculture, only a few models have been developed to simulate individual growth of penaeid shrimp. Growth simulations for penaeid shrimp are based on single-equation models such as the von Bertalanffy (Wang, 1998; Xiao, 1999) and Gompertz growth equations (Jackson and Wang, 1998; Xiao, 1999), bioenergetic models (Mishra et al., 2002) or the Fuzzy Inductive Reasoning (FIR) approach (Carvajal and Nebot, 1998).

The main objectives of the present work are:

(i) To quantify the most important physiological processes involved in growth;
(ii) To analyse the effect of environmental forcing functions on shrimp growth;
(iii) To simulate penaeid shrimp growth by means of an individual growth model;
(iv) To describe how such a model may be integrated into a coupled biogeochemistry–population dynamics model for use in aquaculture management.

2. Materials and methods

2.1. Study site

The model was applied to Maputo Bay (Fig. 1), a large (area: 1200 km^2; volume: 7200×10^6 m^3), shallow (mean depth: 7 m) mesotidal system in southern Mozambique (26° 1′ S, 32° 46′ E), where an important (400 t $year^{-1}$) shallow-water shrimp fishery exists. The

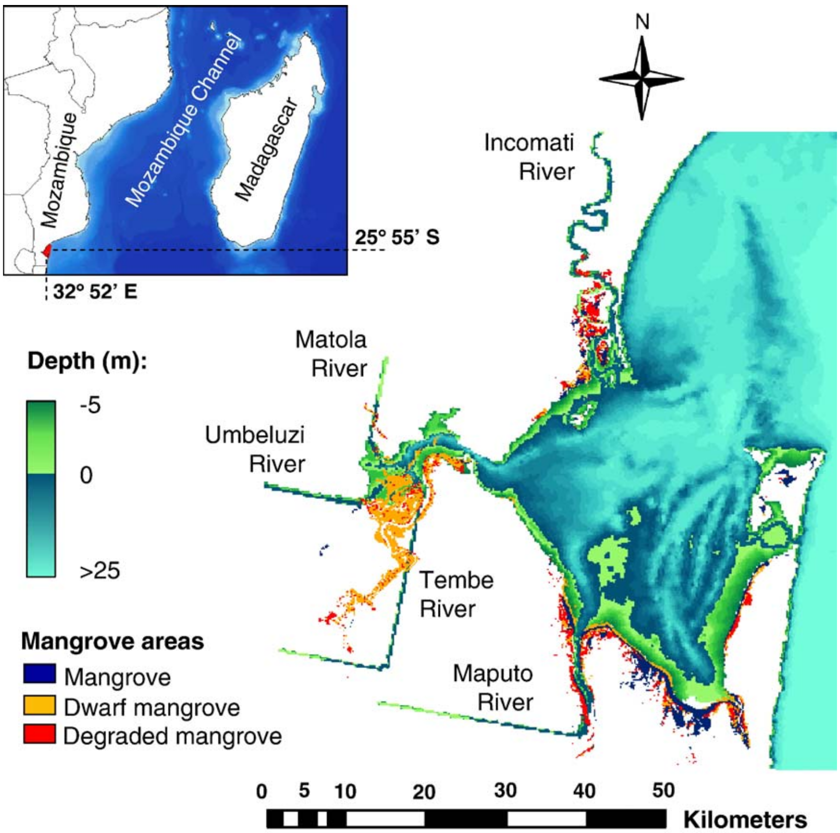

Fig. 1. Location of the study area, showing mangrove areas and bathymetry.