An ecosystem model for optimising production in integrated multitrophic aquaculture systems

Jeffrey S. Ren [a,*], Jeanie Stenton-Dozey [a], David R. Plew [a], Jianguang Fang [b], Mark Gall [a]

[a] National Institute of Water and Atmospheric Research, 10 Kyle Street, P.O. Box 8602, Christchurch 8440, New Zealand
[b] Yellow Sea Fisheries Research Institute, 106 Nanjing Road, Qingdao 266071, People's Republic of China

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ABSTRACT

Integrated multitrophic aquaculture (IMTA) aims to be an ecologically balanced aquaculture practice that co-cultures species from multiple trophic levels to optimise the recycling of farm waste as a food resource. It provides an opportunity for product diversification and an increase in economic return if managed at the optimal stocking densities for each co-cultured species. A generic IMTA ecosystem model, incorporating dynamic energy budgets for a number of co-culture species from different trophic levels was developed to design IMTA farms for optimisation of multispecies productivity. It is based on the trophic similarity in the ecophysiological behaviour of cultured organisms to describe the uptake and use of energy. This approach can accommodate different species within a trophic group and is transferable to IMTA operations based on finfish–shellfish-detritivore-primary producer systems. Model simulations were firstly performed considering the monoculture of mussels and finfish, each "farm" interacting with the natural variability of the local environment. The next step was running the IMTA model with the co-culture groups added in: one run was with finfish as the key species in co-culture with seaweed and sea cucumbers and the other with mussels as the key culture species in association with seaweed and sea cucumbers. Scenario simulations show that conversion from monoculture to IMTA would considerably reduce waste products and increase farm productivity. Although the development of IMTA practices will depend on acceptable levels of waste products, feasibility and profitability of culture operations, the IMTA model provides a research tool for designing IMTA practices and to understand species interactions and predict productivity of IMTA farms. The refinement of the model and its power to predict multispecies productivity depends on emerging data from trial and commercial sea-based IMTA operations.

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1. Introduction

Over the past decade, integrated multitrophic aquaculture (IMTA) has received much attention as a means of practicing sustainable aquaculture by recycling nutrients through co-cultured species from different trophic levels (Chopin et al., 2008). The waste (feed) and by-products (faeces and nutrients) from fed species (e.g. finfish) and filtering feeders (e.g. shellfish) become food for extractive species (e.g. detritivores and seaweed) to reduce farm-derived organic and nutrient loading into the environment. Integrated aquaculture has been practiced for centuries in China, initially through land-based operations which later expanded to include marine systems (NACA, 1989; Yang et al., 2000). Such integrated culture techniques have recently been incorporated into scientific-based experiments which monitor the feeding and growth of a mixture of species from different trophic levels. These studies have shown increases in both farm productivity and the growth rates of co-cultured species, and a reduction in waste products (e.g. Li et al., 1983; Wang, 2001; Chopin et al., 2008; Hughes and Kelly, 2011).

The only commercial scale IMTA operation based on sound scientific research is in the Bay of Fundy in Canada producing salmon and mussels (Chopin et al., 2004; Barrington et al., 2009; Reid et al., 2009). This research commenced in 2001 and at present pilot studies are underway incorporating other species such as sea cucumbers, oysters and sea urchins. Although much of Chilean integrated aquaculture is land-based, the co-culture of blue mussels around open water salmon pens has become common (Soto and Jara, 2007) and trialling of macroalgae culture is also taking place (Buschmann et al., 2008). Being driven by industry rather than scientific research, the placement of the mussel ropes is driven by availability of space as opposed to optimal design (Hughes and Kelly, 2011).

In Scotland there have been a number of experimental/pilot scale trials which have yielded encouraging scientific results, but as yet there is no major commercialisation. Research to date in Scotland has shown that well-designed integrated systems can lead to

* Corresponding author. Tel.: +64 3 3488987; fax: +64 3 3485548.
E-mail addresses: j.ren@niwa.co.nz, jeffrey.ren2012@gmail.com (J.S. Ren).

a reduction in nitrogen emissions from caged fish through harvest of sea urchins and seaweeds but for cultured bivalves, the link to fish culture may only be evident where ambient phytoplankton or seston is limiting (Hughes and Kelly, 2011). This highlights the need to consider the influence natural physical and biological variability of the supporting ecosystem in the design of integrated systems of fish, filter-feeding or grazing invertebrates and seaweed.

Biogeochemical fluxes in surrounding water and sediments play an important role in nutrient cycling and affect internal food supply in farming ecosystems which have been explicitly described in many modelling studies on shellfish aquaculture (e.g. Bacher et al., 1998; Grant et al., 2007; Grangeré et al., 2010). As an IMTA operation is much more complex than monoculture, the biomass and production of each trophic species are difficult to optimise economically through the traditional technique of trial and error and experimentation. This present study offers a model framework that considers the influence of natural biogeochemical fluxes over time on the integrated nutritional pathways between IMTA groups and is designed to predict the optimal stocking biomass at each trophic level to produce an effective economic yield. The model incorporates hydrodynamic processes and metabolic energetics of cultured species with an ecological model to design proximal-balanced ecological IMTA units.

Most ecosystem models strive to relate the distribution and fluctuation in abundance and production of wild living organisms to variations in food conditions, predation and the abiotic environment (Fransz et al., 1991). Similarly the IMTA model aims to map out interactions between co-cultured species and their ecosystem components and predict productive capacity. The impact of cultured species on the environment in coastal systems can also be quantitatively and objectively integrated into the model. A few ecosystem models have been developed to assess environmental impact and carrying capacity of farming systems, but most of the model development has focused on monoculture of bivalves (e.g. Bacher et al., 1998; Dowd, 2005; Grant et al., 2007). Some multi-species modelling work has been attempted to study the carrying capacity of a shellfish polyculture system (Duarte et al., 2003). The functioning of polyculture differs from an IMTA system because species from the same trophic level are included in polyculture (e.g. oysters and scallops used in these studies share the same biological and chemical processes which could potentially impact natural phytoplankton populations). Culturing species at the same trophic level does not mitigate environmental impacts (Chopin et al., 2008). IMTA practices strive to facilitate nutrient recycling and optimise co-culture productivity through bioremediation. To achieve this, biomass stocking densities of the culture species must be optimised by means of ecosystem models.

The main focus of this model is to provide a research tool to fine-tune the design of field trials to optimise yields from each trophic level. Model development followed a number of steps. Firstly, we developed an IMTA model based on dynamic energy budgets (DEB) for each trophic grouping within a finfish–shellfish-detritivore-primary producer profile. Secondly, to test the concept and capability of the model, it was parameterised using potential IMTA species namely, salmon, mussels, sea cucumbers and seaweed. Lastly, IMTA scenario simulations were undertaken to understand the dynamics and potential ecological benefits of IMTA farming.

2. Model description

The IMTA model incorporates an ecosystem model (Ren et al., 2010) with DEB sub-models for each trophic group within the benthic and pelagic components that interact through carbon and nitrogen budgets and nutrient cycling (Fig. 1). The dynamics of
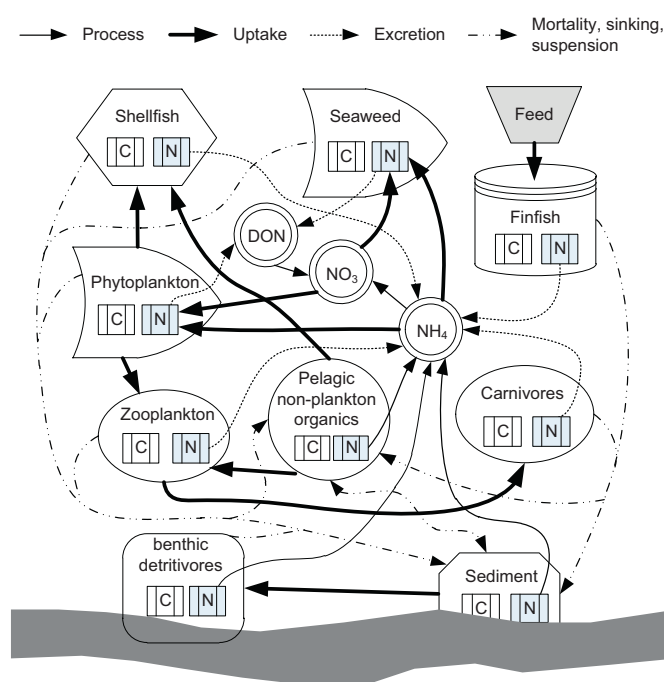

Fig. 1. Conceptual diagram of the IMTA model illustrating the coupling of eco-physiological and biogeochemical processes through carbon (C) and nitrogen (N) pathway between the various compartments. The state variables are defined in Table 1 and rate processes listed in Table 2. The cultured trophic group comprises fed organisms (finfish), suspended filtering feeders (shellfish), nutrient extractive organisms (seaweed) and benthic detritivores (sea cucumber). The pelagic compartment includes phytoplankton, zooplankton, carnivore, dissolved inorganic nitrogen (DIN), dissolved organic nitrogen (DON), pelagic non-plankton organic carbon and pelagic non-plankton organic nitrogen. DIN consists of ammonia nitrogen (NH_4) and nitrate nitrogen (NO_3). The benthic compartment is comprised of carbon sediment and nitrogen sediment.

all biological groups, cultured and non-cultured organisms, are described at the population level. For cultured animals, the population energetics depends on that of individuals. Population dynamics of trophic groups are determined by culture strategies and natural mortality. Individuals are removed when reaching a harvest size. Stochastic events may cause additional mortality but are not included in the model.

Nutrients, pelagic organic matter, phytoplankton, zooplankton and carnivores are exchanged between the farming system and adjacent open waters. This was driven by local hydrodynamic processes where exchange rates were dependent on advection by water currents and turbulent diffusion. These were calculated using a separate hydrodynamic model (see Section 3.4). The IMTA model uses a box model concept with divisions in geographic position. Pelagic variables in the pelagic compartment are assumed to be homogeneous within each box. The biomass exchange of the variables between adjacent boxes is determined by exchange coefficients (day^{-1}), as $dEx_{ij}/dt = k_{ij}(Ex_i - Ex_j)$ with k_{ij} representing the water volume exchanged from boxes Ex_i to Ex_j. The exchange coefficients were based on the results of the 2D hydrodynamic model. A farm ecosystem can be divided into several boxes depending on requirements and local hydrodynamic conditions. The differential equations describing the conservation of state variables are listed in Table 1. The biological intermediate processes are summarised in Table 2 and briefly described below.

2.1. Temperature

The rate processes of biological groups are temperature dependent. A single equation (T_{emp}) is used to describe the temperature