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Pollutant threshold concentration determination in marine ecosystems using an ecological interaction endpoint

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ABSTRACT

The threshold concentrations of pollutants are determined by extrapolating single-species effect data to community-level effects. This assumes the most sensitive endpoint of the life cycle of individuals and the species sensitivity distribution from single-species toxic effect tests, thus, ignoring the ecological interactions. The uncertainties due to this extrapolation can be partially overcome using the equilibrium point of a customized ecosystem. This method incorporates ecological interactions and integrates the effects on growth, survival, and ingestion into a single effect measure, the equilibrium point excursion in the customized ecosystem, in order to describe the toxic effects on plankton. A case study showed that the threshold concentration of copper calculated with the endpoint of the equilibrium point was 10 μg L^{-1}, which is significantly different from the threshold calculated with a single-species endpoint. The endpoint calculated using this method provides a more relevant measure of the ecological impact than any single individual-level endpoint.

1. Introduction

The protection of the structure and function of marine ecosystems are based on the understanding and scientific assessment of the effects of the pollutants on the ecosystems (Chen et al., 2013). However, most of these assessments build upon the extrapolation of single-species effect data to community-level effects (Laender et al., 2008). The use of species sensitivity distribution based on single-species toxic effect tests is the most sophisticated methods (Nelly, 2004). This approach ignores ecological relationships between populations in communities. It has been proved that ecological toxic effects at the community level are determined not only by the inherent sensitivity of the species present, but also by the ecological relationships between the different species (Fleeger et al., 2003). Although large-scale experimental studies, such as mesocosm studies, can account for the ecological relationships during toxic effect assessments, these experiments are too complicated and expensive to be used routinely (Laender et al., 2008).

A practical solution might be the construction of ecosystem models in order to understand the imopacts of the ecological relationships. The reproducibility of ecosystem models with multi-trophic levels, especially those including the higher trophic levels, is quite low owing to their complexity and the difficulty in validating the predicated results experimentally (Carpenter, 1989; Meng et al., 2009; Schindler et al., 1985). However, by considering the widely accepted ‘simplified food web’ and owing to the development in experimental ecology, techniques for simple experimental ecosystems with interspecific competition-grazing relationships have come to maturity (Steele, 1974; Tang, 1999; Xu, 2008). Therefore, ecosystem models with concise ecological relationships, such as ecosystem models including the first and second trophic level only, have relatively few parameters, low difficulty in construction, and can be verified using ecological experiments.

In this paper, we constructed a simplified plankton ecosystem model that has simple interspecific competition-grazing relationships. The toxic effect on each population in this ecosystem was described with multiple endpoints and the optimized concentration–response function for single species. The succession of population biomass dynamics in the constructed model is also discussed. Furthermore, an endpoint representing ecological

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relationships was introduced, and the no-effect concentration for the simplified plankton ecosystem was obtained using this endpoint.

2. Materials and methods

2.1. Simplified plankton ecosystem model

The simplified plankton ecological model consists of two phytoplankton populations and one zooplankton population. The zooplankton grazes on the phytoplankton and phytoplankton fed off an external nutrient source. The model was established based on the logistic growth model and the Lotka-Volterra competition-prey model (Volterra, 1926; Wang et al., 2011), and was constructed using a set of differential equations. Each differential equation describes the growth of a population in terms of its total biomass. The phytoplankton differential equation includes phytoplankton growth, interspecific competition, and grazing by zooplankton. The zooplankton differential equation describes grazing on phytoplankton and mortality. Density restriction in phytoplankton has been taken into account in this model but not in zooplankton. The equations of this model are

$$\frac{dx}{dt} = x(r_1 - a_{11}x - a_{12}y - a_{13}z) \tag{1}$$

$$\frac{dy}{dt} = y(r_2 - a_{21}x - a_{22}y - a_{23}z) \tag{2}$$

$$\frac{dz}{dt} = z(-r_3 + a_{31}x + a_{32}y) \tag{3}$$

where x is the *Prorocentrum donghaiense* biomass (μg mL^{-1}), y is the *Skeletonema costatum* biomass (μg mL^{-1}), and z is the rotifer *Brachionus plicatilis* biomass [individual (ind) mL^{-1}] in this study. r_i ($i = 1, 2$) is the intrinsic growth rate (d^{-1}) under the experimental conditions, 1 representing the *P. donghaiense* and 2 the *S. costatum*. r_3 is the mortality rate of the rotifer *B. plicatilis* (d^{-1}). a_{11} and a_{22} is are coefficients of self-density restriction on *P. donghaiense* and *S. costatum*, respectively. a_{12} is the coefficient of interspecific density restriction of *S. costatum* on *P. donghaiense*, while a_{21} is the coefficient of interspecific density restriction of *P. donghaiense* on *S. costatum*. a_{i3} ($i = 1, 2$) is the amount of algae i ingested by individual zooplankton in unit time. a_{31} ($i = 1, 2$) is the amount of zooplankton into which the algae i is converted in unit density and unit time by the feeding relationship. The equations of a_{ij} are as follows: $a_{11} = r_1/K_1$, $a_{12} = \alpha \cdot r_1/K_1$, $a_{13} = W_1 \cdot F_1$, $a_{21} = \beta \cdot r_2/K_2$, $a_{22} = r_2/K_2$, $a_{23} = W_2 \cdot F_2$, $a_{31} = W_1 \cdot F_1 \cdot h_1/W_3$, $a_{32} = W_2 \cdot F_{21} \cdot h_2/W_3$. K_i ($i = 1, 2$) is the carrying capacity of algae (μg mL^{-1}). α is the interspecific competition parameter of *S. costatum* with *P. donghaiense*, while β is the interspecific competition parameter of *P. donghaiense* with *S. costatum*. F_i ($i = 1, 2$) is the algae filtering rate of zooplankton to algae i (mL ind^{-1} d^{-1}). The filtering rate is proportional to phytoplankton density when phytoplankton density is relatively low, i.e. $F_1 = Fa_1 \cdot x$ and $F_2 = Fa_2 \cdot y$, where Fa_1 and Fa_2 are the filtering rate coefficients (mL^2 cell^{-1} ind^{-1} d^{-1}) (Wei, 2009). h_1 is the transfer efficiency from *P. donghaiense* biomass to *B. plicatilis* biomass (%), while h_2 is the transfer efficiency from *S. costatum* biomass to *B. plicatilis* biomass (%). W_1, W_2, and W_3 are the dry weights of *P. donghaiense* (pg cell^{-1}), *S. costatum* (pg cell^{-1}), and *B. plicatilis* (μg ind^{-1}), respectively.

According to the non-linear dynamics of ecosystems, the simplified plankton ecological model was of ecological significance when x > 0, y > 0, and z > 0, and possessed the only positive asymptotic equilibrium point E^* (x^*, y^*, and z^*) when the model coefficient matrix $\det A\,(a_{ij}) > 0$ (Chen et al., 2009; Wang et al., 1994). In this case, the plankton ecosystem survived continuously and the equilibrium point could be calculated as follows:

$$x^* = \frac{a_{12}a_{23}r_3 + a_{13}r_2a_{32} - r_1a_{23}a_{32} - a_{13}a_{22}r_3}{a_{12}a_{23}a_{31} + a_{13}a_{21}a_{32} - a_{11}a_{23}a_{32} - a_{13}a_{22}a_{31}} \tag{4}$$

$$y^* = \frac{r_1a_{23}a_{31} + a_{13}a_{21}r_3 - a_{11}a_{23}r_3 - a_{13}r_2a_{31}}{a_{12}a_{23}a_{31} + a_{13}a_{21}a_{32} - a_{11}a_{23}a_{32} - a_{13}a_{22}a_{31}} \tag{5}$$

$$z^* = \frac{a_{11}a_{22}r_3 + a_{12}r_2a_{31} + r_1a_{21}a_{32} - a_{11}r_2a_{32} - a_{12}a_{21}r_3 - r_1a_{22}a_{31}}{a_{12}a_{23}a_{31} + a_{13}a_{21}a_{32} - a_{11}a_{23}a_{32} - a_{13}a_{22}a_{31}} \tag{6}$$

2.2. Toxic effect sub-models

The toxicant would have an effect on the plankton ecosystem; some parameters such as r_i, K_i, α, β, and Fa_i would vary, and thus, could be used as toxic effect endpoints. These parameters also caused changes in a_{ij} ($i = 1, 2$, and 3; $j = 1, 2$, and 3). The modified Weibull model was used to describe the response of the parameters serving as endpoints to toxicant concentration (Wang et al., 2011):

$$\frac{u}{u_0} = e^{(-m(c^n - c_0^n))} \quad (\text{if } c \geq c_0)$$

$$\frac{u}{u_0} = 1 \quad (\text{if } c < c_0) \tag{7}$$

where u_0 and u are the values of the parameter used as endpoint in the control and at a toxicant concentration, respectively. m and n are the parameters of Weibull model. c is a toxicant concentration (μg L^{-1}). c_0 is the no-effect concentration, the highest concentration that does not result in toxic effects when a parameter acts as an endpoint, at which u does not show a significant difference from u_0 (Wang et al., 2011).

The change in r_i and a_{ij} would result in the equilibrium point E^* (x^*, y^*, and z^*) of the plankton ecosystem excursing or diverging from the original equilibrium point. Here, the maximum pollutant concentration that does not cause the equilibrium point to diverge from the equilibrium point without pollutant exposure (that is, causes no significant difference) is defined as the equilibrium point threshold concentration (EPTC) of the pollutant.

2.3. Experiments for model parameter determination and model verification

P. donghaiense and *S. costatum* are found widely and occur usually as dominant species in coastal waters in the Chinese Sea (Sun, 2005). They have been cultured successfully and their