The possible effects of climate change on the phytoplankton communities in the Danube river, Hungary

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1 Introduction

Effects of climate change on near-natural ecosystems can be analysed by weather dependent simulation modelling of seasonal community dynamics. Complex models comprising physical, chemical and biological parameters (e.g. nutrients, trophic links) of freshwater systems have been successfully used (Elliott et al. 2005; Mooij et al. 2007; Komatsu et al. 2007). However, in the methodology of modelling approach, which brings relevant findings to the field of climate change research, still there are several unresolved issues. (Sipkay et al. 2009). The basic problem is the lack of combined models and their complicated feasibility. Such models require a large amount of data about environmental parameters. However, there is not enough and adequate information about these parameters. Therefore tactical models are constructed which aims at highlighting the most influential environmental factors (such as temperature), but at the same time a lot of important information is disregarded. Nevertheless, the tactical models could be beneficial if the general functioning of ecosystems is in focus (Hufnagel & Gaál 2005; Vadadi-Fülöp et al. 2008; Sipkay et al. 2008a, 2008b; 2009).

We aimed to develop a discrete-deterministic model answering questions of seasonal dynamics of riverine phytoplankton by using daily temperature data as input parameters. In this way we can get a model of wide applicability concerning global warming related issues. To answer the question how phytoplankton abundance may be affected by global warming by 2100, the data series of climate change scenarios were used as additional input parameters. Predictions of our model, however, are valid only for the Danube River stretch at Göd and for the assumed constancy of disregarded factors. Furthermore the model should be treated with precaution because the scenarios are also products of models (check General Circulation Models and Regional Climate Models, IPCC 2007). In addition, the effect of linear temperature rise was tested.

2 Modelling approach

Long-term series of phytoplankton data are available in the Danube River at Göd (1669 rkm) owing to the continuous record by the Hungarian Danube Research Station of HAS of weekly quantitative samples between 1979 and 2002 (Kiss 1994). Phytoplankton was sampled from the surface water layer of the streamline and expressed as biomass (mg l^{-1}).

The high sampling frequency makes our data suitable for weather driven simulation models. We assume that temperature is of major importance for the seasonal dynamics of phytoplankton. Further, the phytoplankton reaction curve as a function of temperature is taken as the sum of temperature-growth optimum curves. The availability of light is respected, too, as it has also a major influence on the seasonal variation of phytoplankton abundance. Further abiotic and biotic effects are not respected as model parameters but may be implicitly considered by the modelled processes.

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First, a „strategic model”, which is considered as theoretical simulation model, the so-called TEGM (Theoretical Ecosystem Growth Model, Drégelyi & Hufnagel 2009a, 2009b) was used, which involves the temperature optimum-curves of 33 theoretical phytoplankton populations covering the possible spectrum of temperature. This model was adapted to field data from the Danube River (tactical model), considering that excess nutrients varied greatly during the study period (Horváth & Tevanné Bartalis 1999). The “tactical model” is a simulation model fitted to the observed temperature data set. Assuming that excess nutrients represent a specific environment for phytoplankton, two sub-models were developed, one for the period of 1979-1990 with large nutrient excess (sub-model „A”) and one for the period of 1991-2002 with small nutrient excess (sub-model „B”). The two periods reflect the observed reduced nutrient load of the Danube (Behrendt et al. 2005). Both sub-models can be described as the linear combination of 20 theoretical phytoplankton populations. The two versions of the model differ only in the shape of the temperature reaction curves defined by the mean and variance. The tactical model portraying 24 years is derived from the sum of sub-model „A” and sub-model „B”. Biomass (mg l^{-1}) of a certain theoretical phytoplankton population is the function of its biomass measured a day before and the temperature or light coefficient:

$$N_{i,t} = \min(R_T; R_L)^v \cdot N_{i,t-1} + 0.005$$

where

$N_{i,t}$ = biomass of theoretical phytoplankton population „i” at time „t”,

R_T = temperature dependent growth rate, described by the density function of normal distribution,

R_L = light dependent growth rate, including a sine curve representing the scale of light availability within a year,

v = species-specific factor of growth rate,

$N_{i,t+1}$ = biomass of the theoretical phytoplankton population „i” one day after time „t”,

0.005 = a constant for the mass of spores (which was built into the model so as to avoid extinction of the population).

To define whether temperature or light is the driving force, a minimum function was applied. The model was fitted to the daily temperatures of 1979-2002 provided by the Hungarian Meteorological Office by the help of the Solver Optimizer Program of MS Excel. Then, the model was run with the temperatures of climate change scenarios as input parameters. The data base of the PRUDENCE EU project was used (Christensen 2005); these were daily temperatures proposed by the A2 and B2 scenarios of IPCC (2007) which were specified for the period of 2070-2100. Three data series were used including the A2 and B2 scenarios of the HadCM3 model developed by the Hadley Centre (HC) and the A2 scenario of the Max Planck Institute (MPI). The simulated temperatures for the period of 1960-1990 (supplied by the above-mentioned institutes) were taken as control. Each scenario incorporates 31 replicates, i.e. 31 years representing the temperatures of the period around 2070-2100 each containing 365 days. From these 31 replicates we took 24 in order to compare them statistically with those of the 24-year long (1979-2002) observed data. In addition, the effect of linear temperature rise was tested step-wise by increasing the initial temperature by 0.5, 1, 1.5 and 2°C as input variable to the model.

The model outputs were verified by statistical methods using the Past software (Hammer et al. 2001). Yearly total phytoplankton biomass was defined as indicator and calculated as the sum of the monthly average biomass to avoid extreme values. One-way ANOVA was applied to compare means of the model outputs. A post-hoc Tukey test (Tukey’s pairwise comparisons) was applied to test for significant difference between model outputs. Homogeneity of variance was tested with Levene’s test, standard deviations were compared with Welch test (Hammer et al. 2001).

3 Results

The simulated phytoplankton biomass fitted quite well to the monthly average biomass observed ($r = 0.74$, $r^2 = 0.55$) (Figure 1).

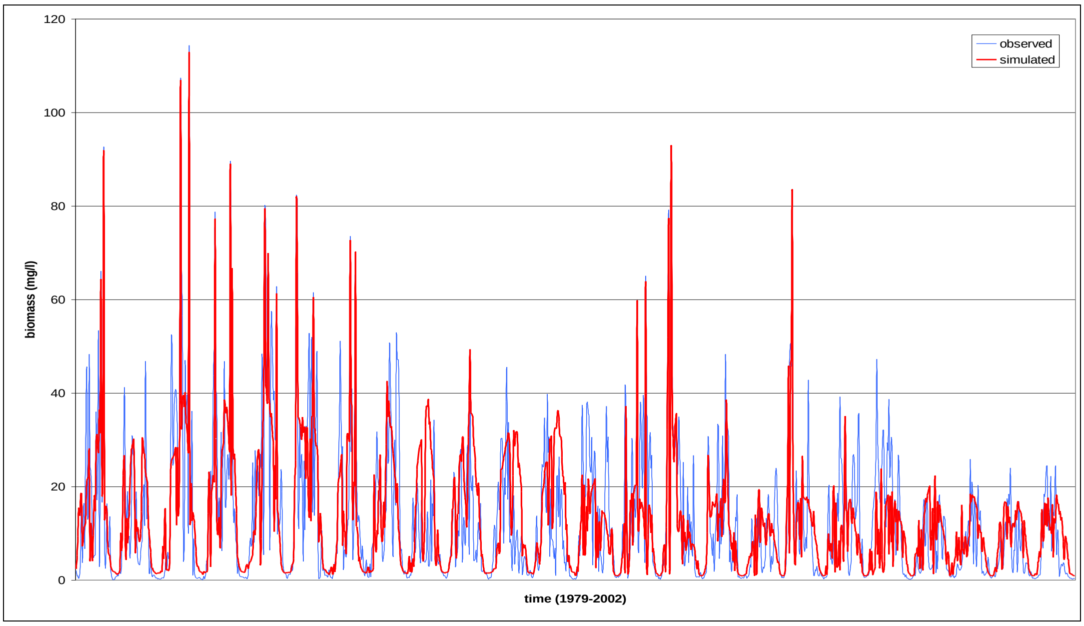

Figure 1. *The Danube Phytoplankton Model fitted to the data series of 1979-1990, including sub-model "A" for the period of 1979-1990 and sub-model "B" for the period of 1991-2002.*

Phytoplankton biomass varied significantly between outputs for scenarios and observed data (one-way ANOVA, $p<0.001$, Figure 2A). Variances were not homogeneous (Levene's test, $p<0.001$) and resulted from the significant differences of standard deviations (Welch test, $p<0.001$). Tukey's pairwise comparisons implied significant differences among the outcomes of A2 scenario (of MPI) and of sub-model „A" ($p<0.05$).

Examining the effect of linear temperature rise revealed also significant differences between outputs (one-way ANOVA, $p<0.001$), and variances were not homogeneous (Levene's test, $p<0.001$); again, this was due to the significant differences of standard deviations (Welch test, $p<0.001$). Tukey's pairwise comparisons indicated that there were significant differences between the outputs for the period of 1979-2002 and outputs at 2°C temperature rise in case of sub-model „A" (Figure 2B). Furthermore, 0.5, 1 and 1.5°C rises in temperatures of sub-model „A" implied significant differences to the outputs of sub-model „B" ($p<0.05$). Despite of these findings the outputs within sub-model „B" showed large-scale similarity ($p=1$). This indicates that at high nutrient load (sub-model „A") phytoplankton communities show a more different response to global warming when compared to low nutrient load (sub-model „B").

It is evident from Figure 2A that biomass increased largely at scenario A2 (MPI); however, biomass output for the period of 1960-1990 increased notably as well (sub-model „A"). Nevertheless, standard deviation was too high in both sub-models. Linear temperature rise caused a drastic biomass increase in sub-model "A", while sub-model "B" yielded not significant changes (Figure 2B).

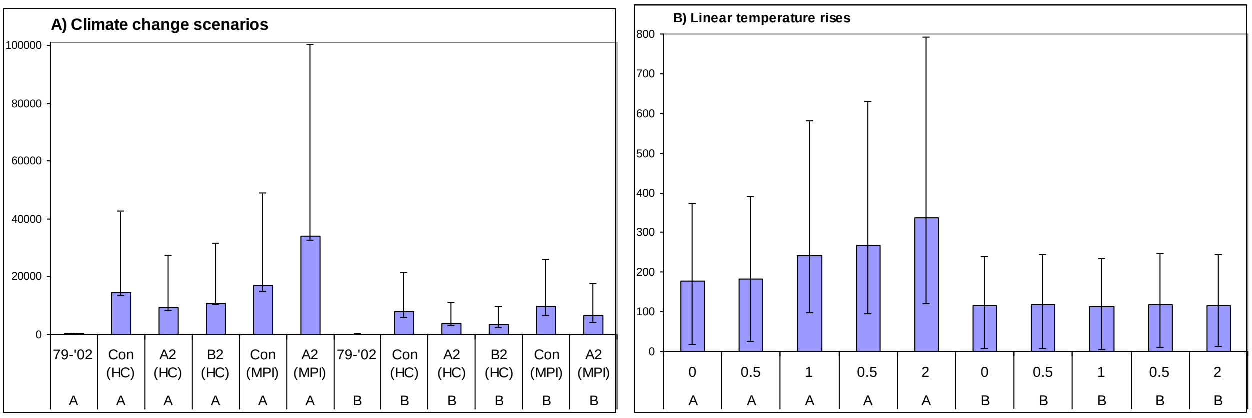

Figure 2. *Monthly means of yearly total algal biomass (mg l^{-1}) for the model outputs for the period of 1979-2002 („79-02"; based on measured data of temperatures) compared with outputs of the model run with the data series of climate change scenarios (A, left) and of linear temperature rises (B, right). Sub-model „A" and „B" are presented separately. HC=Hadley Centre; MPI=Max Planck Institute; A2 and B2 scenarios; Con = control; 0; 0.5; 1; 1.5; 2: degree of linear temperature rise (^{o}C). Columns: mean; vertical lines: SD*

4 Outlook and conclusions

By adapting the TEGM model we managed to develop a model that fits to the measured data quite well. Beyond the indicator of yearly total biomass introduced in this study, further indicators need to be defined in the near future and used in order to get a better understanding of the possible effects of climate change to the phytoplankton of the Danube River.

Interpretation of model outputs for climate change scenarios is rather difficult. The model outputs for the control period of 1960-1990 and the period of 1979-2002 when observed temperature data were used as input parameters showed remarkable differences. Major variation within data series of certain climate change scenarios may account for the high standard deviations observed in the model outputs. This result draws attention to the constraints of applicability of scenarios.

In case of linear temperature rise a clear answer is received: high temperatures result in greater abundance of phytoplankton but only at high nutrient concentration (as it was experienced between 1979 and 1990). Moderate nutrient supply does not favour algae even if temperatures increase by 2°C. Thus, biomass is not expected to increase notably when nutrient loading of rivers has been reduced. Our model suggests that global warming brings drastic changes to nutrient rich environments but would not greatly effect the phytoplankton of nutrient poor water bodies.

Global warming can influence the trophic state and primary productivity of inland waters in a basic way (Lofgren 2002). Bacterial metabolism, rate of nutrient cycling and algal production all increase with rising temperatures (Klapper 1991). Generally, a combination of climate change and anthropogenic pollution enhances eutrophication (Klapper 1991, Adrian et al. 1995). Respective models predicted increased phytoplankton abundance in systems with higher trophic state (Elliot et al. 2005, Mooij et al. 2007, Komatsu et al. 2007). This is in line with our results of linear temperature rise, but valid only in waters with high nutrient concentration.

Looking at the variation of phytoplankton biomass only is not relevant enough if one aimed to explore the effects of climate change. Freshwater food webs show rather characteristic seasonal dynamics, thus, the effect of climate is the function of season (Straile 2005). Further indicators should be included into the model to elucidate seasonal changes of phytoplankton. Such indicators may be the seasonal population peak (e.g. blooms) or the threshold value of 50% of the annual total biomass. Thus, model development and improvement remains a never ending task.

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