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Modeling species richness and abundance of phytoplankton and zooplankton in radioactively contaminated water bodies



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ARTICLE INFO	A B S T R A C T
Keywords: Radioactive contamination Species richness Abundance Modeling Mayak Plankton	Water bodies polluted by the Mayak nuclear plant in Russia provide valuable information on multi-generation effects of radioactive contamination on freshwater organisms. For example, lake Karachay was probably the most radioactive lake in the world: its water contained $\sim 2 \times 10^7$ Bq/L of radionuclides and estimated dose rates to plankton exceeded 5 Gy/h. We performed quantitative modeling of radiation effects on phytoplankton and zooplankton species richness and abundance in Mayak-contaminated water bodies. Due to collinearity between radioactive contamination, water body size and salinity, we combined these variables into one (called HabitatFactors). We employed a customized machine learning approach, where synthetic noise variables acted as benchmarks of predictor performance. HabitatFactors was the only predictor that outperformed noise vari- ables and, therefore, we used it for parametric modeling of plankton responses. Best-fit model predictions suggested 50% species richness reduction at HabitatFactors values corresponding to dose rates of 10^4 - $10^5 \mu$ Gy/h for phytoplankton, and 10^3 - $10^4 \mu$ Gy/h for zooplankton. Under conditions similar to those in lake Karachay, best- fit models predicted 81-98% species richness reductions for various taxa (<i>Cyanobacteria</i> , <i>Bacillariophyta</i> , <i>Chlorophyta</i> , <i>Rotifera</i> , <i>Cladocera</i> and <i>Copepoda</i>), ~ 20-300-fold abundance reduction for total zooplankton, but no abundance reduction for phytoplankton. <i>Rotifera</i> was the only taxon whose fractional abundance increased with contamination level, reaching 100% in lake Karachay, but <i>Rotifera</i> species richness declined with contamination level, as in other taxa. Under severe radioactive and chemical contamination, one species of <i>Cyanobacteria</i> (<i>Geitlerinema amphibium</i>) dominated phytoplankton, and rotifers from the genus Brachionus dominated zoo- plankton. The modeling approaches proposed here are applicable to other radioecological data sets. The results provide quantitative information and easily interpretable mod
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1. Introduction

Chronic exposures to ionizing radiation over multiple cell cycle times or even many organismal generations are highly relevant for human health and ecosystem functioning in a variety of settings. These include long-term consequences of accidents at nuclear power plants (e.g. Chernobyl, Ukraine; Fukushima, Japan) and radioactive waste sites (e.g. Hanford facility, USA), occupational/medical exposures (nuclear industry workers, astronauts, radiotherapy patients), and potential terrorist attacks involving radioactive materials (Beresford et al., 2016a, 2016b; Fredrickson et al., 2004; Xu et al., 2016). However, technical and resource constraints and stringent security measures often limit experimental investigation of protracted irradiation. Therefore, chronic irradiation effects are not as well quantified or understood as those of acute irradiation, which can be defined as exposures lasting for only a brief period (e.g. seconds to minutes). Another important issue that complicates the tasks of predicting and understanding chronic radiation effects arises because radiosensitivity often increases when organisms are irradiated under natural conditions, compared with irradiation under controlled conditions (e.g. in the laboratory) (Garnier-Laplace et al., 2013). This may occur because experimental irradiations are often carried out at nearly-optimal conditions (e.g. favorable temperature and food availability, no interspecific competition) for the studied organisms. In contrast, radioactive environmental contamination acts in conjunction with other stressors (e.g. chemical toxins, seasonal temperature changes) and with interactions between species (Einor et al., 2016; Fredrickson et al., 2004; Møller and Mousseau, 2015; Shuryak, 2017; Shuryak and Dadachova, 2016; Vanhoudt et al., 2012). Consequently, it is important to gather and analyze available information on the effects of chronic exposures under natural conditions.

The water bodies polluted by the Mayak plutonium production

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plant in Russia represent a rich data source for the effects of chronic exposures to several radiation types (gamma, beta and alpha) from a variety of radionuclides on natural freshwater biota. The plant discharged radioactive waste into nearby water bodies for decades, resulting in contamination levels ranging from mild to extremely high. In particular, one of the Mayak waste storage reservoirs (R9), called lake Karachay, was probably the most radioactive lake in the world: its water contained $\sim 7 \times 10^6$ Bq/L of ¹³⁷Cs, $\sim 10^7$ Bq/L of ⁹⁰Sr, $\sim 8 \times 10^4$ Bq/L of alpha-emitting radionuclides, and $\sim 4400 \text{ mg/l}$ of nitrates (Pryakhin et al., 2016). This reservoir was created in 1951 and functioned until 2015, when it was filled with concrete blocks and sand (Atamanyuk, 2016; Pryakhin et al., 2016). Another highly contaminated reservoir R17, called Starove Boloto, was created in 1949 and still operates. Its water contains $\sim 4 \times 10^4$ Bq/L of ¹³⁷Cs, $\sim\! 2\times 10^5$ Bq/L of $^{90}\text{Sr},~\sim\! 2\times 10^2$ Bq/L of alpha-emitting radionuclides, and ~2500 mg/l of nitrates (Pryakhin et al., 2016). Four additional reservoirs, called R3, R4, R10 and R11, have mild to moderate contamination levels, and two nearby reference water bodies -Shershnyovskoye, SR, and Beloyarskoye, BR - have essentially background radioactivity levels and water chemistry (Pryakhin et al., 2016).

Although these water bodies were investigated in numerous ecological studies, e.g. (Atamanyuk, 2016; Atamanyuk et al., 2012; Pryakhin et al., 2016), to our knowledge no quantitative modeling of contamination effects on plankton species richness and abundance was previously conducted. Here we performed such modeling for phytoplankton and zooplankton, and separately for specific taxa: *Cyanobacteria, Bacillariophyta* and *Chlorophyta* among phytoplankton and *Rotifera, Cladocera* and *Copepoda* among zooplankton. We used customized machine learning and parametric techniques that are generalizable to other radioecological data sets.

The main goals of our analyses were to: (1) Identify which water body properties were the strongest predictors of plankton responses. (2) Quantify the shapes and magnitudes of these responses. (3) Derive easily interpretable parameter estimates such as the contamination level needed to reduce species richness or abundance by 50%, and fraction of species richness or abundance predicted to remain under very high contamination. (4) Compare the responses and parameter estimates for different taxa to identify the most sensitive and most resistant ones.

2. Materials and methods

2.1. Dose rate estimation

Average radioactivity levels (in Bq/L) for ¹³⁷Cs, ⁹⁰Sr, all betaemitting radionuclides and all alpha-emitting radionuclides in the water and bottom sediments of each analyzed water body were taken from Pryakhin et al. (2016). The ERICA Assessment tool, version 1.2.1 (www.erica-tool.com), was used to estimate radioactivity levels and radiation dose rates for phytoplankton and zooplankton based on these radionuclide contamination levels. Because concentrations of specific alpha-emitting radionuclides were not reported in Pryakhin et al. (2016), we assumed that total alpha-emitter activity was equally divided between ²³⁸Pu, ²³⁹Pu, ²⁴⁰Pu, ²³⁴U, ²³⁸U, and ²⁴¹Am, as reported in Atamanyuk et al. (2012). Unspecified beta-emissions were assumed to come from ³H, also as reported in Atamanyuk et al. (2012). Missing values of specific radionuclide activities in water or sediments were calculated by default ERICA models. The resulting dose rates are probably accurate to the order of magnitude and illustrate the very wide range of contamination levels from near-background in the reference SR and BR reservoirs to very high values in the most polluted reservoir R9.

2.2. Correlation analysis

The analyzed Mayak-contaminated water bodies were arranged in

ascending order according to the level of radioactive contamination (and dose rates to plankton) as follows: SR, BR, R11, R10, R4, R3, R17 and R9 (Pryakhin et al., 2016). We were interested in quantifying how the species richness and fractional abundance (FA) of each taxon changed as function of this water body contamination ranking because sensitive taxa can decline in FA with contamination level, whereas resistant taxa can show the opposite trend. FA was calculated for each taxon among its plankton type, e.g. Cyanobacteria among phytoplankton or Copepoda among zooplankton. Pryakhin et al. reported the total number of species (abbreviated here as TS for convenience) belonging to each plankton group detected in a given water body in Pryakhin et al. (2016). Because plankton sampling in Mayak-contaminated water bodies was performed repeatedly over multiple years and the numbers of planktonic organisms per water sample are generally very high (Atamanyuk et al., 2012; Pryakhin et al., 2016), these TS measurements are likely to be reasonable representations of species richness. Sampling stations were set up in each reservoir in various parts of the water area and sampling of plankton was carried out at each of the stations during hydrobiological summer from one to three times a year (Pryakhin et al., 2016). Plankton samples (1 L each) were collected from the following water levels: the surface, 0.5 \times S, S, 2 \times S, $(2 \times S + d)/2$ and the bottom; where S is transparency of the water according to Secchi disk, and d is depth of the reservoir at the sampling site (Pryakhin et al., 2016).

For our analysis, we assumed that TS is a Poisson-distributed random variable where the mean is equal to the observed species count in each water body. The Poisson distribution is more appropriate than the Gaussian distribution for integer data, and has been used previously for species richness modeling (Guisan et al., 2002; Mao and Colwell, 2005). When there were 0 observed species, we set the mean to 10^{-6} . We generated 10,000 Monte Carlo simulated data sets based on these assumptions, using Maple 2016^{*} software. In each data set we calculated Spearman's rank correlation coefficient between TS and water body contamination ranking. The 2.5th and 97.5th percentiles of the distribution of correlation coefficients across Monte Carlo simulations were used to approximate 95% confidence intervals (CIs) for the correlation coefficient. These calculations were performed separately for each taxon.

A similar Monte Carlo simulation approach was applied to FA of each taxon. FA was assumed to be a beta-distributed random variable, where the probability distribution BetaPDF had parameters ν and ω and Γ is the gamma function:

$$BetaPDF = FA^{\nu-1}(1 - FA)^{\omega-1}/[\Gamma(\nu) \times \Gamma(\omega)/\Gamma(\nu + \omega)]$$
(1)

We used the method of moments to estimate parameters ν and ω from observed mean fractional abundance FAav and its variance FAvar in each water body, reported in Pryakhin et al. (2016). This was done as follows:

$$\nu = FAav \times \left(FAav \times \frac{1 - FAav}{FAvar} - 1\right), \ \omega = (1 - FAav) \times FAav \times \left(FAav \times \frac{1 - FAav}{FAvar} - 1\right)$$
(2)

The means and variances of beta distributions generated by substituting ν and ω estimates from Eq. (2) into Eq. (1) numerically were quite close to FAav and FAvar values. Consequently, we used this simple analytic approximation to generate 10,000 Monte Carlo simulated data sets and calculate Spearman's rank correlation coefficients between the FA of each taxon and water body contamination ranking.

2.3. Data sets for quantitative modeling of plankton species richness and abundance

Water body size and chemical composition can have important influences on plankton species richness and abundance (Catherine et al., 2016; De los Ríos-Escalante et al., 2011). We extracted the depth and Download English Version:

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