Geophysical Research Abstracts Vol. 20, EGU2018-876-1, 2018 EGU General Assembly 2018 © Author(s) 2018. CC Attribution 4.0 license.



Pico-bioalgorithms – Baltic picoplankton growth model representation

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Significant picocyanobacteria (PCY) contribution to primary production (PP) and their dominance during summer cyanobacteria blooms has been reported in Baltic Sea field studies. According to Stal et al., 2003, PCY contributed more than 50 % to Baltic PP. Mazur-Marzec et al., 2013 reported that single-celled picocyanobacterium comprised from 20 % (in the beginning of July) to 97 % (in late July, August) of cyanobacterial biomass. Moreover, the latest research showed that PCY corresponded to 40-90 % of the total phytoplankton biomass in the Baltic Sea during summer (Paczkowska et al., 2017). The most common PCY genus in Baltic is Synechococcus sp. Despite their great importance in Baltic trophy, these organisms have not been included in phytoplankton functional groups in biogeochemical models for the Baltic Sea, so far. The Authors developed numerical representation of Synechococcus sp. growth. On the basis of previously conducted laboratory experiments, three algorithms (pico-bioalgorithms) were formulated, one for each examined Synechococcus sp. strain (ranked by pigmentation - red: BA-120, green: BA-124 and brown: BA-132). Pico-bioalgorithms account for the response of PCY growth (biological aspect) to different conditions of temperature (T), photosynthetically active radiation (PAR) and salinity (physical aspects). Major physical-biological interactions included in pico-bioalgorithms were as follows: 1) for BA-124, different influence of T on growth rate under different PAR levels; 2) positive impact of salinity on PCY growth with a positive linear dependency on salinity for BA-120 and BA-132; 3) general positive impact of T on Synechococcus sp. growth; 4) the ability of PCY to survive and grow even under low T and PAR; 5) the photoinhibiton of Photosystem II observed for BA-120 at elevated PAR level. Additionally, other features of PCY functioning were also introduced into the algorithms, for instance, PCY being highly effective and competitive to other organisms in nutrients uptake because of their small size and, consequently, a high surface to volume (S/V) ratio.

The pico-bioalgorithms were implemented in 3D Baltic Sea numerical system (biogeochemical model – Ecological Regional Ocean Model hosted in circulation model – Modular Ocean Model). Modelled PCY were compared to literature field data on picocyanobacterium abundance in the Baltic Sea in the last two decades. Model results were also compared to results from model scenarios were PCY were not included. That aimed in pointing to the role of PCY in the whole Baltic ecosystem.

The Authors believe that their work will improve the understanding of picocyanobacterium life cycle and its impact on marine ecosystem functioning.

This work has been funded by the Polish National Science Centre project (contract number: 2012/07/N/ST10/03485) entitled: "Improved understanding of phytoplankton blooms in the Baltic Sea based on numerical models and existing data sets". The Author (AC) received funding from the Polish National Science Centre in doctoral scholarship program (contract number: 2016/20/T/ST10/00214). Funding for MS comes from the statutory funds at IO PAN.