

Protocol of the dissertation thesis defense:

The defense was held in the presence of all designated members of the committee and both opponents.

Introduction of the committee and opponents, passing an attendance list

Introduction of the candidate by his supervisor

Presentation of the dissertation thesis by the candidate in 30 minutes

Supervisor's assessment by Dr. Rohit Ghai

Opponent's evaluation by Dr. Hab. Katarzyna Piwosz – a brief summary, questions: Was it possible to differentiate between DNA and RNA phages in his metagenomes? If so, is there a host preference between them? What experiments would the candidate conduct to verify the phage-mediated ROS defense on cultures and in situ assuming an unlimited growth? Are bacterial temperature generalists represented by identical MAGs or are there some adaptations? Is the marine genus *Pheocystis* known also from the Římov reservoir; was it present in metagenomes? How could be explained the presence of marine *Thalassiosira* in the reservoir? How could be investigated the question of the relative importance of different top-down controls on phytoplankton?

Opponent's evaluation by Prof. Hans-Peter Grossart – a brief summary; questions: Aren't talks about Topic no. 3 being a little out of scope of the thesis? What could be said with more ecological context? Whether everything recovered in metagenome studies is important and what its temporal dynamics and importance might be? How would you answer which MAGs are important at which times? What about linking other OMICs tools? Temperature dependence is a pool of complex interactions, that temp also affects the host. How to figure out which factors are actually important? If you look at the MAGs only, you miss intraspecific variability, how does that translate to your data? How about the effects sample size on the results? Why was a diatom peak missing in the PEG model presented? Is the eukaryotic analysis done biased by sample filtering? How would you like to address the complex interactions in foodweb analysis questions? Did you look for symbiosis or parasitism genes? How would you re-define the PEG model? How would you re-do your study if you could and what are the main conclusions?

Questions from the committee:

How about enzymes carried by viruses (e.g. ROS) and virus specificity?

What is the general virus diversity in the Římov reservoir compared to the MAGs recovered?

What are life strategies of viruses, and if there are bacterial strategies to avoid virus infection?

What is absolute quantification of viruses based on sequences of the MAGs recovered?

Overall assessment: Vinicius Silva Kavagutti has proven his ability to plan and conduct scientific research successfully and satisfactorily responded to all questions in the discussion.

Committee poll: 8 valid ballot papers: passed 8x, failed 0x.