Excessive development of cyanobacterial blooms is a dangerous phenomenon for freshwater ecosystems. Intensification of blooms is associated with anthropopressure processes - e.g. food production and consequent increased transport of nutrients to surface waters, and global climate change - e.g. increased temperatures and short-term intense storms. Consequently, cyanobacterial blooms of *Microcystis* spp. (among other cyanobacterial hepatotoxin-producing organisms) are among the most well-known pervasive plankton communities that significantly develop in summer in temperate climate zones, or occur permanently in tropical climate zones. Their study is of great interest because of the potential threat they represent to biodiversity, human health and socio-economic activities.

However, most studies dedicated to understanding the development and global distribution of *Microcystis* spp. blooms generally focus on the physico-chemical profile of water bodies undergoing accelerated eutrophication. Lately, it has been proposed that occurrence and duration of *Microcystis* blooms in worldwide freshwater ecosystems is strongly influenced by local microbial communities (referred here as the interactome), which may be influenced by land use in the catchment area. There is a dearth of research linking the impact of land use (catchment effect including rural, urban or forest areas) with microbial community changes in lakes, lagoons and reservoirs. Deeper understanding is needed to elucidate the interrelationships of microbial communities that are particularly linked to the occurrence of *Microcystis* blooms, and those that significantly increase the risk and threat of *Microcystis* for the environment. Such negative impacts that will be the subject of the proposed research could include the potential for increased greenhouse gas emissions or the transfer of antibiotic resistance genes by microorganisms.

The proposed studies will include the interactions between methanogenic archaea and methanotrophic bacteria that produce and recycle methane and denitrifying microbial communities that produce and recycle nitrous oxide – the second most important greenhouse gas. Furthermore, *Microcystis* blooms were recently observed to harbor microbial communities with high abundances of mobile genetic elements (MGEs), which are responsible for the dissemination of antibiotic resistance genes (ARGs) resulting in the increase of their associated microbial resistome. Therefore, this aspect will also be the subject of the proposed research.

Research will be carried out on **four different continents and countries: Poland, the USA, Guatemala and Singapore, in different climate zones (temperate and tropical) and in areas with different land use (urban, agricultural or forested catchment).** Physico-chemical parameters of the waters, and the quality and quantity of cyanotoxins will be determined. Above all, however, **functional genes involved in processes related to greenhouse gas production will be searched and gene elements linked to antibiotic resistance will be characterised.** These objectives will be achieved using, inter alia, chromatographic and genetic analyses including next generation sequencing techniques and rt-qPCR.

Consequently, the present research will be a new proposal for knowledge acquisition at a global level, a comprehensive geographical and catchment approach can provide important new knowledge for understanding and prioritising environmental factors affecting environmental quality in the context of cyanoHABs with *Microcystis*.