

Understanding the mechanisms for the evolution of wide-ranging disjunction patterns in living organisms is still one of the major goals of current biogeography. Widely distributed symbiotic organisms are particularly good models for such studies. Intercontinental distribution (disjunctive) ranges of organisms may arise either by separation from formerly unified populations or by long-distance dispersal events. In light of de Bary's definition of symbiosis, both lichen-forming fungi (fungal bionts) and their photobiont partners (green algae or cyanobacteria) are examples of mutualistic symbiosis, and form an iconic model for study from an evolutionary, ecological or biogeographical point of view. The lichens that are the subject of this proposed study are essential components of almost every ecosystem worldwide, and include highly specialized species able to complete their life cycles in aquatic habitats. They are also highly sensitive to human-induced environmental and climatic changes. On the other hand, the global impact of climate change on glaciers has been dramatic because the melting and retreat of ice coverage reached 54% since 1850 and is combined with a regular decrease of yearly snowfall. The project will attempt to study the symbiotic association of fresh-water microorganisms as a model to study the historical mechanisms of intercontinental disjunction patterns and the potential impact of climate change on lichen communities in the glacier forelands. Recent progress in next-generation sequencing technologies provides opportunities for more accurate studies of the population genetics of microorganisms such as fresh-water lichen-forming fungi. The innovative approach and important advantages of this project will be the implementation of metagenomic shotgun sequencing methods in phylogeographic studies of lichen symbioses. Metagenomics is a modern technology widely used to characterize genetic variability and divergence in natural populations on genome-scale, and can be used for large numbers of individuals and populations. These methods have recently been most widely used for the analyses of microbial communities, providing the best combination of read-length, low cost, and highly informative output when compared to traditional sequencing approaches.