



Project acronym: TEGAP

Project title: Genomic basis of climate-change associated brownification/darkwater adaptation in Eurasian perch: the Trans-Eurasian perspective

Project leader: Anti Vasemägi, Swedish University of Agricultural Sciences, Sweden

Discipline: Earth Sciences & Environment: Ecosystems & Biodiversity

Station(s): Kajbasovo Research Station (Russia), Mukhrino Field Station - Nymto Park (Russia)

Climate change is affecting in multiple ways the environment in arctic and temperate lakes, which are important components in the global carbon cycle. For example, during recent decades, an increase of dissolved organic carbon (DOC) has been observed in the Northern Hemisphere leading to brownification of lakes. However, despite the ecological significance of humic substances, very little is currently known how fishes adapt to darker waters.

The main objective of this project is to characterise humic substance-driven selective footprints by whole-genome analysis in perch (*Perca fluviatilis*) at Trans-Eurasian scale. Our preliminary work based on 16 whole genomes has identified hundreds of genomic regions potentially involved in adaptation to humic water. However, analysis of perch across Eurasia is needed to test if the same genes are involved in dark-water adaptation.

We aim to sample perch from dark- and clear-water lakes nearby two research stations in Russia (Kajbasovo Research Station, Mukhrino Field Station – Nymto Park) using fish traps and gill-nets. We will analyse both whole nuclear and mitochondrial genomes of perch to i) identify humic substance-driven selective footprints and characterise the patterns of parallelism and convergence at Trans-Eurasian scale; ii) to further understand the phylogenetic history of perch. By establishing strong collaborative links between the personnel of Kajbasovo and Mukhrino research stations and applicant's group, the current project will contribute significantly to knowledge transfer and training for identifying, understanding, predicting and responding to diverse environmental changes. In addition, the project will significantly contribute to capacity building on modern genomic approaches and DNA sampling procedures.