

" Flexible until it snaps: Dynamics of genes & traits, densities & diversity in communities challenged by environmental change"

Summary

Our results demonstrate the suitability and the potential of molecular approaches to trait-based ecology. The application of molecular traits is often hard to synchronize with traditional morphological and ecophysiological traits.

We demonstrate that

- Proteomics is a quick and relatively cheap technique for analysing shifts in molecular traits but is restricted to the most abundant proteins and requires proper transcriptomes or genomes as reference
- (Meta-)Transcriptomics is a suitable approach to assess molecular trait dynamics in experimental systems
- Different predators cause significantly different transcriptome responses related to the relative importance of grazing and exudation in the protist-bacteria interaction, i.e., to the presence of either the heterotrophic *P. lacustris* or the mixotrophic *C. danica*.
 - o When grazing dominates the interaction, as in the presence of *P. lacustris*, genes acting in stressor response are up-regulated.
 - o when the potential use of algal exudates dominates the interaction, genes affiliated with iron transport are up-regulated.
- Stressors differently affect chrysophytes depending on the prevailing mode of nutrition
 - o Phototrophic strains reacted strongly to silver exposure, whereas light intensity and temperature had only minor effects on growth rates.
 - o For heterotrophic strains, high food concentration toned down the effect of silver, whereas temperatures outside the growth optimum had a combined stressor effect.
 - o The mixotrophic strains reacted differently depending on whether their nutritional mode was dominated by heterotrophy or by phototrophy