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KEYNOTE PRESENTATIONS

Classification of plant communities and alpha and beta diversity of vegetation systems

Enrico Feoli

University of Trieste, Italy

The concept of diversity of vegetation systems is revisited in terms of set theory, fuzzy set theory and similarity theory. It is suggested that the terminology alpha, beta, gamma etc. diversity should be avoided in order to be more coherent with the accepted meaning of diversity, i.e. number of different classes of elements in a collection (richness) and the evenness of the distribution of a given quantity in the classes. In this respect the similarity concept should be used as a supplementary information to characterize the diversity of a collection in a fuzzy way. This suggestion would avoid useless jargon and introduces clarity. It is shown that the so called alpha diversity, gamma diversity and beta diversity may be interpreted in the same way, since every diversity vector can be transformed in a symmetric diversity matrix, of which the Gini-Simpson's index is the average similarity, while the index of Shannon is the entropy of its eigenvalues. It is concluded that rather to be worried about measuring diversity it would be more fruitful to be worried about why we are willing to measure it.

Ecological networks

Jens M. Olesen

Aarhus University, Denmark

Ecological networks are typically complex constructions of species and their interactions, although other kinds of node such as individuals also are used. During the last decade, the study of networks has moved from static to dynamic analyses, and has attained a deeper insight into their internal structure, heterogeneity, and temporal and spatial resolution. I review, discuss and suggest research lines in the study of the spatio-temporal heterogeneity of networks and their hierarchical nature. I will use several case studies, e.g. from the arctic Zackenberg in Greenland. I focus upon temporal dynamics, linkage constraints, habitat borders, network modularity, and super networks that integrate different network types. Few studies have explicitly examined temporal change in networks, and I present examples that span from daily to decadal change. Network structure is commonly constrained by phenological uncoupling (a temporal phenomenon), abundance, body size and population structure. Some potential links are never observed, that is they are 'forbidden' (fully constrained) or 'missing' (a sampling effect), and their absence can be just as ecologically significant as their presence. Many networks are hierarchically structured, with modules forming the basic building blocks, which can result in self-similarity. Finally, by scaling up to a higher level of organization, it is possible to combine different network types (e.g. food webs and mutualistic networks) to form super networks. I conclude by listing a set of research topics that I see as emerging candidates for ecological network studies in the near future.

Is ecology predictable?
Lessons from experimental microbial ecosystems

Owen Petchey

University of Zürich, Switzerland

Forecasts of ecological dynamics in changing environments are increasingly important, and are available for a plethora of variables, such as species abundance and distribution, community structure, and ecosystem processes. There is, however, disagreement about whether ecological dynamics are predictable, and therefore whether researching ecological forecasting is worthwhile. I will show how combining of models and experimentation can play a key role in resolving this debate. Initial results suggest a resolution based on recognising and understanding scaling of ecological predictability, for example with organismal features such as body size, and with level of ecological organisation, as well as a resolution based on a more nuanced view of ecological predictability and its aims.

How to monitor community diversity from space?

Duccio Rocchini

University of Trento, Italy

Remote sensing is one of the most cost-effective approaches to identify biodiversity hotspots and predict changes in species community composition. This is because it allows for complete spatial coverages of the Earth's surface under study over a short period of time. Furthermore, remote sensing provides repeated measures, thus making it possible to study temporal changes in biodiversity. In this talk I will provide a concise review of the potential of remotely sensed imagery to help track changes in species diversity, and provide an overview of the potential pitfalls associated with the misuse of such imagery to predict species diversity.

Contribution of communities to ecosystem functioning in aquatic systems

Ursula Scharler

School of Life Sciences, Durban, South Africa

Communities in ecosystems contribute to ecosystem function in different ways. When communities are investigated from an energy throughput and connectivity point of view, it becomes apparent how the different communities participate in ecosystem function. In ecosystems, functional groups and communities display a large range of energy throughput, displaying the obvious decreasing trend from small to large organisms, but depending on the community biomass present in the ecosystem. Further, trophic connectivity of groups often differs, especially between mid-trophic levels groups compared to low- or high-trophic level groups, but also between groups of the same trophic levels. Through this discrepancy in energy throughput and connectivity, the functional groups and communities occupy a certain niche in the system in terms of their dominance regarding energy efficiency. Some communities therefore contribute a considerable proportion of an ecosystem's energy efficiency, whereas others may play a comparatively small role, even though they are an integral part of a particular food web and an important food web component *per se*. The role of the various communities may change over time to varying degrees as is apparent from time series of ecological networks depicting the energy flow of the food web. Even if the contribution of certain communities changes, it does not necessarily mean that attributes of the entire ecosystem also digress - often, there is no apparent change on the ecosystem level when the contributions of the individual functional groups and communities differ substantially. In conclusion, the hierarchical connection between functional groups or communities, and the ecosystem is not straightforward, as the ecosystem does not respond in a linear fashion to changes of its components. However, certain patterns of community contribution especially with regards to energy throughput and connectivity are apparent throughout aquatic food webs.

The food web implications of plankton body size

Ulrich Sommer[*], *Maria Moustaka-Gouni*

*GEOMAR, Kiel, Germany

Open water food webs have traditionally been considered a typical representation of the principle that large eat the small. Predator : prey size ratios of 10:1 to 1000:1 have been considered for the lower trophic levels, e.g. mm-sized Daphnia feeding on 1 µm to 30 µm sized phytoplankton, mm-sized copepods feeding on 5 to 100 µm sized phytoplankton, 1 cm to 10 cm-sized small pelagic fish feeding on mm-sized crustacean zooplankton. The resultant image was a relatively short (4 to 5 links) food chain from primary producers to top-predators, such as marine mammals and sharks. Combined with the classic assumption of a 10% ecological efficiency this was well compatible with the observation that fish production equals ca. 1% of primary production.

This image was seriously shaken with the discovery of the “microbial loop” through which often >50%, sometimes even >90% of primary production are channeled towards the metazoan plankton. Usually, 2 trophic levels were inserted between the smaller fractions of phytoplankton and the mm-sized planktonic metazoans. Heterotrophic nanoflagellates (2-20 µm) feeding on picoplankton (<2 µm; bacteria and the smallest phytoplankton) and heterotrophic, protistan microzooplankton (20 – 200 µm) feeding both on autotrophs and heterotrophs <20 µm. However, this was not the end of increasing complexity. A detailed study of feeding relationships of heterotrophic nano- and picoflagellates identified a complex food web within this guild, containing chains with up to 5 links and predator : prey size ratios sometimes close to 1:1.

While considerations of size make it is easily conceivable to squeeze numerous trophic levels into a food web, energetic constraints probably place more serious limits. Already putting zooplanktivorous fish on TL 5 (i.e. 1 extra trophic level for HNF and for microzooplankton) and retaining the primary production : fish production ratio of 100:1 would require an average ecological efficiency of ca. 0.4, or external food subsidies, or it would cast doubts on the estimates of primary or fish production.

ORAL PRESENTATIONS

Biodiversity and ecosystem functioning

Phytoplankton functional diversity shifted gradually due to global warming, human impacts and oligotrophication in the Danube River at long-term scale

András Abonyi[1*], *Éva Ács*[1,3], *András Hidas*[1], *István Grigorszky*[1], *Gábor Várbíró*[2,3], *Gábor Borics*[2,3], *Angéla Földi*[1,3], *Keve Tihamér Kiss*[1]

[1]MTA Centre for Ecological Research, Danube Research Institute, Department of Hydro- and Plant Ecology, Budapest, Hungary
[2]MTA Centre for Ecological Research, Danube Research Institute, Department of Tisza River Research, Debrecen, Hungary
[3]MTA Centre for Ecological Research, GINOP Sustainable Ecosystems Group, Hungarian Academy of Sciences, Tihany, Hungary
[*]E-mail: abonyi.andras@okologia.mta.hu

Keywords: climate change, Europe, large rivers, river plankton, trend analysis

Long-term dynamics of phytoplankton have been addressed in marine and lake systems, but rarely in rivers. However, large rivers are highly human-impacted, whereas global warming may further affect the functioning of phytoplankton at long-term scale.

In the middle section of the large European Danube River, long-term decrease in Chl-*a* and increase in species diversity have formerly been revealed. The functional community composition that directly relates to ecosystem functioning has not been addressed previously. We analyze a 34-year long phytoplankton dataset from the middle river section at Göd (N-Budapest), Hungary. We focus on gradual changes in the functional composition and functional diversity components based on the functional trait and functional group approaches.

We hypothesized that long-term gradual changes in major environmental constraints should be followed by gradual shifts in dominance relationships among functional traits and functional groups of phytoplankton. We further hypothesized that functional shifts were highlighted by gradual changes in functional diversity components: evenness, divergence, and dispersion.

The most frequent water discharge values shifted from above of 2000 m^3s^{-s} to below of this value. High-flows increased significantly in values with shortening tendency in duration and altered seasonality. The concentration of N- and P- forms, as well as total suspended solids decreased significantly. Water temperature increased significantly, especially in summer. In the phytoplankton, single-celled eutrophic centric diatoms decreased in relative abundance, but flagellated, elongated, and filamentous forms increased. A clear functional shift was the dominance decrease of planktonic taxa and the relative abundance increase of benthic diatoms.

Functional evenness and dispersion increased significantly based on both functional approaches. Functional divergence decreased based on functional traits, but increased based on functional groups. Functional evenness increased in summer and autumn independently of the approach, but it decreased in winter and spring based on the functional group composition.

Long-term increase in functional diversity components would indicate enhanced ecosystem functioning of phytoplankton in the middle section of the Danube. However, we argue that the observed increase in functional diversity is related to a gradual shift from high-biomass communities with the dominance of eutrophic centric diatoms towards the relative abundance increase of numerous low-biomass elements. These include a few planktonic algae well adapted to altered conditions, diatoms with benthic origin, and dispersed limnophilic taxa.

We show first evidences for a long-term phytoplankton functional regime shift in a European large river. Global warming, human impacts and oligotrophication may increase the functional diversity of large river phytoplankton, but the origin and functional role of taxa should be carefully considered. Our results may further indicate altered food web structure of the middle section of the Danube River at long-term scale.

Settlement in hard-bottom communities under climate change: seasonal constrains and opportunities opened up by future warming

Francisco R. Barboza[*], *Marco Scotti, Markus Franz, Maysa Ito, Martin Wahl*

GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany
[*]E-mail: fbarboza@geomar.de

Keywords: settlement patterns, climate change, environmental filtering, long-term experiment

Biological communities are undergoing dramatic transformations in the course of climate change. Phenology, the seasonal timing of life cycles, is the process on which more observational evidence has been generated on the early impacts of climate change. However, experimental evidence on how future warming impact on species phenology will be translated at the community level are missing in marine ecosystems. The present work experimentally evaluated the impact of a predicted warming scenario on the settlement patterns of Baltic hard-bottom communites and discussed changes in their structure. During a 10-month experiment conducted in benthic outdoor mesocosms, two treatments were implemented: (1) ambient, with natural field temperatures and (2) warm, with field temperatures increased by 4 °C. Settlement was registered by exposing PVC panels in the mesocosms on a monthly basis. Generalized additive and linear models were combined to evaluate differential seasonal changes in species richness, species turnover in time and species occurrence among treatments. Obtained results showed higher settlement rates in the warm treatment during winter, due to the relaxation of the filter imposed by cold temperatures. Settlement rates strongly increased in the ambient treatment during spring months, overcoming the richness of the

warm treatment in summer. The earlier settlement during cold months and the stressful conditions registered in summer could explain the slower temporal species turnover observed in the warm treatment. Beyond species characteristic responses, patterns at the community level were mainly driven by autotrophs. Algal settlement since early winter under warming conditions reshaped natural phenological patterns and altered the balance between autotrophic and heterotrophic processes in different seasons. Warming modified the timing and functional identity of settlement, potentially affecting intra-annual changes in structure and functioning of resulting hard-bottom communities.

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Increased temperatue disrupts biodiversity-ecosystem functioning relationships

Elodie C. Parain[1,2*], *Rudolf P. Rohr*[1*], *Sarah M. Gray*[1], *Louis-Félix Bersier*[1]

[1]University of Fribourg, Department of Biology – Ecology and Evolution, Fribourg, Switzerland
[2]Yale University, Department of Ecology and Evolutionary Biology, CT, USA
[*]E-mail: elodie.parain@yale.edu

Keywords: global warming, Biodiversity-Ecosystem Functioning, Lotka Volterra mechanistic model, competition, Sarracenia purpurea communities

Gaining knowledge of how ecosystems provide a large quantity of services to humans is of primary importance, especially with the current threat of climate change. Yet, little is known about how increased temperature will impact the Biodiversity-Ecosystem Functioning (BEF) relationship. In this study, we tackled this subject theoretically and experimentally. We developed a BEF theory based on mechanistic population dynamic models, which allows the inclusion of the effect of temperature. The model predicts that temperature increase will intensify competition and consequently the BEF relationship will flatten or even become negative. We conducted a laboratory experiment with natural microbial microcosms and the results were in agreement with the model predictions. The experimental results also revealed that an increase of both temperature average and variation had a more intense effect than an increase of temperature average alone. Our results indicate that, under climate change, high diversity may not guarantee high ecosystem functioning.

Response of species diversity to disturbance and environmental variability depends on how it is measured

Yong Cao

A recently proposed framework allows one to calculate a family of species-diversity measures, “effective number of species” or ENS by changing the weights of common vs. rare species (*q*-value). ENS has been frequently referred to as the “true” or most robust measure of species diversity and is being quickly adopted. However, its applications to biodiversity monitoring and resource management have been little explored. In this study, we used simulated assemblages and a field dataset to examine how ENS responded to stress and was related to landscape environments when the *q*-value was progressed increased, and how the weighting scheme affected the accuracy and precision of ENS estimates. The true value of ENS (i.e., based on the entire assemblage) with all species weighted equally, i.e., species richness, steadily decreased as stress increased. With common species given more weight (higher *q*-value), the responses of ENS to stress became weak and diverged among assemblages, decreasing less in some, but increasing in others. Estimates of ENS based on samples were even less successful to detect stress. With increasing *q*, the accuracy of ENS estimates improved, but the precision decreased. R^2 in a regression of ENS of stream fish assemblages with environmental variables steadily decreased with increasing *q*-value. In conclusion, incorporating relative abundance into species diversity as in implemented in ENS weakened its ability of detecting stress and its environmental interpretability. Ecologists need to consider how to better incorporate species abundance in measuring species diversity.

Multiple factors affecting prediction accuracy in stacked species distribution models – a ”virtual ecologist” approach

Rui F. Fernandes[1*], *Daniel Scherrer*[1] *and Antoine Guisan*[1,2]

[1]Department of Ecology and Evolution, University of Lausanne, Biophore building, 1015 Lausanne
[2]Institute of Earth Surface Dynamics, Geopolis, University of Lausanne, 1015 Lausanne
[*]E-mail: rui_fff@msn.com

Keywords: community ecology, virtual species, species distribution models, sample size, prevalence, species pool

Important questions have been raised in the field of community ecology over the past years. Particular focus has been given to understanding why and how composition and richness of biological communities change in space and time. What’s the exact distribution of communities and which methods should be used to determine those distributions? These questions are increasingly important under the growing negative impacts of global changes affecting biodiversity (e.g. habitat fragmentation, biological invasions, climate and land-use change). It is therefore essential to create methods that allow us to understand and predict the distribution and composition of communities in a region, to mitigate impacts. Species distribution models (SDMs) are a correlative approach establishing a statistical relation between species distribution data (that can be obtained through field observations of a specific site) and available environmental data from those locations. Therefore, SDMs can be useful tools to predict species distribution across a region and under changing environmental conditions. Here, using a ”virtual ecologist” approach and SDMs, we assess how different factors (sample size, sampling prevalence, species pool and modelling technique) might affect the prediction accuracy of modelled virtual communities (obtained through stacked-SDMs; S-SDM), to determine under which conditions one can obtain accurate species assemblage predictions when precise and known species distribution data is available. Learning how the accuracy of S-SDM predictions are affected by these factors might help to understand the level of uncertainty that can be expected, even when “perfect” and known data is used. It can also help determine an acceptable level of uncertainty when predicting species assemblages with real data. We started by creating 291 virtual species distribution maps that were used to randomly select three sets of 100 species (our regional species pools). For each set, the distribution maps of all species were stacked and the resulting binary maps (bS-SDM) were considered as our “true” communities. The occurrences of all the virtual species present in the “true” communities were sampled using different sample sizes and different occurrence sampling methods. The sampled occurrence data was then used to fit SDMs for all single species in each set (the species were fitted using GLM, GAM or BRT). From our original sets of 100 species we randomly selected additional species pools with 25 and 50 species, to assess the effects of regional species pool size. The binarised projections for our species in each set were stacked together to create predicted communities that were compared with our initial “true” communities. We observed that: (1) the proportion of species correctly predicted as present/absent increases with sample size; (2) sampling prevalence has mainly an effect on the prediction of species assemblages at low sample sizes; (3) different sizes of species pools or different modelling techniques do not seem to differently influence prediction accuracy. However, even with high sample sizes, and using a complete known truth, residual uncertainty remains in the predictions, as caused by the simulated sampling process. This means that even with complete knowledge of the distribution of virtual species and with very large sample sizes (3200 sites), one cannot obtain “perfect” predictions from community models. Therefore, when evaluating the accuracy of community predictions from stacked-SDMs fitted with real field data, one would never reach the maximum possible accuracy, and high values (e.g. around 0.8-0.9 for Sørensen) could already be seen as the best possible predictions. If originally based on original field data, using virtual simulations as presented here could be used in future studies to inform on the accuracy level that one can expect given the species prevalences, the size of the species pool and the number of sampled sites in a dataset.

Long-term records of Baltic hard-bottom communities: the role of metapopulational processes in compensating climate variability

Markus Franz[1*], *Francisco R. Barboza*[1], *Maysa Ito*[1], *Martin Wahl*[1]

[1]Benthic Ecology, Helmholtz Centre for Ocean Research Kiel, Germany
[*]E-mail: mfranz@geomar.de

Keywords: hard-bottom communities, benthic, biodiversity, long-term monitoring, climate variability, functional diversity, ecosystem engineer

The systematic monitoring of biological communities is the most valuable approach to study their dynamics, register and predict regime shifts in their structure, and evaluate the ecological effects of climatic processes whose signal can only be detected through multi-annual/decadal surveys. In the context of global change, the rate of environmental transformations is predicted to be faster in the Baltic than in other seas, stressing the urgent requirement to generate reliable baselines in this marine ecoregion. With this objective in mind, we are generating and analyzing historical records of hard-bottom communities in the SW Baltic Sea. The results of annual samplings over 10 years in the Kiel and Lübeck bights showed both, stable communities as well as regime shifts accompanied with the loss of habitat forming taxa. The obseverd differential shifts in community composition and the cumulative consequences that local, regional and global drivers have on benthic communities, highlight the role that biological processes might have in compensating these effects.

The impact of increasing temperatures on the diversity-dispersal relationship in metacommunities

Sarah M. Gray[1*], *Elodie C. Parain*[1,2], *Louis-Fèlix Bersier*[1]

[1]University of Fribourg, Department of Biology – Ecology and Evolution, Fribourg, Switzerland
[2]Yale University, Department of Ecology and Evolutionary Biology, CT, USA
[*]E-mail: sarahmarie.gray@unifr.ch

Keywords: diversity-dispersal relationship, metacommunities, temperature, microcosmos, succession

Dispersal is key for maintaining biodiversity at local and regional scales in metacommunities. However, little is known about the combined effects of dispersal and climate change on biodiversity. Theory predicts that alpha-diversity is maximized at intermediate dispersal rates and that this hump-shaped relationship will flatten when competition increases. In the rising part of the temperature performance curve, attack rates and ultimately interspecific competition are predicted to increase with temperature; thus we predict that the hump-shaped relationship will also flatten with warming. We explored this question using aquatic communities of *Sarracenia purpurea* from early- and late- successional stages. With increased dispersal, the hump-shape was observed only in late-succession communities. Increased temperature did not flatten this relationship, but instead decreased diversity globally. In early-succession

communities, diversity increased monotonically with dispersal, and these communities were little affected by temperature. Here, temperature may have little additive effect on competition, and experimental dispersal rate may be too low to observe the hump-shape. For late communities, the absence of flattening and the decrease in species gamma-diversity is due to higher extinction rate with temperature, which mostly affects small-bodied species. Consequently, temperature modifies dispersal dynamics through species-specific impacts at the metacommunity level.

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Persist or produce: A community trade-off tuned by species evenness

Rudolf P. Rohr[1*], *Serguei Saavedra*[2], *Guadalupe Peralta*[3], *Carol M. Frost*[4], *Louis-Félix Bersier*[1], *Jordi Bascompte*[5], *Jason M.Tylianakis*[6,7]

[1]Department of Biology – Ecology and Evolution, University of Fribourg, Switzerland
[2]Civil and Environmental Engineering, Massachusetts Institute of Technology, Cambridge, USA
[3]Centre for Integrative Ecology, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
[4]Department of Forest Ecology and Management, Swedish University of Agricultural Sciences, Skogsmarksgränd, Umeå, Sweden
[5]Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland
[6]Centre for Integrative Ecology, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
[7]Department of Life Sciences, Imperial College London, Silwood Park Campus, Ascot, United Kingdom
[*]E-mail: rudolf.rohr@unifr.ch

Keywords: biodiversity, competition systems, demographic stochasticity, ecosystem functioning, niche theory, species coexistence

Understanding the effects of biodiversity on community persistence and productivity is key to managing both natural and production systems. Because rare species face greater danger of extinction, species evenness, a measure of how similar abundances are across species in a community, is seen as a key component of biodiversity. However, previous studies have failed to find a consistent association of species evenness with species survival and biomass production. Here we provide a theoretical framework for the relationship among these three elements. We demonstrate that the lack of consistent outcomes is not an idiosyncratic artifact of different studies but can be unified under one common framework. Applying a niche theory approach, we confirm that under demographic stochasticity evenness is a general indicator of the risk of future species extinctions in a community, in accordance with the majority of empirical studies. In contrast, evenness cannot be used as a direct indicator of the level of biomass production in a community. When a single species dominates, as expressed by the constraints imposed by the population dynamics, biomass production depends on the niche position of the dominating species and can increase or decrease with evenness. We demonstrate that high species evenness and an intermediate level of biomass production is the configuration that maximizes the average species survival probability in response to demographic stochasticity.

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Food webs

Structure and dynamics of food webs: a large-scale comparative study

Anett Endrédi[*], *Vera Senánszky, Ferenc Jordán*

[1]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[*]E-mail: endredi.anett@okologia.mta.com

Keywords: food web, keystone species, centrality, network analysis

One of the most important aims of conservation ecology is to quantify the relative importance of species and to find keystone species within ecosystems. Since the importance of species may be associated with their interactive partners, a possible approach for this problem is network perspective. Network analysis focuses on the interaction structure of food webs and it helps to mathematically quantify the positional importance of species and to identify candidate keystone groups. Although a wide range of different structural and dynamical network indices can be used to characterize and compare ecological communities, the relationships among them are not well-known. As a consequence, it can be difficult to choose the most adequate ones for certain ecological problems.

The aim of this study was to examine the correlation between the most popular structural network indices (i.e. trophic level, centralities, , status, the components of the keystone index and topological overlap) and Libralato's keystoneness index which had been suggested to be the best proxy for network dynamics.

Results (1) show different centrality ranks for different network indices, calculated for the same set of aquatic food webs, (2) quantify the similarity of particular indices, (3) help to match adequate tools to particular problems and thus (4) contribute to a more efficient systems-based conservation framework.

Detecting early signs of stress in a benthic system by carbon flows analysis

Maysa Ito[*], *Marco Scotti, Francisco R. Barboza, Markus Franz, Martin Wahl*

GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany
[*]E-mail: mito@geomar.de

Keywords: grazing, seaweed, temperature gradient, trophic analysis

Marine ecosystems are exposed to changing conditions worldwide, and one of the main drivers of change is temperature. Therefore, assessing at an early stage how species respond to changing temperatures is crucial. The interactions between species have often been neglected in past studies, leading to unreliable predictions on how they behave in the community. The goal of our work is to understand how temperature impacts energy flow between primary producer and grazer. The study focused on the primary producer *Fucus vesiculosus* and the

grazer *Idotea balthica* since they represent important compartments in the Baltic system. The interactions between these compartments were depicted as flows of carbon. In September 2016, we collected the algae and the grazers in the Kiel fjord. They were placed in tanks and gradually acclimatized to the target temperatures (5, 10, 15, 20, 22 and 25 °C). After target temperatures were attained, the experiment lasted four weeks. Once per week we measured net primary production of *F. vesiculosus*, quantified respiration and biomass of *F. vesiculosus* and *I. balthica*, and collected fecal pellets of *I. balthica*. The results of the measurements were converted into grams of carbon per day and square meter. Starting from 20 °C each compartment showed decreasing physiological rates. However, connecting the data through the analysis of carbon flows we detected imbalance between the carbon input by algae primary productivity and the loss of carbon by respiration of the grazer already at 15 °C. This means the consumption of grazers exceeded the production of the macrophytes. The analysis of the interactions showed that at 5 and 10 °C the system was balanced and productive, while at 15 °C *F. vesiculosus* was in the stress state threshold due to grazing. From 20 °C to 25 °C physiological rates of both, *F. vesiculosus* and *I. balthica*, were reduced since a stressful temperature level was reached. Our results highlight the need to study interactions between relevant compartments rather than looking at single species responses to sufficiently predict community responses towards future environmental changes.

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Quantifying temporal variability in food-web structure: are environmental drivers more important than network position?

Phil Jellyman[1*], *Shannan Crow*[1], *Doug Booker*[1]

[1]National Institute of Water and Atmospheric Research, Christchurch, New Zealand
*E-mail: phillip.jellyman@niwa.co.nz

Keywords: fish communities, invertebrates, rivers, New Zealand, flow variability, ecology

Spatial organisation of species assemblages is one of the most influential factors affecting food-web structure. In lotic (i.e., running water) ecosystems, the availability of space is primarily determined by river flow. Flow has long been considered the ‘master variable’ (sensu Poff et al. 1997) in lotic ecosystems as it determines the availability of space and can limit the abundance and distribution of freshwater species. However, the hypothesis that variation in the flow regime is the major driver of temporal variability in food-web structure has not been examined. We tested this hypothesis in the South Island of New Zealand where the maritime climate of this island leads to an unpredictable flow regime (i.e., floods can occur during any month of the year). Geographic isolation combined with variable environmental conditions has led to the structure of the riverine fish fauna being driven by diadromous movements between the ocean and fresh water. Most of the diadromous movements are caused by juvenile recruitment into fresh water, which suggests that the riverine food webs near the coast could

differ markedly from the food webs of inland rivers. However, food webs at any location in the river network could be subjected to unpredictable flooding. We hypothesised that the relative importance of flow on food-web structure would vary based on distance inland, with flow being a more important driver of inland food webs (where the predatory fish fauna is largely composed of non-migratory species) compared to coastal food webs that are primarily structured by diadromous fish recruitment dynamics. We compared inland and coastal food webs from three replicate rivers on the east coast of the South Island, New Zealand. The six sites were sampled on 25 occasions over three and a half years to examine temporal variability in food-web structure. Food webs across all sites were generally characterised by inverted biomass pyramids although predator-to-prey mass ratios were capable of being bottom-heavy pyramids or ‘stacks’ depending on the antecedent flow conditions or time-of-year. We found that inland food webs were typically simplified (i.e., reduced richness and trophic links) versions of coastal food webs with inland food webs comprising a subset of generalist species recorded rather than suite of specialist species. Evaluation of our initial hypothesis was complicated by unexpected stream-drying at some sites that typically flow year-round; unsurprisingly, drying produced the most striking between-year differences in food-web structure, irrespective of network position, because of the severe species deletions for food webs in drying streams (McHugh et al. 2015). The recovery of lower trophic levels from environmental flow extremes experienced during the study (i.e., floods or droughts) was similar at coastal and inland sites. However, the recovery of predatory fish communities was significantly delayed at inland sites. This presentation will conclude with a summary analysis comparing the relative importance of environmental drivers versus network position for contrasting food webs and also highlight some of the analytical difficulties that exist when examining complex spatially and temporally replicated food-web datasets.

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Classic allometric trophic network (ATN) models overestimate trophic transfer efficiency in food webs

Nadja J. Kath[1], Alice Boit[1], Christian Guill[1], Ursula Gaedke[1]*

[1]Ecology and Ecosystem Modelling, University of Potsdam, Potsdam, Germany
*E-mail: nkath@uni-potsdam.de

Keywords: allometric trophic network model (ATN), food chain, trophic transfer efficiency

Allometrically scaled trophic network models (ATN) assume that general models with few allometrically scaled metabolic parameters are still able to capture resource-consumer dynamics (Yodzis & Innes, 1990). Because of their generality and simplicity, these models are widely used in food web and network studies (Schneider et al., 2016). However, doubts concerning the energetics were raised when the classic ATN failed to reproduce the seasonal plankton succession of Lake Constance (Boit, Martinez, Williams, & Gaedke, 2012).

We compared the classic version (Brose, Williams, & Martinez, 2006) to an adjusted version with improved energetics (Boit et al., 2012) using a theoretic food chain of four trophic levels to investigate the energetics of the ATN. Our target parameter is the trophic transfer efficiency (TTE), which is defined as the ratio between predator production and prey production.

In the classic version, the TTE of the top predator often exceeded the maximum energetically possible TTE of 43% (assuming an assimilation efficiency of 85%), whereas it always remained in a realistic range in the adjusted version (Fig. 1). The unrealistically high TTE in the classic ATN is mostly due to the fact that only losses due to maintenance (i.e. basal respiration) but not activity respiration is not accounted for. If the top predator's prey is only weakly top-down controlled, its biomass is high, but its production is very low. At the same time, the combination of high prey availability and the lack of activity respiration means that the top predator can sustain a high mortality rate, i.e., its production rate is high. This results in an unreasonably high TTE at the top of the food chain. In the adjusted version of the ATN we propose conceptual changes in the individual bio-energetic processes by including activity respiration, which limits the production capacity of the top predator and thus yields lower and more realistic values of its TTE. Including activity respiration is particularly relevant when unicellular organisms and invertebrates dominate as their activity respiration may strongly surpass their basal respiration.

The potential for (too) high TTE and the resulting accumulation of biomass in the upper trophic levels in the classic ATN affects the distribution of biomass along the food chain. This affects the intensity of top-down vs. bottom-up control and therefore may alter simulated ecological dynamics. As the adjusted version is able to predict the correct energetics, it can be recommended for new simulation studies.

Figure

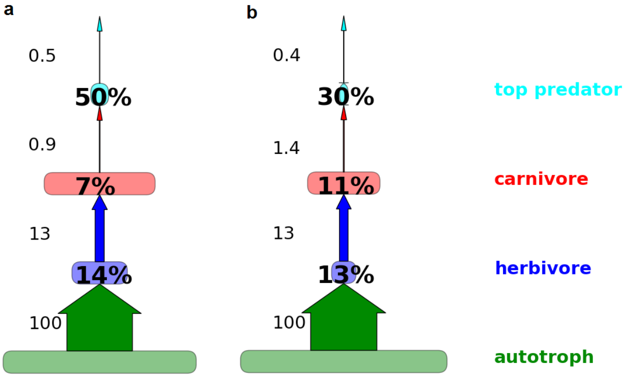

Fig. 1: Comparison of the energy transfer and biomasses within a food chain between the classic ATN model (a) and the adjusted ATN model version including activity respiration (b). Included values are production (numbers above the boxes) and trophic transfer efficiency (bold large numbers, defined as production ratio of two adjacent trophic levels). The production is standardized to autotroph's production of this chain as 100%, so that wider arrows indicate larger values. Box widths are scaled with the species' biomasses individually for each chain.

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Single-species MSY-assesments as a predictor for multi-species fisheries? The additivity of pairwise perturbations in food webs

Ágnes Móréh[1*], *Anett Endrédi*[1], *Ferenc Jordán*[1,2]

[1]Danube Research Institute, MTA Centre for Ecological Research, Karolina 29, 1113, Budapest, Hungary
[2]Wissenschaftskolleg zu Berlin, Berlin, Germany
*E-mail: moreh.agnes@okologia.mta.hu

Marine ecosystems are expected to feed more and more people, while we want to minimize the disturbance on them. The solution may be the improvement of maximum sustainable yield (MSY) assessments by putting them into multi-species context.

In spite of frequent critiques, single-species approaches are routinely used in determining MSY ignoring any interactions between species. However, it is clear that fish stocks are interdependent and should be considered simultaneously. The behavior of species depends on the context of the community, for example, on their position in a food web. To make strides for improving the multi-species approaches we need to better understand how local or non-local are the effects of changing the elements of a large interaction network.

We analyzed a hypothetical food web topologically and determined the key nodes, built a dynamical model and performed sensitivity analysis on it. After determining the community response to all single-species and all pairwise combinations of double-species perturbations, we quantified the additivity of effects for particular pairs of species.

Our results suggest that additivity is higher if both species have stronger indirect interactions, are quite central in the network and are involved in larger trophic flows. In these cases, predictability is quite high and single-species MSY is useful in the context of multi-species fisheries.

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Size compartmentalization in soil food webs

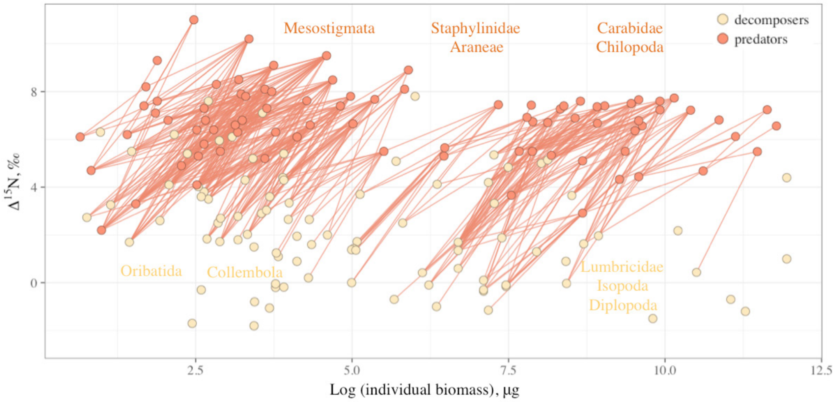
Anton Potapov[1,2*], *Alexei Tiunov*[2], *Stefan Scheu*[1]

[1]University of Göttingen, J.F. Blumenbach Institute of Zoology and Anthropology, Göttingen, Germany
[2]Russian Academy of Sciences, A.N. Severtsov Institute of Ecology and Evolution, Moscow, Russia
[*]E-mail: apotapo@gwdg.de

Keywords: stable isotopes, predator-prey, soil fauna, trophic interactions, mesofauna, macrofauna

Food webs are known to be size-structured with consumers having larger body size than their prey (Cohen et al. 1993). In marine food webs prey size of predators is constrained by predator gape size and therefore the trophic position increases continuously with body size. In contrast, soil food webs are based on size-unconstrained basal resource (detritus) and contain numerous primary consumers (detritivores) of very different body size. This suggests weak relationships between body size and trophic position. To prove this prediction, we compiled published data on the nitrogen stable isotope values (as measure of trophic position; Post 2002) and compared it with body masses of soil animals of temperate forests. The dataset included species from virtually all dominating groups of soil fauna, ranged from 1.9 µg (*Prozercon fimbriatus*) to 154 mg (*Porcellio scraber*) in individual dry biomass and from -1.8 (*Ceratoppia bipilis*) to 11.0‰ (*Zerconopsis remiger*) in litter-normalized Δ^{15}N values. Despite the size ranging over five orders of magnitude, there was no correlation between the body mass and trophic position of soil animals (see Figure). Within the high-order taxa the correlation was weakly positive only in Mesostigmata (Spearman $R^2 = 0.11$, $p = 0.038$), but not for other predators. In contrast, the correlation between body mass and trophic position was negative across all detritivores ($R^2 = 0.10$, $p = 0.003$), likely because smaller animals feed selectively on microorganisms rather than on dead plant material. As indicated by similar Δ^{15}N values, predatory micro-, meso- and macrofauna occupy similar trophic levels. This empirical observation suggests that soil food webs in fact harbor many trophic chains of similar length composed of soil animal species of different size classes. Size compartmentalization can serve as important mechanism fostering the stability of soil food webs.

Figure



Trophic level (Δ^{15}N values) as related to individual body mass of 181 species across dominating groups of soil fauna from temperate forests. Red lines represent trophic links based on Δ^{13}C, Δ^{15}N and body mass ratios of predators and their potential prey.

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Comparison of predator–parasitoid-prey interaction models for different host plant qualities

Carolina Sanchez[1], Manuel Gamez[2], Francisco J. Burguillo[3], József Garay[4], Tomás Cabello[1]*

[1]Department of Biology and Geology, University of Almeria, Almeria, Spain
[2]Department of Mathematics, University of Almeria, Almeria, Spain
[3]Department of Physical Chemistry, University of Salamanca, Salamanca, Spain
[4]Department of Plant Systematics, Ecology and Theoretical Biology, L. Eötvös University, Budapest, Hungary
[*]E-mail: carolflor83@hotmail.com

Keywords: phytophagous-parasitoid-predator system, Lotka-Volterra model, cultivar, *Nesidiocoris tenuis*, *Bemisia tabaci*, *Trichogramma achaeae*

Population dynamics models suggest that the over-all level of resource productivity can play important roles in community dynamics. One of them may be the quality of the host plant that can determine the effectiveness of entomophagous (predatory and parasitoids species) by altering the growth rate of the phytophagous population via effects on fecundity, survival, and rate of development. These effects have been studied in relation to the distribution of host plants as their physiological state. However, few studies have taken into account the differences between plant cultivars.

The objective of this study was to find a continuous-time dynamic model, appropriate to describe the effects of different tomato cultivars on a one predator-two prey model. The experimental part was carried out under greenhouse conditions in three tomato cultivars, with the predatory species *Nesidiocoris tenuis* (Reuter) (Insecta, Hemiptera, Miridae) and two prey species: the phytophagous species *Bemisia tabaci* (Gennadius) (Insecta, Hemiptera, Aleyrodidae) and the parasitoid species *Trichogramma achaeae* Nagaraja & Nagarkatti (Insecta, Hymenoptera, Trichogrammatidae), the latter as intraguild-prey.

Applying the software SIMFIT we found that a three-dimensional Lotka-Volterra type system could be well fitted to the data, estimating the phytophagous growth rate, the parasitoid and predator mortality rates, the predation and parasitism rates, the parasitoid emergence rate according to the cultivar type.

In the results, it was found that there is a very important effect of the host plant quality, according to the cultivar, on the intraguild predation that results in important changes in the dynamics of phytophagous populations. These results are also discussed in relation to their importance in the biological control of pest species in greenhouse crops.

The effect of phenology on the structure of a benthic food web

Marco Scotti[1*], *Agnes Mittermayr*[1,2], *Ulrich Sommer*[1]

[1]GEOMAR Helmholtz Centre for Ocean Research Kiel, Düsternbrooker Weg 20, 24105 Kiel, Germany
[2]Center for Coastal Studies, 5 Holway Avenue Provincetown, MA 02657, USA
[*]E-mail: mscotti@geomar.de

Keywords: biodiversity, body size, food web topology, functional traits, life cycle, network analysis

Food webs are binary representations of who eats whom in ecosystems. Their interactions can be modelled as a function of body size differences between prey and predators (especially in marine systems). The study of food web structural and dynamical properties can provide clues on the relationship linking biodiversity to community stability. Thus, food web modelling consists of a powerful tool for better understanding the effects on ecosystems of various human impacts that alter biodiversity (e.g. climate change). Due to costs and time consuming samplings most of the food webs refer to an average annual picture. Such average representation impairs the chances of modelling the phenology and its consequences on food web assembly.

Here we present the network analysis of a benthic food web from the Baltic Sea (Falckenstein Beach in the inner Kiel Fjord, Germany). Samples were collected on a biweekly basis, from the beginning of March until the end of September 2011. Feeding preferences were determined with triple stable isotope analysis (δ13C, δ15N and δ34S) and body size of consumers recorded. Altogether, 15 food webs were constructed starting from species feeding preferences. Network analysis revealed that in summer: (1) species are less omnivore and feed at lower trophic levels than in spring; and (2) high levels of trophic specialization are associated with low trophic similarity. Body size trends observed for some species of polychaetes and amphipods are coherent with changes in the food web structure. Indeed, the size-frequency distribution of some invertebrates with annual life cycle is dominated by large individuals during spring, while the young individuals born in summer belong to small size classes. Therefore, it is not surprising having omnivore feeding behaviors associated to large individuals in spring, while small size individuals display herbivore feeding habits during summer. We emphasize how these changes would have remained hidden with the construction of an average annual food web. Also, we suggest that body size trends provide a way to connect phenology to food web structure. This connection might turn to be particularly useful to investigate the consequences of climate change on phenology and, indirectly, on food web stability.

Chrysophyte algae-zooplankton interactions in lakes: effects on secondary production and diversity

Csaba F. Vad[1*], *Dunja Lukić*[1,2], *Zsófia Horváth*[1], *Martin J. Kainz*[1], *Robert Ptacnik*[1]

[1]WasserCluster Lunz, Lunz am See, Austria
[2]Department of Limnology and Bio-Oceanography, University of Vienna, Vienna, Austria
[*]E-mail: csaba.vad@wcl.ac.at

Keywords: climate change, phytoplankton, zooplankton, feeding ecology

Global change-mediated shifts in the plankton of eutrophic lakes are widely discussed, while in nutrient-poor lakes, they receive little attention. Chrysophyte algae are predicted to increase in contribution in oligo- and mesotrophic lakes, largely due to their mixotrophic nutrition. There is indication for detrimental dietary effects on zooplankton growth and reproduction but our understanding on their effect on secondary production is fragmentary. By using a colonial (*Dinobryon divergens*) and a unicellular (*Ochromonas tuberculata*) chrysophyte, we tested for dietary effects on zooplankton performance by using cladoceran (*Bosmina longispina*, *Daphnia longispina*) and copepod (*Eudiaptomus gracilis*) grazers to reveal species-specific responses. *D. divergens* proved to be grazing resistant against cladocerans already when provided in single cells and very small colonies. In contrast, adult *E. gracilis* was able to ingest it with a similar rate as the reference food *Cryptomonas*. However, *Eudiaptomus* discriminated against *D. divergens* in mixed diets. In a 2-week incubation, pure *Dinobryon* diet reduced egg production and survival of the copepod significantly compared to the reference food *Cryptomonas*; this difference disappeared when supplementing it with *Cryptomonas* (1:1 mixture). *Ochromonas* did not support *E. gracilis* nauplii to reach adult stage, while cladocerans were able to reach maturity. However, the pure diet reduced all their life history parameters. We can conclude that the dominance of chrysophytes is able to impair secondary production and might alter the composition of zooplankton communities. Cladocerans seem to be more prone to physical interference than copepods, while copepods seem to be more sensitive to chrysophyte nutrient quality. Therefore, chrysophyte blooms may affect energy flow in pelagic food webs.

Metacommunities

Plant metacommunity system in the islands of the Tuscan archipelago

Alessandro Chiarucci[1], *Giulia Finotti*[1], *Enrico B.L. Cerabolini*[2], *Bruno Foggi*[3],
Daniele Viciani[3], *Simone Fattorini*[4]

[1]BIGEA, Alma Mater Studiorum University of Bologna, Bologna, Italy
[2]DISTA, University of Insubria, Varese, Italy
[3]BIO, University of Florence, Italy
[4]MESVA, University of L'Aquila, L'Aquila, Italy

Biogeographical patterns of metacommunities at archipelagic level are still poorly understood because of the lack of information at different geographical scales (i.e. within islands vs. between islands). The availability of large datasets contained in vegetation databases offeres new opportunities for testing explicitly formulated hypotheses based on theoretical metacommunity assumptions using local data from relevès and floristic data from the whole islands. In this work the plant communities and entiere floras from the seven major islands of the Tuscan Archipelago (Italy): Elba, Giglio, Capraia, Montecristo, Pianosa, Giannutri and Gorgona. Our aims were to test: (1) if plant species composition at the metacommunity level was more affected by local conditions (i.e. the abiotic characteristics at single sampling sites) or by the island where sampling sites were located, and (2) how island species pools influenced local species diversity. For these purposes, we assembled a large data set including all phytosociological relevés available in published and unpublished sources, from the year 1973 to present.

The final database included 1334 relevès, for a total of 790 species and subspecies. Multivariate analyses, sample-based rarefaction curves, regression techniques and beta-diversity analyses were used to test the role of island belonging and local abiotic factors in controlling variation in plant community.We found that the sampling effort (represented by the number of available relevès and hence the sampled area) was affected by temporal and spatial biases, which can explain some biogeographical inconsistencies. However, we found a positive relation between the overall floristic richness known from each island and the biodiversity patterns emerged from relevès. We also found that local factors and island belonging interact in a complex way in generating beta-diversity patterns.

Root-symbiotic fungal communities on remote islands are diverse but functionally distinct

John Davison[1*], *Mari Moora*[1], *Maarja Öpik*[1], *Martti Vasar*[1], *Teele Jairus*[1], *Martin Zobel*[1]

[1]Institute of Ecology and Earth Science, University of Tartu, Tartu, Estonia
[*]E-mail: john.davison@ut.ee

Keywords: dispersal, island biogeography theory, microbes, microorganisms, trait-environment relationship

Island biogeography theory is one of the most influential paradigms in ecology. That island characteristics, including remoteness, can profoundly modulate biological diversity has been borne out by studies of animals and plants. By contrast, the processes influencing microbial

diversity, life history and function in island systems are largely unknown. We sequenced arbuscular mycorrhizal (AM) fungal DNA from plant roots collected on 13 islands worldwide and compared AM fungal diversity on islands with existing data from mainland sites. AM fungal communities on islands were as diverse as mainland communities and diversity was maintained even on the remotest islands (c. 6000 km from the closest mainland). Thus, in contrast to the patterns recorded among macro-organisms, efficient dispersal appears to outweigh the effects of speciation and extinction in regulating AM fungal diversity on islands. Nonetheless, AM fungal communities on more distant islands comprised a higher proportion of ruderal taxa and taxa with large spores, indicating that tolerance of significant environmental stress may be required during the dispersal and establishment process.

Varying patterns on varying scales: A metacommunity analysis of nematodes in European lakes

Birgit Dümmer[1*], *Walter Traunspurger*[1]

[1]Department of Animal Ecology, Bielefeld University, Germany
[*]E-mail: birgit.duemmer@uni-bielefeld.de

Keywords: metacommunity, nematodes, EMS-Analysis

Ecological community patterns are often extremely complex and the factors with the greatest influence on community structure have yet to be identified. In this study we used the elements of metacommunity structure (EMS) framework to characterize the metacommunities of freshwater nematodes in 16 lakes located in northern Germany and southern Sweden. Lakes varied in their trophic state. The analysis was applied at four geographical scales (radius ranging from 80 m to 360 km). The site characteristics associated with site scores indicative of the structuring gradient were identified using Spearman rank correlations.

The metacommunities of the 174 nematode species included in this analysis mostly had a coherent pattern. The degree of turnover increased with increasing scale. Ordination scores correlated with geographical variables on the larger scales and with the trophic state index on a regional scale. The association of the structuring gradient with spatial variables and the scale-dependent increase in turnover showed that nematode dispersal was limited. The different metacommunity patterns identified at the increasing geographical scales suggested different, scale-related mechanisms of species distribution, with species sorting dominating on smaller and mass effects on larger geographical scales.

This study shows that meiobenthic organisms provide great benefit for metacommunity analysis due to their high abundance and diversity on small and large scales of analysis.

Isolation drives the strength of species sorting across multiple taxonomic groups in alpine lakes

Zsófia Horváth[1*], *Csaba F. Vad*[1], *Mia M. Bengtsson*[2], *Theresa Lumpi*[3], *Christian Preiler*[1], *Blake Matthews*[4], *Robert Ptacnik*[1]

[1]WasserCluster Lunz, Lunz am See, Austria
[2]Institute for Microbiology, University of Greifswald, Greifswald, Germany
[3]Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden
[4]Department of Aquatic Ecology, EAWAG, Kastanienbaum, Switzerland
[*]E-mail: zsofia.horvath@wcl.ac.at

Keywords: metacommunity, species sorting, dispersal limitation, plankton

Understanding how landscape topography and isolation affects local community assembly currently represents one of the most intriguing issues in metacommunity ecology. Mountain ridges can pose a physical isolation barrier for several terrestrial taxonomic groups, while we know less about how it affects dispersal among lake communities. High elevations can result in lower numbers of neighbouring lakes due to topographic reasons, contributing to the remoteness of individual lakes. As lakes along elevational gradients are rarely studied in metacommunity ecology, we miss information on their levels of isolation by dispersal limitation. For passively dispersing organisms such as plankton, dispersal among lakes can happen both overland and through waterways. As community patterns are commonly investigated based on overland distances, we are largely unaware of the relative importance of waterways for connectivity, which might increase with topographic complexity that hinders other potential overland vectors.

Our aim was to investigate whether isolation by dispersal limitation in alpine lakes can affect the strength of species sorting in plankton communities, and to better understand the role of overland and watercourse dispersal in multiple taxonomic groups.

We studied bacterio-, phyto- and zooplankton in lakes along the northern fringe of the Alps in Central Europe (Austria, Germany, Switzerland). We quantified the degree of isolation for each lake as the number of all nearby lakes along a spatial scale ranging from 5 to 500 km. We calculated environmental match as a proxy for the strength of local species sorting at the local habitats and related it to scale-dependent isolation. We also analysed metacommunity patterns based on both overland and watercourse distances in a variation partitioning approach along the same spatial scale.

Our results showed that species sorting was strongly affected by isolation in all planktonic groups. Its spatial scale dependence showed a close relationship with body size, and implied that dispersal limitation acts already over shorter distances for larger sized (zooplankton) than for smaller sized taxa (bacteria). The relative importance of overland against watercourse dispersal was scale-dependent, with the importance of watercourse dispersal increasing with distance. Bacteria, protozoa, and phytoplankton showed highly similar patterns, while spatial patterns in zooplankton were always explained better by watercourse distance.

These results imply an overall strong dispersal limitation in alpine lakes for multiple microscopic taxa.

Drivers of stream diatom beta-diversity from local to global scales

Thibault Leboucher[1*], *William R. Budnick*[2], *Aurélien Jamoneau*[1], *Sébastien Boutry*[1], *Janne Soininen*[3], *Wim Vyverman*[4], *Sophia I. Passy*[2] *& Juliette Rosebery*[1]

[1]Aquatic Ecosystems and Global Changes Research Unit, IRSTEA, 50 avenue de Verdun, 33612 Cestas, France
[2]Department of Biology, University of Texas at Arlington, Arlington, TX 76019, USA
[3]Department of Geosciences and Geography, University of Helsinki, PO Box 64, Helsinki, FIN-00014, Finland
[4]Laboratory Protistology & Aquatic Ecology, Ghent University, Krijgslaan 281 S8, 9000 Gent, Belgium
[*]E-mail: thibault.leboucher@irstea.fr

Keywords: biogeography, metacommunities, anthropogenic impacts, environmental heterogeneity, spatial processes, stream networks

The taxonomic composition of a community results from an interplay of regional (dispersal and species pool) and local (species sorting) processes and a key question in community ecology is to understand the relative influence of these processes along gradients. β-diversity might represent a potential key to contribute to this question.

Diatoms play a central role in aquatic ecosystems and more and more researchers focused their attention on finely understanding the mechanisms that govern their community assembly. It is now accepted that the biogeographical distribution of stream diatoms depends mainly on environmental heterogeneity, anthropogenic impacts and dispersal-related processes.

Today we only have a limited understanding of how species sorting and dispersal-related processes interact to affect diatom species distribution, and of how these potential interactions are modulated by the geographic scale (environmental heterogeneity) and by anthropogenic stressors. In this study, we explored the β-diversity evolution of stream diatom communities from local to global scales, across different levels of nutrient enrichment, with a dataset encompassing 3000 samples from France and the US. According to the arguments developed before, we tested four main hypotheses: (1) β-diversity in diatom communities increases from local to larger scales, as environmental heterogeneity increases. (2) β-diversity in natural conditions is always higher than β-diversity in communities under high nutrient levels, regardless of scale. (3) In unimpacted conditions, β-diversity is mainly controlled by species-sorting and the relative contribution of this process is expected to increase from local to larger scales. (4) In impacted conditions, species-sorting influence should be tenuous and constant across spatial scales, allowing to detect the signal of dispersal-related processes.

Our results highlight that beta-diversity increases from local to global scales and is always higher in unimpacted conditions than in impacted ones. After extracting the effect of gamma diversity with null models, we detected significant changes in the relative impact of local community assembly processes vs. regional processes according to the scale of observation. The relative importance of species-sorting increases simultaneously with the scale and this phenomenon is particularly pronounced for unimpacted environments. In impacted conditions, species-sorting influence is weakened and we detected the signal of dispersal-related processes. Our results generate novel insights into the main mechanisms driving beta-diversity patterns.

Secondary propagule dispersal by waterbirds

Ádám Lovas-Kiss[1*]*, Attila Molnár V.*[1]*, Casper H.A. van Leeuwen*[2]*, Maria Ovegård*[3]*,*
Andy J. Green[4]

[1]Department of Botany, University of Debrecen, Egyetem sq. 1, Debrecen H-4032, Hungary
[2]Department of Aquatic Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands
[3]Department of Aquatic Resources, Swedish University of Agricultural Sciences, Skolgatan 6, SE-742 42 Öregrund, Sweden
[4]Estación Biológica de Doñana, EBD-CSIC, Américo Vespucio 26, 41092 Sevilla, Spain, Seville, Spain
[*]E-mail: epipactispalustris@gmail.com

Keywords: *Larus fuscus*, *Phalacrocorax carbo*, endozoochory, secondary seed dispersal

Secondary dispersal of propagules can be even more important for the dispersed organisms than primary dispersal. Recent studies showed the importance of mammals (bats, foxes etc.) as secondary vectors, but we lack knowledge about the role of waterbirds. In our research we focused on a piscivore (great cormorant, *Phalacrocorax carbo* L.) and an omnivore (lesser-black backed gull, *Larus fuscus* L.).

Cormorants regurgitate pellets daily, and we collected 112 pellets from seven European locations which examined for intact propagules. One-third of pellets contained ≥ one intact plant seed, with seeds from 16 families including plants from a broad range of freshwater, marine and terrestrial habitats. Of 21 plant species, only two have an endozoochory dispersal syndrome, compared to five for water and eight for unassisted dispersal. One-fifth of the pellets contained ≥ one intact propagule of aquatic invertebrates from seven different taxa (crustaceans and bryozoans). Network analysis suggested associations between particular fish species and plant or invertebrate species.

Lesser-black backed gull samples were collected from ricefields. The birds were feeding on the red swamp crayfish *Procambarus clarkii*, originally from North America, which is one of the world's worst aquatic invaders. In the ricefields of Doñana, south-west Spain, we collected excreta (N = 76 faeces, 14 pellets) of lesser-black backed gull in December 2014 and November 2015. Diaspores from at least 12 plant species (seeds from 11 angiosperm taxa, and charophyte oogonia) were recovered from gull excreta, together with eggs of 12 aquatic invertebrate taxa. Seven of the plant species are important agricultural weeds, and two are alien to Spain. Diaspores from six plant taxa were germinated. We collected propagules from the outside of 13 crayfish captured as they moved out of ricefields during harvest, and found a similar set of plants and invertebrates, suggesting that propagules in gull excreta were ingested inadvertently with their crayfish prey.

Our results confirm that secondary dispersal by waterbirds can be of great importance, both when feeding on different fish species or an alien crayfish. This dispersal mode can promote the expansion of both native and alien species. Secondary dispersal pathways associated with complex food webs must be studied in detail if we are to understand species movements in a changing world.

Acknowledgments
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Effects of forest fragmentation on seed dispersal networks in Brazilian Atlantic rainforest

Emma-Liina Marjakangas[1], *Nerea Abrego*[2], *Vidar Grøtan*[3], *Milton Ribeiro*[4], *Mauro Galetti*[5], *Renata de Lara Muylaert*[6], *Richard Stevens*[7], *Laurence Culot*[8], *Lucas Pereira*[9], *Erica Hasui*[10], *Fernando Lima*[11], *Paulo Inácio Prado*[12], *Alexandre A. Oliveira*[13], *Ricardo Bovendorp*[14], *Carolina Bello*[15], *Renato de Lima*[16], *and Otso Ovaskainen*[17]

[1] Norwegian University of Science and Technology, Norway
[2] University of Helsinki, Finland
[3] Norwegian University of Science and Technology, Norway
[4] Universidade Estadual Paulista, Brazil
[5] Universidade Estadual Paulista, Brazil
[6] Universidade Estadual Paulista, Brazil
[7] Museum of Texas Tech University, U.S.A.
[8] Universidade Estadual Paulista, Brazil
[9] Universidade Estadual Paulista, Brazil
[10] Universidade Federal de Alfenas, Brazil
[11] Universidade Estadual Paulista, Brazil
[12] Universidade de São Paulo, Brazil
[13] Universidade de São Paulo, Brazil
[14] Universidade Estadual Paulista, Brazil
[15] Universidade Estadual Paulista, Brazil
[16] Universidade de São Paulo, Brazil
[17] University of Helsinki, Finland
[*]E-mail: emma-liina.marjakangas@ntnu.no

Keywords: community structure, co-occurrence, functional connectivity, joint species distribution model, species interaction

Forest cover loss and degradation due to land use activities is one of the principal causes of global biodiversity loss. Deforestation rates are disproportionally high in tropical biodiversity-rich areas. Indirectly, forest fragmentation can reduce biodiversity by disrupting species interaction networks. Species interaction networks, such as pollination or seed dispersal networks, are fundamental in maintaining ecosystem functioning. In tropical forests, frugivorous animals act as the most important means for seed dispersal and thus are one of the main agents of forest regeneration. The long-lasting anthropogenic defaunation of tropical forest ecosystems has strongly altered the interaction networks of seed dispersers,

which has in turn affected the composition of plant communities and important ecosystem services, such as carbon storage. Moreover, recorded observations on seed dispersal interactions are usually biased taxonomically, temporally and geographically. Therefore, knowledge on potential interactions and on a more mechanistic perspective on the processes behind observed changes in community composition are called for. The objectives of this study were to examine how fragmentation-related factors affect interactions between and among seed dispersers and trees in highly fragmented Brazilian Atlantic rainforest. We used spatially and taxonomically comprehensive data sets on frugivorous animal (including bats, birds, large mammals, primates and rodents) and tree occurrences within Brazilian Atlantic rainforest biome. We fitted a spatially explicit joint species distribution model to each taxonomical group occurrence data to combine information on traits, environmental covariates, phylogenetic correlations, and the spatially explicit data structure. The models were fitted separately for each taxonomical group. To examine the co-occurrence associations among the taxonomical groups, we first used the group-specific models to generate predicted communities spanning over the entire biome. We then used the predicted species communities to produce spatial maps on species richness, regions of common profile in community composition, and trait composition over the biome. On average, fragmentation, topography and climatic factors had equally strong effects on the variation in community structure, but the effect of fragmentation was smaller in avian frugivore groups. Positive interactions within the taxonomical groups were scarce after accounting for shared environmental requirements, whereas negative interactions were nearly non-existing. This could be due to the manifold indirect interactions among the species at the same trophic level. Species richness and the number of interactions links were higher in areas with larger overall forest cover. This highlights the importance of area conservation over individual species conservation.

Viral metacommunities of bats and rodents

Fabiola Nieto-Rabiela[1*], *Gerardo Suzán*[1], *Anuwat Wiratsudakul*[2], *Oscar Rico-Chávez*[1]

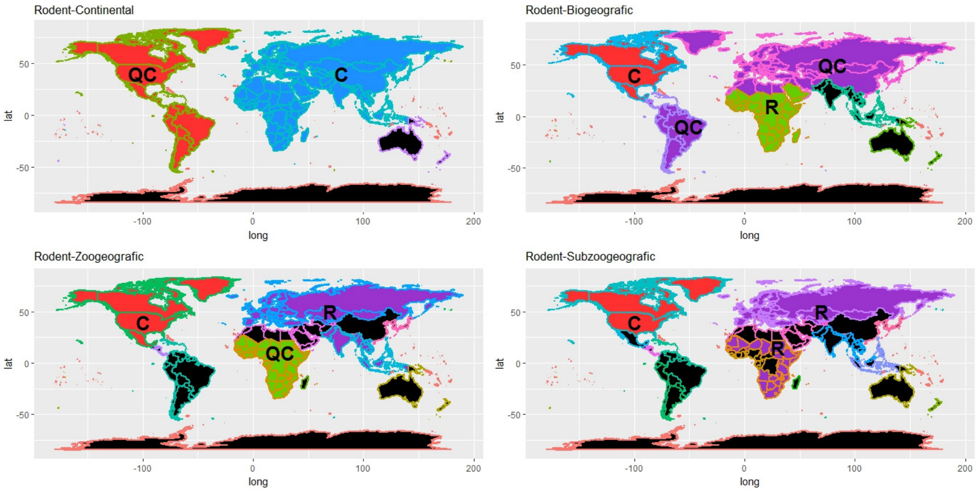
[1]Departamento de Etología, Fauna Silvestre y Animales de Laboratorio, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, México
[2]Department of Clinical Sciences and Public Health, Faculty of Veterinary Science, Mahidol University, Nakhon Pathom, Thailand
[*]E-mail: fabyz00nr@gmail.com

Keywords: niche theory, functional diversity, phylogenetic diversity, diseases ecology, host environmental filtering, biogeographic, zoogeographic

Identifying the mechanisms that modulate the diversity of symbionts associated with wildlife is fundamental for a better understanding of the factors that modulate the assemblages of multi-host and multi-pathogenic systems. Small mammals represent an ideal system for exploring the structures of viral assembly associated with their hosts. The objective of the present work was to analyze the contribution of phylogenetic and functional factors to the assembly and structure of viral metacommunities associated with rodents and bats at different spatial scales and in viral taxonomy scales. It is necessary highlight that each scale

represent a historical processes influenced over the biodiversity along the time within regions and depending the surface size to be analyzed, the migration capability of both the host and virus is also affected. A meta-analysis was performed using a database of virus reports by molecular methods grouping them in different regions 1) continental: America, Oceania and "Big Mass" including Europe, Africa and Asia; 2) Biogeographic: Neotropical, Neotropical, Palearctic, Afrotropical, Oriental and Australian and 3) Zoogeographic: Neotropical (Na1, Na2), Panamanian, Neotropical (No1, No2), Palearctic, Afrotropical (A1, A2), Oriental), Sahara-Arabic, Sino-Japanese and Australian. For each region, the metacommunity structure was determined both at the level of viral species and viral family. The contribution of phylogeny, and host traits as body mass, litter size, number of layers per year and trophic guild to the metacommunity assembly for each region was calculated using a redundant analysis of canonical ordering (RDA). The following metacommunity structures were detected in rodents: three Clementsian, four quasi-clementsian and three randomly, showing a tendency toward Clementsian structures, which indicate a restricted distribution of viruses through their hosts, which, when complemented with RDA results, assume that in the American continent, more specifically in the Nearthic region, this restricted distribution refers to the predilection for clades, since 29% and 10% phylogenetic contributions were obtained as maximum values, respectively. While in bat dominated random structures due to the presence of cosmopolitan viruses, with presence of up to 75% of virus species such as rabies, which disrupt such structures. In spite of this, bats are more coherent at the viral family level, with the emergence of four quasi-clementsian structures and 1 checkboard. In contrast, rodents share viruses among families, overlapping and presenting more coherence at the viral species level. The results indicate that the assemblage of viral diversity associated with rodents and bats responds to phylogenetic and functional characteristics, which alternate between regions depending on the predominant historical processes. Therefore we can conclude that the viral metacommunities associated with chiroptera and rodents are predominantly Clementsian and respond to environmental filters of the host, offering us tools to recognize patterns of virus-host association. Approaching the understanding of the rules of virus-host association and providing tools to make better decisions in epidemiological cases on surveillance, control and even prediction of viral distribution and dissemination.

Figures

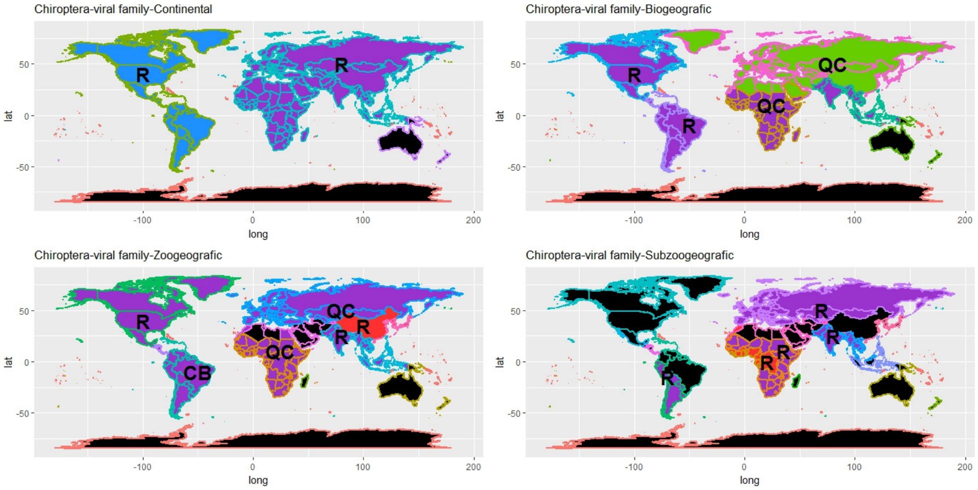

Rodent-Continental

Rodent-Biogeografic

Rodent-Zoogeografic

Rodent-Subzoogeografic

Figure 1. Rodent results - Viral species


Chiroptera-viral family-Continental

Chiroptera-viral family-Biogeografic

Chiroptera-viral family-Zoogeografic

Chiroptera-viral family-Subzoogeografic

Figure 2. Chiroptera results - Viral Family

Table

ROEDENTS											
Continental Host/Virus	Structure	RDA	Biogeographic region Host/Virus	Structure	RDA	Zoogeographic region Host/Virus	Structure	RDA	Subzoo-geographic region Host/Virus	Structure	RDA
America 57X49	Cuasi-clementsian	29% Phylo 0.14% Phylo+Fun	Neartic 41X42	Clementsian	10% Phylo 6.64% Fun				Na1 38X40	Clementsian	10.78% Phylo 6.75% Fun
									Na2	INSUFFICIENT	
			Neotropical 41X27	Quasi-clementsian	0.9% Phylo+Fun	Panamian	INSUFFICIENT				
		0.14% Phylo+Fun				Neotropical	INSUFFICIENT		No1	INSUFFICIENT	
									No2	INSUFFICIENT	
Big Mass 48X44	Clementsian	0.26% Fun	Paleartic 41X34	Quasi-clementsian	0.9% Phylo+Fun	Paleartic 28X24	Random	1.6% Phylo+Fun			
						Sinho-Arabic	INSUFFICIENT				
						Sinho-Japaness	INSUFFICIENT				
			Afrotropical 27X24	Random	0%	Afrotropical 27X24	Quasi-clementsian	0%	A1 22X14	Random	19% Phylo+Fun
									A2	INSUFFICIENT	
			Oriental	INSUFFICIENT		Oriental	INSUFFICIENT		O1	INSUFFICIENT	
									O2	INSUFFICIENT	
			Australian	INSUFFICIENT		Australian	INSUFFICIENT				

Table 1. Rodent results - Viral species

Chiroptera											
Continental Host/Virus	Structure	RDA	Biogeographic region Host/Virus	Structure	RDA	Zoogeographic region Host/Virus	Structure	RDA	Subzoo-geographic region Host/Virus	Structure	RDA
America 61X25	Random	0.88% Fun	Neartic 37X14	Random	2.39% Phylo+Fun	Neartic 39X15	Random	2% Phylo+Fun	Na1 27X12	Random	9% Phylo+ Fun
									Na2	INSUFFICIENT	
			Neotropical 46X20	Random	1.71% Phylo+Fun	Panamian	INSUFFICIENT				
						Neotropical 40X13	Random	1.28% Phylo+Fun	No1 35X11	Random	0%
									No2	INSUFFICIENT	
Bigg Mass 103X82	Quasi-clementsian	0.83% Phylo+Fun	Paleartic 75X84	Random	1.73% Phylo 0.69% Phylo+Fun	Paleartic 33X44	Random	0.65% Phylo+Fun			
						Sinho-Arabic	INSUFFICIENT				
						Sinho-Japaness 49X50	Random	6.09% Fun 5.32% Phylo			
			Afrotropical 50X38	Random	6.12% Phylo+Fun	Afrotropical 40X36	Random	7.41% Phylo+Fun	A1 29X20	Random	19% Phylo+ Fun
									A2 19X22	Random	9.62% Phylo+ Fun
						Madagascan	INSUFFICIENT				
			Oriental 18X25	Random	8.96% Phylo+Fun	Oriental 18X25	Random	8.96% Phylo+Fun	O1	INSUFFICIENT	
									O2	INSUFFICIENT	
			Australian	INSUFFICIENT		Australian	INSUFFICIENT				

Table 2. Chiroptera results - Viral Species

Chiroptera- Viral family											
Continental Host/Virus	Structure	RDA	Biogeographic region Host/Virus	Structure	RDA	Zoogeographic region Host/Virus	Structure	RDA	Subzoogeographic region Host/Virus	Structure	RDA
America 61X14	Random	0.8% Fun	Neartic 37X10	Random	2.41% Phylo+Fun	Neartic 39X10	Random	2.02% Phylo+Fun	Na1	INSUFFICIENT	
									Na2	INSUFFICIENT	
			Neotropical 46X13	Random	1.7% Phylo+Fun	Panamian	INSUFFICIENT				
						Neotropical 40X10	Check-board	1.28% Phylo+Fun	No1 35X9	Random	2.46% Phylo+Fun
									No2	INSUFFICIENT	
Bigg Mass 103X23	Random	1.78% Phylo+Fun	Paleartic 75X26	Quasi-clementsian	0%	Paleartic 33X20	Quasi-clementsian	0.83% Phylo+Fun			
						Sinho-Arabic	INSUFFICIENT				
						Sinho-Japaness 49X20	Random	7.5% Phylo 6.09% Fun			
			Afrotropical 50X17	Quasi-clementsian	6.28% Phylo+Fun	Afrotropical 40X17	Quasi-clementsian	8.01% Phylo+Fun	A1 29X8	Random	1.79% Phylo+Fun
									A2 19X15	Random	4.19% Phylo 2.22% Fun
						Madagascar	INSUFFICIENT				
			Oriental 18X12	Random	11.42% Phylo+Fun	Oriental 18X12	Random	11.42% Phylo+Fun	O1 10X11	Random	28.76% Phylo+Fun
									O2	INSUFFICIENT	
			Australian	INSUFFICIENT		Australian	INSUFFICIENT				

Table 3. Chiroptera results - Viral Family

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Effect of field sampling design on variation partitioning in a dendritic stream network

Péter Sály[1*], *Tibor Erős*[2]

[1]Department of Hydrobiology, University of Pécs, Pécs, Hungary
[2]MTA Centre for Ecological Research Balaton Limnological Institute, Tihany, Hungary
[*]E-mail: psaly@gamma.ttk.pte.hu

Keywords: metacommunity, fish assemblage, species distribution modelling, network topology, Moran's eigenvector maps (MEM), relative importance of space and environment

Variation partitioning is one of the most frequently used method to infer the importance of environmental (niche based) and spatial (dispersal) processes and dispersal limitation in metacommunity structuring. However, the reliability of the method in predicting the role of the major structuring forces is less known. We studied the effect of field sampling design on the result of variation partitioning of fish assemblages in a stream network. Along with four different sample sizes, a simple random sampling from a total of 115 stream segments (sampling objects) was applied in 400 iterations, and community variation of each random sample was partitioned into four fractions: pure environmentally (landscape variables) explained, pure spatially (MEM eigenvectors) explained, jointly explained by environment and space, and unexplained variance. Results were highly sensitive to sample size. Even at a given sample size, estimated variance fractions had remarkable random fluctuation, which can lead to inconsistent relative importance of the environmental and spatial variables structuring of metacommunities. Interestingly, all the four variance fractions correlated better with the number of the selected spatial variables than with any design properties. Sampling interval proved to be a fundamentally influential sampling design property because it affected the number of the selected spatial variables. Our findings suggest that the effect of sampling design on variation partitioning is related to the ability of the eigenvectors to model complex spatial patterns. Hence, properties of the sampling design should be more intensively considered in metacommunity studies.

Effect of niche characteristics and site position on occupancy frequency distribution of stream macroinvertebrates

Ildikó Szivák[1], *Pál Boda*[2], *Gábor Várbíró*[2], *András Csercsa*[3], *Eszter Á. Krasznai*[2,4], *Arnold Móra*[1,5], *Diána Árva*[6], *Mónika Tóth*[1], *Tibor Erős*[1]

[1]Balaton Limnological Institute, MTA Centre for Ecological Research, Tihany, Hungary
[2]Duna Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[3]Department of Biology of Ecosystems, University of South Bohemia, Ceske Budejovice, Czech Republic
[4]Doctoral School of Chemistry and Environmental Sciences, University of Pannonia, Veszprém, Hungary
[5]Department of Hydrobiology, University of Pécs, Pécs, Hungary
[6]Research Institute for Fisheries and Aquaculture, National Agriculture Research and Innovation Centre, Szarvas, Hungary
[*]E-mail: szivak.ildiko@okologia.mta.hu

Keywords: metacommunity theory, niche and dispersal-related processes, occupancy frequency distribution, freshwater insects

One approach to examine patterns in the distribution of species in nature is the occupancy frequency distribution (OFD), which can delineate rare and common species. A number of ecological mechanisms have been associated with different forms of OFD. At one extreme end, there are generalists and common species with broad niches and wide regional distribution; those patterns are driven mainly by the dispersal-related processes. At another extreme end, there are specialist and rare species with small ecological niches and restricted distribution, that patterns are influenced mainly by niche-related processes. For stream insects the unimodal right-skewed OFDs are common, implying that most species are very rare. This pattern indicates that the assemblages are under environmental control and are driven by niche-related processes caused by the high environmental variability and geographical isolation of habitats. Beside niche-based processes, dispersal-related processes may also account for species distribution patterns and predict bimodal OFD in which most species are widespread or extremely restricted. In stream assemblages the bimodal OFD is rare, and it can be seen in the case of generalist and widespread species groups. The relative role of niche and dispersal-related processes can be varying depending on the positioning within the stream network and environmental heterogeneity. Furthermore, within the same assemblage, the role of niche and dispersal-related processes can have different effects on the distribution pattern of species with different ecological traits (specialist vs. generalist).

We deconstructed entire insect assemblages by ecological traits and compared the form and modality of the OFDs of specialist and generalist species for streams and rivers in Hungary. The sampling sites were surveyed twice (spring and late summer) during one year period to determine the seasonal influence.

We found mainly right-skewed OFDs implying the importance of niche-related processes in both streams and rivers. Notable differences were detected in the form of OFDs between species groups with different niche characteristics. Specialist species showed strongly right-skewed OFDs implying the importance of niche-related processes, while generalist species showed much variation in OFDs (e.g. bimodality in spring in streams) indicating the effect of both dispersal and niche-related processes. We found differences in OFD patterns depending on habitat position only for specialist species. Specifically, niche-related processes were less pronounced in the stream than river sites in summer. Finally, the influence of seasonality appeared only in stream sites: niche-related processes were slightly more significant in spring than in summer for both specialist and generalist species. In conclusion, the form of OFDs was considerably influenced by the niche characteristics of species; and the variation in the OFDs of species cannot be clearly related to network position.

Statistical ecology

Design-based mapping of natural resources and their diversity

L. Fattorini[1]*, M. Marcheselli*[1]*, C. Pisani*[1]*, L. Pratelli*[2]

[1]University of Siena, Italy
[2]Naval Academy, Livorno, Italy

Spatially explicit information is needed in many ecological studies. In most cases, the extent of the study region render impractical, perhaps even impossible, to completely census the entire region. Thus, the survey variable is measured only for a sample of points. In these situations, estimation criteria are necessary to estimate the values of the survey variable within non-sampled sites and obtaining wall-to-wall maps depicting the spatial pattern of the survey variable throughout the whole study region. Until now, methods adopted to reconstruct population maps lie in the realm of model-dependent inference, i.e. the sampled units are held fixed (as if they were purposively selected) and the values of the survey variable at points are supposed to be random variables generated from a spatial process (super-population). Under model-dependent approaches, the probability distribution of any sample statistic is determined from the uncertainty entailed by the super-population which has been supposed to generate the population values, conditional on the sampled points. In model-dependent approach, the most common techniques are the kriging predictors. Throughout the years, kriging has become a standard procedure for the interpolation of spatially distributed data in several disciplines (geology, climatology, meteorology, etc.). Other methods adopted to reconstruct population maps exploit the auxiliary information which may be available for all the sites of the population, e.g. the auxiliary variables related with the survey variable achieved for all sites from remote sensing sources. Widely adopted techniques of this kind are cokriging, regression kriging, locally weighted regression and k-nearest neighbour methods. In this paper we attempt map reconstruction in a design-based framework, i.e. population values are viewed as fixed constants and the probability distribution of any sample statistic is determined from the uncertainty entailed by the probabilistic sampling scheme adopted to select sites. Values at single unsampled sites are estimated by means of a spatial interpolation, adopting a weighted function of the sample data. Weights decrease with the distance of the sample sites from the site under estimation. The design-based asymptotic properties of the interpolator are considered as the number of sampled sites increased. Conditions ensuring design-based asymptotic unbiasedness and consistency are derived. These conditions essentially require the existence of a continuous and bounded surface onto the study area and the use of spatially balanced sampling designs to select sites. A very portable mean squared error estimator is adopted. The results of a simulation study from artificial and real populations are reported to confirm the theoretical results. An application of the method for mapping the coverage of holly oak and white violet in the protected area of "Montagnola Senese" (Central Italy) is reported.

Structural equation models account for ecological complexity

Sonia Lombardi[1,2*], *Simona Imperio*[3], *Stefano Focardi*[2], *Antonello Provenzale*[3]

[1]CNR- ISC (The Institute for the Complex Systems),Via Madonna del Piano, 10, 50019,
Sesto Fiorentino (FI), Italy
E-mail: sonia.lombardi@fi.isc.cnr.it
[2]Department of Biology - University of Florence, Via Madonna del Piano, 6, 50019, Sesto Fiorentino (FI), Italy
E-mail: stefano.focardi@isc.cnr.it
[3]CNR-IGG (Institute of Geosciences and Earth Resources),Via Moruzzi, 1, 56124, (PI), Italy
E-mail: simona.imperio@igg.cnr.it

Empirical studies of ecological communities need to account for a large number of reciprocal effects among the components of the studied ecosystem. It is of the uppermost interest to disentangle these relationships, to discriminate causal effects from spurious correlations and deal with observational errors, which, in studies performed under natural conditions may be large and have the potential to bias our conclusions. More and more studies make use of structural equations models (SEM) to deal with complex ecological systems. Here we review this literature and discuss pros and cons of this statistical methodology as compared with standard generalised linear models. Further, we demonstrated the use of SEM using a 100-years-long time series relative to the abundance of three sympatric species of wild ungulates (roe deer, wild boar and fallow deer) and we demonstrate the use of an innovative methodology (Generalised SEM) which has a great potential for analysing complex networks characterised by non-normal distributions and by categorical variables. We tested two main hypotheses: i) the complexity level of the ungulate community affects the strength of intra- and inter-specific competition; ii) intra- and inter-specific interactions are stronger than climate forcing in a Mediterranean environment.

Confronting existing knowledge with data: trait based modeling of macro-invertebrate community composition in Swiss rivers under multiple stressors

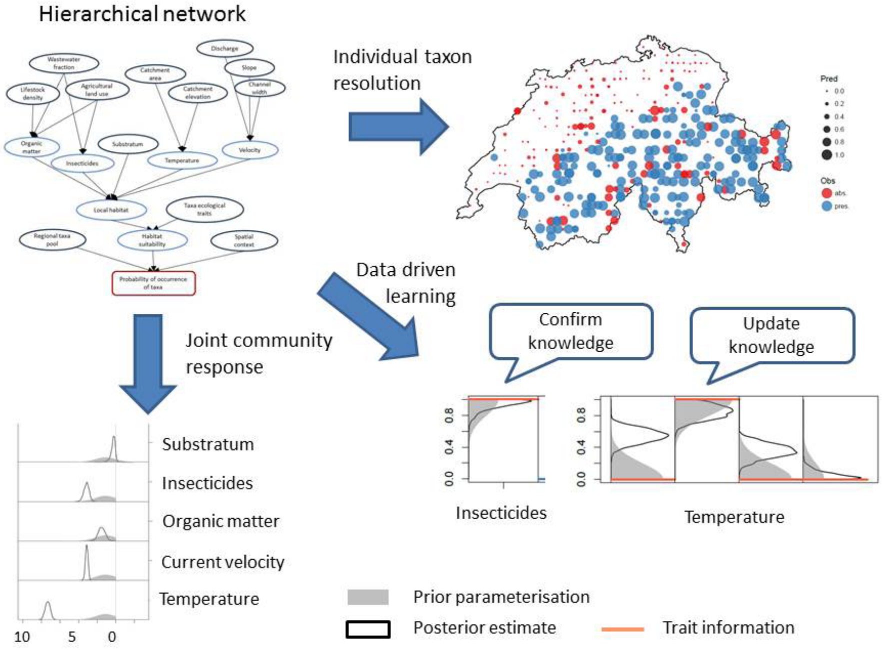
Peter Vermeiren[1*], *Peter Reichert*[1], *Nele Schuwirth*[1]

[1]Department Systems Analysis, Integrated Assessment and Modelling, EAWAG, Duebendorf, Switzerland
[*]E-mail: peter.vermeiren@eawag.ch

Keywords: Hierarchical model, Bayesian network, land use, river management, ecological traits

Multiple human and natural influence factors affect invertebrate communities in rivers, with knock on effects on ecosystem functioning and goods and services provisioning. Despite well-developed knowledge on invertebrate-environment interactions and the availability of Swiss wide biomonitoring data, critical issues remain in disentangling effects of multiple stressors and moving towards understanding that is applicable across river basins with different taxonomic compositions. We aimed to test and improve current understanding of how community composition or macro-invertebrates in rivers is influenced by environmental factors that change across natural and anthropogenic gradients. Therefore, we formalized expert knowledge on invertebrate-environment interactions, available in trait databases, to predict the probability of occurrence of taxa within characteristic communities at sites throughout Switzerland. We derived direct environmental factors that describe local habitat conditions from indirect environmental factors including land use, pollution sources, river morphology and topography. Local environmental conditions were then combined with data on trait preferences for each taxon to derive a habitat suitability for each environmental factor and taxon at each site. Additional factors such as the spatial context of the site, the regional species pool and observation errors will be taken into account. The model was calibrated with monitoring data using a generalized linear model and Bayesian inference was used to validate and improve knowledge on trait preferences of individual taxa. The model allows a test of cause-effect relationships for different human stressors and allows synthesis, testing and improvement of current trait knowledge. We aim to apply the model in decision support for river management

Figure



Overview of the hierarchical model with results at individual and community level, and an example of data-driven learning of trait information of individual taxa.

Plant ecology

Post-exclosure community dynamics in acidic sandy grasslands: cryptogams, phanerogams and soil seed bank

Rebeka Balogh[1*], *Edit Farkas*[2], *László Lőkös*[3], *Beáta Papp*[3], *Tibor Novák*[4], *Gábor Matus*[1]

[1]Department of Botany, University of Debrecen, Debrecen, Hungary
[2]HAS Centre for Ecological Research, Institute of Ecology, Vácrátót, Hungary
[3]Hungarian Natural History Museum, Budapest, Hungary
[4]Dept. for Landscape Protection and Environmental Geography, University of Debrecen, Debrecen, Hungary
[*]E-mail: beca002@gmail.com

Keywords: Corynephoretum, Festucetum vaginatae, grazing, lichens, mosses, vascular plants, soil seed bank

Open grasslands may differ in their sensitivity to management change. In eastern part of the lowlands of Carpathian Basin open sandy grasslands of *Pannonic inland dunes* are enlisted in EU Habitat Directive (no. 2340) as communities seriously endangered of disappearance. Due to the widely practiced plantation with black locust these have suffered a large scale habitat loss in the last decades. Unfortunately, little is know about their spontaneous dynamics or best management practices. This especially holds for cryptogams, a usually neglected segment in vegetation dynamics, though these compose a significant part of biomass and that of diversity in this community type. Vegetation dynamics of Corynephoretum canescenstis and that of Festucetum vaginatae, the two characteristic vegetation types of the Nyírség's sand region shared by Hungary and Romania, has been monitored in grazed and experimentally fenced stands. Fencing was used to model the prevailing trend of falling stocking densities. Vegetation change of grazed and fenced permanent plots has been surveyed from 2007 to 2016. Soil seed banks have been analysed right away at fencing in 2009 then repeated in 2015. Biomass of cryptogams has been sampled in 2013, five years after grazing exclosure, then hand-sorted into species. Spot tests as well as HPTLC has been applied to identify critical lichen taxa. Soil analyses have taken place at the beginning and closing of the project. Composition and dominance of cryptogams has been correlated with microtopography and selected soil traits. Fencing has led to a generally increased cover and biomass in vascular plants soon after fence was built and the same in cryptogams a few years latter due to their slower growth rates. Large dicots (*Centaurea biebersteini*, *Thymus degenianus*) reacted positively while small vasculars either perennials (*Poa bulbosa*, *Corynephorus canescens*) or annuals (*Digitaria ischaemum, Minuartia viscosa*) have adversely been affected by the exclosure. The colonist moss *Syntrichia ruralis* and the strong competitor grass, *Festuca vaginata* proved hardly influenced by management change. Response of *Cynodon dactylon* proved ambiguous as it increased its dominance in Corynephoretum whereas decreased in Festucetum vaginatae. As a rule, biomass of mosses exceeded those of lichens irrespective of the community or management. Overall cryptogamic biomass tended to be significantly lower in Corynephoretum than in Festucetum vaginatae as well as lower in grazed stands than

in fenced ones. Most cryptogams (e.g. *Brachythecium albicans, Cladonia rangiformis*, *C. rei* and *Polytrichum piliferum*) were among supported species. Lichens in general benefited relatively more from exclosure than did the mosses. The only cryptogam apparently favoured by moderate grazing has been the legally protected lichen *Cladonia magyarica*. A drawback of fencing has been that it seems to support the invasive *Ambrosia artemisiifolia* and *Conyza canadensis*. Out of the totally redorded 58 seed bank species only a handful had dense (>500/ m^2) viable seed populations (in decreasing rank dominants were *Rumex acetosella, Minuartia viscosa, Scleranthus annuus* and *Conyza canadensis*). Composition and dominance of seed bank of grazed-fenced pairs in both community proved very similar. No proof for changing soil seed banks has been gathered within the studied period possibly because persistent seed banks tend to accumulate during decades. We concluded that Corynephoretum is more sensitive to management change (more grazing steressed) than the abiotically more stressed Festucetum vaginatae. Long-term grazing exclosure is likely to promote the spread of some invasive aliens or even lead to spontaneous forestation and brings the decline of characteristic annuals. Some short spells of low intensity grazing or patchy grazing are, however, likely to promote cryptogam biodiversity and avoid denudation.

Impact of the invasive *Impatiens glandulifera* on the growth of co-occurring native plants

Judith Bieberich[1, 2*], *Marianne Lauerer*[1], *Maria Drachsler*[1,] *Julian Heinrichs*[1],
Stefanie Müller[1], *Heike Feldhaar*[2]

[1]Ecological Botanical Garden, University of Bayreuth
[2]Department of Animal Ecology 1, University of Bayreuth
[*]E-mail: judith.bieberich@uni-bayreuth.de

Keywords: plant invasion, allelopathy, competition, growth experiment, seedlings, juvenile plants

The success of invasive plant species might be facilitated by allelopathy (novel weapon hypothesis) and a strong competitive effect. *Impatiens glandulifera*, an alien plant species in Europe, produces 2-Methoxy-1,4-naphthoquinone (2-MNQ) and can suppress the growth of natives. To date it is not known, (1) if really 2-MNQ is responsible for the growth suppression of native plants, (2) if this effect depends on the plant's developmental stage and (3) if *I. glandulifera* is tolerant to its own chemical weapons.

We investigated the impact of *I. glandulifera* on seedlings and juvenile plants of three native European species often co-occurring with *I. glandulifera* in the field. Germinated seeds of the target species were grown for six days on agar together with seeds of *I. glandulifera* or on agar containing 2-MNQ. Impact on growth of juvenile plants was investigated in a pot experiment. Four week old plants were grown for ten weeks together with *I. glandulifera* plants (interspecific competition), together with plants of the own species (intraspecific competition) or as single plant watered with 2-MNQ. Several growth parameters of all target plants were quantified.

The impact of *I. glandulifera* depended on the target species and on the plant's developmental stage. *I. glandulifera* juveniles were surprisingly not tolerant to 2-MNQ and to intraspecific competition. In conclusion this may regulate growth within *I. glandulifera* populations. Regarding the native seedling experiments only *Urtica dioica* was negatively affected. In the juvenile stage 2-MNQ reduced the growth of *U. dioica* and *Geum urbanum* but not of *Filipendula ulmaria*. In competition with *I. glandulifera* the growth of all natives was reduced, most of all *U. dioica* up to 86 %. However the competitive effect of *I. glandulifera* mostly was not stronger than the intraspecific competition. In conclusion *I. glandulifera* has a similar part in the ecosystems than the investigated dominant native plants without eliminating them but reducing their cover. Species specific reactions to *I. glandulifera* further may result in changed species compositions in native plant communities.

Acknowledgments
We thank the Cusanuswerk for financial support and the gardeners of the Ecological Botanical Garden for their advice in plant cultivation.

Functional variation of *Brachypodium genuense* (DC.) Roem. *et* Schult in sub-Mediterranean grasslands

Alessandro Bricca[1*], *Federico Maria Tardella* [2], *Karina Piermarteri* [3] , *Nicola Postiglione* [3], *Andrea Catorci*[2]

[1]Department of Science, University RomaTre, Rome, Italy
[2]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy
[3]School of Advanced Studies, University of Camerino, Camerino, Italy
[*]E-mail: alessandro.bricca@uniroma3.it

Keywords: intra-specific functional trait, grassland invasion, fast-slow growing strategies

Semi-extensive farming cessation and settlement abandonment are threatening European pastoral landscapes and their biodiversity, affecting species assemblage and ecosystem functioning. At community level, this process typically involves the spread of coarse tall grass species able to dominate the community thanks to particular sets of traits. In this sense *Brachypodium genuense* (DC.) Roem. *et* Schult. is a problematic species occurring in the semi-natural grasslands of the Italian peninsula over 1,200-1,400 m a.s.l. Its spread decreases the light irradiance at the ground level, besides soil pH, temperature and water content as well as species diversity and richness. In addition, *B. genuense* dramatically reduces the nutrient value of pastures negatively affecting both shepherding and habitat suitability for wild herbivores. Consequently, understanding the ecological factors that allow for its spread, and the relationship between its functional features and environmental constraints, is a primary goal for biodiversity and socio-economic issues. Since traits reflect the trade-offs among different functions within a plant and variations in resource availability have been shown to determine their inter- and intra-specific variations.

We hypothesized that *B. genuense* was able to spread and dominate the sub-Mediterranean grassland communities (Monti Sibillini, central Italy) subjected to a wide range of environmental conditions, thanks to its broad spectrum of performances. In fact, it showed large plasticity, mirrored by high variations of Specific Leaf Area (SLA), plant height and tussock cover values.

We found that in more productive conditions (deeper soil, medium/high pH values, north-facing slopes, and "conservative" landforms) populations of *B. genuense* had higher SLA, plant height and cover values. This underlies a fast-growing strategy based on high resource rate of acquisition and use, as well as higher competitive ability for aboveground resources (e.g. light). In unproductive/dry conditions (south-facing slopes, shallow soils, lower pH values) *B. genuense* had lower SLA, plant height and cover values, underlying a slow-growing strategy with low rate of resource acquisition and high rate of resource conservation. In addition, we found that very high nitrogen amount might have a detrimental effect on *B. genuense* individuals decreasing the SLA values, thus requiring the plant to change the growth strategy.

We also inferred that the invasive/dominant behavior of competitive-stress tolerant tall grasses is related not only to clonal integration strategy, plant height, litter deposition, etc., but also to the morphological plasticity of leaves, allowing plants to maintain the coordination of multiple resource capture and, hence, to sustain dominance.

Acknowledgments
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The effects of habitat type and precipitation on *Quercus robur* seedling emergence and survival

László Erdős[1*], *Gábor Ónodi*[1], *György Kröel-Dulay*[1]

[1]Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary
[*]E-mail: erdos.laszlo@okologia.mta.hu

Keywords: forest-steppe, spatial heterogeneity, pedunculate oak, by commas

The existence of forest-steppes depends on a subtle balance of several environmental factors, thus even minor modifications in some parameters can result in considerable vegetation changes. As forest-steppes of the Carpathian Basin are located at the western edge of the biome, they may be particularly sensitive to environmental changes.

In the Carpathian Basin, mean annual temperature is likely to increase and summer precipitation to decrease with climate change. Oaks are usually expected to react negatively to these changes. However, the frequency of extreme precipitation events will probably increase, which may have positive effects for oak regeneration. Unusually wet seasons or years may be of particular significance, and may benefit oak germination and seedling establishment. This, in turn, can have fundamental effects on community structure and composition. In this study our aim is to investigate how artificial watering changes oak performance in different micro-habitats.

The precipitation manipulation experiment is being conducted in the Kiskunság National Park, near Fülöpháza. *Quercus robur* acorns were collected within a near-natural oak forest in the region. To exclude acorns with a reduced viability (e.g. aborted, insect-infected), we carried out visual inspection and the float test. We selected 16 forest patches. For each patch, 6 acorns were planted within the forest interior, 6 acorns in the north-facing forest edge, and 6 ones into the neighbouring grassland.

We applied two precipitation treatments: control acorns received ambient precipitation, while the second group received additional water from April till September (approximately 15 mm each time at a biweekly resolution). A total of 288 acorns was used in the experiment (3 habitats × 16 replicates × 2 treatments × 3 acorns). Soil moisture was measured biweekly, other background factors (e.g. light availability, herb layer cover, leaf litter) were estimated once. Seedlings were censused biweekly, and their performance (e.g. height, number and size of leaves) was registered in September.

Background factors differed significantly among the three habitats. Light availability was the highest in grasslands, the lowest in forest interiors, and intermediate in edges, while soil moisture showed a reverse pattern. The cover of the herb layer was the largest in edges, while that of mosses was highest in grasslands. Leaf litter cover was considerable in both the forest interiors and the edges.

Seedling emergence and survival was very similar for the forest interiors and the forest edges. In both cases, seedling number was increasing rapidly with the additional watering, while there was a lag-phase with the controls. From the second half of June, however, there was virtually no difference between the two treatments. Results were quite different for the grasslands, where seedling performance was weak compared to the forest and edge habitats. Seedling number was low throughout the study period in the control group, while it was significantly higher in the group with additional watering. From June-July onwards, there was a decrease in seedling number, although some individuals later re-sprouted.

Leaf number per seedling was the highest in the edges, and a bit lower in forest interiors. Seedlings were higher in forest interiors than in edges. Leaf size did not differ considerably between the forest interior and edge habitats. Differences between the control and the watered groups were minor or non-existent for all the above cases. For all these parameters, grasslands tended to have the lowest values.

We conclude that both habitat type and precipitation can have a great effect on oak seedling emergence and survival. Despite the marked differences in habitat parameters, forest interiors and edges are almost equally suitable for oaks, while oaks heavily depend on additional watering in grasslands. The moderate differences between the two treatments in the case of forest interiors and edges may have been caused by the unusually wet growing season in the study year.

Changes of assembly rules with time and restoration treatments in an old-field succession

Melinda Halassy[1*], *Zoltán Botta-Dukát*[1], *Anikó Csecserits*[1], *Katalin Török*[1]

[1]Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary
[*]E-mail: halassy.melinda@okologia.mta.hu

Keywords: carbon amendment, dry grassland, ecological filters, mowing, plant traits, seeding

Community assembly was recently suggested as principle guide for ecological restoration. Our basic hypothesis is that old-field succession is dominantly a trait-driven process with significant changes of assembly rules with time and by understanding these changes, adaptive management can help to achieve restoration target. We carried out microscale field experiments to test the following hypotheses: i. early seeding of a limited number of species results in a long-lasting impact on vegetation composition (priority effect); ii. dry climate and low productive soil represent an environmental stress that results in increasing convergence of traits useful in the adaptation of species to stress (stress-dominant hypothesis); iii. reducing nutrient availability in restoration further strengthens trait convergence; iv. as the canopy closes in old-field succession, competition between species results in the divergence of traits related to resource acquisition (limiting similarity hypothesis); v. mowing decreases trait divergence because it opens the canopy and thus decreases competition.

The study was conducted in the Kiskunság inland sand dune area in the center of the Pannonian biogeographic region, Europe. The target of restoration efforts was the drought limited sand grassland (Festucetum vaginatae danubiale Soó 1929) on former arable lands. Restorative interventions focused on the manipulation of the dispersal, abiotic and biotic filters including early seeding of five target species (Dianthus serotinus, Euphorbia segueriana, Festuca vaginata, Koeleria glauca, Stipa borysthenica) to overcome dispersal limitation; carbon amendment to lower soil available nitrogen as abiotic constrain; and mowing with hay removal to manipulate biotic interactions. The distribution of 11 traits was compared with null-model and the effect of time and treatments were tested with linear mixed effect models.

We found changes in assembly rules with time only for three traits (life form, lead dry matter content, seed bank) when spontaneous succession was allowed to work (control plots), the rest were either random, convergent or divergent throughout the studied six year period. From the treatments applied, seeding had the most visible impact on both species and trait composition. Seeding resulted in an increased diversity for five traits and a decreased diversity for three traits. The most significant changes in time as a result of seeding are the conversion of the seed bank trait distribution from convergent to divergent and that of maximum plant height from divergent to convergent. We have found converging trait patterns for specific leaf area and duration of flowering for the studied period. Carbon amendment resulted in increased trait convergence for maximum plant height and duration of flowering. Trait divergence was found for plant height and leaf size for the studied period, and divergence established from the second year on for leaf dry matter content. Mowing decreased trait divergence for maximum plant height, end of flowering and life form.

We conclude that the dispersal filter is crucial after nudation, and early seeding of species with selected traits can direct restoration outcome. Trait convergence and divergence can be further manipulated by restorative interventions that aim at tightening or widening the mesh size of the abiotic and biotic filters in order to achieve target assembly.

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Chemical and physical properties act as filters on aquatic river plant communities: A trait-based study

Balázs A. Lukács[1*], *Tibor Erős*[2], *Attila Molnár V.*[3], *Anna E.-Vojtkó*[1,4], *Lars Götzenberger*[5]

[1]Department of Tisza Research, MTA Centre for Ecological Research-DRI, Debrecen, Hungary
[2]Department of Hydrozoology, MTA Centre for Ecological Research-BLI, Tihany, Hungary
[3]Department of Botany, University of Debrecen, Debrecen, Hungary
[4]University of South Bohemia, České Budějovice, Czech Republic
[5]Institute of Botany, Czech Academy of Sciences, Třeboň, Czech Republic
*E-mail: lukacs.balazs@okologia.mta.hu

Keywords: macrophytes, hydrophytes, trait, environment filtering, community assembly

Trait-based plant community ecology has grown exponentially in the last decades. However, the majority of the related theories has been developed and tested predominantly in the terrestrial ecosystem. Previous studies investigating the functional trait composition of aquatic plant communities and their environmental determinants remain scarce, and even those few studies published on the topic applied categorical trait attributes, instead of more precise continuous traits.

We used community-weighted means and functional diversity to identify how plant functional traits respond to environmental gradients in streams and rivers and how these relationships vary between aquatic and riverbank species. We studied the processes governing community assembly along major environmental gradients related to carbon and nutrient limiting factors (pH, and chemical variables of water and substrate) as well as physical strain (current velocity). Values of six continuous traits (leaf area, specific leaf area, leaf dry matter content, seed mass, seed shape, woodiness) were collected from the LEDA database. We calculated community weighted mean (CWM) and standardised effect size (SES) of functional diversity (FD) for each community. We used stepwise regression analyses for each trait along the environmental gradients to test which environmental factors best explain the changes in CWM and FD. All analyses were done for aquatic and riverbank species pool.

The relative importance of habitat filtering differed between rivers and streams. We found pH and soil properties as the main environmental drivers of aquatic plant community assembly. Our study showed that a filtering mechanism acts on certain functional traits of river macrophytes along environmental gradients, thus shaping the assembly of communities. We found that the effect of habitat filtering significantly increased toward higher pH, which imply the response of functional traits to carbon limitation. The strength of habitat filtering differed among hydrophyte and riverbank species along the productivity gradient. Our results showed that higher productivity of streams lead to trait convergence among riverbank species, and the larger functional dissimilarity among hydrophyte species is likely to increase the diversity of resource acquisition strategies, by which communities can greatly increase their primary productivity.

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Intermediate anthropogenic perturbations determine plant species composition and diversity of Indian dry tropical forest communities

R. Sagar

Department of Botany, Institute of Science, Banaras Hindu University, Varanasi-221005, India
*E-mail: sagarbhu@gmail.com

The dry tropical forest communities are more threatened than the moist or wet forest communities due to a long history of intense biotic pressure. Because of such biotic threats these forest communities of India are being converted into dry deciduous scrub, dry savanna and dry grassland communities. The size, duration and severity of disturbance inhibit the regeneration and species diversity of dry tropical forest communities. In this study, we compare species composition and plant diversity of protected area with that of non protected area experiencing biotic disturbances. We explore the possible restoration strategies for dry tropical species diversity against the chronic and acute disturbances. Remotely sensed data of Odisha forests for years 1935 and 2010 showed temporal conversation of dense forest communities into the non forested areas due to increased population pressure over the years. Similarly, the Andhra forest communities have decreased at rate of 0.22 Km^2yr^{-1} between years 1930 and 2011. The ground level studies from Vindhyan forests showed that the biotic perturbations governed the species composition, species distribution within and outside the protected areas. In such area tree stem density and basal area significantly decreased along the increasing order of disturbance, while within the protected area they increased, although poorly. Outside the protected area, disturbance intensity reduced the species richness, evenness, and Shannon index of the forest communities. On the other hand, these indices increased monotonically due to increased disturbance intensity within the protected area. Thus, moderate level of disturbance could be a real option to promote the species diversity of dry tropical forest communities. For example, for high accumulation of species diversity, the forest communities of protected areas need to experience a limited level of continued biotic exploitation, while forest communities outside the protected forests, will benefit from such management practices that increase the availability of fuel and fodder in the nearby human habitations. This will reduce the pressure of grazing, illegal tree felling and lopping for fuel and fodder.

Functional response of graminoid species to changing summer water availability: insight into the effects of climate change in sub-Mediterranean meadows

Federico Maria Tardella[1*], *Alessandro Bricca*[2], *Karina Piermarteri*[3], *Nicola Postiglione*[3], *Irina Goia*[4], *Stefano Chelli*[1], *Giandiego Campetella*[1], *Roberto Canullo*[1], *Andrea Catorci*[1]

[1]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy
[2]Department of Sciences, University of RomaTre Roma, Italy
[3]School of Advanced Studies, University of Camerino, Camerino, Italy
[4]Faculty of Biology and Geology, University of Babes-Bolyai, Cluj-Napoca, Romania
[*]E-mail: dtfederico.tardella@unicam.it

Keywords: specific leaf area, leaf dry mass, leaf area, climate change, sub-Mediterranean meadows

Climate change models predict modification of existing precipitation regimes and an increasing summer drought in Mediterranean regions. Especially in fragmented landscapes as semi-natural pastures, climate change has the potential to overwhelm the capacity for adaptation in many plant populations. The consequences are likely to include unpredictable changes in the abundance of species within communities and reduction in their ability to resist and recover from further environmental perturbations. Consequently, understanding adaptation strategies of plants to changes in water availability is of key importance in predicting the response of sub-Mediterranean grasslands to climate change. The main research aim was to investigate how dominant graminoids in sub-Mediterranean meadows (central Apennines, Italy) respond to the variability of weather events, through the assessment of key functional traits that reflect species ecological strategies: specific leaf area (SLA, one-sided leaf area per unit of dry mass) and plant height (the shortest distance between the upper photosynthesizing leaf on a plant and the ground level).

In different fenced plots, we artificially imposed lower and higher summer water availabilities than the average of the previous 30 years; while other plots received only ambient rainfall. We measured leaf area, dry mass and plant height and calculated SLA on randomly collected leaf samples of dominant graminoid species in each plot (three replicates for each treatment), at three times of one growing season, and tested the effect of treatments on these variables, controlling for phenological state of plant, leaf state and time of data collection.

We found that in some perennial late spring/early summer-flowering species (i.e. *Cynosurus cristatus* and *Lolium perenne*), reduced rainfall, jointly with phenological phase and time, affected in the same direction both leaf area and dry mass, leaving SLA values substantially unchanged during the growing season. Additional rain increased significantly SLA in *Cynosurus cristatus*, due to a higher increase in leaf area than in dry mass. In other perennial species (i.e. *Arrhenatherum elatius* and *Elymus repens*) with later reproductive cycle, increase in drought caused a significant decrease in SLA, associated to a reduction in leaf area, especially at the end of the treatment (summer end), indicating a shift of plant strategy to a lower efficiency in resource acquisition and use. Contrariwise, the increase in drought within a growing season, had a modest influence on plant height. These results suggest that response patterns of leaf traits to reduced water availability are species-specific and are probably linked to species' functional structure. This requires further research to understand the relation between leaf traits and other plant traits, including those related to plant flowering strategy. Moreover, as species with high SLA have also a higher nitrogen concentration, the lower SLA associated to drough events would worsen the nutritional value of pastures, representing a threat to livestock rearing.

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The intersection of diversity metrics and spatial mapping: new insights into regional vegetation patterns for complex communities

David Tierney

Office of Environment and Heritage, PO Box 1967 Hurstville, NSW 2220, Australia
E-mail: David.Tierney@environment.nsw.gov.au

Keywords: beta (β) diversity, zeta (ζ) diversity. multivariate analyses, vegetation classification, scale, predictive modelling, regional

Can we combine diversity metrics and mapping to better understand plant community patterns at regional scales for complex plant communities? Diversity metrics (β; ζ; multivariate dispersion) were measured and spatial mapping undertaken and intersected (an approach hitherto not undertaken) as a novel method for assessing complex vegetation patterns. Data from two contrasting survey designs from 69 randomly selected swamps (over 800 quadrats) across a large region with high species diversity and complex vegetation patterns at small spatial scales were used for these analyses. Vegetation patterns at the regional scale were then compared using a novel classification procedure (hybrid classification) informed by small-scale floristic variability as an alternate to a standard classification. It was determined that: 1. Estimates of spatial structure were biased when using standard approaches to survey design (both β and ζ overestimated). 2. The levels of spatial structure among swamps (as measured by β and ζ) were such that swamps were largely unique. 3. A skewed pattern of floristic assemblages (types) was determined such that there were few common floristic assemblages but many uncommon assemblages. 4. Floristic assemblages previously mapped as occurring in discrete parts of the region were found to be widespread. 5. A poor relationship exists between a standard classification approach and a hybrid classification informed by within swamp variability. Small-scale floristic patterns within swamps largely drove regional diversity. These floristic patterns had little relationship to previous classification and mapping for the region using standard mapping procedures based on regional scale variables. The intersection of diversity metrics and spatial mapping can provide critical insights into regional vegetation patterns that otherwise remain obscure. The use of regional scale variables linked to standard mapping techniques can create vegetation mapping that is largely an artefact of survey and classification limitations in these complex communities.

Figures

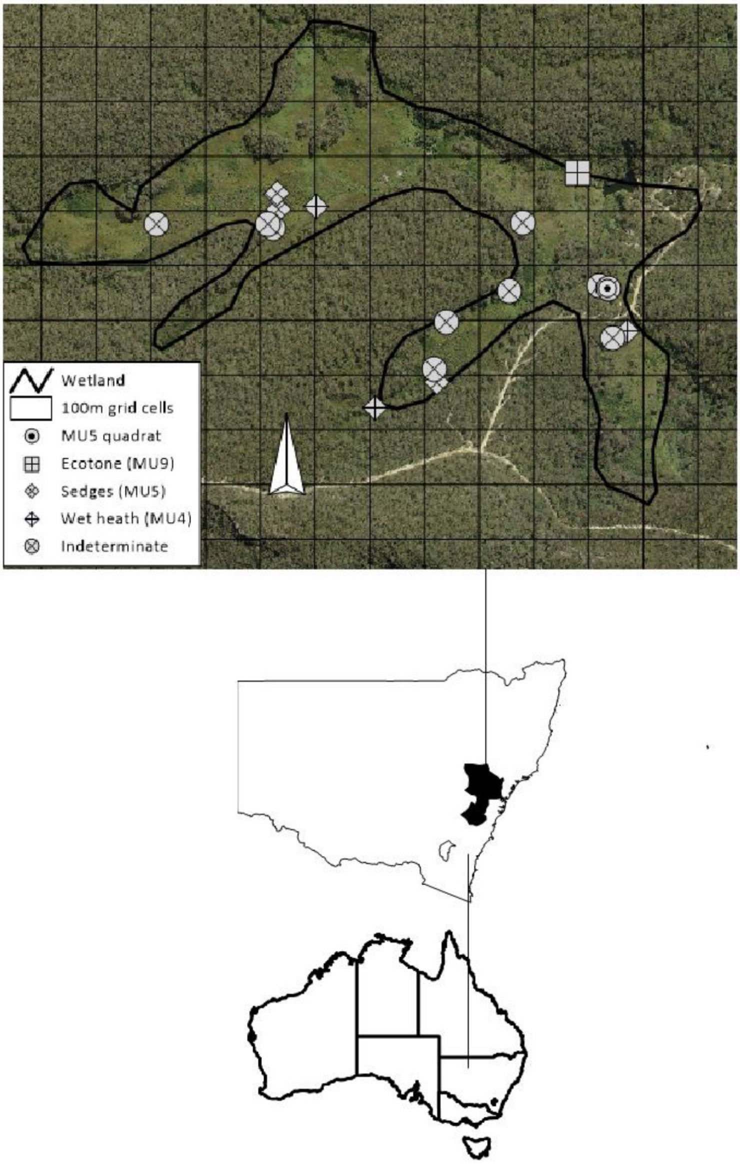

Figure 1. The location of the Study Area (The Greater Blue Mountains World Heritage Area – shaded black) in eastern Australia with an aerial photograph of one previously sampled wetland from the area (mapped as a sedge dominated swamp) with sampled plots consisting of ecotones, sedges, wet heath and indeterminate vegetation types with only the sedges floristically consistent with the single 400 m^2 quadrat (shown as MU5 quadrat). Likely affinities with map units defined by Tierney *et al*. 2015 shown in brackets.

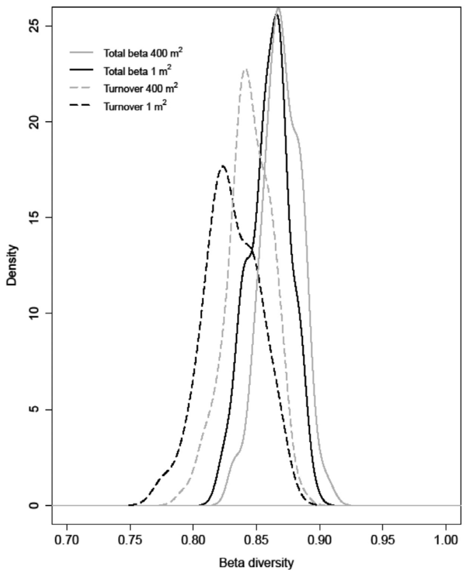

Figure 2. Beta diversity for small / 1 m^2 (black) and large / 400 m^2 (grey) plots with total beta (solid line), turnover (dashed line). Density scored out of 100; beta diversity scaled from 0 – 1.0.

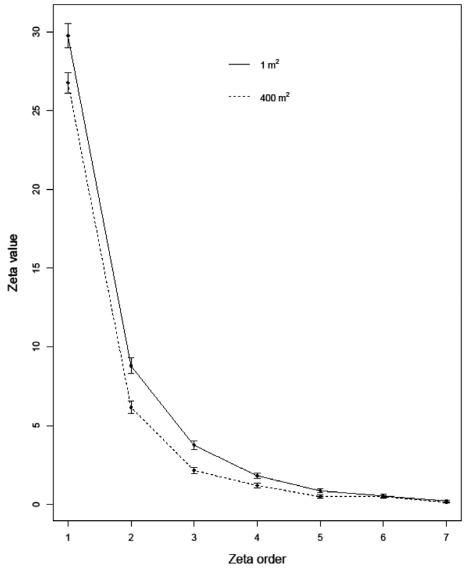

Figure 3. Mean Zeta decline ± standard error for small / 1 m^2 (solid line) and large / 400 m^2 plots (dashed line).

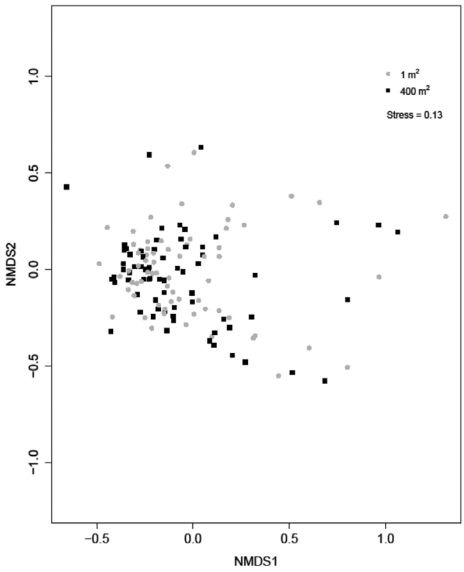

Figure 4. MDS for small / 1 m^2 (grey circle) and large / 400 m^2 plots (black square) across 69 surveyed wetlands spanning 10 significantly different vegetation types.

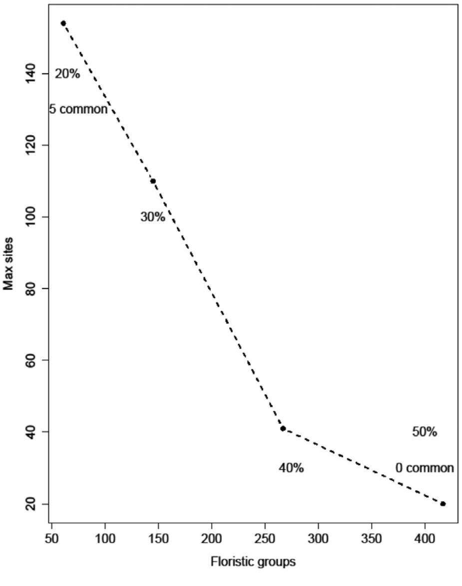

Figure 5. The number of floristic groups against the maximum number of sites occupied by a floristic group at the four similarity levels investigated (20%; 30%; 40%; 50%) with the number of floristic groups classified as "common" shown at the 20% and 50% Similarity level.

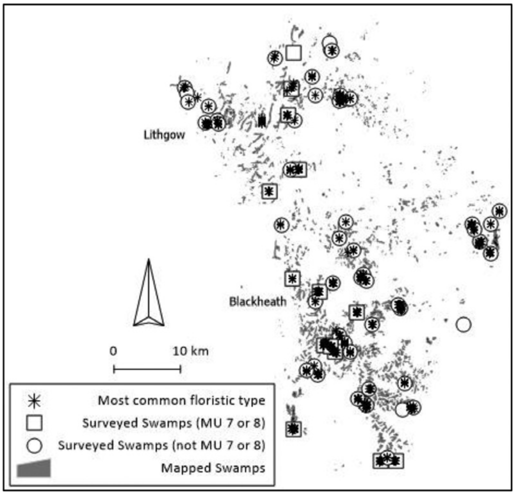

Figure 6. The distribution of the most common floristic type across the region overlaid on the location of all mapped swamps and swamps previously mapped to be this floristic type (MU 7 and 8 of Tierney et al. 2015) in the region.

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Ecological theories provide strong support to habitat restoration: A conceptual framework

Török P.[1], *Helm A.*[2]

[1]MTA-DE Lendület Functional and Restoration Ecology Research Group, Egyetem sqr. 1,
H-4032 Debrecen, Hungary
[2]University of Tartu, Institute of Ecology and Earth Sciences, Lai 40, 51005 Tartu, Estonia

Species-rich landscapes and natural habitats are facing large-scale degradation caused by the intensified land-use. The loss of biodiversity also strongly affected the landscape functionality via the decreased levels of pollination and biological pest control. Habitat restoration is a powerful tool to counteract degradation by the recovery of former species richness and area of natural habitats and by creating a habitat network and connectivity in landscapes dominated by human influence. Thus, habitat restoration has a top priority both in scientific research and in practice. There is a strong demand to seek cost-effective habitat management and recovery strategies, because of the high costs of technical restoration. Incorporating findings of theoretical ecology into practical restoration can address this request. Our ultimate goal was to develop a conceptual framework and to link biodiversity conservation, sustainable management and restoration in order to meet the major challenges related to land use, climate change adaptation and human well-being.

Drivers of plant diversity in urban green spaces

Béla Tóthmérész[1,2*], *Bernadett Hüse*[2], *Balázs Deák*[1]

[1]MTA-DE Biodiversity and Ecosystem Services Research Group, Debrecen P.O. Box 400,
H-4002 Hungary
[2]University of Debrecen, Department of Ecology, Debrecen P.O. Box 400, H-4002 Hungary
[*]E-mail: tothmerb@gmail.com

Keywords: urbanisation, species-area relationship, alien species, cosmopolitan species, urban flora

Urbanization considerably changed the landscape worldwide; habitat loss and changes in the abiotic environment have been seriously affected urban biodiversity (Magura et al. 2010, Hüse et al. 2016). Studying urban green spaces we tested the following hypotheses: (i) species richness increases with increasing patch area in urban landscapes (ii) lower species richness, higher ratio of weeds and disturbance-tolerant species are present in the city centre characterised by a high level of disturbance, (iii) the ratio of warm-and nutrient-demanding species increases, while the ratio of moisture-demanding species decreases towards the city centre, (iv) there is an increase in cosmopolitan and alien species and a decrease in species of the natural flora towards the city centre.

We surveyed the spontaneous vegetation along an urbanisation gradient in urban parks, vacant lots and peri-urban areas in the city of Debrecen, East-Hungary, using five plots of 5×5 meters in every site.

We found a positive species-area relationship for the urban parks and peri-urban areas (permanent habitats), while no relationship was found for vacant lots (Deák et al. 2016). Surprisingly, urban parks harboured the lowest number of species likely due to the high level of urbanisation. The ratio of weeds and disturbance-tolerants was the highest in the city centre likely due to the high-intensity trampling and soil disturbances. Plant species of the city centre characterised by a warmer and drier urban climate were more drought-tolerant compared to peri-urban areas. Likely due to the high nutrient deposit in the cities, the ratio of nutrient-demanding species was the lowest in the urban parks and the highest in the peri-urban areas. The ratio of alien and cosmopolitan species was high both in vacant lots and peri-urban areas.

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Grassland recovery on linear landscape elements – Promising example to restore natural vegetation

Orsolya Valkó[1], Balázs Deák[1], Péter Török[2], András Kelemen[1,3], Tamás Miglécz[1,3], Réka Kiss[2,] Béla Tóthmérész[1,2]*

[1]MTA-DE Biodiversity and Ecosystem Services Research Group, Debrecen, Hungary
[2]Department of Ecology, University of Debrecen, Debrecen, Hungary
[3]MTA's Post-Doctoral Research Programme, Budapest, Hungary
[*]E-mail: valkoorsi@gmail.com

Keywords: alkaline grassland, drainage ditch, grassland restoration, spontaneous succession, target species, weed

Restoration of grasslands is a high priority in the European biodiversity strategy (Valkó et al. 2016). Open landscapes have been negatively affected by large-scale drainage and amelioration to support agricultural production in many parts of Europe. In continental alkaline grasslands, amelioration and establishment of drainage channel systems were typical in the 1950s and 60s (Deák et al. 2015). Drainage channels caused a considerable fragmentation and degradation of natural grasslands; thus several projects aimed at eliminating these linear landscape elements. In a multi-site study, we explored the drivers of grassland recovery after soil-filling of drainage channels in landscape-scale restoration projects in Hortobágy National Park, East-Hungary. Channel embankments, formerly built from the excavated soil, were used to fill the 8 m wide channels and grazing was applied to facilitate the recovery of grasslands similar to the surrounding matrix. Three age classes were selected for the study: 1-, 6- and 8-year-old filled channels; with nine sites per age group, surrounded by three grassland types (27 channels in total). We recorded the percentage cover of vascular plant species in 18 plots per channel, 486 plots in total. We found that the species pool of the filled channels became more similar to the reference grasslands with increasing successional age and increasing distance to the central zone of the channel regardless of grassland type. Species richness of the filled channels became more similar to that of the reference grasslands with increasing successional age. However, we found that several target species, especially salt-tolerant pioneers, could establish even in the first year. Grassland recovery was most successful in sites adjacent to dry grasslands characterised by soils with high salt content, which favoured specialist species and suppressed non-target species. Cover of non-target species was higher in wet meadows with moist, nutrient-rich soils which favoured generalists and non-target species. Our study revealed that passive restoration after soil filling of disused drainage channels can effectively support grassland recovery even within less than ten years, when restoration sites are surrounded by natural grasslands (Valkó et al. 2017).

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Process strengths determine the forms of the relationship between plant species richness and primary productivity in plant community

Zhenhong Wang
School of Environmental Science and Engineering, Chang`an University, Xi`an, China
E-mail: w_zhenhong@126.com

Keywords: plant diversity, ecosystem functions, richness-productivity relationship, selection effects, combination model, humped forms, density effects, competition stress, ecological dynamics

The current rates of biodiversity loss have exceeded the rates observed during the earth`s major extinction events, which spurs the studies of the ecological relationships between biodiversity and ecosystem functions, stability and services to determine the consequences of biodiversity loss. The plant species richness-primary productivity relationship (SRPR) is crucial to the understanding of these relationships. Although most of ecologists have widespread consensus on loss of plant diversity undoubtedly impairing ecosystem functions, and proposed many processes to explain the SRPR, none of the studies has satisfactorily resolved the issue of the forms and mechanisms clarifying the SRPR due to inconsistent results in the SRPR observation and the long-term debates on ecological processes suggested to explain the SRPR. Here, I have developed a simple model that combines the positive and/or negative effects of sixteen ecological processes on the SRPR and models that describe the dynamics of complementary-selection effect, density effect and the interspecfic competitive stress structured by other ecological processes. I can regulate the strengths of the effects of these ecological processes to derive the asymptotic, positive, humped, negative and irregular forms of the SRPR, and verify these forms using the observed data. The results demonstrated that the different strengths of the ecological processes determine the forms of the SRPR and the forms of the SRPR can change with the variation of the strengths of these ecological processes. The dynamic characteristics of the complementary-selection effect, density effect and the interspecfic competitive stress on the SRPR are diverse, and are dependent on the strengths and variation of these ecological processes. This report explains the diverse forms of the SRPR, clarifies the integrative effects of the different ecological processes on the SRPR and partially deepens our understanding of the interactions that occur among these ecological processes.

Space and landscapes

Habitat management and agricultural vs. forested landscape context determine butterfly and bird diversity in orchard meadows and calcareous grasslands

Lunja M. Ernst[1], *Teja Tscharntke*[1], *Péter Batáry*[1,2*]

[1]Agroecology, University of Goettingen, Göttingen, Germany
[2]GINOP Sustainable Ecosystems Group, MTA Centre for Ecological Research, Tihany, Hungary
[*]E-mail: pbatary@gmail.com

Keywords: biodiversity, conservation management, extensive management, farmland species, Germany, habitat abandonment, species richness, woodland species

Calcareous grasslands and orchard meadows are among the most species-rich semi-natural habitats in Europe and of high conservation importance, but they are severely threatened by intensified land use and abandonment. Here, we focus on the effects of management (by grazing or mowing) vs. abandonment of these grasslands in agricultural vs. forest-dominated landscapes of Germany.

We recorded butterflies and birds in 20 calcareous grasslands and 20 orchard meadows, each in 10 agricultural and 10 forested landscapes. Both taxa were classified in farmland and woodland species according to their habitat preferences.

Species richness and abundance of farmland butterflies were higher on calcareous grasslands than orchard meadows and benefited from forested landscapes in case of orchard meadows. Species richness of woodland butterflies was much lower than that of farmland butterflies, but higher on abandoned than managed grasslands, independent of habitat type and landscape context.

Species richness and abundance of woodland birds were higher than that of farmland birds in the studied grasslands. Richness and abundance of farmland birds benefitted from managed and not abandoned orchard meadows, and in addition, they were more abundant in agricultural landscapes. On calcareous grasslands, however, the abandonment led to higher richness and abundance of farmland birds. Woodland birds exhibited higher species richness in abandoned than managed grasslands, especially in orchard meadows.

Woodland birds and butterflies appeared to be less affected by habitat type, management or landscape context than farmland species. Calcareous grasslands were much more important for butterfly diversity than orchard meadows, but suitability of orchards for butterflies was improved when embedded in forested landscapes. In contrast to butterflies, bird diversity benefitted more from orchard meadows than calcareous grasslands, which had higher diversity when management was abandoned. Hence, short-term abandonment can improve habitats for birds and butterflies, but of course, long-term abandonment would destroy the identity of these openland habitats and their associated community. Landscape context can shape communities in these two grassland habitat types, so conservation management should consider reserves in both agricultural and forested landscapes and thereby, diversify regional biota.

Successional patterns of ecosystem engineers at the upper altitudinal limit of the Dry Puna (Peru): a facilitation cascade process

Andrea Catorci[1*], *Federico Maria Tardella*[1], *Karina Piermarteri*[2], *Luca Malatesta*[2]

[1]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy
[2]School of Advanced Studies, University of Camerino, Camerino, Italy
[*]E-mail: andrea.catorci@unicam.it

Keywords: tropical alpine environments, plant interactions, facilitation cascades, nurse species, habitat amelioration

Facilitation processes constitute basic elements of vegetation dynamics in harsh systems. Recent studies in tropical alpine environments demonstrated how pioneer plant species, defined as “ecosystem engineers”, are capable of enhancing landscape-level richness by adding new species to the community through the modification of microhabitats, and also provided hints about the alternation of different ecosystem engineers over time. Nevertheless, most of the existing works analysed different ecosystem engineers separately, without considering the interaction of different ecosystem engineers. Therefore, these studies do not consider, at the scale of plant communities, the whole process of possible patch creation, alternation, coalescence and senescence, by means of the interaction of different ecosystem engineers and the degradation of microhabitat patches, that are key processes of vegetation dynamics in harsh environments.

Focusing on the altitudinal limit of Peruvian Dry Puna vegetation, we hypothesized that positive interactions structure plant communities by facilitation cascades involving different ecosystem engineers, determining the evolution of the microhabitat patches in terms of abiotic resources and beneficiary species hosted. To analyze successional mechanisms we used a “space-for-time”substitution to account for changes over time, and analyzed data on soil texture, composition, and temperature, facilitated species and their interaction with nurse species, and surface area of engineered patches by means of chemical analyses, indicator species analysis, and rarefaction curves. A successional process, resulting from the dynamic interaction of different ecosystem engineers, which determined a progressive amelioration of soil conditions (e.g. nitrogen and organic matter content, and temperature), was the main driver of species assemblage at the community scale, enhancing species richness. Cushion plants act as pioneers, by starting the successional processes that continue with shrubs and tussocks. Tussock grasses have sometimes been found to be capable of creating microhabitat patches independently. The dynamics of species assemblage seem to follow the nested assemblage mechanism, in which the first foundation species to colonize a habitat provides a novel substrate for colonization by other foundation species through a facilitation cascade process.

Factors affecting species composition of isolated grasslands – the role of kurgans in preserving steppe vegetation

Balázs Deák[1*], *Orsolya Valkó*[2], *Péter Török*[2], *Béla Tóthmérész*[1,2]

[1]MTA-DE Biodiversity and Ecosystem Services Research Group, Debrecen P.O. Box 400, H-4002 Hungary
[2]University of Debrecen, Department of Ecology, Debrecen P.O. Box 400, H-4002 Hungary
[*]E-mail: debalazs@gmail.com

Keywords: habitat fragmentation, landscape protection, specialist species, weeds

Land use intensification during the past centuries resulted in a considerable loss and isolation of grassland habitats in Europe. In intensively used agricultural landscapes remnants of natural flora usually could remain in small habitat islands embedded in a hostile matrix such as arable land. In Eurasia burial mounds, so-called 'kurgans', have a great potential to preserve remaining natural habitats and act as biodiversity hotspots (Deák et al. 2016a). Given their special micro-topography kurgans are characterised by a specific soil development and micro-climate, which makes them adequate habitats for several steppe specialist plant species. They are proper objects to study factors driving biodiversity in isolated habitat fragments, which are crucial for understanding ecological processes shaping the vegetation and also for designing their protection strategies (Deák et al. 2016b). We surveyed the vegetation of 44 isolated kurgans in East-Hungary and studied the effects of habitat area, slope, recent disturbance, past destruction and woody encroachment on the species richness and cover of grassland specialists and problem species. We used model selection techniques and linear models for testing relevant factors affecting specialist species in grassland fragments. We found that the biodiversity conservation potential of kurgans is supported by their steep slopes, which provide adequate habitat conditions and micro-climate for steppic specialist plant species. By harbouring viable population of several grassland specialist species, kurgans have a great potential for preserving species pool of grassland habitats in agricultural landscapes, and can mitigate the negative consequences of landscape level human disturbances. We found that specialist species are threatened both by recent disturbances and encroachment of alien woody species, especially black locust. Factors that supported specialist species suppressed problem species by providing unfavourable environmental conditions and putting them at a competitive disadvantage. Woody encroachment and current disturbances affect vast majority of kurgans, posing a serious threat to grassland specialist species. Thus, there is an urgent need to integrate active conservation measures into the current passive protection of kurgans (Deák et al. 2016a, b).

Acknowledgments

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Advancing versus retreating fronts: the fine-scale dynamics of treeline shifts

Beáta Oborny[*], *Dániel Zimmermann*

Department of Plant Taxonomy, Ecology and Theoretical Biology, Eötvös Loránd University, Budapest, Hungary
[*]E-mail: beata.oborny@ttk.elte.hu

Keywords: spatial population dynamics, ecotone shift, environmental gradient, climate change, phase transition

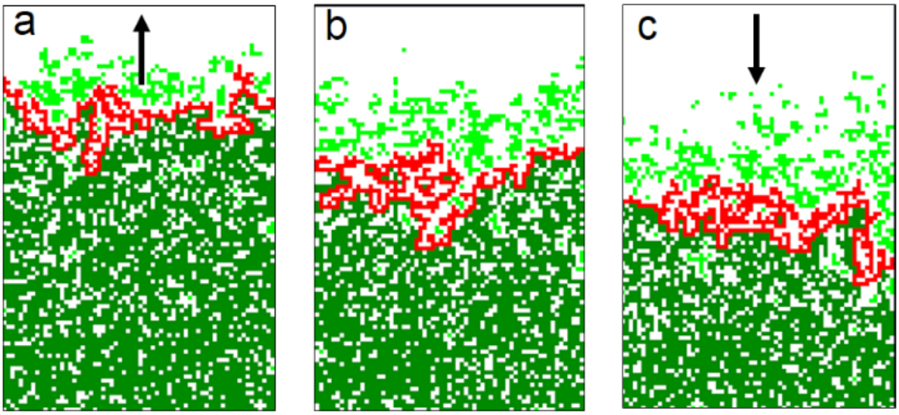
Climate changes can cause considerable shifts in the positions of the treelines across altitudinal, latitudinal or moisture gradients. These shifts generally influence the survival and spatial distribution of many other species; therefore, understanding the dynamics of treeline movements is vital for the long-term protection of wildlife in these transition zones. The geometry of treelines is usually complex; thus, it is not trivial how to distinguish random fluctuations from trend-like shifts. Another challenge is to detect when restructuring occurs instead of a simple spatial shift of the original structure.

We studied the geometry and movement of treelines by spatially explicit computer simulations. The elementary processes were colonization and local extinction on the fine scale of individual trees. We assumed that the colonization and/or extinction rate changed along an environmental gradient, and we analysed the emergent treeline pattern. Then we introduced a systematic change in the local rate of colonization or extinction over time. In case of a favourable/unfavourable change, the treeline advanced/retreated, so that we could study the leading/trailing edge of the range.

The simulations showed that simple colonization-extinction dynamics can produce relatively sharp treelines across smooth environmental gradients. This sharpening can be explained by a critical phase transition from the living to the extinct state. The phenomenon may be considered as a minimal (most parsimonous) explanation for the emergence of vegetation zones across altitudes or latitudes.

The hull, i.e., the boundary of the continuous forest cover, had a characteristic fractal structure: the fractal dimension was 7/4 at fine spatial scales, independently from the details of colonization and extinction, and from the gradient. When we assumed a climate change, the fractal dimension of the hull remained the same even in the case of relatively fast advance or retreat. This suggest that the hull is a robust structure, that shifts in a predictable manner in case of an environmental change. In general, the theory of critical phase transitions can provide a firm theoretical background for the study of treeline shifts, as it helps to find invariable characteristics concerning the length and width of the hull.

Figure



Example for an a) advancing, b) standing, and c) retreating front. Dark green and red: continuous forest cover. Red: the hull. Light green: fragmented groups of trees.

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Protecting landscape connectivity: Multi-node selection of key habitat patches based on fragmentation and reachability

Juliana Pereira[*] *– Ferenc Jordán*

MTA Center for Ecological Research, Danube Research Institute, Budapest, Hungary
[*]E-mail: julianapereira.mailto@gmail.com

Habitat connectivity is of major importance in biodiversity conservation, and is one of the key aspects to be taken into consideration in the spatial design of networks of protected areas. Network analyses provide efficient tools for modelling habitat connectivity and defining priority areas for protecting it [1]. Widespread prioritization approaches are based on rankings of the centrality (or importance) of individual habitat patches. However, it has been noted that the set of nodes selected as key for conservation through individual ranking may depart from the optimal or most efficient group of nodes [2]. Multi-node analyses calculate the combined centrality of a set of *n* habitat patches in order to identify groups of patches that maximally complement each other in order to increase the protection of connectivity for the whole network. We apply multi-node analyses to the prioritization of habitat patches for five vulnerable bird species in Catalonia, Spain, using two different approaches to connectivity, based on fragmentation and reachability. Groups of patches based on fragmentation are usually concentrated on core areas, while reachability groups are widely spread. Fragmentation sets have higher centrality value for low-mobility species, and reachability sets for long distance dispersers. The protection of the networks against fragmentation requires fewer patches, allows for more gradual implementation and is currently better accounted for by the Natura 2000 network of protected areas, while the protection of reachability is less costly and more efficient in terms of area requirements. Our work contributes to the inclusion of multi-node approaches in landscape graph analysis for reserve design.

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Forest ecology

Relationship between avian communities and vegetation structure in secondary forest and betel nut plantation in Taiwan

Chia-Hao Chang[1], *Fu-Hsung Hsu*[1], *Jo-Szu Tsai*[1,*]

[1]Institute of Biodiversity and Department of Biological Resources, National Chiayi University, Chiayi, Taiwan
[*]E-mail: ross.tsai@mail.ncyu.edu.tw

Keywords: bird communitites, betel nut, secondary forest, foraging guilds

With the development of lowland and hillside area, original forest has been replaced by secondary forest and economic crops. Betel nut tree (*Areca catechu*) has become one of the most common crops in central Taiwan. However, betel nut plantation has caused soil erosion and changed the ecosystem function. The ecological impacts of the industry are poorly studied with respect to bird communities. We sampled 40 betel nut and 40 forest plots in central Taiwan, and conducted five 50m-radius point count surveys in each plot and recorded all the species seen or heard from March to May in 2015 and 2016. We used Mann-Whitney *U* test to compare species richness, abundance, and densities by foraging guild. To understand the relationship between environmental factors and bird communities, a distance-based redundancy analysis (dbRDA) was used. Our results showed that species richness in forest was higher than in betel nut plots (P=0.001), but overall abundance was similar (P=0.32). For foraging guilds, the densities of aerial sallying insectivores and shrub insectivores are higher in forest than in betel nut plots. For arboreal omnivores, we found White-eared Sibia (*Heterophasia auricularis*) and Taiwan Barbet (*Psilopogon nuchalis*) had higher densities in forest than in betel nut plots, while Light-vented Bulbul (*Pycnonotus sinensis*) and Japanese White-eye (*Zosterops japonicus*) had a reverse pattern. From dbRDA, aerial sallying insectivores and arboreal insectivores prefer plots with more trees, and shrub insectivores prefer plots that have high coverage and complicated structure. The different preferences of foraging guilds between betel nut and forest suggested that the vegetation structure and thus the resources the habitat can provide have some effects on the avian communities. The evidence from this study suggests that betel nut and secondary forest hold different biodiversity in richness and foraging guild.

Natural and artificial renewal of pine trees as a place for occurrence of ground beetles and spiders

Agnieszka Kosewska

In habitats itensively transformed by human, it is very important to maintain biodiversity of the largest possible invertebrate groups, which is a condition for the sustainability of ecosystems. Especially the presence of non-specialized predators, including the ground beetles and spiders, in many ecosystems, including in the forests, reduces the risk of potential pests and is an important bioindication factor associated with anthropopression.

The aim of the study was quantitative and qualitative analysis of entomofauna and arachnofauna on the natural and artificial regeneration of pine.

The study was conducted in two Forest Districts in Northeastern Poland. Barber traps were placed on research fields designed to the natural and artificial regeneration of pine, to trap epigeic entomofauna.

Research areas consisted of three combinations:

– N- renewed naturally pine - plots without preparation of soil
– N + P- renewal of natural pine with traditional soil preparation (LPZ plow)
– renewal of artificially pine with seedlings from container and traditional production.

As a result of the research, it was found that natural and artificial pine regeneration can influence the increase of entomofauna diversity in the forests. The most beneficial variant for entomofauna such as carabid beetles and spiders is the natural renewal of the pine without preparation of the soil.

The effects of forestry treatments on the community structure of different organism groups

Péter Ódor[1,2]*, Gergely Boros*[1,2]*, Ferenc Samu*[3]*, Réka Aszalós*[1,2]*, Flóra Tinya*[1]*, Bence Kovács*[1]*, Zoltán Elek*[4]

[1]MTA Centre for Ecological Research, GINOP Sustainable Ecosystem Group, Tihany, Hungary
[2]MTA Centre for Ecological Research, Institute of Ecology and Botany, Vácrátót, Hungary
[3]MTA Centre for Agricultural Research, Agricultural Institute, Budapest, Hungary
[4]MTA-ELTE-MTM Ecology Research Group, Budapest, Hungary

Keywords: forest management, biodiversity

There is a paradigm shift in Central Europe from the traditional forestry systems towards continuous cover forestry that provides a diversification of possible management practices. In a mature, temperate sessile oak-hornbeam forest in Northern Hungary, four different forestry treatments were modeled within the framework of an open-field forestry experiment, which belong to rotation system (preparation cutting, clear-cutting, retention tree group) and selection forestry (gap creation). The effects of these treatments were studied on the community structure, diversity and abundance of vascular plants, enchytraeid worms, ground beetles and spiders. The experiment following a complete block design with six replicates was established in 2014, and the short-term (2014-2016) responses are summarized.

One of the major findings is that plant cover increased significantly in all treatments, especially in the gap and clear-cut. The abundance of worms decreased in some treatments belonging to the rotation system such as the clear-cut and retention tree group. The abundance of spiders and ground beetles were unaffected by treatments. The effect of treatments on the species richness of the various taxa were not revealed, except for worms, they were less species rich in the retention tree group. The treatments had a consistent effect on the species composition for all studied organism groups. Generally, plants and the immobile soil organisms showed the highest sensitivity to the altered microclimatic condition of the forestry treatments.

Based on this short observation period we can conclude that fine scaled forestry treatments like gap creation had only moderate effect on forest site, which is favourable for conservational perspectives.

Acknowledgements
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The indicator side of tree microhabitats: a multi-taxonomic approach

Yoan Paillet[1,2*], *Solène Du Puy*[1], *Frédéric Archaux*[1], *Christophe Bouget*[1], *Vincent Boulanger*[3], *Nicolas Debaive*[3,4], *Olivier Gilg*[4], *Frédéric Gosselin*[1], *Eric Guilbert*[2]

[1]Irstea, UR EFNO, Nogent-sur-Vernisson, France
[2]MECADEV, UMR 7179 MNHN/CNRS, Paris, France
[3]Office National des Forêts, Département Recherche et Développement, Fontainebleau, France
[4]Réserves Naturelles de France, Dijon, France
[*]E-mail: Yoan.Paillet@irstea.fr

Keywords: birds, bats, saproxylic beetles, large trees, strict forest reserves, cavities

Forest biodiversity assessment relies mostly on indirect indicators based on elements of forest structure used as a surrogate for species. However, most of those indirect indicators used in national and international evaluation processes lack scientific evidence documenting their quantitative link with the biodiversity they are supposed to assess. In addition, those for which the link is established generally concern only one taxon and are rarely considered at the community level. In this context, tree microhabitats – defined as tree-borne singularities such as cavities, conks of fungi or bark characteristics – have recently gained attention as a potential forest biodiversity indicator for species that depend on them for at least a part of their life cycle and that are difficult to detect. However, like most other potential indicators, precise quantitative information on the link between biodiversity indices and microhabitat variables remains scarce.

We explored the link between the richness of three taxonomic groups (bats, birds, and saproxylic beetles) and microhabitat indices using a nation-wide multi-taxonomic sampling design comparing 213 plots located inside and outside forest reserves. We hypothesized that the positive effect of setting aside forest reserves on biodiversity conservation was indirectly due to the increase in the proportion of large structural elements (living trees and standing deadwood) which in turn favoured the quantity and diversity of microhabitats. We also hypothesized that microhabitat indices would be better indicators than large and standing dead tree densities, two classical and often used indirect forest biodiversity indicators. We first analysed the response of total species richness and species richness of different groups and guilds (e.g. red-listed species, forest specialists, cavity dwellers...) to several microhabitat indices (density, diversity) to identify the best microhabitat metric. We then used confirmatory structural equation models to assess the indirect effects of management, large structural elements and microhabitats on the diversity of the target species.

We first showed that microhabitat indices based on diversity better described biodiversity than indices based on abundance. Structural equation models confirmed that setting aside forest reserves increased the quantities of large trees and standing deadwood, which in turn drove higher quantities and diversity of microhabitats. This significantly increased the richness of several taxonomic groups including notably total richness and cavity dweller richness of both birds and bats. However the magnitude of the link between microhabitat indices and species richness was relatively small. Conversely, the biodiversity of saproxylic beetles was not driven by microhabitat indices and, for this taxon only, models involving direct effects of large structural elements or management performed better.

Tree microhabitats appear to be an indicator for part of the taxonomic groups we analysed, but do not constitute a universal biodiversity indicator. They rather have a complementary role compared to large structural elements. Currently, their moderate correlation with biodiversity, as well as thei sensivity to other factors not taken into account in this study (e.g. observer effects), question their transferability to management and policy. Finally, this study calls for replicable and standardized multicriteria methods to validate biodiversity indicators.

Transformation of lowland rainforest into plantations: Changes in the diversity and composition of trophic groups of protists

Garvin Schulz[1*], *Dominik Schneider*[2], *Nicole Brinkmann*[3], *Stefan Scheu*[1],
Valentyna Krashevska[1]

[1]J.F. Blumenbach Institute of Zoology and Anthropology, University of Goettingen, Germany
[2]Genomic and Applied Microbiology, University of Goettingen, Germany
[3]Department of Forest Botany, University of Goettingen, Germany
[*]E-mail: gschulz3@gwdg.de

Keywords: Illumina sequencing, land-use, environmental DNA, Indonesia, microbial eukaryotes, 18S rDNA

Large areas of lowland rainforests of Sumatra, Indonesia, are converted into agro-ecosystems, such as jungle rubber, intensive rubber and oil palm plantations. Land-use changes are connected with tremendous changes in biotic and abiotic factors that alter biodiversity and functioning of converted systems. Effects of land-use change on diversity and community composition of bacteria, fungi and different invertebrate groups has been investigated, but information on soil protists is lacking. To fill this gap of knowledge, we investigated the effects of land-use change on soil protist communities using state-of-the-art molecular methods. Protists are an abundant and diverse group of soil microbial eukaryotes, which belong to very different phylogenetic and trophic groups and are important players and indicators of ecosystem functioning.

Soil eukaryotic community composition and diversity were assessed by Illumina sequencing of environmental DNA targeting the hypervariable V4 region of 18S rDNA using universal eukaryotic primers. The overall dataset comprised 5,204 operational taxonomic units at species level (97% genetic identity). After subsampling of 2,300 sequences per sample, OTUs were categorized according to literature into five trophic groups: symbionts, photoautotrophs, phagotrophs, animal and plant parasites. Total protist richness was similar in rainforest, jungle rubber and oil palm plantation but significantly lower in intensive rubber plantations. In contrast, the relative abundance of protists was at maximum in the rainforest and declined with land-use intensity in the order jungle rubber > intense rubber > oil palm plantation. The most abundant trophic group were phagotrophs (58%), followed by animal parasites (27%), photoautotrophs (14%), plant parasites (1%) and symbionts (<1%). The relative abundance of photoautotrophs increased significantly with land-use intensity. This was similar but less pronounced for the relative abundance of symbionts. Animal and plant parasites decreased with increasing land-use intensity. The relative abundance of phagotrophs was lowest in rainforests and significantly higher in arable systems. Also community compositions and the factors affecting the structure of individual trophic groups differed between land-use systems. Overall, the results suggest that protists richness, relative abundance and community composition of tropical lowland rainforest differed drastically from converted systems and this likely is associated with marked changes in ecosystem functioning. Further, the results support earlier suggestions that protists are powerful indicators of land-use systems reflecting changes in the functioning of ecosystems transformed from rainforest into plantations.

Macroecology

Comparison of the trophic ecology of two mammals: the Wild boar *Sus scrofa* and the porcupine *Hystrix cristata* in the northern slope of Djurdjura (north of Algeria).

Par Mansour Amroun[1*], *Ben Ammar Ania*[1]

[1]Université de Tizi-Ouzou, Faculté des Sciences Biologiques et des Sciences Agronomiques, 15000 Tizi-Ouzou, Algérie
[*]E mail: mansouramroun@gmail.com

Keywords: *Sus scrofa, Hystrix cristata,* diet analysis, overlap, Djurdjura, Algeria

This work suggests approaching the trophic ecology of two mammals the wild boar *Sus scrofa* L. 1875 and the porcupine *Hystrix cristata* L. 1875 in the National park of Djurdjura (Algeria). The diet of both mammals was studied from the analysis of 315 feces collected from September, 2011 till August, 2012.

The analysis of the food spectrum of both mammals in this locality shows that the wild boar and the porcupine have a very large diet with a tendency to frugivory. It appears that *S. Scrofa* and *H. cristata* presents a selective behavior not only towards the species of plants which they consume, but also parts of plants which they take. Other fleshy fruits (wild cherries / cherries, figs and apples / pears) for the greater part complete the diet of the wild boar and the porcupine. Fruits occupy respectively more than 36, 33 % and 34, 34 % at the wild boar and the porcupine.

The use of the Chi square reveals a highly significant difference between both global diets (khi ^{2} = 132,68; p-value=9,48; ddl=4). This is partially due to the over-representation of the air and subterranean vegetables at the porcupine and that of mushrooms and earthworms at the wild boar. The use of the Pianka's index ($\geq$ 0.85 in any period except in spring where it is = 0.67), show a very high overlapping of trophic niches of both species.

Our results highlight a regular consumption (over all year) of earthworms with a very considerable percentage, they participate in the global diet with a 37, 5 % rate at the wild boar. We notice that the consumption of fruits (including acorns) evolves according to the same trends to both species, and that the latter filter in mainly on acorns in winter to the detriment of the other food items.

Congruency across taxa and spatial scales: Are we asking too much of species data?

*Rafael B. de Andrade**[1], *Sabina Burrascano*[1], *Yoan Paillet*[2], *Péter Ódor*[3], *Gloria Antonini*[4], *Christophe Bouget*[2], *Thomas Campagnaro*[5], *Frédéric Gosselin*[2], *Philippe Janssen*[6], *Anna Maria Persiani*[1], *Juri Nascimbene*[7], *Francesco Maria Sabatini*[8], *Tommaso Sitzia*[5], *Carlo Blasi*[1]

[1]Dept. of Environmental Biology, Sapienza University of Rome, Rome, Italy
[2]Irstea, UR EFNO, Nogent-sur-Vernisson, France.
[3]MTA Centre for Ecological Research, Institute of Ecology and Botany, Vácrátót, Hungary
[4]Dept. of Biology and Biotechnologies Charles Darwin, Sapienza University of Rome, Rome, Italy
[5]Dept. of Land, Environment, Agriculture and Forestry, Università degli Studi di Padova, Padova, Italy
[6]Irstea, UR EMGR, Grenoble, France
[7]Dep. of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy
[8]Dept. of Geography, Humboldt-Universitätzu, Berlin, Germany
*E-mail: rafsbio@yahoo.com.br

Scale dependency is one of the main factors causing the variability of correlations among species diversity parameters. Recent syntheses demonstrated how both extent (the geographical area comprised by the survey or total sample) and grain (the scale of each sampling unit) have a significant effect on cross-taxon congruency. These results, however, do not represent a definitive framework to understand this variation across spatial scales, since this was only indirectly analyzed, by comparing the results of different studies. Our goal is to assess if and how cross-taxon congruency vary across different spatial scales in European temperate forests. Our general hypothesis is that cross-taxon congruency in species richness and composition in European temperate forests increases together with the scale of analysis. We account separately for differences in spatial grain and extent, and evaluate the relationships between all the possible pairs of taxonomic groups. We use a comprehensive set of field data encompassing Italy, France and Hungary (Fig. 1), and including species diversity information for six taxonomic groups: vascular plants, bryophytes, birds, epiphytic lichens, saproxylic beetles, and wood-inhabiting fungi. We calculated effect sizes for species richness and community composition correlation at three different spatial scales of grain and extent: (i) plot grain - site extent, (ii) plot grain - continental extent, and (iii) site grain - continental extent. No pair of taxa had their species richness consistently correlated (either positively or negatively) in all three combinations of grain and extent analyzed (Fig. 2). However, birds and bryophytes, and fungi and lichens had the highest correlation of species richness when sampled at a plot-level grain and site extent. When analyzing congruent patterns of species composition, plants resulted as the best surrogates for other taxa, even across different spatial scales (Fig. 3). We demonstrate that diversity congruency relationships among taxa in European temperate forest are for the most part, scale-dependent. Our results support that increasing database extent and sampling grain masks local patterns of congruency and highlights those due to common response to broad environmental and biogeographic factors that covary across the European continent. We suggest the results presented in this study to be taken into serious consideration when developing indicators of sustainable forest management for the conservation of forest biodiversity.

Figures

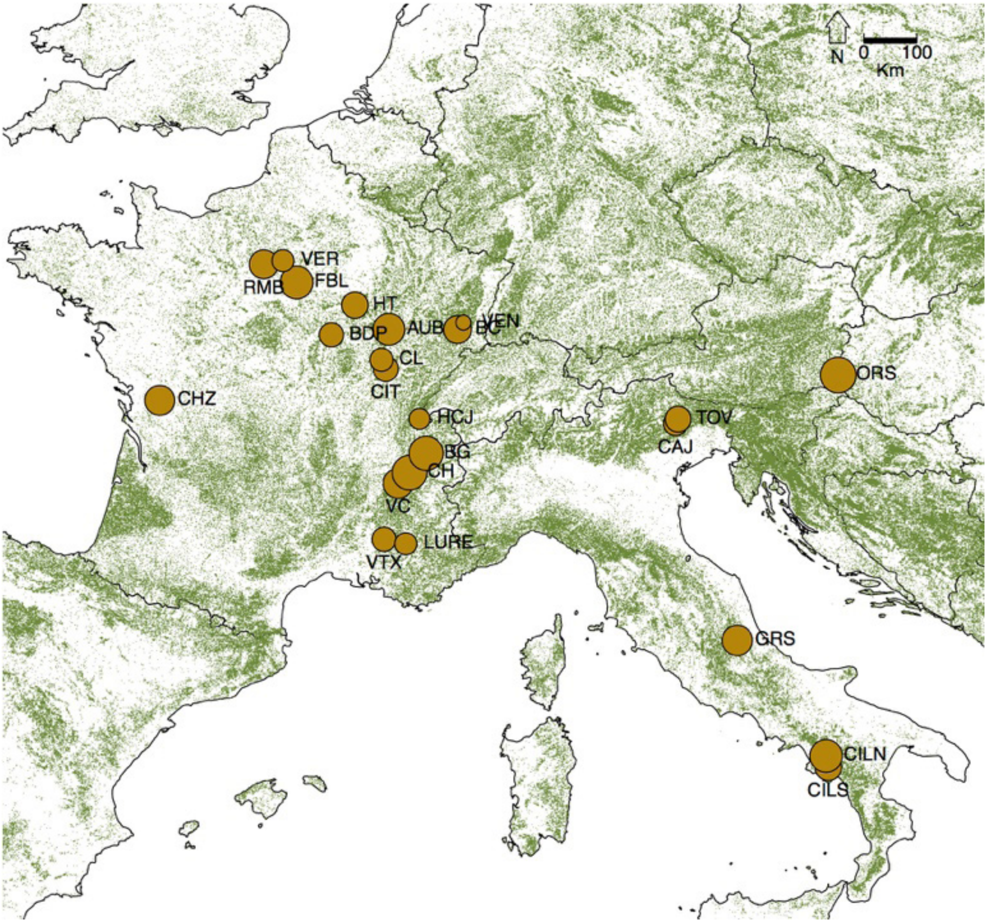

Figure 1. Sampling sites and forest cover (in green, from the joint Research Centre http://forest.jrc.ec.europa.eu). The size of the dots is log-proportional to the number of plots at each site.

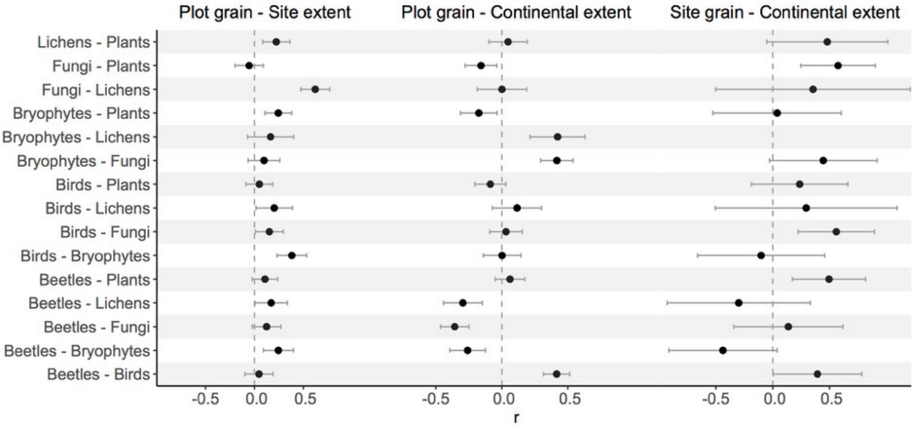

Figure 2. Effect size estimations and 95% confidence intervals for Pearson's correlation coefficients among species richness of different taxa in Temperate European forests.

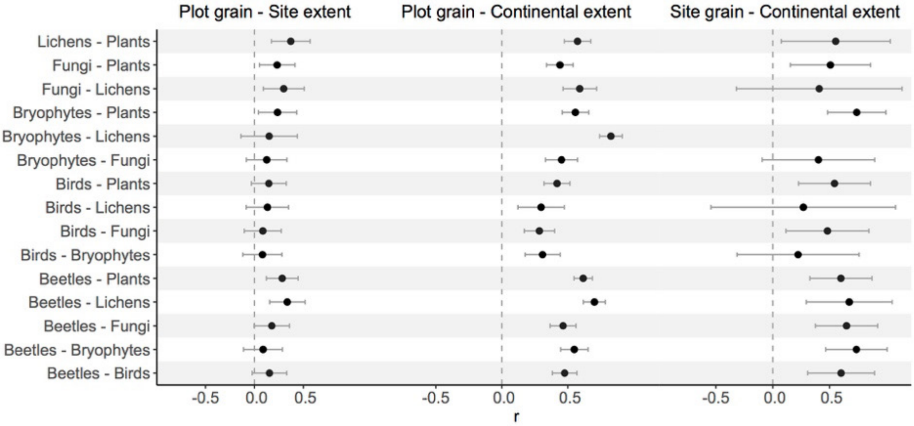

Figure 3. Effect size estimations and 95% confidence intervals for correlation coefficients among spatial patterns of community composition (derived from Mantel correlation test) of different taxa in Temperate European forests.

Which traits predispose species to extinction? A review

Filipe Carvalho[*1], *Aino Juslén*[1], *Pedro Cardoso*[1]

[1]Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland
[*]E-mail: filipe.chichorrodecarvalho@helsinki.fi

Keywords: extinction risk, vulnerability, life-history traits, review

Biodiversity is shrinking rapidly and despite our efforts, only a small part of it has had their risk of extinction evaluated. Identifying the traits that make species vulnerable might help us predict the outcome for those less known. We gathered information on trait responses to extinction risk from over than a hundred publications, across all taxa, spatial scales and geographical regions, in what we think it is the most complete compilation up to date. Vertebrates, and specially mammals and birds, are unsurprisingly the most studied taxa. In terms of traits, geographical range size is by far the overall best, and habitat specialization the intrinsic best, predictor across all taxa. Several traits for which we lack data for most species often rank high. Body size is the most popularly tested trait aside from range size. The "bigger is bad" rule is however not very supported across all taxa, but fortunately this trait becomes usually very informative in those studies that investigate its interaction with extrinsic and other intrinsic traits. Further studies should analyse interactions between traits and sources of threats, but we recognize that such analyses are very data-thirsty. Modelling virtual species, i.e., with agent based models, might be a good workaround for this lack of real data.

A method to make quantitative predictions on global community quantities with incomplete information on model parameters

Hugo Fort[1*]

[1]Department of Physics, Universidad de la Republica, Montevideo, Uruguay
[*]E-mail: hugo@fisica.edu.uy

Keywords: quantitative Lotka-Volterra competition theory, biodiversity–ecosystem functioning experiments

The capacity of community ecology for making quantitative predictions is often limited by incomplete empirical information which precludes obtaining reasonable estimates of model parameters. This is particularly the case for communities with large species richness S since it is practically impossible to perform the S monoculture experiments (to obtain the species carrying capacities) plus the Sx(S-1)/2 pairwise experiments (required to estimate the entire set of interspecific interaction coefficients of the interaction or community matrix). However quantitative predictive tools are vital for understanding the fate of ecological communities.

Here we derive an analytical approximation for predicting the relative yield total (or equivalently the mean relative yield) as a function of the mean intensity of the interspecific competition and the species richness. The rationale is that with incomplete information on model

parameters it seems more reasonable to attempt to predict global or mean quantities, defined for the whole community of competing species, rather than making detailed "microscopic" predictions, like species abundances.

This method, with only a fraction of the model parameters (carrying capacities and competition coefficients), is able to predict accurately empirical measurements covering a wide variety of taxa − algae, plants, protozoa, etc.

Our aim with this approach is to contribute in making community ecology a more quantitative and predictive science. We argue that such parsimonious modeling is preferable than more realistic theories involving additional parameters which can be very difficult to measure.

Three-dimensional image processing to survey productivity and dynamics of pasture communities in the Pollino National Park (Southern Italy)

Domenico Gargano[1,2], Liliana Bernardo[1,2], Aldo Schettino[3], Maurizio Muzzupappa[4], Antonio Lagudi[4], Nicodemo G. Passalacqua[2]*

[1]Department of Biology, Ecology and Earth Science, University of Calabria, Rende (CS), Italy
[2]Museo di Storia Naturale della Calabria ed Orto Botanico University of Calabria, Rende (CS), Italy
[3]Pollino National Park, Rotonda (PZ), Italy
[4]Department of Mechanical, Energetics and Management Engineering, University of Calabria, Rende (CS), Italy
[*]E-mail: domenico.gargano@unical.it

Keywords: community productivity, pastures, structure-from-motion, vegetation dynamics

Image-based three-dimensional reconstruction (Structure-from-Motion, SfM) has been widely applied in geosciences research and cultural heritage documentation, restoration and conservation. SfM represents a low-cost methodological alternative to laser-based systems (1). Recently, the use of SfM is growing also in vegetation science. Indeed, this tool was used to perform landscape-scale analyses of dryland vegetation (2), and to evaluate tree canopy structure from remote-sensed (3). Instead, the potentiality of SfM for fine-vegetation structure modelling was little explored in high-diverse terrestrial systems as the Mediterranean mountain pastures. In such communities the application of SfM can undergo various technical limitations, as the canopy heterogeneity caused by the high species diversity (>30 specie x m^2), and the adverse field conditions constraining the procedures of image acquisition. Nonetheless, the availability of a low-cost fine surveying methodology would strongly improve knowledge and management of these valuable plant communities. We tested SfM for reconstructing vegetation structure and evaluating productivity and seasonal dynamics in 1 m^2 plots representing Mediterranean pastures. Our main goals consisted in evaluating the effectiveness of SfM to produce estimates of vegetation productivity (i.e. vegetation volumetric variations) in alternative to traditional biomass measures. This would limit the method-

ological drawbacks originated by the vegetation removal, which can constrain some analyses like multi-temporal monitoring. In addition, we tested the reliability of SfM in analysing multiseasonal variations of vegetation structure. To this end, we compared data obtained from SfM models with the coenological variability observed by floristic recognitions. Our preliminary results confirm that SfM can provide some reliable proxies of community productivity, by also offering new opportunities for analysing patterns of vegetation structure, composition and dynamics.

Acknowledgments

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Aquatic ecology

Associations of amphipods of the South-Southeastern Brazilian Continental Shelf

Natalia Joana Rebello da Cunha[1*], *Tito César Marques de Almeida*[1]

[1]Laboratório de Ecologia de Comunidades Aquáticas, Univali, Itajaí, Brasil
[*]E-mail: nataliacunha@edu.univali.br

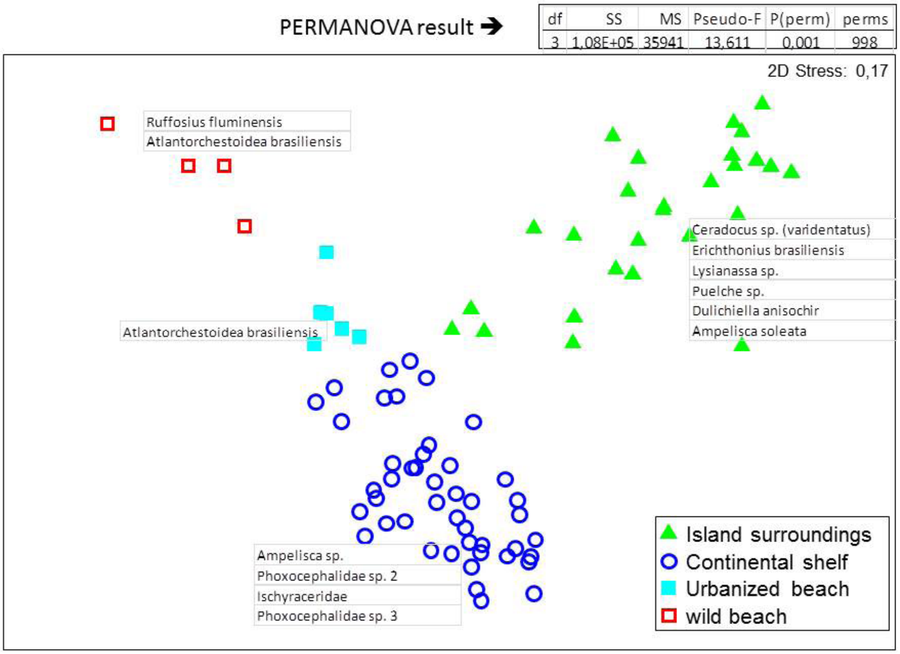
Keywords: ecology, communty, Amphipoda

Amphipods perform important ecological role as indicators of environmental quality, cycling organic matter, and participating in the food chain of many species of economic interest. This word aimed to analyze amphipods associations of the South-Southeastern Brazilian continental shelf, from the external shelf to sand beaches in 76 sampling stations. Sediments samples were washed in 0,5 mm mesh sieves, organisms were fixed in 4% formalin solution, identified in stereoscopic microscopes, and conserved in 70% alcohol solution. PERMANOVA was conducted in a Bray-Curtis similarity matrix after a nMDS. 2987 individuals from 16 families were recorded, and *Ruffosius fluminensis*, *Dulichiella anisochir* and *Ceradocus sp* were the most abundant species. Four distinct associations were observed according to the habitat.

Ampelisca sp., Ischroceridae sp.,Phoxocephalidae sp. 2, and Phoxocephalidae sp. 3 represented the associations of the external shelf, while Ceradocus sp., Erichtonius brasiliensis, Lysianassa sp., Puelche sp., Dulichiella anisochir and Ampelisca soleata were the associations found in the island surroundings. The urbanized beach had Atlantorchestoidea brasiliensi as the dominant species, while Ruffosius fluminensis and Atlantorchestoidea brasiliensis were the most abundant in the wild beach associations.

We speculate that Sediments' characteristics due to hydrodynamic patterns are the main aspects that drove the association of the amphipods of the South-Southeastern Brazilian Continental Shelf.

Figure



PERMANOVA result ➔

df	SS	MS	Pseudo-F	P(perm)	perms
3	1,08E+05	35941	13,611	0,001	998

Identified associations representation from the similarities analyzes

Spatiotemporal variation of pelagic fish assemblages across neotropical lakes in a subtropical wetland

Alexandre Garcia[1*], *Marlise Bemvenuti*[1], *João Vieira*[1], *Mario Condini*[1], *Rodrigo Bastos*[1], *Bianca Possamai*[1], *Lucia Rodrigues*[2], *David Motta-Marques*[2]

[1]Instituto de Oceanografia, Universidade Federal de Rio Grande, Rio Grande, Brazil
[2]Instituto de Pesquisas Hidráulicas, Universidade Federal do Rio Grande do Sul, Rio Grande, Brazil
[*]E-mail: amgarcia.ictiofurg@gmail.com

Keywords: species diversity, species composition, spatial heterogeneity, habitat complexity

Current approaches in community ecology aim to explain the patterns of distribution and abundance of species, linking processes that occur at different spatiotemporal scales. In the present work, we investigated intra- and interannual variation in fish assemblages across lakes with contrasting sizes and embedded in a complex wetland located at subtropical latitudes (32ºS) of the Neotropics. Fish collections were carried out at Taim Hydrological System (2,254 km^2) in the southernmost region of Brazil (Fig.1). The regional climate is subtropical (Cfa type) with annual average air temperatures of 16ºC and precipitation between 1800 and 2200 mm. Fishes were sampled using gillnets in pelagic waters (>1.5m) of four lakes during 14 field surveys between 2001 and 2004. Lakes varied in surface areas ranging from comparatively small ('Jacaré': 1.45km^2, 'Nicola': 2.58km^2), intermediate (Flores: 11.30km^2) and large ('Mangueira': 820 km^2). Lakes and sites were coded as FLO (Flores), Nicola (NIC), Jacaré (JAC), and Mangueira's due to its largest size was divided into two sampling stations located at its northern (MAN) and southern (MAS) reaches. Similarities in species composition and abundance among lakes were analyzed using nonmetric multidimensional scaling (NMDS) and analysis of similarities (ANOSIM). Diversities components (richness and evenness) were evaluated using rarefaction method and Evar index, respectively. A total of 9,014 individuals and 32 species were recorded, with the largest lake Mangueira (MAN and MAS combined) showing the higher number of individuals (5,408) and species (28), whereas the intermediate size lake (FLO) had the lowest capture (470 and 19, respectively). Species richness and evenness had contrasting trends across lakes. The average number of species per field trip significantly increased from FLO to MAS ($F_{4,63} = 5.23$, $p < 0.001$). Post hoc multiple comparisons (Newman-Keuls test, $\alpha = 0.05$) showed that FLO lake had lower average number of species (7.7) than JAC (10.8) and both Mangueira sites (MAN: 12.0 and MAS: 11.0). However, when differences in sample sizes were taken in account by the Rarefaction method, such trend was not statistically significant ($F_{4,63} = 1.51$; $p > 0.20$). In contrast with species richness, FLO had the highest evenness value (0.68) when compared with the other lakes, which ranged from 0.36 (MAN) to 0.45 (JAC) (Newman-Keuls test, $\alpha = 0.05$). These among-lakes differences in assemblage attributes (species richness, evenness, and average number of fish per sample) were not correlated with lake's surface area ($p>0.05$). MDS plots showed higher similarities among fish assemblages of FLO, NIC and JAC lakes, when compared to MAN and MAS. The higher average dissimilarity occurred between the northernmost (FLO, 58.41%) and the southernmost site (MAS, 58.51%). SIMPER analysis revealed that seven species accounted for approximately 70% of the dissimilarity in the pair-wise comparisons between Mangueira and the other lakes (Fig.2). These findings could be explained by spatial heterogeneity across the studied lakes. For instance, habitat complexity derived from lake-wetland interface changes markedly among the studied lakes. Lakes up north of the study gradient (FLO, NIC, JAC) closer to the wetland area, had a tendency to have lower water transparency and higher turbidity probably due to input of nutrients and organic matter from the wetland. On the other hand, the larger southern lake (MAN and MAS sites) is characterized by higher water transparency and relative abundance of submerged macrophytes. Therefore, spatial heterogeneity related with changes in habitat complexity seems to be an important factor structuring pelagic fish assemblages in subtropical lakes.

Figures

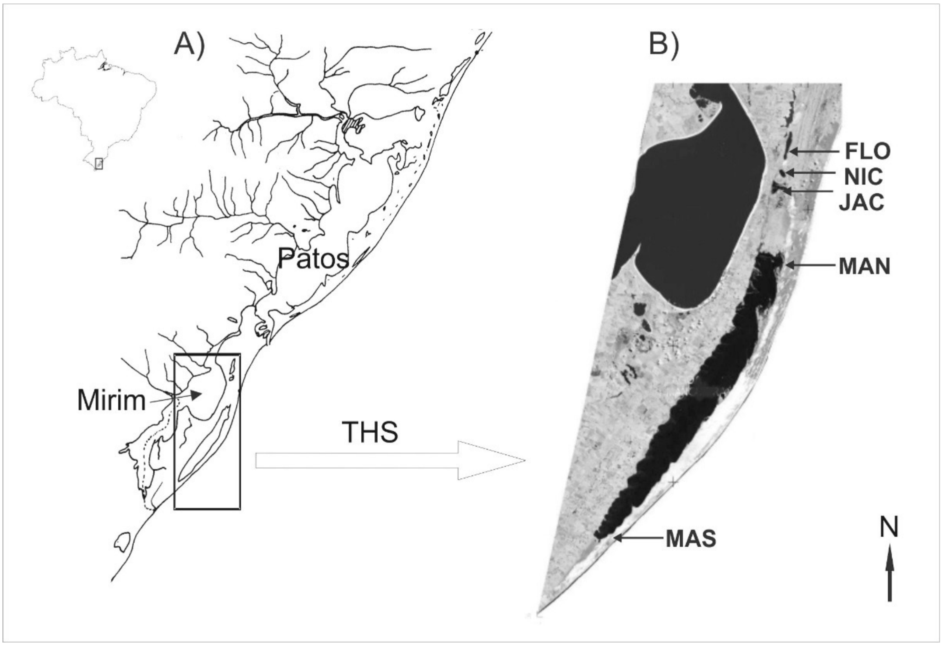


Figure 1. Patos-Mirim drainage basin in southern Brazil (A) and the Taim Hydrological System, THS (B) with the sampled lakes and sampling stations: Flores (FLO), Nicola (NIC), Jacaré (JAC) and Mangueira (MAN and MAS.

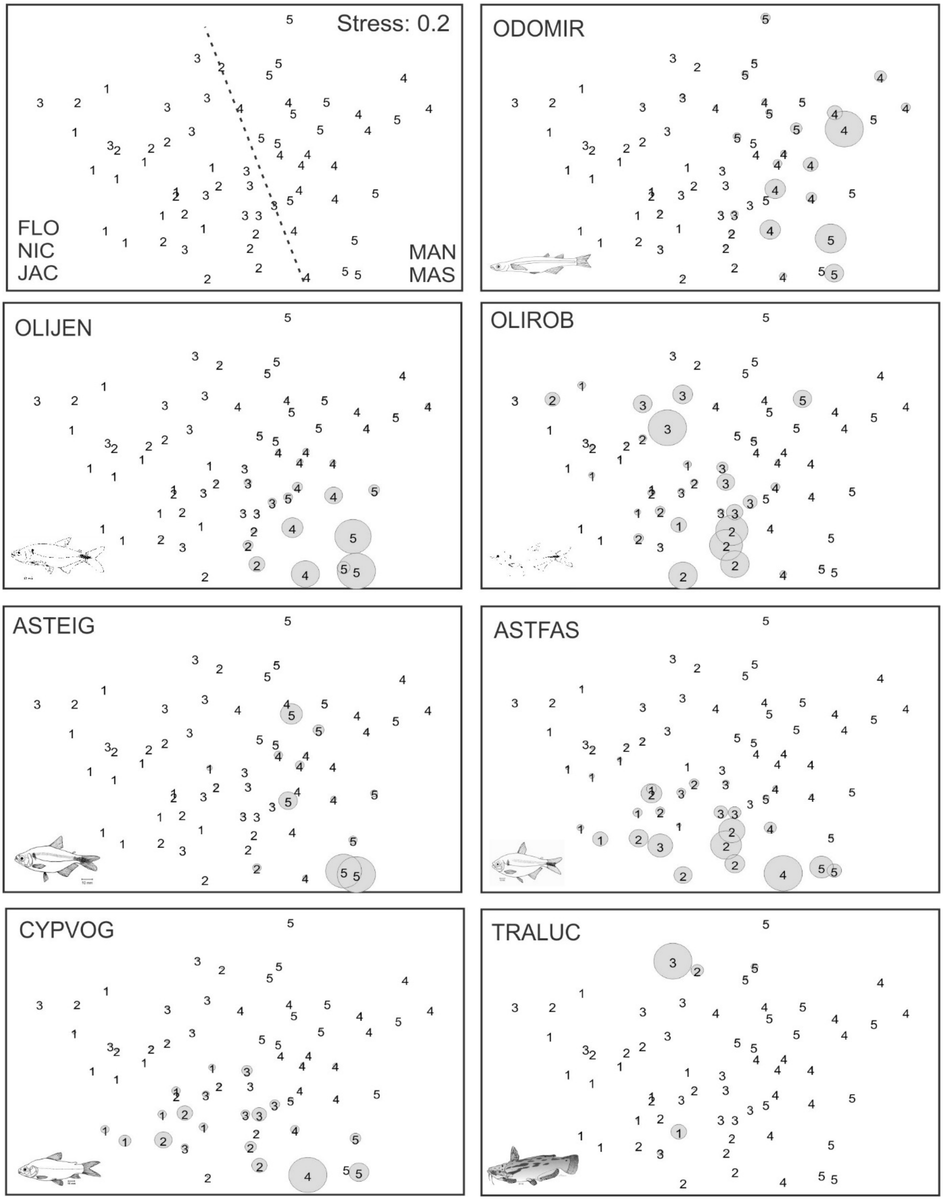


Figure 2. MDS ordination of sample sites based on the species composition of Flores (1), Nicola (2), Jacaré (3), and northern (4) and southern (5) sites of Mangueira lake. Mean CPUE data were square-rooted transformed and Bray-Curtis similarity was used as similarity index. Species codes: OLIJEN: *Oligosarcus jenynsii*, OLIROB: *Oligosarcus robustus*, ASTEIG: *Astyanax eigenmanniorum*, ASTFAS: *Astyanax fasciatus*, ODOMIR: *Odonthestes mirinensis*, ODOPER: *Odonthestes perugiae*, CYPVOG: *Cyphocharax voga*, TRALUC: *Trachelyopterus lucenai*.

Phytoplankton functional niches in fluvial ecosystems

Zsolt Nagy-László[1*], *Gábor Borics*[2], *András Abonyi*[3], *Judit Padisák*[4], *Gábor Várbíró*[2]

[1]Department of Limnology, University of Pannonia, Veszprém, Hungary
[2]Department of Tisza Research, MTA Centre for Ecological Research, Danube Research Institute, Budapest, Hungary
[3]Department of Hydro- and Plant Ecology, MTA Centre for Ecological Research, Danube Research Institute, Budapest, Hungary
[4]MTA-PE Limnoecology Research Group, Veszprém, Hungary
[*]E-mail: nagyzs@gmail.com

Keywords: functional niches, niche characteristics, modelling, environmental variables, riverine phytoplankton

The niche concept can be considered a cornerstone in community ecology and has a revival under climate change. Functional concepts of phytoplankton have received considerable amount of interest recently. Two complementary functional approaches have been developed based on 1) trait characteristics of taxa (functional traits), and 2) based on characteristic occurrence of species groups (functional groups) according to distinguished set of environmental conditions.

Here, we demonstrate that phytoplankton functional groups *sensu* Reynolds (FGs) can be characterised by distinct niche characteristics (position and width) in fluvial ecosystem, and also that how niche-based modelling provides an effective tool in better understanding the functional organization of phytoplankton along the longitudinal axis of rivers. To test our hypotheses, we used a large dataset regarding the Hungarian section of the Tisza River from the period 2007-2012. By using a niche-based modelling (niche position – marginality and niche width – tolerance) of FGs, we identified the main environmental constraints along which the phytoplankton functional niches could be separated. Our results suggest that nutrients and water temperature are important variables shaping the distribution of FGs in niche space. The effects of other environmental variables are also discussed.

Based on the niche delimitation, functional phytoplankton niches can be categorized as 1) FGs with non-marginal position and large niche-breath; 2) FGs with marginal position and niche-breath; and 3) FGs with non-marginal position and narrow niche-breath.

Our result suggests that niche based delimitation:

1. can be considered a promising tool for establishment of main driving constraints that separate phytoplankton functional niches;
2. can also be used for characterisation of habitat demands of phytoplankton FGs in fluvial ecosystems;
3. is a useful tool for comparing the distribution of phytoplankton functional niches along the longitudinal axis of individual rivers;
4. is a promising approach for comparing the niche distribution of individual functional groups among different type of potamal rivers.

Patterns of top-down regulation along an enrichment gradient for a series of marine lakes and lagoons

Sabine Wollrab[1*], *Philippe Pondaven*[2], *Stephan Behl*[2,3], *Beatriz Beker*[2], *Herwig Stibor*[2,3]

[1]Department of Experimental Limnology, Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany
[2]Laboratoire des Sciences de l'Environnement Marin, Université de Bretagne Occidentale, Plouzané, France
[3]Department Biologie II, Ludwig-Maximilians-Universität München, Planegg-Martinsried, Germany
[*]E-mail: wollrab@igb-berlin.de

Keywords: top-down control, bottom-up control, trophic interactions, food web, marine plankton

While theoretical food web studies highlight the importance of alternative energy pathways in shaping community response to bottom-up and top-down forcing, empirical insight on the relevance of the predicted patterns is largely lacking. In marine plankton food webs differences in food size spectra between ciliates and copepods lead to alternative energy pathways, one expanding from small phytoplankton over ciliates to copepods, the other from large phytoplankton directly to copepods. Predation pressure by copepods leads to an increase of small phytoplankton through top-down control of copepods on ciliates, but to a decrease of large phytoplankton through direct predation by copepods. Due to these opposite response patterns, food web theory predicts a shift from dominance of large to small algae along an enrichment gradient. However, if copepods are under top-down control by strong predation through planktivores such as fish or jellyfish, dominance of large algae is expected throughout the enrichment gradient. These predictions clearly deviate from the general assumption of a shift from small to larger phytoplankton taxa with increasing nutrient availability. We tested these predictions by analyzing the phytoplankton composition from numerous marine lakes and lagoon sites located on the archipelago of Palau covering a wide range of nutrient levels, comparing sites lacking large numbers of higher trophic levels (jellyfish, pelagic fish) with sites harboring high densities of jellyfish. The observed patterns strongly support that higher trophic levels influence the phytoplankton size distribution along a nutrient enrichment gradient, highlighting the importance of alternate energy pathways in food webs for community responses.

Acknowledgments
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Human systems

A neighbourhood landscape design framework for enhancing ecosystem services in the urban area

Chan Zi Ching Jane[1*], *Agnieszka O. Guizzo*[1], *Liao Kuei-Hsien*[2]

[1]Department of Architecture, National University of Singapore, Singapore
[2]National Taipei University, New Taipei City, Taiwan
[*]E-mail: akiczcj@nus.edu.sg

Keywords: ecosystem services, landscape, landscape architecture, design framework, neighbourhood, urban area

The profession of landscape architecture, which has a tradition to apply ecology to open space design, is increasingly embracing the concept of ecosystem servcies. In recent years scholars in design and planning have started to explore the integration of ecosystem services into landscape design. In this paper we present a design framework for neighbourhood landscape for enhancing ecosystem services in the urban areas. Neighbourhood landscape, or residental landscape, refers to the open space in the residential neighbourhood. Neighbourhood landscape accounts for a substantial amount of the total green areas in the city. It represents the most common form of urban nature – or urban ecosystem – to which urban dwellers are exposed on a daily basis. Its omnipresence also suggests its importance in affecting the overall ecological conditions of the city, through the way it is designed, used, and maintained. Despite so, the design of neighbourhood landscape receives relatively less attention compared to other more natural forms of landscape, such as natural reserves and parks, with regards to urban sustainability and resilience. We argue that it is important to integrate ecosystem services into the design of neighbourhood landscape, which could potentially help to enhance the overall ecological quality of the city. To provide guidance to neighbourhood landscape designers in designing with ecosystem services, we have developed the Neighbourhood Landscape Design Framework (NLDF) through an interdisciplinary and participatory process involving researchers, landscape architecture practitioners, public housing residents, and relevant public agencies. NLDF addresses 17 urban ecosystem services, with a suite of integrated design strategies provided for each service. NLDF also includes a set of design targets for optimizing each service and performance indicators for assessing the effectiveness of design. The integrated design strategies, design targets, and performance indicators in NLDF are based on extensive review of relevant literature on all 17 ecosystem services, as well as on practical experiences.

Acknowledgments
This material is based on research/work supported by the Singapore Ministry of National Development and National Research Foundation under L2 NIC Award No. L2NICCFP1-2013-10 to Tan P.Y.

Carbon and water cycle in grassland ecosystems of diverse water availability – Modelling with Biome-BGCMuSo

Eszter Lellei-Kovács[1*], *Zoltán Barcza*[2], *Dóra Hidy*[3], *Ferenc Horváth*[1], *Roland Hollós*[1], *Gábor Ónodi*[1], *Miklós Kertész*[1]

[1]MTA Centre for Ecological Research, Institute of Ecology and Botany, Vácrátót,
[2]Eötvös Loránd University, Department of Meteorology, Budapest
[3]MTA-SZIE, Plant Ecology Research Group, Gödöllő
[*]E-mail: lellei-kovacs.eszter@okologia.mta.hu

Biogeochemical cycles of grassland ecosystems are highly sensitive to changes in land use and climate change. Simulation of the biogeochemical cycles of managed grasslands may help in identifying and quantifying the main processes, contributing to changes in their productivity. In our work we used the latest version of Biome-BGCMuSo model, the modified version of the widely used biogeochemical Biome-BGC model, with structural improvements to simulate herbaceouos ecosystem carbon and water cycles more faithfully.

Our sampling areas were in five different grassland types in the Kiskunság, Hungary, as open and closed sand grasslands, mesic meadow, wet meadow and marshland. Different soil texture and changing water table level, consequently highly different water conditions are characteristic in these ecosystems, influencing the developement and productivity of vegetation, and also the potential for animal husbandry. Hence, for the meadows and the marshland ecosystems we included mowing management in the simulations. For the comparison of the ecosystems and studying their functions we simulated ecosystem variables, as ecosystem respiration, standing and harvested aboveground biomass etc.

We found that ecosystems of higher water availability are more sensitive to changes in water conditions, and their productivity is more variable between years. By calibration processes using projected leaf area and aboveground biomass we aim to further specify our findings.

Biome-BGCMuSo is available as a standalone model, but also through virtual laboratory environment and Biome-BGC Projects database (http://ecos.okologia.mta.hu/bbgcdb) developed within the BioVeL project (http://www.biovel.eu). Scientific workflow management, web service and desktop grid technology can support model optimization.

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Effects of the biological life and mankind on the Earth (mainly between 1778 and 2015)

Béla Ralovich

Ministry of Welfare (retired), Budapest, Hungary

Components and events of timeless and endless Universe are consequences of permanent flow of energy and substance in accordance with the laws of eternal Nature which will never be totally known by man kind. All components of the Universe have lived their own physical life. The life of our Earth is exceptional because of the presence of *biological life*. The biological life is a biological phenomenon of a *living unit* which lasts till its own death. The living unit is a substantial matrix which is bordered by a permeable membrane/wall. Inside the unit and through its membrane/wall an organized and directed engergy and substance transport flows. The living unit has been affected by the outside effects and it can accomodate to those only between the borders of its own life requirements. In the same time it influences on its environment, too. Now it seems that the living unit is only present in the Bio-sphere of our Earth which is a *closed system* for it. In the case of any kind of closed systems it is *obligatory permanently to ensure* the specific life conditions which are necessary for a *continuous life* and *reproduction* of a living unit. It seems that the appearance of biological life and mainly that of men have fundamentally effected on the Earth. In consequence of the effects different *periodes* can be determined in the life of our Earth. It is necessary to know about these periods because each of them had/have special energetic and substantial processes which had/ have biological consequences. Now we shall only deal with a short piece of the period of the life of our Earth which has started in 1778.

The Environment-Microbiota-Health axis; how acquired microbial communities affect host immunity

Lasse Ruokolainen[1]*

[1]Department of Biosciences, University of Helsinki, Helsinki, Finland
*E-mail: lasse.ruokolainen@helsinki.fi

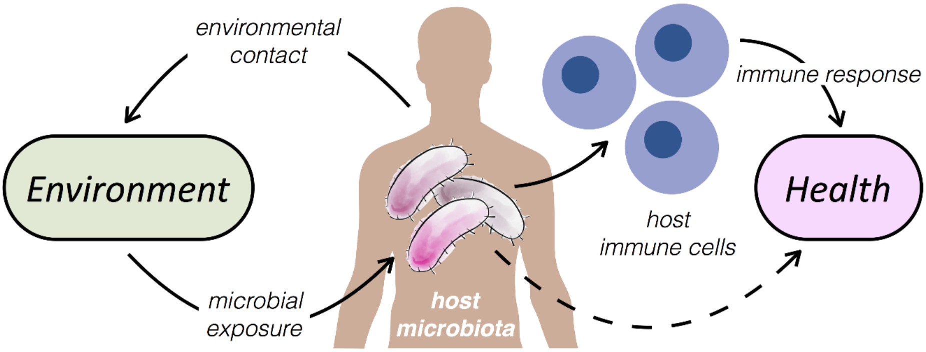
Keywords: allergy, biodiversity hypothesis, microbial community

There is increasing interest in the ecology of host microbial communities, which can be relatively easily studied with modern sequencing methods. A particularly rapidly developing field considers the role of microbiota in host health. After birth, important symbionts colonise the body, transmitted vertically from the mother, and horizontally from other individuals and the surrounding environment. It follows that the mode of birth, social behaviour, and the living environment all influence the assembly and subsequent dynamics of host microbial communities. Microbes encountered in early life have an important role in inducing the development of immune structures in the body and educating the immune system to differentiate between harmful and harmless invaders. Imbalance in the immune tolerance is one of the key reasons behind the rising epidemic of allergic diseases in the world.

Several lines of evidence suggest that lack of immune tolerance is associated with a reduced contact with natural environments, which is in turn associated with urbanisation and the loss and fragmentation of natural ecosystems, as well as abandonment of traditional lifestyles. We have shown that increasing proportion of green space in the living environment is associated with reduced risk of allergic sensitisation. More broadly, urban environment and lifestyle tend to increase the prevalence and severity of allergies in both humans and their dogs. Differences in living environment and lifestyle can also be associated with patterns in the composition of host microbial communities. A clear example is provided by a comparison between the Finnish and Russian Karelia, differing considerably in socio-economical structure, as well as allergy prevalence. Furthermore, differential exposure to environmental microbes is evident in contrastingly different commensal microbiotas between these areas.

Local exposure to specific microbes via the skin, airways, and gut have been shown to exert systemic effects in the host to prevent inflammatory responses, by interacting with the host immune cells. Still, it is unclear how widely such effects are distributed in the host microbial communities. A picture is emerging that to promote health, we need to preserve biodiversity in the environment and make sure a microbial part of this diversity, colonises our bodies. This also bares consequences to, e.g., urban planning, agricultural practices, and child care.

Figure



A schematic illustration of the Environment-Microbiota-Health axis.

Acknowledgments
I would like to thank Jenni Lehtimäki, Antti Karkman, Nanna Fyhrquist, and Tari Haahtela.

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Ecological networks

Multiplex networks: expanding our view of species interactions

Andrew J. Davis

Institute of Chemical Ecology, MPG, Jena, Germany & Institute of Zoology, Goettingen University, Goettingen, Germany
E-mail: adavis@ice.mpg.de

Keywords: facilitation, competition, mutualism, trophic relations, food webs

Ecology is complex, no doubt about it, but interaction networks provide a means of visualizing and analysing much of this complexity. But for too long, for at least the more than 40 years since Bob May's seminal contribution, different types of interactions have been examined separately. This is not real life. In real life all interactions operated together and simultaneously and we ecologists have to get to grips with this reality. I therefore present evidence, largely from my work with *Drosophila*, for some of the less studied interaction types. Then I critically review published attempts to combine different interaction types and analyse them together. I conclude by suggesting ways of producing multiplex networks that capture and make more amenable the reality of co-occuring simultaneous species interactions.

Acknowledgments
I thank in particular Uli Brose, Ferenc Jordán, Sonia Kéfi, Wei-cheung Liu and Volker Loeschcke. I thank collectively the very many other people from whom I have learned in developing these ideas.

Modeling the influence of aquatic-terrestrial coupling on aquatic biodiversity patterns

Rajat Karnatak, Sabine Wollrab

Aquatic and terrestrial ecosystems are connected through energy flow and the movement of material and organisms. These movements are determined by the structure, spatial configuration and connectivity of these different ecosystems. From a meta ecosystem perspective, studies in past have introduced spatially realistic models which have mostly ignored the underlying connection structure. In this presentation, we will introduce a theoretical model which is inspired by dynamical networks, and the spatially realistic Levin's model formulated by Ovaskanien & Hanski [1]. The goal of the model is to provide a better dynamical understanding regarding the role of aquatic-terrestrial coupling in determining the aquatic biodiversity patterns and processes seen in nature.

Reference

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Turbidity mediates the relative importance of herbivory and carnivory in a fairy shrimp

Dunja Lukić[1,2,*], *Csaba F. Vad*[1], *Robert Ptacnik*[1], *Zsófia Horváth*[1]

[1] aWasserCluster Lunz, Lunz am See, Austria
[2] Department of Limnology and Bio-Oceanography, University of Vienna, Vienna, Austria
[*]E-mail: dunjalkc@gmail.com

Keywords: anostraca, trophic ecology, turbidity, temporary ponds

Intraguild predation is defined as predation on a potential competitor. It is widespread in food webs, where its presence can significantly decrease top-down effects. Experimental studies usually focus on direct manipulation of the food web structure, while the effect of the local environment on food web structure is less studied. Temporary waters are usually very shallow habitats. Mixing by wind may induce high levels of abiotic turbidity in such systems. For filter feeders inhabiting such systems, turbidity may have direct implications for food uptake. Here we tested whether turbidity affects the feeding mode in the fairy shrimp *Brachinecta orientalis*, a key species of astatic soda pans. Live specimens were collected from soda pans in eastern Austria and subjected to short-term, feeding experiments. Unicellular algae and copepods were offered as food either separately or in combination. The prey type treatments were crossed with turbidity levels in a factorial design. There was a pronounced decrease in the ingested biomass of algae with increasing turbidity. Conversely, predation efficiency was less affected by turbidity. Our results suggest that turbidity shifts their diet from more herbivorous in transparent to more predatory in turbid waters. Thus, turbidity directly affects the intraguild feeding relationship among Anostraca and their prey. Our study species, *B. orientalis*, exhibits high densities in its natural habitats and therefore might have a strong effect on the co-occurring planktonic species. By determining the strength on an intraguild predation relationship, turbidity might also affect community composition.

Acknowledgments

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Diversity

Taxonomic and functional diversity patterns of stream-fish assemblages from Brazilian Atlantic Rain Forest

Mauricio Cetra

Disentangling the hierarchical structure of river systems and multi-scale environmental effects is important for understanding the freshwater fish community. We sampled 70 stream stretches to investigate how the taxonomic and functional composition and diversity of fish assemblages respond to environmental taking into account a hierarchical organization of streams in three watersheds. Species composition had high correlations between two stretches on the same watershed. Functional diversity had low intra-correlations values, showing that the functioning of the streams fish communities were independent from the watershed. The most important environmental variables were substrate gradient and depth. The species richness was high in poor surrounding environments, but this situation can be explained by tolerant and generalist species in streams with poor habitat quality. In streams with consolidated substrate, taxonomic and functional evenness were low in consequence of invertivores abundance, showing the need to preserve this type of substrate. Our results highlight the importance of local environmental filters shaping streams fish assemblages across different basins, which is more evident when functional descriptors of assemblages are analysed, reinforcing the importance of the approach based on traits as a powerful tool to elucidate local community assembly processes in broader spatial scales.

Phenological variation in urban *Arabidopsis thaliana* populations under natural habitat and controlled conditions

Anke Frank[*], *Juliette de Meaux, Gregor Schmitz, Andrea Schrader, Anja Linstädter*

Institute of Botany, University of Cologne, Cologne, Germany
[*]E-mail: anke.frank@uni-koeln.de

Keywords: urban population ecology, *Arabidopsis thaliana,* natural population adaptations, natural and standard growth conditions, phenological characteristics

Knowledge on the phenological characteristics of natural populations required to understand the relationship between the environment and genetic setup of a species is still sparse. To improve our understanding we investigated phenological patterns and events of variation, both among and within eight naturally occurring urban populations of the annual plant *Arabidopsis thaliana. A. thaliana* is an ideal study plant due its small genome, wealth of genetic and physiological information and rapid identification of gene function (The 1001 Genomes Consortium 2016). Adaptation to contrasting environments has been studied in this species

mainly on a wide geographic scale (e.g. Montesinos et al. 2009) but information about adaptation to different habitats in close proximity is scarce.

First, we observed the phenology of eight populations in their natural urban habitats. From early March to June 2017, we visited the natural populations twice per week (31 visits) and recorded for initially almost 180 permanently marked individuals rosette diameter, bolting event, inflorescence length, number of flowers and fruits. Second, we monitored some of these phenological traits for five of these populations under standard conditions (in a growth chamber). This approach enables us to compare the variation of phenology under standard and natural conditions.

For the natural populations, we give an overview of the within and among population variation of key phenological traits using GLMs to explore the magnitude of natural variation. For the comparative approach, we analyse coefficients of variation, both, within and between populations, in matching phenological traits.

Our results show that different phenological characteristics varied substantially within and among populations as found in other studies (e.g. Méndez-Vigo et al. 2013). However, while the onset of phenological events (i.e. first occurrence of events in a population) can be very similar across populations, peak times and spread of events differed quite strongly within and among populations. Our match of phenological data from individuals of natural and growth chamber populations is currently in progress. Next steps we will be to relate phenology to plant fitness parameters between our natural individual and individuals grown under different controlled conditions. The focus will be the growth rates of inflorescences and number of seeds. To our knowledge, this is the first study to directly compare phenological characteristics of urban *A. thaliana* populations under natural habitat and growth chamber conditions. Our ultimate goal is to identify genetic mechanisms responsible for adaptation in natural populations (Mitchell-Olds & Schmitt 2006; Bomblies et al. 2010)

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Pathogen predators can encapsulate and isolate environmental pathogen reservoirs

Tommi Mononen[1*], *Lasse Ruokolainen*[1]

[1]Department of Biosciences, University of Helsinki, Helsinki, Finland
[*]E-mail: tommi.mononen@helsinki.fi

Keywords: metacommunity, disease dynamics, free-living pathogens, pathogen predators

We are modelling evolutionary host-pathogen dynamics of free-living pathogens in a spatio-temporal landscape using a metacommunity perspective. Each community in a habitat patch network consists of host, pathogen and pathogen consuming predator populations (except pathogen reservoirs). The communities are connected by host dispersal, and infected hosts act as pathogen vectors between patches.

Pathogens are assumed to survive and reproduce in every habitat patch in a network, but there are special reservoir patches that are unsuitable for predators (for example, predators that can survive either in water or in soil environment, but not both). This kind of a reservoir patch becomes a pathogen source in a patch network. Pathogens will spread by infecting dispersing hosts visiting the patch. However, in neighboring patches, where the predatory species can survive, local predator populations become large and they isolate the source patch from the rest of the network (if pathogens cannot gain resistance against the predators). This kind of reservoir patch has only local effects in the network, if infected hosts are not effective dispersers and their disease recovery time is short.

On the other hand, if the pathogen is able to gain resistance against predation, encapsulation becomes harder and infected hosts can spread pathogens throughout the whole network from a pathogen reservoir. We assume that resistance ability is costly for the pathogen; pathogen growth will decrease along to resistance gain. When the trade-off is low, pathogens can achieve resistance without large costs, which leads to global spreading and prevents the encapsulation. When the cost of resistance is high, dynamics converge towards the non-resistance case, because either pathogens are weak to reproduce or will be eaten by pathogen predators surrounding the reservoir patch. This again leads to encapsulation and isolation.

Based on these results, it is possible that the pathogen reservoirs of free-living pathogens—acting as potential pathogen sources—can have only limited impact on network-wide dynamics. However, partly resistant pathogens are potentially capable of spreading across space.

Functional diversity along altitudinal gradients: a multi-taxa approach in the Western Alps

Cristina Tha[1,2*], *Cristiana Cerrato*[1], *Ramona Viterbi*[1], *Antonello Provenzale*[3]

[1]Gran Paradiso National Park, Turin, Italy
[2]Department of Plant Protection Biology, SLU – Swedish University of Agricultural Ecology, Alnarp, Sweden
[3]Italian National Research Council, Pisa, Italy
[*]E-mail: cristina.tha92@gmail.com

Keywords: functional diversity, altitudinal gradient, species turnover, multi-taxa approach

Loss of biodiversity results in a loss of ecosystem services. Functional diversity (FD) has been shown to be a biodiversity component that may be used as a practical, sensitive tool to predict community responses to a changing environment. Within this framework, our study aims to provide an explorative analysis on the feasibility of a trait-based approach in mountain ecosystems and how this can improve the understanding of how FD is distributed along altitudinal gradients and in time.

Using data from two sampling seasons (2006–2008 and 2012–2013) the FD of birds, butterflies, spiders and beetles (carabids and staphylinids) was examined along altitudinal transects (between 500 - 2600 m a.s.l.) in NW Italian Alps. As a first step, a functional database was created for each taxon and FD assessed using different metrics. Subsequently, we evaluated the relationship between FD indices and species richness comparing the results between the two sampling seasons. Additionally, via variation partitioning and β-diversity analyses, we examined which environmental variables most influence the observed changes and whether these are likely due to the natural species turnover or are the result of environmental changes.

Our results suggest that alpine FD studies, whilst promising, are not without constraints, specifically for occasions where for rare and endemic species biological and ecological information is lacking. Furthermore, the quality of FD indices results to be negatively affected by species-poor communities. Different components of FD have different relationships with species richness. Here, the Michaelis-Menten saturation curve provides a regression model that better fits the observed relationship. The multi-taxa approach we employed and the possibility to analyse the changes in the FD indices that occurred between the two sampling periods suggest different responses between taxa to environmental variations. Despite the short time frame, some FD changes were observed and they appear to be related to species richness modifications. Temperature and altitude result to be the environmental factors that most influence the alpine community functional structure.

This study provides a starting point to develop further in-depth spatial-temporal analyses to investigate the distribution of functional traits and their main drivers and to analyse functional redundancy within communities. Moreover, it underlines how investigating FD indices can enhance our knowledge of the functional structure of communities, an approach that has a great predictive value when evaluating responses to climatic and environmental changes. From a conservation perspective, it will also help in detecting the most vulnerable areas, indicating where sustainable management strategies are necessary in order to maintain overall ecosystem functions.

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The effect of habitat hierarchy on testate amoeba communities: additive partitioning of biodiversity

Andrey N. Tsyganov[1*], *Alexander A. Komarov*[1], *Edward A.D. Mitchell*[2,3], *Satoshi Shimano*[4], *Yuri A. Mazei*[1,5]

[1]Depatment of Zoology and Ecology, Penza State University, Krasnaya str. 40, 440026 Penza, Russia
[2]Laboratory of Soil Biology, Institute of Biology, University of Neuchâtel, rue Emile Argand 11, CH-2000 Neuchâtel, Switzerland
[3]Jardin Botanique de Neuchâtel, Pertuis-du-Sault 56-58, CH-2000 Neuchâtel, Switzerland
[4]Science Research Center, Hosei University, 2-17-1 Fujimi, Chiyoda-ku, 102-8160 Tokyo, Japan
[5]Department of Hydrobiology, Lomonosov Moscow State University, Leninskiye Gory, 1, 119991 Moscow, Russia
*E-mail: andrey.tsyganov@bk.ru

In order to better understand the distribution patterns of terrestrial eukaryotic microbes and the factors governing them, we studied the diversity partitioning of soil testate amoebae across levels of spatially nested habitat hierarchy in the largest European old-growth dark coniferous forest (Pechora-Ilych Biosphere Reserve; Komi Republic, Russia). The variation in testate amoeba species richness and assemblage structure was analysed in 87 samples from six biotopes in six vegetation types using an additive partitioning procedure and principal component analyses. The 80 taxa recorded represent the highest value of species richness for soil testate amoebae reported for taiga soils so far. Our results indicate that testate amoeba assemblages were highly aggregated at all levels and were mostly controlled by environmental factors rather than dispersal processes. The variation in species diversity of testate amoebae increased from the lowest to the highest hierarchical level. We conclude that, similarly to macroscopic organisms, testate amoeba species richness and community structure are primarily controlled by environmental conditions within the landscape and suggest that metacommunity dynamics of free-living microorganisms are driven by species sorting and/or mass effect processes.

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Mazzoleni course

Inhibitory effect of extracellular DNA: from models and theoretical reasoning to experimental evidence

Stefano Mazzoleni

Dept. of Agricultural Sciences, University of Napoli Federico II, via Università 100, 80055, Portici (Na), Italy

Theoretical modelling work demonstrated that the build-up of plant-soil negative feedback could explain gradients of species diversity and the spatial patterns of both vegetation and individual plants. Extensive review work on plant facilitation in terrestrial ecosystems provided indirect evidence supporting the counterintuitive concept of “autotoxicity”.

Throughput metabolomic characterization by nuclear magnetic resonance (NMR) methods of a large set of plant litter materials at different decomposition stages showed the correlation between the accumulation of extracellular DNA and the rise of species specific inhibitory effects.

The direct inhibition by conspecific extracellular DNA was demonstrated in lab experiments on several plants, but also in other organisms including bacteria, fungi, algae, protozoa and insects.

These findings revealed a new unexpected function of extracellular DNA at the ecosystem level and its possible role in self-recognition processes.

Ongoing research is now focusing on the mechanisms of such inhibitory effects at both cellular and molecular levels. Moreover, the role of DNA self-inhibition in successional dynamics, plant-pathogen interactions and species coexistence and patterns is under investigation.

POSTER PRESENTATIONS

Estuary – inner continental shelf coupling and polychaete assemblages in southern Brazil

Tito Almeida

E-mail: titoalmeida2008@gmail.com

Estuaries are ecosystems of great ecologic and economic importance and many are altered as they enable human settling worldwide. We aimed to compare the structure and composition of polychaete assemblages in an urbanized estuarine region from southern Brazil and its adjacent inner shelf; both affected by port activity and related dredging operations. We also explored their relationship with environmental characteristics. Three areas were determined for sampling design: 1) a dredged estuarine area (DEA), 2) a non-dredged estuarine area (NDEA) and 3) the inner shelf (IS). Two stations were sampled in each area along seven random surveys between 2002 and 2004. For each sample, ecological descriptors were calculated and differences between assemblages under our experimental design were tested by a mix of univariate and multivariate permutational analysis of variance (PERMANOVA) approaches. Water and sediment variables were measured/collected for each campaign and analyzed though Principal Components Analysis (PCA). We also tested for correlations between the multivariate species matrix and the sediment data through a Canonical Analysis of Principal Coordinates (CAP). A total of 1663 polychaetes were identified, grouped into 16 families, represented by 23 species. *H. similis* was responsible for almost 75% of all sampled organisms but *N. fluviatilis, N. brasiliensis*, *M papillicornis, M. posterelongata and P. tricuspis* were also among the most representative. Two distinct associations were identified represented by IS with higher species richness and by the estuarine (DEA and NDEA) with dominance of *H. similis* and *N. fluviatilis.* Our results indicate the effect of urbanization and dredging activities on the polychaete assemblages, which showed composition and distribution patterns typical of altered areas.

Comparative study of the *Fomes fomentarius* and *Trametes gibbosa* beetle community in Hidegvízvölgy

Réka Andrési[1*], Katalin Tuba[1]

[1]Institute of Silviculture and Forest Protection, Faculty of Forestry, University of Sopron, Sopron, Hungary
[*]E-mail: andresi.reka@gmail.com

Keywords: tinder fungi, white rot, *Octotemnus glabriculus*, *Sulcacis nitidus*

The insect community of mushrooms has already been discovered in Hungary. However, the examination of tinder fungus insect community has not been addressed in greater depth. In this study, two different fungal species (*Fomes fomentarius* and *Trametes gibbosa*) were collected from the identical area: Hidegvízvölgy of Sopron. In Hidegvízvölgy the two types represent the two extremes of fungus. Both species belong to the *Polyporaceae* family. In terms of their structure, *F. fomentarius* is perennial, mostly single, sessile, ungulate, while *T. gibbosa* is annual, rather durable, occasionally occurring in groups, often with a hump at the base. Both fungi cause white rot of wood and usually both species are found on beech (*Fagus sylvatica*) (Domanski et al. 1973, Igmándy 1991).

The main objective of this study was to compare the beetle community of *F. fomentarius* and *T. gibbosa*, which were collected from trees in the same location. Tinder fungi, 4 pieces *F. fomentarius* and 4 pieces *T. gibbosa* were collected in April of 2013, from different beech trees. The fungi were collected without bark and uncleaned because we wanted to keep our target groups and conserve this complex biome. Each fungus was packed in paper sack. In every 8th week, the beetles were collected from the bags. The tinder fungi were held in the laboratory of the Institute of Silviculture and Forest Protection under special conditions, which means 20±1 °C, 60% humidity and 16 hours of lighting and 8 hours of darkness.

We found 105 beetle specimens in the *Fomes fomentarius* samples, while in the *Trametes gibbosa* samples by a hundredfold, 10998 beetles. Four beetle species were identified from *F. fomentarius*, and eight species from *T. gibbosa*. In both fungus species, we found *Octotemnus glabriculus* and *Sulcacis nitidus*. In the *F. fomentarius* the largest number of individuals were 95 and the average number were 26,25. The maximum numbers of beetle species were 2 in the sample fungus. However, the average number of species was 1,5. In *Trametes gibbosa* the maximum number of individuals were 3612, while the average in a fungus were 2749,5. The maximum number of species was 6, while the average was 5. The average volume of the *F. fomentarius* is 288,6 cm^3, so an individual fungus beetle has 10,99cm^3 space. The average volume of a *T. gibbosa* is 102,2 cm^3, thus a fungus feeder beetle could use 0,04 cm^3 space on average. The fruiting bodies of the two species have a different structure. *T. gibbosa* has a thinner body than *F. fomentarius*, in spite of that it provides more room and nutrition for species. Both fungus were examined regarding which part of their body was liked by the fungus beetle. In *Fomes* the beetles begin to consume under the bark and they proceed to the tubular part. In case of *Trametes* species were consumed between the meat and the tubular part. Presumably, they consuming in both directions simultaneously. It is interesting that at the base of the fungi the beetles only consumed when they were eaten the other parts.

In conclusion, despite the fact that the tinder samples were collected at the same time and location from *Fagus sylvatica* trees, *Fomes fomentarius* and *Tramates gibbosa* have a significantly different number of beetle species and specimens. Presumably, the difference could be caused by the structure of fruiting bodies. The *Fomes* has a harder body. It can be feed only by a few beetle species. *Trametes gibbosa* has a thinner meat, but nonetheless it has more fungus consumers. Probably they are different species and they are not competitors of each other.

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Comparative study of ground beetle and ground-dwelling spider assemblages

<u>László Bali</u>[1], Dániel Andrési[2], Csaba Szinetár[3], Katalin Tuba[1]*

[1]Institute of Sylviculture and Forest Protection, Faculty of Forestry, University of Sopron; Sopron, Hungary
[2]KEFAG Kiskunsági Erdészeti és Faipari Zrt.; Kecskemét, Hungary
[3]Institute of Biology, Faculty of Natural Sciences, Eötvös Loránd Univerity; Szombathely, Hungary
[*]E-mail: bali.laszlo@uni-sopron.hu

Keywords: *Carabidae*, *Araneae*, pitfall trapping, deadwood, gap

In our study, the data of two common forest floor arthropod groups, ground beetles (*Coleoptera: Carabidae*) and ground-dwelling spiders (*Araneae*) were compared. Species of both groups are considered abundant, generalist predators in forest ecosystems [1, 2]. These taxa are well-known indicator organisms [3-5]. They react sensitively to changes in environmental parameters, vegetation structure [1, 2, 6-13], anthropogenic disturbances [14] and deadwood abundance [15-17].

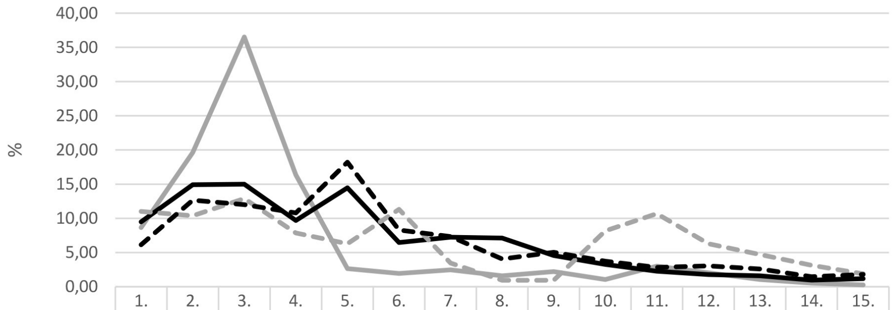
Our goals were to compare the area's ground-dwelling spider and ground beetle assemblages and to assess the effects of artificial gap opening and lying deadwood presence.

To this end, we carried out surveys in Vép 32/D forest sub-compartment, in Gyöngyös-plain [18]. The sub-compartment's stand is homogenous *Quercus cerris* (L.); its age is 69 years. Two of the stand's artificial gaps and their surroundings were surveyed with Barber-type pitfall traps [19-21]. The traps were planted in two 70 m long transects (transect 1 and 2), along the gaps' longitudinal axis, with 15 traps in each transect, 5 m from each other. Traps #5 and #11 are at the edges of the gaps. The installation of the traps took place in April 2013. They have been active during 2 years (for 414 days). In each year, we collected the samples fortnightly, during 8 months. The quantity and quality of the lying deadwood in the traps' 2.5 m vicinity were also measured, using the Ódor method [22].

In our two-year survey, we collected 12842 individual arthropods (11393 spiders and 1449 ground beetles), representing 146 species (115 spiders and 31 ground beetles) (Table 1).

Pardosa alacris (C. L. Koch) and *Calosoma inquisitor* (L.) were the most abundant species. Both groups were most abundant at May and June. The difference between the ground beetle's two graphs are probably caused by geometer caterpillar (*Lepidoptera*: *Geometridae*) outbreak in 2013 (Fig. 1). Both groups had more species and specimens in 2013. The species and specimen numbers of the spiders are higher in the inner parts of the transects (Table 1). The Shannon-diversity values of the ground beetles are generally lover and show higher deviations, which is presumably caused by their lower species and specimen numbers. However, the respecting values do not show high alterations between years or transects (Fig. 2). In the ordination analysis, we summarized the data of the two years and two transects and evaluated by both taxa. The corresponding ST values are inside the confidence interval [23]. The results show two distinct clusters in both cases. The groupings on the spiders' graph consist distinctly of the transects' inner and outer traps, which could indicate community differentiation between habitats. On the ground beetles' graph, 10 traps show high degree of similarity, while the other 5 are distinctly separated (Fig 3). In our opinion, this anomalous pattern is caused by trap destroying big game activity. Since the ground beetles had much lover specimen and species numbers, their data is more sensitive to such disturbances. The correlation analysis show positive significant connections between ground beetle specimen numbers and deadwood quantity, and spider and ground beetle species number. Furthermore, there are negative significant connections between both group's species number and deadwood decay degree (Table 2). However, we have to note, that since deadwood was only present in low quantities (Table 1); the results of this analysis could be inaccurate.

In conclusion, according to our data, the stand's ground-dwelling spider community is richer and more diverse than the ground beetle assemblages are, and it is more affected by the gap openings. These can be the result of the fact that while the ground-dwelling spiders do not leave their forest floor habitats, some ground beetles (i.e. *Calosoma* species) can and will migrate between forest levels.



	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.
13 B	8,66	19,63	36,52	16,36	2,65	1,95	2,48	1,59	2,21	1,06	3,01	2,03	1,06	0,53	0,27
13 S	9,48	14,91	14,99	9,69	14,47	6,46	7,24	7,12	4,57	3,26	2,27	1,78	1,60	0,97	1,18
14 B	11,01	10,38	12,89	7,86	6,29	11,32	3,46	0,94	0,94	8,18	10,69	6,29	4,72	3,14	1,89
14 S	6,14	12,65	12,01	10,79	18,21	8,30	7,34	4,06	5,04	3,73	2,83	3,04	2,59	1,47	1,80

Figure 1. Catching results through the years (from April until November) in relation to the taxa's yearly total specimen numbers (13: 2013, 14: 2014, B: ground beetles, S: spiders).

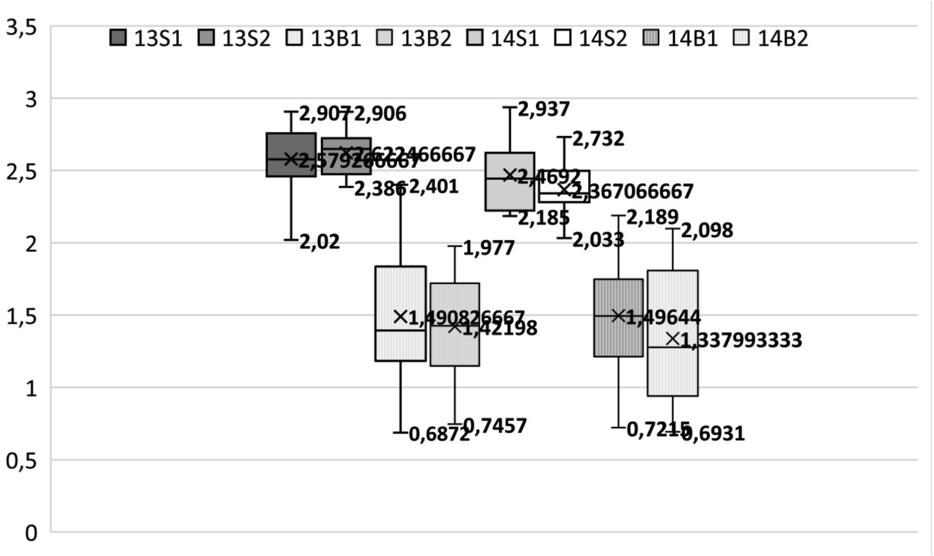
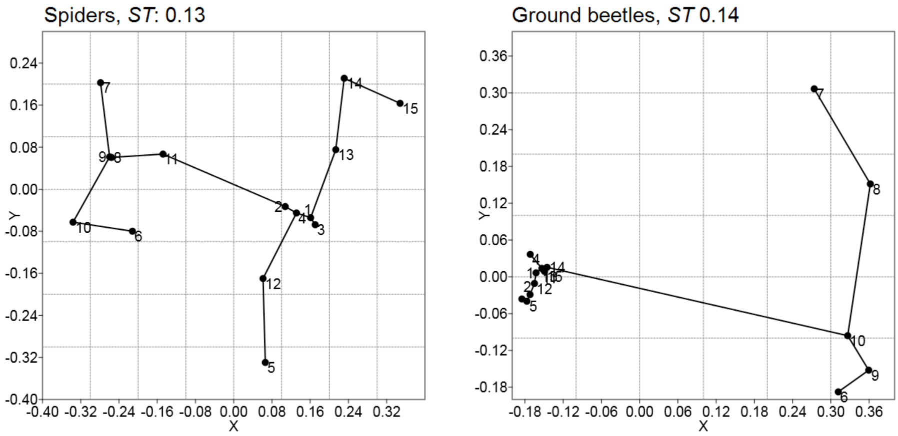


Figure 2. Box-plots depicting differences in Shannon-diversity values in the different years and transects (13: 2013, 14: 2014, S: spiders, B: ground beetles, 1: transect 1, 2: transect 2).


Spiders, *ST*: 0.13

Ground beetles, *ST* 0.14

Figure 3. Ordination analysis. The numbers represent trap numbers, whose data have been summarized by transects, and years; in addition, the lines represent the minimum spanning tree.

Table 1. Survey results by sample collection times (upper half) and by traps (lover half) (S: spiders, B: ground beetles, DW: lying deadwood in the 2,5 m vicinity of the traps, n: specimens, Av.: average).

Sample collections				1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.	Σ
2013	**Spider specimens**			597	939	944	610	911	407	456	448	288	205	143	112	101	61	74	**6296**
	Beetle specimens			98	222	413	185	30	22	28	18	25	12	34	23	12	6	3	**1131**
2014	**Spider specimens**			313	645	612	550	928	423	374	207	257	190	144	155	132	75	92	**5097**
	Beetle specimens			35	33	41	25	20	36	11	3	3	26	34	20	15	10	6	**318**
	Traps			**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**Σ**
2013	**S**	**Taxa**	**1**	26	30	27	16	29	37	34	33	33	39	33	27	21	16	17	**86**
			2	27	28	28	35	32	26	38	35	31	25	29	33	23	26	26	**81**
		n	**1**	230	264	203	110	159	245	197	250	261	258	214	205	81	37	63	**2777**
			2	178	187	241	241	380	310	301	226	216	232	229	215	241	140	182	**3519**
	B	**Taxa**	**1**	8	10	9	9	10	10	12	8	8	13	10	10	10	4	5	**27**
			2	5	7	7	9	11	8	9	9	9	8	9	9	11	7	8	**23**
		n	**1**	45	70	69	27	58	26	27	29	23	21	38	57	50	34	40	**614**
			2	26	40	41	36	61	33	16	19	22	22	44	48	34	36	39	**517**
	DW	**Total d [cm]**	**1**	42.0	-	-	-	-	49.5	-	-	-	-	-	-	-	6.5	-	**98.0**
			2	-	-	-	5.0	-	-	-	-	11.0	-	-	-	-	-	-	**16.0**
		Av. decay degree	**1**	4.6	-	-	-	-	2.0	-	-	-	-	-	-	-	6.0	-	**3.4**
			2	-	-	-	2.0	-	-	-	-	2.0	-	-	-	-	-	-	**2.0**
2014	**S**	**Taxa**	**1**	16	25	23	24	22	27	27	28	27	23	20	25	16	22	23	**64**
			2	18	11	20	24	23	29	27	26	20	24	24	29	25	22	16	**67**
		n	**1**	132	184	193	161	154	237	198	221	239	110	137	137	62	109	136	**2410**
			2	86	72	87	179	199	162	232	173	116	193	267	353	254	190	124	**2687**
	B	**Taxa**	**1**	5	7	5	4	5	8	4	3	6	6	4	6	8	4	11	**24**
			2	4	5	4	2	5	3	8	4	2	8	4	7	7	9	5	**25**
		n	**1**	8	10	12	12	7	13	8	12	9	9	14	17	19	4	27	**181**
			2	7	7	7	2	15	7	11	10	4	16	11	13	16	13	14	**153**
	DW	**Total d [cm]**	**1**	42.0	-	-	-	-	49.5	-	-	-	-	-	-	-	6.5	-	**98.0**
			2	-	-	-	5.0	-	-	-	-	11.0	-	-	-	-	-	-	**16.0**
		Av. decay degree	**1**	4.6	-	-	-	-	2.0	-	-	-	-	-	-	-	6.0	-	**3.4**
			2	-	-	-	2.0	-	-	-	-	2.0	-	-	-	-	-	-	**2.0**

Table 2. Spearman Rank Order Correlations. Upper half shows data of 2013, lower half shows data of 2014 (DW: lying deadwood quantity, Decay: average decay degree, DxD: deadwood weighted by decay degree, S: spider T: taxa, n: specimens, B: ground beetles; significant correlations are bold).

	DW	Decay	DxD	ST	Sn	BT	Bn
DW	-	-0.111803	0.800000	0.300000	0.400000	0.410391	-0.200000
Decay	-0.111803	-	0.447214	**-0.894427**	-0.670820	**-0.917663**	0.447214
DxD	0.800000	0.447214	-	-0.200000	0.100000	-0.153897	0.300000
ST	0.000000	-0.447214	-0.300000	-	**0.900000**	**0.974679**	-0.300000
Sn	0.400000	-0.670820	0.100000	0.600000	-	0.820783	0.100000
BT	0.820783	0.229416	0.872082	0.205196	0.410391	-	-0,461690
Bn	**0.974679**	0.057354	0.872082	0.051299	0.359092	**0.921053**	-

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Quantifying biotic filter effects in old field succession

Andraž Čarni[1], Nina Juvan Mastnak[2], Andrej Paušič[3], Gábor Szabó[4], Zita Zimmermann[4], Sándor Bartha[4]*

[1]Research Centre of the Slovenian Academy of Sciences and Arts, Jovan Hadži Institute of Biology, Novi trg 2, 1000 Ljubljana, Slovenia
[2]Research Centre of the Slovenian Academy of Sciences and Arts, Anton Melik Geographical Institute, Novi trg 2, 1000 Ljubljana, Slovenia
[3]University of Maribor, Faculty of Agriculture and Life Sciences, Pivola 10, 2311 Hoče, Slovenia
[4]MTA Centre for Ecological Research, Institute of Ecology and Botany, H-2163 Vácrátót, Alkotmány Str. 2-4, Hungary
[*]E-mail: carni@zrc-sazu.si

Keywords: distinctiveness, dominant species, Kras region, succession, spatial dependence, subordinate species

Dominant matrix species put strong constraint on the colonization and establishment of subordinate species in secondary succession. The related biotic filter effects might play key role in the rate and direction of regeneration processes. Dominant species often form heterogeneous patchworks in middle successional stages. Few studies have addressed the relative role of dominants in filtering subordinate species. Here we applied two methods exploring the spatial associations between dominant and subordinate species for quantifying biotic filter effects in an old field succession on the Kras Plateau (SE Slovenia).

Seven sites (representative successional stages) were selected with different ages (1, 3, 6, 9, 13, 15 and more than 100 years) after the abandonment of croplands but they were still mown once a year and therefore scrub and forest could not develop. At each stage we sampled the presence of vascular plant species in 5x5cm microquadrats along 52 m circular transects (1040 microquadrats per transects) and these high extent and high resolution samples were used for exploring spatial relationship between dominant and subordinate species.

One method based on information theory models assessed multiple spatial associations between focal dominant and all subordinates in particular stages of vegetation development. Because spatial associations are scale dependent we used a series of plot sizes (between 5cm up to 5m) for assessing spatial dependence at increasing spatial resolution. Another information theory measure (called local distinctiveness) was used to quantify the spatial heterogeneity of dominant species.

The other methods used were analysis of life forms, chorotypes (origin of species), species behaviour (synsystematic affiliation) that were adapted for analysis of differences within stands of different age.

The strongest biotic filter effects appeared in intermediate stages of old field succession (between 9 and 15 years) when dominant matrix species formed the highest spatial heterogeneity. Significant differences were found between the filter effects of particular dominant grass species that have important implication for restoration management.

How do belowground organisms affect the yield and secondary metabolite production of marjoram (*Origanum majorana* L.)

Krisztina Bereczki[1], *Gergely Boros*[1], *Krisztina Szabó*[2], *Tünde Takács*[3], *Rita Engel*[2]

[1]MTA Centre for Ecological Research, GINOP Sustainable Ecosystems Group, 8237 Tihany, Klebelsberg Kuno u. 3.
[2]MTA Centre for Ecological Research, Institute of Ecology and Botany, Alkotmány u. 2-4, H-2163 Vácrátót, Hungary
[3]MTA Centre for Agricultural Research, Institute for Soil Scinces and Agricultural Chemistry, Herman Ottó u. 15, H-1111 Budapest, Hungary

Links between the below- and aboveground communities have been the focus of growing number of studies in the last decades. The potential effect of soil processes on the plant performance has long been known, however recent studies showed that in addition to the yield, the production of secondary metabolites can be also influenced by certain members of soil fauna, such as arbuscular mycorrhizal fungi (AMF) and earthworms. To better understand how soil communities affect attributes of plant communities, we need complex, experimental approaches. In the present study, we conducted a mesocosm experiment to study the combined effect of AMF fungi and earthworm on the growth and polyphenol content of marjoram (*Origanum majoranana* L.), a member of *Lamiaceae* family. We had five treatments in sixteen replications: 1. control: sterile soil; 2. sterile soil + AMF inoculum (INOQ-top) contains one fungi species (*Glomus intraradices*); 3. sterile soil + AMF inoculum, which is a mixture of several Glomus species (Symbivit); 4. sterile soil + earthworms; 5. sterile soil +

INOQ-top + earthworm. According to our results, mycorrhization increased significantly the yield of biomass in marjoram. In terms of polyphenol content the effect of treatments was similar in each examined phenolic compounds (rosmarinic acid, lithospermic acid isomer, apigenin-6,8-di-*C*-glucoside, luteolin-7'-*O*-glucuronide, apigenin-glucuronide): the highest increase was observed by the combined presence of AMF and earthworms, while the separate effect of AMF and earthworms was also significant. These results suggest that the combined application of AM fungal inoculum and earthworms can be a potential to improve the quantity and quality of commercially important medicinal plant and thereby can play an important role in sustainable agriculture.

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Scale sensitivity of the relationship between alpha and gamma diversity along alpine elevation gradient of central Nepal

Kuber P. Bhatta

E-mail: kuber.bhatta@uib.no

Aim Components of scale, such as grain, focus, and extent, influence the spatial patterns of alpha and gamma diversity and their relationships. We explore these scale issues by testing if gamma diversity can predict alpha diversity independent of scale and whether the elevational patterns of herbaceous and woody species richness are dependent on scale.
Location Langtang National Park, central Nepal.
Methods We estimated richness for the woody and herbaceous plant species along an elevation gradient (3900–5000 m a.s.l.) in nested plots of 1, 16, and 100 m^2 and the regional species pool (gamma diversity) from written sources. Generalised Linear Modelling was used to analyse the alpha and gamma diversity and their correspondence at different grain-sizes.
Results Elevational gamma diversity confidently predicts the alpha diversity patterns for both life-forms at all grain-sizes. The concordance tends to increase with larger grain-size and area of species pool, especially for the monotonously decreasing elevational gamma and alpha diversity patterns of the woody species. The hump-back patterns of the elevational gamma and alpha diversity for the herbaceous species also concord significantly, but here the concordance between alpha diversity and local species pool is stronger. Elevational patterns of alpha diversity are consistent across grain-sizes, although the deviance explained by the elevation gradient increases with larger grain-size, especially for woody species.
Main conclusions The correspondence of elevational gamma and alpha diversity is basically scale-invariant at the extent of scales studied here, although it tends to be stronger at a coarse grain and with a larger area for the species pool, especially for woody life-forms. For herbaceous species, local species pool is a better predictor of alpha diversity than the regional gamma diversity. The elevational patterns of species richness are almost independent of grain and focus; however, the patterns become more prominent at the coarser grain-sizes.

Major plant lineages can be more informative than phylogenetic corrections

Martin Bitomský[1*], *Jan Mládek*[1]

[1]Department of Ecology and Environmental Sciences, Palacký University, Olomouc, Czech Republic
[*]E-mail: bitomsky.martin@gmail.com

Keywords: asterid, grassland, monocot, phylogenetic bias, rosid, trait-based ecology

There is heated debate about controlling for phylogenetic bias in trait-based ecology because it is not always necessary correction and could sometimes lead to deceptive interpretations. Current ecology now has two options: either focus on methods which filter phylogenetic bias (confounding effects) or use phylogenetic dependence of species for addressing ecological questions. However, ecologists may struggle to correctly conduct phylogenetically informed analyses because it requires advanced knowledge of other disciplines like molecular biology, bionformatics and statistics. Here, we present very simple and clearly intrepretable approach that effectively accounts for phylogeny without the need of creating phylogenetic trees or using advanced statistical techniques. It is based on affiliation to major plant lineage (asterid, rosid, monocot). We compared the outputs of our approach and classic ecophylogenetic methods addressing three common research questions at species and community level. Using data from seminatural grasslands we showed that this lineage approach provided similar results as widely used methods with phylogenetic correction. In general, results suggest that our lineage approach (phylogeny coded as categorical variable) is not oversimplification but relevant treatment capturing interesting ecological phenomena which are not detectable by classic phylogenetic corrections. We suggest that in some situations only using information about major plant lineages (without using phylogenetic tree) could be sufficient for trait-based ecological study and can even improve the interpretation and attraction of results.

Changing the relative importance of environmental filtering and mass effect along a productivity gradient

Zoltán Botta-Dukát[1,2,*], *Barbara Lhotsky*[1], *Anikó Csecserits*[2], *Bence Kovács*[2],
Miklós Kertész[1,2], *Attila Lengyel*[1], *Gábor Onodi*[2], *Tamás Rédei*[1,2]

[1] GINOP Sustainable Ecosystems Group, MTA Centre for Ecological Research, Tihany, Hungary
[2] Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary
[*]E-mail: botta-dukat.zoltan@okologia.mta.hu

Keywords: community assembly, traits, maximum entropy approach

It is widely accepted that assembly of local plant communities is neither fully deterministic or fully stochastic process: non-random local niche-based processes interact with random dispersal and demographic stochasticity. However, on the relative role of these processes we have only scarce information.

Modelling observed abundances by the maximum entropy approach (Community Assembly by Trait Selection) developed by Shipley (2010, Shipley et al. 2006, 2012) allows statistical decomposition of total information content that are attributable to environmental trait filtering, mass effect and demographic stochasticity. We applied this method to 103 grassland plots sampled in the same site along productivity gradient from wetlands to open sand grassland. Trait data consisted of species' means of 5 continuous traits (height, leaf size, SLA, LDMC and seed weight) and categorization of species according to other six traits (growth form, ability to re-flower, leaf distribution, shoot growth form, age at first flowering, lateral spread). NDVI were measured in each plot as proxy of productivity.

Our main result is that there is a strong habitat selection at the unproductive end of our gradient, but its role steeply decrease with increasing productivity. The role of dispersal from the meta-community is slightly increase with productivity, while their joint effect is negligible along the whole gradient. Variation unexplained by trait selection or dispersal is moderate in the low-productivity plots, but can exceed 80% in the high-productivity plots.

Acknowledgments
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The influence of catchment- and site-scale variables on taxonomic and trait composition of insect assemblages in neotropical savanna streams

Diego M. P. De Castro[1*], *Sylvain Dolédec*[2], *Marcos Callisto*[1]

[1]Institute of Biological Sciences, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil
[2]CNRS, UMR 5023 – LEHNA, Biodiversité et Plasticité dans les Hydrosystèmes, Université Lyon 1, Villeurbanne, France
[*]E-mail: diegobioufla@gmail.com

Keywords: traits, aquatic insects, spatial scale, land use

Identifying the influence of spatial scales that most influences the species-environment relationships is a major goal in community ecology. We evaluated the importance of geographic location, catchment and site scales and associated environmental variables in shaping taxonomic and functional composition of Ephemeroptera, Plecoptera and Trichoptera (EPT) assemblages in neotropical savanna headwater streams. Using co-inertia analyses and 1760 samples collected in 160 stream sites, we investigated the relationships between the catchment- and site-scale habitat variables and the taxonomic and trait composition of insect assemblages. Sites were associated with catchment-scale variables that depicted land cover and land use. Site scale was characterized by variables describing habitat hydromorphology, substrate, flow, canopy, in-stream cover, and water quality. EPT traits were assessed using 28 categories of 7 biological traits. Catchment and site-scale variables both explained significant variation of EPT taxa and trait composition. Substrate, hydromorphology, and land use were most influential to the taxonomic composition whereas trait composition was mainly affected by land use. Geographic location accounted for a significant part of assemblage variation, suggesting the folowing alternative hypotheses: (i) species have evolved in ecologically divergent ways in the different locations, not ignoring that geography and environmental variables may be correlated, (ii) EPT evolutionary history may have constrained the colonization of various locations, and (iii) weak dispersal capabilities of neotropical EPT have prevented them from overcoming geographic barriers. Identification of variables driving the taxonomic and functional structure of macroinvertebrate assemblages is of critical importance to determine the scale at which efforts for protection and/or rehabilitation would best be directed to improve and/or maintain appropriate environmental and ecological conditions.

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Phytoplankton cell size indicates nutrient sensitivity and vulnerability to grazing

Evangelia Charalampous[1], Birte Matthiessen[1], Maria Moustaka-Gouni[2] and Ulrich Sommer[1]

[1] GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany
[2] School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece
*E-mail: echaralampous@geomar.de

Keywords: phytoplankton, size, nutrient response, grazing

Environmetal conditions are altered due to the rapid climate change and the functional impacts of the upcoming changes are not yet definied. Phytoplankton is the basis of the pelagic food webs and its cell size is predicted to decline due to increased grazing and decreased nutrient availability. However, the consequenses of this size decline still needs to be investigated. On such a content we experimentally tested whether (i) individual size determines the plankton's vulnerability to grazing, and (ii) a community wide size shift affects phytoplankton's response to nutrient enrichment and depletion.
An indoor mesocosm experiment (February-March 2016) was conducted using a natural plankton community from the Kiel Bight (Baltic Sea). The plankton was first treated with a gradient of six copepod (Acartia tonsa) densities (0, 10, 20, 40, 80, 160 ind/L) for seven days in order to test for (i) and shift the community size structure. After the removal of grazers three of the pre-grazed (0, 40 and 160 ind/L) communities were treated with two different nutrient levels (ambient conditions, 16N/1P) to assess the community response (ii).

The results show that phytoplankton individual size can determine its vulnerability of being consumed by mesograzers. Grazing pressure was highest on medium (mainly nanoplankton) sized phytoplankton. The effect was weaker for smaller and bigger sized cells or even positive for pico-plankton (<10 μm^3) due to release from competitor or protozoan grazers (Fig1). Grazing, however, also differently affected single species that belonged to the same size class. Nutrient addition increased phytoplankton growth. This effect was reduced for those communities that were pre-treated with grazers (Fig2). Larger cells generally responded stronger to nutrient addition. Individual species response to nutrients, however, could deviate from the mean response of their size class. Among the size classes pico-plankton were the least nutrient limited.

We conclude that with some deviations, cell size can be used as an indicator for phytoplankton responses to growth, i.e. nutrients, and loss, i.e. grazing, factors.

Figures

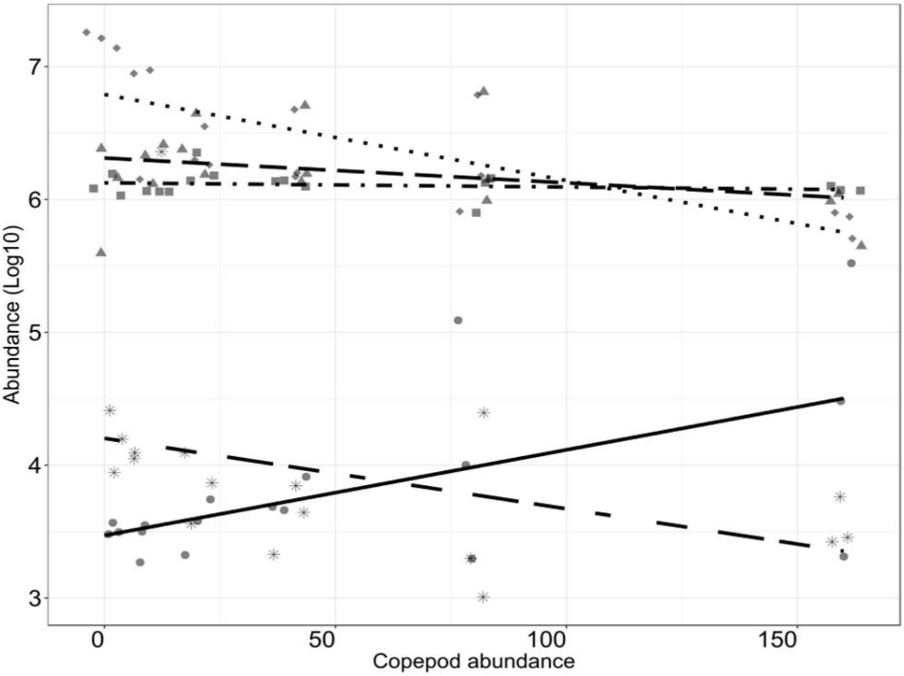

Figure 1. Size class response after 7 days of copepod grazing. x-axis: cell abundance (log10), y-axis: copepod abundance in the treatments. Size class: <10 μm^3 (shape: circle, line: solid), 10-100 μm^3 (shape: triangle, line: longdash), 100-1000 μm^3 (shape: rhomb, line: dotted), 1000-10000 μm^3 (shape: square, line: dotdash), >10000 μm^3 (shape: star, line: long and short dash)

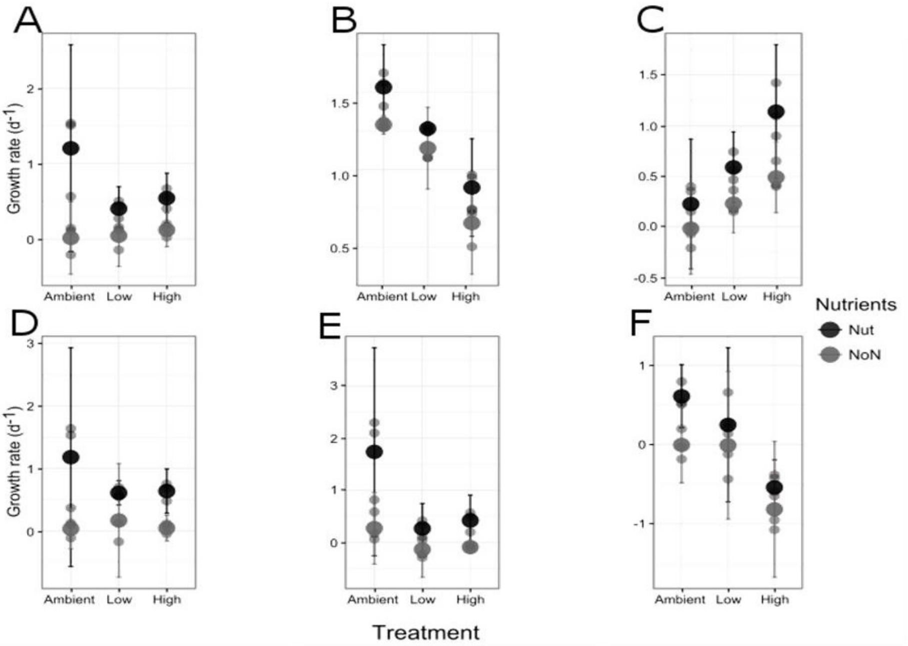

Figure 2. Growth rate of the plankton community (A) and the size classes <10 µm3 (B), 10-100 µm^3 (C), 100-1000 µm^3 (D), 1000-10000 µm^3 (E), >10000 µm^3 (F) at the first 3 days of the nutrient manipulation phase. Ambient: non grazed pre-treatment, Low: pre-treatment of 40 ind/L, High: pre-treatment of 160 ind/L

Interspecific variability in isotopic composition (δ^{13}C, δ^{15}N) of congeneric mullet species in marine and estuarine zones

Adna Ferreira Silva Garcia[1*], *Alexandre Miranda Garcia*[1], *Sabrina Radunz Vollrath*[1], *Ítalo Jesus Marchetti*[1], *João Paes Vieira*[1]

[1]Programa de Pós-graduação em Biologia de Ambientes Aquáticos Continentais, Universidade Federal do Rio Grande, Rio Grande, Brazil

[*]E-mail: adnaferreira@gmail.com

Keywords: diet, trophic ecology, isotope niche, trophic position, Mugilidae, *Mugil*, south Brazil

Mullets constitute dominant species in estuarine fish assemblages from tropical to temperate zones. Their diet is usually characterized by large amounts of detritus, and the consumption of benthic invertebrates, green filamentous macroalgae, plankton and other suspended organic matter can vary according to the species. Microscopic analysis of their stomach contents have been traditionally used to describe their diet composition. Although may achieve high taxonomic resolution, this method can be biased due to the impossibility to determine the origin of detritus and the true assimilation of the ingested microorganisms. In the past decades, stable isotope analysis (SIA) has been considered a suitable tool to better understand food assimilation and trophic ecology, particularly for detritivorous species as mullets. In the present work, we compared stable isotope ratios of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) of three species (*Mugil curema*, *Mugil liza* and *Mugil* sp.) in a marine surf-zone and after their recruitment into an estuarine zone of subtropical coastal system in south Brazil (29ºS). All analyzed specimens (n=61) were immature individuals with total length (TL,mm) lower than 100, with exception of *M. liza* that ranged from 23 to 341. Despite of the larger body size variation in this species, no statistically significant correlation ($p > 0.05$) were found between body size and isotopic composition in both habitats. There were interspecific and between-habitat differences in average carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope ratios. A two-way ANOVA revealed statistically significant interaction in $\delta^{13}C$ values between species and habitat ($p < 0.00$), with distinct patterns for each species: no differences between marine (-18.60) and estuarine (18.28) for *M. curema*, higher values at the estuarine (-14.55) than marine (-19.12) site for *M. liza* and the opposite pattern (-14.13 vs. -16.02) for *M*. sp.. There were no statistically significant interaction in $\delta^{15}N$ values between species and habitat ($p > 0.65$), with higher values in the marine surf-zone compared to the estuary regardless of the species. *Mugil* sp. had that highest average $\delta^{15}N$ values compared with the other two mullet species in both marine (12.80 vs. 10.29 and 9.8 for *M. curema* and *M. liza*, respectively) and estuarine (10.62 vs. 8.78 and 7.56 for *M. curema* and *M. liza*, respectively) habitats. Accordingly, estimation of trophic position (TP) considering $\delta^{15}N$ values of consumers and the nitrogen isotopic baseline (average $\delta^{15}N$ values of particulate organic matter in suspension and in the sediment in each habitat), revealed higher TP for *M*. sp. in the marine (2.72) and in the estuary (2.22). In contrast, average TP values of *M. curema and M. liza* were comparatively lower both in the marine (1.48 and 1.33, respectively) and in the estuary (2.18 and 1.82). Isotopic niches based on isotope ellipses containing 95% of data (SEAc) also changed markedly among species and between habitats. *Mugil curema* and *M. liza* had much higher values of SEAc (3.68 and 3.37, respectively) than *M*. sp. (0.80) in the marine, whereas more similar values were observed in the estuary, but with higher isotope niche for *M*. sp (8.89) than for the other species (*M. curema*: 6.10 and *M. liza*: 6.18). Isotope niche overlap also changed substantially between habitats. There was no overlap in SEAc ellipses between *M*. sp. and the other mullet species, which showed overlapped of 60.7% between them. In contrast, all mullet species showed some degree of isotope niche overlap in the estuary, with lower values found between *M. liza* and *M. curema* (16.7%) and higher values between *M. curema* and *M*. sp. (28.1%). These findings suggest food resource partitioning in the mullet community inhabiting this subtropical coastal system. In the studied area, *M. curema* and *M. liza* are positioned on the base of the food chain potentially consuming detritus and microphytobenthos, whereas *M*. sp. is positioned comparatively higher in the food chain probably due to greater consumption of animal preys, such as zooplankton or microinvertebrates over the substrate.

Meeting of a monodominant species with diverse species assemblages

Krishan Kaushik[1*], *Kinga Rudolf*[2], *Viktoria Szalontai*[1], *Tamás Morschhauser*[1]

[1] Institute of Biology, University of Pécs, Hungary
[2] Dept. of Plant Production and Plant Protection, Univ of Kaposvar, Hungary
[*]E-mail: kkmerry@gamma.ttk.pte.hu

Keywords: *Allium ursinum*, transect method, density profile

There are strong competitor species which can destroy the vegetation structure and decrease the biodiversity. These alterations in composition of vegetation may occur due to native or alien plants. This investigation is looking for the interaction between a monodominant species and diverse species pool at fine scale in the forest herb layer. The study was carried out with candidate monodominant plant -*Allium ursinum* in deciduous oak-hornbeam forest vegetation type in the Mecsek hills SW of Hungary in 2016-17. Six study sites were selected with two different types of understorey vegetation: the *Melica uniflora* and the *Carex pilosa* facies of *Asperulo taurinae-Carpinetum.* The objective of our study was to describe how the species of this background vegetation are excluded by the increasing density of *A. ursinum* from the edge towards the monodominant situation. Different criteria for sites selection were: to avoid strong ecological abiotic gradients and strong biotic interactions. A transect was arranged in 25cm x 25cm quadrat up to 20m in eight parallel lanes touching each other per site. By first meter it spans from high species diversity but lacking *Allium ursinum* presence to monodominance of *Allium ursinum* near its 20th meter. Collected data types include presence/absence and cover data. Density profiles of species are presented to characterize the order of competitor species at fine scale.

The species numbers of examined transects were between 22-31. On the basis of density profiles the species can be characterized into different categories along the transects. There are differences in the order of species among the various study sites may be due to abiotic and biotic factors.

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Co-occurrence pattern of ground beetle (Coleoptera, Carabidae) assemblages along pollution gradient in scotch pine forest

Renata Kędzior[1*], *Artur Szwalec*[1], *Paweł Mundała*[1], *Tomasz Skalski*[2]

[1]Department of Ecology Climatology and Air Protection, University of Agriculture, Kraków, Poland
[2]Biomantis sp. z o.o., Jagiellońskie Centrum Innowacji, Kraków, Poland
[*]E-mail: r.kedzior@ur.krakow.pl

Keywords: heavy metal contamination, Carabid beetles, forest specjalists, C-score index, community disassembly

Over the last 30 years there has been a great deal of interest in investigating patterns of species co-occurrence across a space and time which may be shaped by interspecific competition for shared resources. Good model of co-occurrence mechanisms is developed among predatory animals along pollution gradient where the shared resources along contamination become more limited and energetic budget for detoxication is much higher. Field observation and laboratory experiments of Carabid beetles may suggest that ecological interactions, such as decreased competition for resources at polluted sites, can counterbalance the costs of detoxification. Community disassembly by heavy metal pollution may occurs when the presence of toxic elements shifts co-occurrence patterns of species from structured to random. On the other hand however, limited resources on pollution gradient should lead to higher competition between dominated species. Disassembly can imply a loss of existing co-evolved interactions among species, which has ramifications for community dynamics and quality of polluted ecosystems functioning.

We expect that an assemblage dominated by competitive species interactions would exhibit a significant segregation of taxa, whereas one dominated by mutualistic or syntrophic interactions would exhibit an aggregation of taxa.

Responses of Carabidae co-occurrence patterns to heavy metal concentrations were investigated in scotch pine gradient of the zinc smelter in the Olkusz District (southern Poland) on 18 localities. The amplitude of Zinc concentration in the humus layer varied between 108 mg kg^{-1} dw to 6150 mg kg^{-1} dw. We used C-score index, which is based on the average number of checkerboard units (CUs) between all possible species pairs in a matrix. We simulated in EcoSim 5000 random matrices testing differences between the randomized and observed scores for carabid co-occurrences.

There was strong co-occurrence segregation of species in space between localities as well as along seasonal dimension in heavy metal gradient. Dominants from reference sites such as *Carabus violaceus*, *C. glabratus* and *C. auronitens* were replaces by smaller *Carabus arcensis*, *Pterostichus oblongopunctatus* and *Pt. niger* along higher concentration of heavy metals. Ground beetle assemblages from reference sites showed also significant segregation pattern. Community disassembly occurred only among assemblages from heavily polluted sites. On most of the polluted sites, random distribution as an effect of extinction and recolonization occurred. Our data suggest that increased pollution alters both higher extinction of sensitive forest specialists with higher competition abilities, leading to replacement by less sensitive generalists and the occurrence of species on heavily polluted sites is a result of unstable community relationships between species.

Biosorption potential of the coenobial freshwater green algae *Pseudopediastrum boryanum* var. *longicorne* for the removal of chromium(VI) ions from polluted aquatic ecosystems and industrial wastewaters

Małgorzata Sutkowy[1*], *Grzegorz Kłosowski*[1]

[1]Department of Biotechnology, Kazimierz Wielki University, Bydgoszcz, Poland
[*]E-mail : sutkowy@ukw.edu.pl

Keywords: *Pseudopediastrum boryanum,* biosorption, hexavalent chromium, heavy metals

Industrial waste water and sediment containing heavy metals cause many ecology- and health-related problems. It is well known that different types of metals can be accumulated by aquatic organisms and transferred to humans through the food chain. Many conventional methods have been used to decontaminate the environment from the adverse effects of these pollutants, but most of these methods are very expensive and far from their optimal performance. The capability of microorganisms to bind metal ions is a well-known phenomenon. Contamination of the environment by a wide spectrum of heavy metals is a form of pollution that usually results from industrial and mining drainage. Environmental pollution with heavy metals is particularly relevant in aquatic media, since heavy metals are usually rare elements in such ecosystems. The idea of using microorganisms, especially microalgae, as biosorbents of heavy metals deserves particular attention due to their natural biosorbent properties and the relatively simple and inexpensive methods of obtaining their biomass. The effectiveness of elimination of metals from aqueous solutions by microalgae depends on their structure and thus their taxonomic classification (class, genus, species), as well as the conditions in which biosorption is conducted. An example of microalgae with desirable biosorption characteristics are the cosmopolitan green algae of the *Pseudopediastrum* sp., commonly occurring in freshwater, with a structure of the coenobium composed of many cells which endows it an exceptionally large sorptive area in relation to its volume.

The aim of the study was to evaluate the suitability of dried biomass of the microalgae *Pseudopediastrum boryanum* var. *longicorne*, derived from an optimized bioreactor culture, for the biosorption of toxic chromium(VI) ions. Significant increase in the growth rate of *P. boryanum* was obtained by selecting the appropriate culture medium (L-S2T2), light intensity (4000 lx), daily photoperiod (12 h darkness / 12 h light) and addition of carbon dioxide to the medium (6% v/v). The effect of the most important biosorption process parameters, i.e. pH and the initial concentrations of Cr(VI) ions and biosorbent, on the effectiveness of ion removal and sorptive capacity of the microalgae was analyzed. Biosorption was conducted in Erlenmeyer flasks containing dry biomass of the microalgae (0.5–2 g/L) to which 250 cm^3 of Cr(VI) ion solutions at selected concentrations (10–200 mg/L) and pH (2–6) were added. The effect of pH was analyzed at a chromium concentration of 10 mg/L, the effect of the biosorbent concentration was analyzed at pH 2 and a chromium concentration of 10 mg/L, while the effect of the initial chromium concentration was analyzed at a biosorbent concentration of 1 g/L and pH 2. The entire system was mixed on a shaker at a constant mixing rate of 250 rpm, at 22.0 ± 2.0°C, for 180 min.

The experiment demonstrated effective use of the dried biomass of *Pseudopediastrum boryanum* var. *longicorne* for the biosorption of Cr(VI) ions from aqueous solutions. The highest percentage of removal of Cr(VI) ions was obtained at pH 2 and a biomass concentration of 2 g/L, at which the lowest sorption capacity of the microalgae was observed. With the increase in the initial concentration of Cr(VI) ions, sorption capacity increased and the percentage of their removal from the solution decreased.

Evaluating the relative importance of methodological decisions in sampling and analysis of functional beta diversity along an environmental gradient

Attila Lengyel[*], *Anikó Csecserits, Miklós Kertész, Bence Kovács, Barbara Lhotsky, Gábor Ónodi, Tamás Rédei, Zoltán Botta-Dukát*

MTA Centre for Ecological Research, Tihany/Vácrátót, Hungary
[*]E-mail: lengyel.attila@okologia.mta.hu

Keywords: beta diversity, dissimilarity, productivity, similarity, traits

Explaining functional beta diversity by environmental variables has been gaining focal interest of ecologists for several years. Studies published until now vary considerably in how significant and what type of functional signal is detected along particular gradients. During the analytical process aiming at the quantification of the relationship between functional composition and environment several methodological decisions have to be made, including the delimitation of the statistical population, the selection of the traits and the choice of the beta diversity measure. In this study we evaluate the relative importance of methodological decisions on the outcome of analyses inspecting the relationship between functional beta diversity and an environmental gradient. We compare the between-experiment variation attributed to four methodological decisions: i) the position and ii) the breadth of the range sampled along the main environmental gradient, iii) the trait selected, and iv) the functional beta diversity index.

The study site is in the Kiskunság Sand Ridge region, a part of the Hungarian Great Plain, central Hungary. The soils are rich in calcareous sand, and their low water retention capacity, coupled with uneven precipitation, makes water the main limiting resource for vegetation. The land surface is undulating, with semi-arid open grasslands on the top of dunes and more productive reed-beds and marsh-like vegetation in the depressions. The data set included 101 vegetation plots of 4 sq-meters sampled in different types of herbaceous vegetation along the productivity gradient. In each plot, vascular plants were recorded. For each species the following trait values were measured in field or acquired from literature: growth form, age of first flowering, clonal height, leaf size, specific leaf area, leaf dry matter content, lateral spread, life span, leaf distribution, shoot growth form, seed weight, generative height. The productivity of each plot was characterized by NDVI field measurement.

A schematic data analysis comprised of four steps: 1) selection of a 20-plot subsample from the data set; 2) selection of a plant trait; 3) calculation of a dissimilarity matrix containing pair-wise functional beta diversities; 4) calculating Spearman's correlation between dissimilarities and between-plot NDVI differences. Methodological decisions required for steps 1 to 3 were made randomly. Then, the correlation value was modelled as a function of the mean and the range of NDVI values in the subsample, the trait and the beta diversity index selected. The importance of these variables was analysed by variation partitioning.

The trait alone explained the biggest part of the total variation (21%), with considerable variation attributable to NDVI range alone (10%) and shared between trait and NDVI range (8%). Mean NDVI had no significant effect alone, and it explained only 3% together with the NDVI range. Beta diversity index was attributed to 4% alone and 3% shared with NDVI range.

Our results suggest that the most important decision in the analysis of the relationship between functional beta diversity and an environmental gradient is the selection of the trait, followed by the gradient length covered by the sample. In comparison with these sampling decisions, the selection of the functional beta diversity index has low importance.

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Changes in terrestrial animal communities following grassland restoration

Szabolcs Lengyel

Hungarian Academy of Sciences, Centre for Ecological Research, Danube Research Institute,
Budapest-Debrecen, Hungary

Ecological restoration has long been used as testing grounds for hypotheses in community ecology. However, much of this knowledge comes from studies based on plants and vegetation and we know little on how restoration affects animal communities. Here I synthesize results from a landscape-scale restoration project to contribute to our understanding of how terrestrial animal communities assemble following restoration. Grassland restoration was carried out on 760 hectares of former cropland in Hortobágy National Park (E Hungary) between 2005-2009. We used both chronosequence-based and repeated-measures approaches to quantify changes in several invertebrate and vertebrate taxa. The diversity and abundance of wild bees, invertebrates with mostly predatory species (carabid beetles, spiders) and amphibians usually increased in early stages and decreased in later stages of restoration to levels typically found in the natural (target) grasslands. In contrast, the diversity and abundance of herbivorous invertebrates (e.g. grasshoppers) and some vertebrates (birds, small mammals) usually increased after restoration. Species composition in several invertebrate groups changed rapidly towards that of natural grasslands in only a few years but was modified by extreme weather events such as unusually high precipitation. Top predators such as birds specializing on herbivorous insects increased considerably and preferred landscape structure rich in habitat types with abundant prey, rather than landscape structures with diverse habitat types. Our studies provide evidence for the overwhelming importance of local (biotic) filters such as food availability and suggest less important roles for dispersal-related or environmental (abiotic) filters in the assembly of animal communities in restored grasslands.

Invasive bivalves in neotropical reservoirs increase the complexity of benthic communities

Marden Seabra Linares[1], Marcos Callisto[1], João Carlos Marques[2]*

[1]Laboratório de Ecologia de Bentos, Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade de Minas Gerais, Av. Antônio Carlos 6627, Belo Horizonte, Brazil
[2]MARE – Marine and Environmental Sciences Centre, Department of Life Sciences, Faculty of Sciences and Technology, University of Coimbra, Portugal
*E-mail: mslx@hotmail.com

Invasive bivalves are among the most successful invasive species in freshwater ecosystems, having colonized a wide range of aquatic environments, exhibiting high densities and constituting a major fraction of benthic macroinvertebrate assemblages. As ecosystem engineers, invasive bivalves generally cause physical alterations in the ecosystems which they establish themselves (Linares *et al*. 2017), but the effects over benthic macroinvertebrate assemblages are less clear. Thus, the objective of this study was to characterize the ecological effects of the invasive bivalves *Corbicula fluminea* and *Limnoperna fortunei* on the structure of benthic macroinvertebrate communities in neo-tropical reservoirs. We tested the hypothesis that invasive bivalves increase the complexity of benthic macroinvertebrate assemblages. For that we used eco-exergy and specific eco-exergy, thermodynamic indicators that can be used to capture an assemblage's capacity for self organization (Marchi *et al*. 2010). We used data from 160 sampling sites from four reservoirs, each site sampled once in each area, during the dry season from 2009 to 2012. Our results showed that benthic macroinvertebrate assemblages presenting invasive bivalves showed significantly higher eco-exergy and specific eco-exergy, which corroborate our hypothesis. South American aquatic ecosystems historically lacked powerful suspension feeders able to provide a direct link between the benthic an water column components of the ecosystem (Karatayev *et al.* 2007), role eventually undertaken by the establishment of *Corbicula fluminea* and *Limnoperna fortunei*. Resources produced in the water column captured by these invasive bivalves may then become available to benthic assemblages. Therefore, invasive bivalve establishment may open new energetic pathways for benthic macroinvertebrate assemblages in neotropical reservoirs, making available resources that otherwise would not be and increasing the assemblages' complexity.

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Aquatic macroinvertebrates, functional diversity and water quality in the Sinaloa river, Mexico, a basin with predominant agricultural land use

Eugenia López-López[1*]*, Erick Mendoza-Martínez*[1]*, Andrea Gómez-Ruiz*[1]*,*
Jacinto Elías Sedeño-Díaz[2]

[1]Laboratorio de Evaluación de la Salud de los Ecosistemas Acuáticos, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México
[2]Coordinación Politécnica para la Sustentabilidad, Instituto Politécnico Nacional, Ciudad de México, México
[*]E-mail: eulopez@ipn.mx

Keywords: agricultural region, aquatic invertebrates community, Sinaloa river, Mexico

Sinaloa State is the main agricultural region in Mexico. The use of agrochemicals such as pesticides and fertilizers is very common, and the agricultural runoff reach the waterways (rivers, streams), and finally they arrive at the sea in the form of a mixture of pollutants, which is potentially toxic. Aquatic organisms are sensitives to this mixture of contaminants and their communities can be affected. Biological communities have a functional role in aquatic ecosystems the health condition of ecosystems also, can be affected if these functions are altered. We studied the functional diversity of the aquatic macroinvertebrates (AM) of Sinaloa river, which are exposed to leached of agrochemicals, and their relationship with water quality parameters. Seven study sites were selected to characterize water quality through 22 parameters and sampling of AM. The study was carried out in two season (dry and rainy) during 2016. Functional diversity was measured using the functional divergence and functional regularity indices. Our results show that the highest score of functional divergence occurred during the dry season in study sites from upper reaches of Sinaloa river, while the lower values occurred during the rainy seasons in study sites of the medium reach of Sinaloa river, and they are associated to highest concentration of biochemical oxygen demand. Functional regularity index show its highest values also during the dry season but in study sites of the lower reach of Sinaloa river. Agricultural runoff is evident during the rainy season because chemical forms of nitrogen and phosphorus are associated to study sites during this season. The rainy season with their agricultural runoff is causing stochastic alterations in the AM community and decrease the values of functional diversity. On the other hand, functional diversity is increased during the dry season due to a base flow of the river and a decrease of the agricultural runoff to the river.

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Sheep endozoochory in a small protected area: benefit or harm to a vulnerable community?

Gábor Matus, *Rebeka Balogh*

Department of Botany, University of Debrecen, Debrecen, Hungary
*E-mail: matus.gabor@science.unideb.hu

Keywords: viable seeds, seed germination, sheep, sandy grassland

Quantitative data on seed dispersal by large herbivores are important for agriculture as well as for conservation. Dispersal biological data of invasive plants also have a great economic significance. We have been out to quantify the endozoochorus disperal potential of the only domestic animal in a small reserve through the year. We were interrested in whether sheep can contribute more to dispersal of native or weedy (including invasive) plants and how is it reflected in soil seed banks. The study area was a small and ill-proportioned Natura 2000 site in East-Hungary (southern segment of HUHN20025) with a relatively well explored flora. Its size is 130 ha (perimeter 6.3 km) and is covered by open sandy grasslands, fallow lands, mesophilic meadows and marshes, *Robinia pseudacacia* and *Pinus sylvestris* plantations and borders with arables and ruderal sites. The study has been conducted on a small dune covered with Corynephoretum grassland (*Corynephorus canescens, Polytrichum piliferum*). Vegetation of 25 permanent plots of $4m^2$ size has been surveyed three times a year (specific cover at 4 m^2 and presence at 1 m^2) through 2011 and 2012. Soil seed banks have been analysed using the germination method. A flock of sheep visiting the study area on a daily basis consisted of 140 ewes and their offspring during the study. All dung has been collected monthly from each vegetation plot (altogether 13 times, on average at 30.8±1.7 days intervals). Data from the very first collection date (March 2012), also containing older dropings of unknown age, have been excluded from analyses. Samples have been air-dried, weighed then germinated on sterilized potting soil in a heated greenhouse for nine months. Accidental seed rain has been monitored in pots containing only sterilized soil. Seedlings have regularly been identified then removed while unidentified specimens have been transplanted then grown till flowering. The totally collected 535 g of sheep dung has yielded 2305 seedlings (4.3 viable seeds/g on average) the 99.6% of which has been identified to the species level. Altogether 74 plant species (8 to 34/month) have been identified (forming 18.9% of the local flora). The composition well reflected habitat diversity. The total seed input from sheep dung has made up $23.05/m^2/yr$. All above characteristics have shown a pronounced seasonal pattern with lows from winter to early spring and highs from midsummer to late autumn corresponding to seasonal changes of seed offer. Similarly, species composition of dung has shown cyclic seasonal changes and different width of dispersal windows (only 5 months for *Spergula pentandra* but round the year for *Cynodon dactylon*). Few species of the studied community have been detected among dispersed ones and *Spergula pentandra* itself has been one of the few detected ones with any conservation interest (NT in IUCN rank). Many more weedy species (e.g. *Amaranthus retroflexus*, *Capsella bursa-pastoris*, *Chenopodium album*, *Portulaca oleracea*, *Urtica dioica*) have been recorded, often in large quantities. Seven of dispersed species are considered as invasive and one of them, *Phytolacca americana* was among the frequent ones suggesting a strong preference of sheep for its fleshy berries. Sheep dispersal also strongly favoured small seeded species. Distribution of seed size classes have differed significantly between dispersed and undispersed species of local flora. A further overrepresentaion has been detected when size class distribution of dispersed species was compared to that of the dispersed seeds. However it is not known whether dominance of small seeded species in dung is a result of their higher survival rates in sheep gut and/or is a consequence of their higher seed offer. Amount of dung as well as that of seed input have negatively been correlated with relative height of the source plot. Yearly seed input proved as low as 0.4% of persistent seed banks of plot soil samples (ca. 5,500 seeds/m^2 till the depth of 10 cm). In spite of the limited extension and short time of sampling a remarkable portion of local flora has been detected underlining the significance of endozoochory both in quantities and in terms of linking different habitats but with little support for conservation targets.

Forest cover positively affects social wasp communities in Brazilian agricultural landscapes

Hugo Reis Medeiros[1,2*], *Milton Cezar Ribeiro*[2], *Yuri Campanholo Grandinete*[3], *Ciro Abbud Righi*[1,4]

[1]Postgraduate program in Applied Ecology, University of São Paulo, Piracicaba, Brazil
[2]Spatial Ecology and Conservation Lab - LEEC, São Paulo State University, Rio Claro, Brazil
[3]Aculeata Lab – Systematics and Evolution, São Paulo State University, São José do Rio Preto, Brazil
[4]Department of Forestry Science, University of São Paulo, Piracicaba, Brazil
[*]E-mail:hugorm@usp.br

Natural and semi-natural habitats play a key role in maintaining a high level of animal diversity and ecosystem services in farmlands (Fahrig et al. 2011), however, this issue is scarcely known in Neotropics. Social wasps (Vespidae, Polistinae) were used as a model group to investigate how local communities of social insects respond to landscape context. We hypothesized that (a) species richness, abundance and diversity of social wasps foraging in agroecosystems increase with increasing forest cover in the surrounding landscape, and that (b) landscape diversity and local factors such as microclimate and crop management are less important for explain the patterns. Social wasps were sampled in 16 coffee plantations located across a gradient of forest cover (2.8 % to 59.3 %) in the border between Minas Gerais and São Paulo States, southeast Brazil. In each coffee plantation we used four traps (1 Malaise trap and 3 attractive traps) to sampling wasp communities. Traps remained open during seven consecutive days (from 19 to 26 September 2016) and were fixed within coffee fields at a distance of 100 meters from any forest edge. Landscape composition and configuration surrounding of coffee plantations –forest cover, forest connectivity, edge density and habitat diversity – were calculated at four spatial extents: 250 m to1000 m, with intervals of 250 m. At local scale, we used the following explanatory variables: altitude, average temperature, average humidity, average luminosity, coffee field size and the number of applications of insecticide, herbicide and fungicide. Using a competing hypothesis and model selection approach we evaluated the contribution of local and landscape explanatory variables on local

wasp communities by using the Akaike Information Criterion (AIC). Generalized Linear Models (GLM) were used for fit the models. We captured 631 specimens representing 28 species within 11 genera. Species richness, abundance and diversity of wasps increased with increasing forest cover at all spatial extents. Additionally, abundance was positively affected by forest connectivity. Wasps forage in coffee plantations, but probably use adjacent forest fragments as nesting habitats and refuges against the constant environmental disturbances in agricultural matrix such as harvest and pesticide applications. Therefore, environmental schemes designed to preserve biodiversity and ecosystem services in Neotropical farmlands should promote conservation, restoration and functional connectivity of tropical forests at landscape level.

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Influence of temporal diversification on invertebrate communities in a long-term crop-rotation experiment

Michael Meyer[1], Heinz-Josef Koch[2], Christoph Scherber[1]*

[1]Institute of Landscape Ecology, Westfälische Wilhelm-Universtät, Münster, Germany
[2]Institute of Sugar Beet Research, Göttingen, Germany
[*]E-mail: micmeyer@uni-muenster.de

Keywords: crop rotation, agricultural landscape, arthropod communities, memory effect

In agricultural production systems, aboveground invertebrate communities that provide neither economic benefits as pollinators nor act as pest species, have so far been rarely investigated. In particular, data on arthropod biodiversity in crop rotation systems are lacking.

To evaluate the impact of temporal diversification on invertebrate communities, we performed extensive sampling in a long-term crop rotation experiment close to the village of Harste (North of Göttingen, Lower Saxony, Germany). We monitored seven rotation systems containing five different crops (silage maize SM, winter wheat WW, oilseed rape OR, sugar beet SB and grain pea GP), ranging from monocultures to one six-year-rotation including four crops. Sampling was conducted during the vegetation period from late April until harvest at the end of July 2016 using pitfall traps, pan traps and sticky traps.

We found that species groups are differentially sensitive to the current crop and the history of cultivated crops. Web-building spiders occurred preferentially in structurally rich crops as OR, whereas they showed low density in SM and SB. Ground-dwelling hunting spiders occurred ubiquitously. Granivorous or phytophagous Carabid beetles also reached highest densities in OR, whereas carnivore or omnivore species reached highest densities in other crops, especially in WW.

OR in the previous year enhanced activity density of herbivorous Carabid beetles in WW fields. Myriapods also reached maximum values in plots that had been planted with OR the year before, whereas OR in the investigated year showed no positive influence on this species group. The signal was even detectable if OR had been grown two years ago.

Crop identity in a rotation system is likely important for community composition than the amount of different crops within one rotation, since the crops directly affect prey availability, vegetation structure and microclimate. On a broader landscape scale, temporal diversification may lead to a higher invertebrate diversity because a higher variety of crops provides habitat and food resources for more invertebrate species.

Change of diversity of macrofungi and vascular plants in succession of wood pasture

Kinga Rudolf[1], Ferenc Pál-Fám[1], Richard Hoffmann[1], Tamás Morschhauser[2]*

[1]Kaposvár University, Institute of Plant Science
[2]University of Pécs, FS, Institute of Biology
*E-mail: rukinga@freemail.hu

Keywords: Belső-Cserehát, macrofungi and vegetation, Rényi's diversity profile, change of diversity

In the Belső-Cserehát the abandoned wood pastures and grazed forest preserving the formerly widespread traditional form of land use have significant natural values. Due to the mosaic structure these habitats have of great importance for preservation of biodiversity. These areas remaining after the abandonment of the grazing become more and more conspicuous as protected areas nowadays, Europe wide. Hungarian wood pastures are scarcely studied from mycological and botanical point of view in spite of their significant natural values. The study area was the abandoned wood-pasture of Irota village (48°24′N, 20°52′E) in the Cserehát hills, in North-Eastern Hungary. It has been formed from *Quercetum petraeae-cerris* and *Carici pilosae-Carpinetum* forests by deforestation and grazing. In the eighties after the abandonment of grazing, the area went through a spontaneous afforestation. The myco- and phyto-coenological survey of the Irota wood pasture was made in 2004-2005 which was repeated in 2014-2016. The myco- and phyto-coenological samples were made according to the Zürich-Montpellier method with plots of 25×25 m^2. Macrofungi species were sampled on the basis of fruit bodies, the cover of the vascular plants were estimated visually in the herb, shrub, and canopy layers separately. Fungi were sampled in September and October. In the plots the diversity of macrofungi and vascular plants was compared at two different time (10 years deviation). The numbers of fruit bodies of terricolous- and lignicolous macrofungi were analyzed separately because of the different properties of these groups. A scale-dependent characterization of diversity, based on the data of sampling plots, was carried out by Rényi's generalized entropy-type diversity profile calculation.

These last 10 years the Irota wood pasture went through a spontaneous afforestation, in its stand with decreased rate of patches of grass. The present stand of wood pasture can be characterized by an alternation of old Turkey oak trees in small groups or standing alone and patches of grass, partially dense scrub layer and a herb layer rich in species. The comparison of Rényi's diversity profile of macrofungi on the basis of species set of full, terricolous and lignicolous macrofungi showed increasing of diversity compared to the situation the 10 years ago. Whereas, the diversity of vegetation decreased on the basis of full species set. In this habitat the rate of woody species increased significantly because of succession which increased the diversity of macrofungi whereas, the diversity of vascular plants decreased.

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Evolution of flammability in Brazilian cerrado and seasonal forest communities

Catarina G D Netto[1], Johannes H. C. Cornelissen[2], Marco A. Batalha[1]*

[1]Department of Botany, Federal University of São Carlos, São Carlos, Brazil
[2]Faculty of Earth and Life Sciences, Systems Ecology, Vrije Universiteit Amsterdam, The Netherlands
[*]E-mail: catarina_netto@yahoo.com.br

Keywords: fire, functional trait, phylogenetic signal, savanna, trait evolution

Wildfires have occurred on Earth since the early evolution of land plants. The very origin of fire is linked to the origin of plants, which provide fuel and oxygen, two of the three essential elements to fire occurrence (1). As a consequence, fire has played a key role in the distribution of most terrestrial biomes (2). Since the origin of savannas, with the increase of C_4 grasses, fire has established an important positive feedback with this group of plants, under the strong seasonality typically found in tropical savannas (3). Considering the importance of fire on the ecology and evolution of savanna plant species, changes in fire regimes are very likely to alter community structure, composition, and functioning (4). The Brazilian cerrado presents a wide physiognomic range, going from grassland to woodland, but with most of its physiognomies within the definition of tropical savanna, hosting the world's most diverse flora of all tropical savannas with a high rate of endemism (5). A popular theory for the cerrado origin and evolution considers fire as a trigger prompting the evolution of some species lineages (6).

Furthermore, the fact that some fire-adapted life forms of cerrado species are rare or absent in sister lineages growing in adjacent seasonal forest reinforces the role of fire in the evolution of the cerrado particular flora (7). Within the cerrado, scattered patches of semi-deciduous seasonal forest emerge, which are generally found in fertile valleys. However, the negative effects of fire on the establishment and growth of forest species constrain the expansion of forests (8). One ecological mechanism with which fire can act on the evolution of plant species is by filtering. Environmental filters such as fire select those species that can persist in a community on the basis of functional traits that enhance their tolerance to the abiotic conditions. Species that are both tolerant of or resilient to fire and are also highly flammable, may not only pass the environmental filter but also reinforce it through the mentioned positive feedback, thereby having important impacts on the community functions and services and functions (9, 10). If flammability is indeed adaptive through such feedback, it may show phylogenetic patterning A phylogenetic perspective has been widely used in functional traits studies at levels ranging from individuals to communities. As phylogenetic theories become available for many groups of organisms, studies in community ecology can benefit from the knowledge of evolutionary relationships among coexisting species (11).

To understand the evolution of flammability on plants species of cerrado and the role of fire on community structure and distribution, we sampled 30 cerrado plots and 20 seasonal forest plots in Santa Rita do Passa Quatro, São Paulo State, southeastern Brazil.. We built a phylogenetic tree for the 67 vascular species sampled in the cerrado and another phylogenetic tree for the 27 species sampled in the seasonal forest. We measured three flammability traits in dry leaves: time to ignition, total combustion time, and mass consumption during burning (12). We used Blomberg's K (13) to test for phylogenetic signal. For the cerrado, the low values for the K statistics (Table 1) indicated phylogenetic overdispersion, meaning that more distant related species were more similar than expected by chance considering flammability traits. Since fire is frequent in the cerrado and acts as an environmental filter, similar values may have arisen independently in distant clades, leading to the phylogenetic overdispersion. In the seasonal forest community, K values were higher, but non-significant (Table 1), indicating an absence of phylogenetic signal, that is, a random distribution of flammability values across the phylogeny. This might be linked to a stronger influence of competitive exclusion acting as an ecological force (11), since fire is not frequent in the seasonal forest (14). Thus, we corroborated the idea that, even under the same climate, cerrado and season forest species evolved through different paths due to different environmental pressures exerted on them.

Table 1. Blomberg's K values for phylogenetic signal on cerrado and seasonal forest species. Values significantly ($P < 0.05$) lower than 1 indicate phylogenetic overdispersion and are in bold.

Trait	Cerrado	Seasonal Forest
Time To Ignition	**0.078**	0.409
Combustion Time	**0.101**	0.128
Mass Consumption	**0.119**	0.184

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Can population of *Ephemera danica* (Müller 1764) mayfly be an indicator of the effects of the restoration of a small lowland river?

Krystian Obolewski[*], *Joanna Sawczyn, Martyna Bąkowska*

Department of Hydrobiology, Kazimierz Wielki University, Bydgoszcz, Poland
[*]E-mail: obolewsk@ukw.edu.pl

Keywords: restoration, community structure, ecological indicator, spatio-temporal variability

In the 21st century, river restoration treatments were carried out throughout the world, and in Europe they were particularly intensive in Great Britain, Austria and France. In Central Europe one of the first complex reconstructions of the river bed was carried out in the River Kwacza, a tributary of the River Słupia (northern Poland).

To economize further investments, it is necessary to assess the effectiveness of the implemented solutions leading to the highest environmental benefits. For this purpose, the so-called bioindicators are increasingly used. The aim of this study was to determine the possibility of using a mayfly species *Ephemera danica* as a indicator of the changes brought about by the restoration of a small lowland river in a temperate climate.

Population structure was compared before (2007=T+0) and after the restoration of the river (2008, 2012-2014). The data on abundance, biomass and size of the larvae (Dc - total length, Dca - length without antennae and cerci, Fig.1) were collected in a 2.5 km stretch of the river, at 30 sampling sites. Their location was associated with the position of particular hydro-technical solutions (sills, deflectors, stone groynes, etc.). The organisms were collected (n=1214) in a 20 cm frame, identified and meastured in the laboratory.

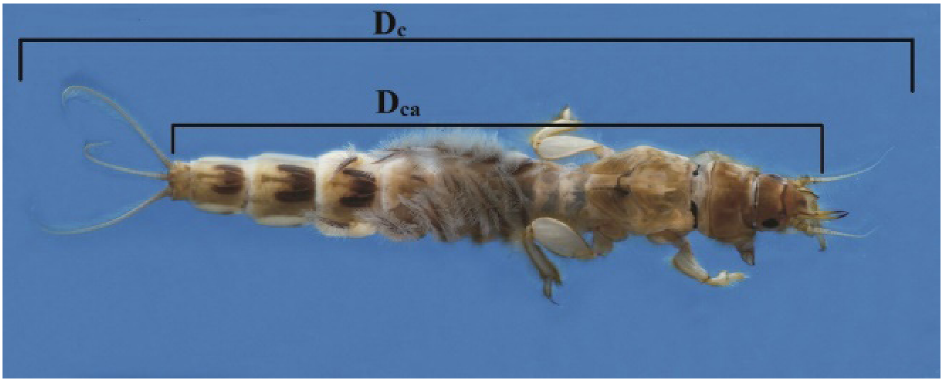

Fig. 1. Determined the length of the body

A total of 1214 organisms were collected: 155 before and 1059 after the restoration Kwacza River. After the restoration, the average number of *E. danica* larvae increased two-fold, especially at the places of installation of baffles and stone islands, while their average biomass decreased almost two-fold, especially at the places where stability thresholds were constructed. The body length of the larvae also decreased. Larvae with longest bodies occurred close to the stone islands and in the exposed parts of the riverbed. All analyzed parameters of the population of *E.danica* in the renatured section of the Kwacza River differed significantly during the study period ($p<0.0001$), reaching maximum values at T + 7.

The number of mayflie larvae was most markedly affected by the installment of the baffles and, in the long-term, by cutting off of the old riverbed. Consistent increase of the mass of individuals occurred in the fragments with semi-palisades, bank revetments, stability thresholds, and stone islands, but eventually (T + 7) the highest values were recorded at the baffles. By the end of the study period, mayflie body lengths (Dc and Dca) reached highest values in the exposed parts of the channel (felling of trees). The Dc value increased near the stone islands and to a lesser degree near the bank revetments. Near the baffles, body lengths of individual *E. danica* decreased, and reached stable values near the semi-palisades. The variability of the length of individuals without antennae and cerci (Dca) was consistent with the Da values; the increase of the body length also concerned the reference place K10.

Detailed analysis of the changes in the population structure of *E. danica* indicates the possibility of the use of this species in the monitoring of the ecological effects of river restoration treatments.

Measuring fractions of beta diversity of plants along a cronosequence of eucalypt plantations in the pampas of Argentina

Pamela Eugenia Pairo[1,3*], *Estela Rodriguez*[2], *Pablo Aceñolaza*[3], *M. Isabel Bellocq*[1]

[1]Laboratorio de Ecología de Comunidades y Macroecología, Instituto de Ecología, Genética y Evolución de Buenos Aires (IEGEBA-CONICET), Ciudad Autónoma de Buenos Aires, Argentina
[2]Centro Regional de Geomática (CEREGEO-UADER), Provincia de Entre Ríos, Argentina
[3]Centro de Investigaciones Científicas y Transferencia de Tecnología a la Producción, CONICET, Provincia de Entre Ríos, Argentina
[*]E-mail: pamepairo@gmail.com

Keywords: plant diversity, spatial turnover, Eucalyptus grandis, cronosequence

Human activities produce landscape with natural and modified habitats (Vallejo et al. 2016). Typically, majority of studies on the effects of eucalypt plantations on biodiversity consider mature plantations (Zhang et al 2014). However, they experience changes in environmental conditions related to age (e.g. canopy closure, increased depth of the leaf litter). Thus, these changes affect species differently, according to their habitat preferences, and may result in differences in diversity, structure and species composition between ages (Bunn et al., 2010). In addition, studies on the effects of eucalypt plantations on biodiversity in grassland are surprisingly scarce in Argentina, considering the spread of these plantations in Mesopotamic pampean. The aim of this study is to assess beta diversity (nestedness and turnover components) between plant communities in natural habitats (grasslands) and each age along eucalypt chronosequence (*Eucalyptus grandis*) and their relationship with environmental variables. The study was carried out from December 2015 to January 2016. To represent chronosequence, nine ages were chosen and grassland sites in Entre Ríos Province, Argentina. At each age and grassland, there were 3 replicates. We established at each replicate 3 plots ($16m^2$) to record all plant species present. Plots were placed at least 15m away from the edge of the communities to avoid edge effect. In each replicate, we estimated environmental variables that we thought would change with age (pH, N, P, wood density, humidity, %canopy, depth of the leaf litter and average height of eucalypt tree).We have selected grassland as habitat reference and calculated β_{sor} (dissimilarity in terms of the Sorensen index) into two additive fractions, β_{sim} (dissimilarity due to species replacement) plus β_{nes} (dissimilarity due to nestedness). In addition, we performed a principal component analysis (PCA) on the environmental variables measured in eucalypt plantations and calculated Pearson coefficient between age and PCA axis. Then, we calculated the linear regression between dissimilarity (β_{sor} and their components) and PCA axis 1. This axis ordered replicates according eucalypt chronosequence (Fig. 1) and positively correlated with age ($r=0.88$, $p<0.001$). We found that dissimilarity taxonomic (β_{sor}) significantly decreased with age (intercept=0.87, slope=0.2, both P<0.01) (Fig. 2A). Spatial turnover is responsible for the most taxonomic dissimilarity between the plant diversity of grassland and each plantation age, which reflects species replacement (β_{sim}= 0.64, β_{nes}=0.23) (Fig. 2B y C). Our results showed that regional species pool is negatively affected by eucalypt plantations in grassland context. The differentiation of the spatial turnover and nestedness components of beta diversity indicates that less species grassland is conserved within eucalypt plantations due to increased depth of the leaf litter, height of eucalypt tree canopy and decrease in pH and wood density.

Figures

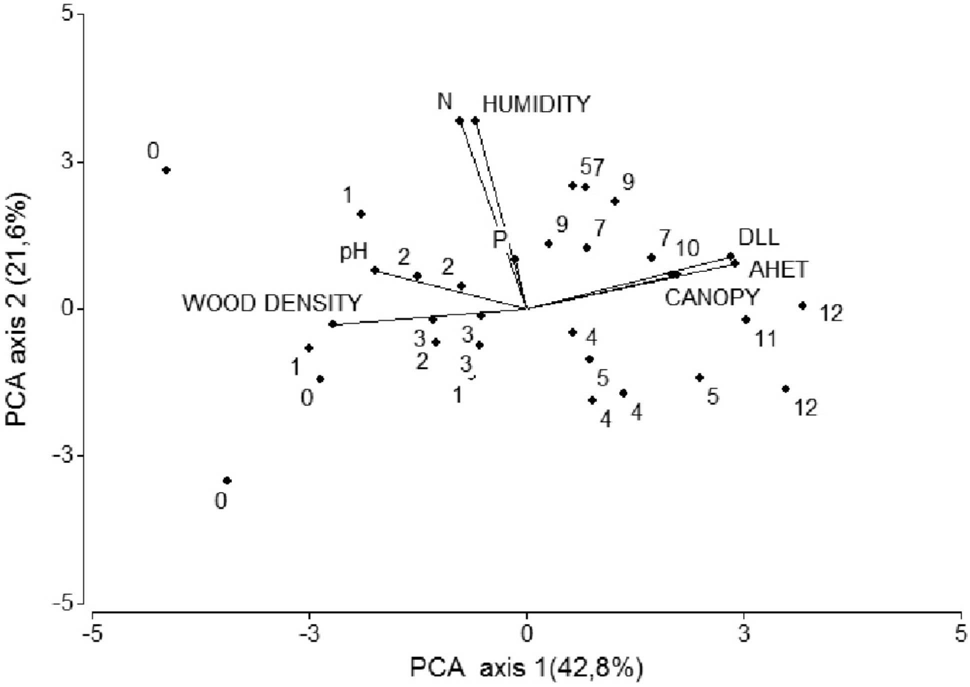

Figure 1: Principal component analysis (PCA) of environmental variables in eucalypt plantation:wood dendity,pH, N, P, % humidity, depth of the leaf litter (DLL), %canopy and average height of eucalypt tree(AHET). Numbers represent the ages.

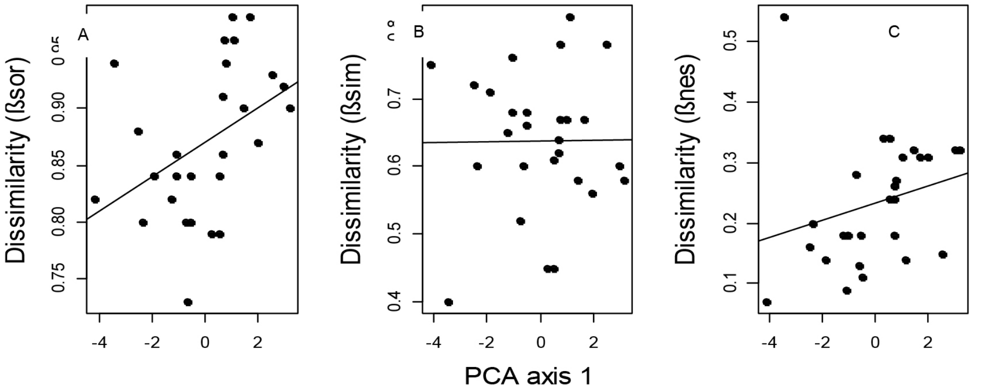

Figure 2: Relationship between taxonomic dissimilarity (βsor, βsimand βnes) and PCA axis 1.

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Testing the viability of the steady-state satiation equation adopting a Bayesian framework

Nikos E. Papanikolaou[1*], *Dimitrios P. Papachristos*[1], *Dimitrios C. Kontodimas*[1], *Theodore Kypraios*[2]

[1]Laboratory of Agricultural Entomology, Benaki Phytopathological Institute, Athens, Greece
[2]School of Mathematical Sciences, University of Nottingham, Nottingham, UK
[*]E-mail: nepapanikolaou@yahoo.gr

Keywords: Bayesian inference, functional response, handling time, mechanistic models

Functional responses, i.e. the relationship between prey density and per capita prey consumption rate by a predator, are central to predator-prey theory and are typically classified according to their shape. If the consumption rate of a predator rises linearly with prey density, we speak of a linear functional response. Such a response can theoretically be seen if both handling and digestion time are negligible. In practice, however, linear functional responses are rare, as digestion time is hardly ever negligible. If consumption rate first rises linearly with prey density but remains constant once a threshold prey density has been reached, we speak of a type I functional response. In type II functional responses, density dependence occurs via a continuously decelerating feeding rate (type II), and a type III functional response is sigmoid. The plateaus of type II and III responses are typically determined by handling or digestion time.

Type II functional responses appear to be the most common in nature, first described by the well-known disc equation. Thereafter, several modelling approaches for type II functional responses have been pursued with respect to the attack rate. The discrimination of these models is typically based upon their assumption on predation limitation. The limitation regarding the number of prey attacked at higher densities is often attributed to satiation or handling time constraints. However, although digestion and handling prey are discrete phenomena, digestion must be considered as a background process, acting in parallel to handling (attacking and eating) prey, which influences the predator's hunger level and consequently its probability of searching for prey. This leads to further examination of functional response models and an argument about their mechanistic basis. In this task, a handy mechanistic functional response model that realistically incorporates attacking and eating prey has been presented, the steady-state satiation (SSS) equation (Jeschke et al. 2002). The application of the SSS equation model is underutilized so far in the ecological literature, probably due to its complexity relative to the simpler disc equation.

Our aim was to test the viability of the SSS equation model adopting a Bayesian framework for estimating parameters in ordinary differential equation models, in order to quantify the uncertainty of the estimates in a coherent, probabilistic manner. In this task, short- and long- term functional response experiments were performed using a ladybird beetle-aphid predator-prey system. The SSS equation model fitted to the long-term functional response data using a Bayesian approach in which all the unknown model parameters are treated as random variables. In order to overcome issues of practical non-identifiability, we used the posterior distribution of the handling time parameter which was obtained from the fitting the disc equation to the short-term functional response data, as we expect that digestion effects should be negligible in this short time period.

The SSS equation model fitted to the data well, indicating its viability. Further research in its mechanistic basis could lead to a clearer understanding of predators feeding behaviour using mathematical models.

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Secondary succession in the abandoned North Adriatic Karst grasslands from functional and phylogenetic perspective

Nataša Pipenbaher[1*]*, Marco Antonio Batalha*[2]*, Branko Bakan*[1]*, Sonja Škornik*[1]*,*
Mitja Kaligarič[1]

[1]Department of Biology, Faculty of Natural Sciences and Mathematics, University of Maribor, Maribor, Slovenia
[2]Department of Botany, Federal University of São Carlos, São Carlos, Brazil
[*]E-mail: natasa.pipenbaher@um.si

Keywords: Assembly rules, Functional diversity, Karstic vegetation, Phylogenetic diversity, Slovenia

Grasslands in the North Adriatic Karst are among the richest grasslands in the world and harbor the highest small-scale density of plant species found in terrestrial habitats. Land abandonment of these grasslands has been driving their replacement by woodlands. Along this successional gradient, intensively studied for last forty years, environmental conditions constantly change and community assembly rules might change accordingly. We sampled 56 grassland plant communities in different successional stages. Following new approaches to account for ecological differences - one based on trait differences (functional diversity) and another based on evolutionary history (phylogenetic diversity) – we combined both in our study. Thus, using the functional-phylogenetic distances we got insights on the process of community assembly along a successional gradient from active from grasslands to woodlands. We found 146 species, for which we measured functional traits and built a phylogenetic tree. The three successional stages were floristically different, with grasslands related to harsher and woodlands to milder soil conditions. All communities presented higher functional than phylogenetic distances, implying that pairwise evolutionary relationships were divergent. If more importance was given to functional distances, most grassland communities and some scrublands were under-dispersed; when more importance was given to phylogenetic distances, only one grassland community was under-dispersed and one woodland community was over-dispersed. Combining functional and phylogenetic distances provided us with better estimates of ecological differences along the succession, where environmental filter seems to be the dominant force in early stages. In that case, a competitive exclusion become likely more important toward late stages. Taking into account that grasslands, scrublands, and woodlands are assembled by different rules is essential to conserve them and to understand how they will behave under future environmental scenarios.

Functional diversity in aquatic macroinvertebrates assemblages in the arid basin of Río Grande, a natural protected area, Mexico

Jacinto Elías Sedeño-Díaz[1*]*, Valeria Alejandra Perdomo Zúñiga*[2]*,*
Emilio Martínez Ramírez[3]*, Eugenia López-López*[2]

[1]Coordinación Politécnica para la Sustentabilidad, Instituto Politécnico Nacional, Ciudad de México, México
[2]Laboratorio de Evaluación de la Salud de los Ecosistemas Acuáticos, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Ciudad de México, México
[3]Centro de Interdisciplinario de Investigación para el Desarrollo Integral Regional, Unidad Oaxaca
[*]E-mail: jsedeno@ipn.mx

Keywords: River of arid zones, Water Quality Index, Divergence and regularity indices

Functional diversity is the variety of ecological attributes that organisms play in communities and ecosystems and may be summarized using different specific indices or by means of indices related to biodiveristy. In aquatic macroinvertebrates (AM), a functional feeding group (FFG) is referring to the way in which a group AM acquire food considering their morphological or behavioral characteristics. Respiratory modes (RM) refer to the anatomical and physiological characteristics to perform the breathing process. In Mexico, the Tehuacán Cuicatlán Biosphere Reserve, is very important by their characteristic arid vegetation; however, there is not a systematically monitoring program of their water courses, and also, is considered as an area of scientific unknown in terms of their water recourses an their aquatic biota. The aim of this work is to analyse the relation between water quality (through physicochemical variables) and functional diversity of AM. We quantify the functional diversity of MA through GFA and RM using functional divergence and functional regularity indices and correlated it with water quality. The Rio Grande basin is located in the southern portion of the Tehuacán Cuicatlán Biosphere Reserve. The work was carried out during the dry and rainy seasons of 2015, in 11 study sites along the Río Grande basin. Water and air temperature, dissolved oxygen (DO), turbidity, salinity and conductivity was measured *in situ*, and water samples were obtained for microbiological and physicochemical analyses. The AM samples was carried out with a kick neet and a spoon net. In the laboratory, the samples were processed and the Water Quality Index (WQI) and the taxonomic and functional identification of the AM were calculated. A Principal Component Analysis (PCA) was performed with environmental factors, FFG, RM and functional diversity estimators for each sampled site, and sampling season. The order PCA result in three groups: The first one corresponded to the study sites dominated by the highest WQI scores, highest concentration of DO, NO2, NO3, gill and aerial RM, and FFG of predators, filterers and scrapers. The second group was characterized by high concentrations of sulphates, orthophosphates and total nitrogen. The predominant FFG was piercing, and the RM was cutaneous. The latter group was characterized by the highest concentration of total phosphorus, and sharing with the second group the major richness and diversity, as well as the gill and special MR. Gill MR and Predator FFG were associated with the highest water quality, while the Special RM and Detritivore FFG were associated with the lowest WQI scores and the presence of coliforms.

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Trophic networks: comparative analyses and methodological problems

*Vera Senánszky**, *Anett Endrédi, Ferenc Jordán*

Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
*E-mail: senanszkyvera@gmail.com

Keywords: food webs, network analysis, DAG, hierarchy

Food webs are key objects of community ecology since decades. Food web research provided a lot of information about the structure, dynamics, stability, vulnerability of ecological communities. A number of experimental, descriptive and modelling studies exist, yet, the most basic methodological issues are still open and intensely debated.

One of the possible solutions for many of the problems is the comparative approach. Spatial and temporal gradients of food webs as well as different versions of the same food web described under different conditions may help to better understand the similarities and differences among food web data. We show a large food web database and discuss the methodological challenges of comparative analysis. We discuss the consequences of directed loops and what is the advantage of not having them in DAGs (directed acyclic graphs). We discuss how to consider the weights and direction of trophic links and how to match methods to data in a meaningful way. In many cases the devil is in the details, so the importance of high-quality databases and good database management cannot be overestimated.