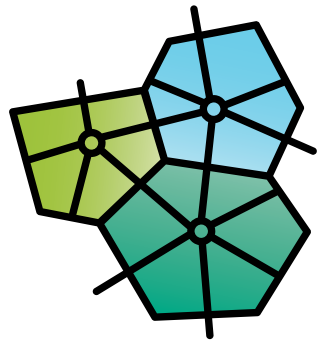

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CONTENTS

Plenary

Endemism in ecosystems – Exploring the role of community assembly and turnover

Carl Beierkuhnlein[1,2,3]

[1]Chair of Biogeography, University of Bayreuth, Bayreuth, Germany
[2]Geographisches Institut Bayreuth GIB, Bayreuth, Germany
[3]Bayreuth Center of Ecology and Environmental Research BayCEER, Bayreuth, Germany
E-mail: carl.beierkuhnlein@uni-bayreuth.de

Keywords: island biogeography, speciation, Canary Islands, La Palma, beta-diversity, single-island endemics, ecological isolation, oceanic islands, ecosystem functioning, assembly rules

Islands and archipelagos are considered as classic laboratories to study speciation and diversification. Established approaches relate these processes to biological aspects such as phylogenies of taxa or diversity within taxonomic groups and to geographical aspects such as isolation, distances to other habitats or island size and elevation. Besides spatial isolation, obviously ecological isolation is effective as climatic conditions play an important role for endemism (Irl et al. 2015, Steinbauer et al. 2016, Irl et al. 2017). The increasing proportion of endemism with elevation hints at diversifying processes resulting from ecological isolation. However, ecological isolation is also effective between ecosystems. It is evident that plant species are not uniformly distributed accross isolated islands but rather linked to specific communities and ecosystems. Within islands closely related endemic species occur with different habitat requirements. However, the contribution of ecological isolation effects and available area for speciation in ecosystems as well as biotic interactions within ecosystems is widely ignored in island biogeography that is mostly focused on physical aspects.

Here, I disentangle the patterns of endemism as well for single island endemics as for archipelago endemics at the scale of ecosystems. Ecosystems are considered as functional units within islands that differ considerably in species assemblages and community structure. The spatial extend of major ecosystem types was calculated for all islands, and all plant species were assigned to ecosystems for every single island. Plant species are classified into native (non-endemic), archipelago endemics, single island endemics, and alien species.

The spatial extend of ecosystems within islands plays a minor role. Extensive ecosystems such as Canary Pine forest can host less species than the laurel forest, but surprisingly show a higher proportion of endemism. It is rather the type of ecosystem (e.g. fayal-brezal) that is linked on all islands with a high proportion of endemism. Harsh environments at the coast exhibit a high proportion of native species, but less endemics and alien species.

Acknowledgments
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Community ecology in deep-sea ecosystems: The boundaries of the extremes

Roberto Danovaro[1,2]

[1]Stazione Zoologica Anton Dohrn, Villa Comunale Napoli, 80121, Italy
[2]Department of Life and Environmental Sciences (DiSVA), Polytechnic University of Marche, Via Brecce Bianche, 60131 Ancona, Italy
E-mail: r.danovaro@staff.univpm.it

Deep-sea ecosystems represent Earth's major ecological research frontier. The extreme conditions present in these ecosystems (an average depth of approximately 4.2 km and thus >400 atm, near total darkness and lack of photosynthesis, from very cold to extremely hot temperatures) challenge major ecological hypotheses and constrain community ecology and species interactions. We now recognize that their complexity is far higher than expected in the past and the new ecological interactions are present in systems exploiting alternative sources of dark energy. We also acknowledge functional hotspots and complex community composition that contradict a food-poor, metabolically inactive, and minor component of global carbon cycles. Symbioses appear widespread, revealing novel adaptations. Populations show complex spatial structure, large scale connectivity and evolutionary histories. The novel findings accumulating on deep-sea ecology allow us to define new rules for the comprehension of the community ecology in these extreme ecosystems and to better understand their contribution to the global biosphere functioning.

Eco-engineering: Making space for nature in the Anthropocene

Louise B. Firth

School of Biological and Marine Sciences, University of Plymouth, Plymouth, UK
E-mail: louise.firth@plymouth.ac.uk

Keywords: intertidal ecology, eco-engineering, non-native species, biolotic homogenization

Coastal defence structures are proliferating as a result of rising sea levels and stormier seas. With the realisation that most coastal infrastructure cannot be lost or removed, research is required into ways that coastal defence structures can be built to meet engineering requirements, whilst also providing relevant ecosystem services - ecological engineering. This approach requires an understanding of biological communities, species interactions and the identity and functioning of the organisms that colonise these novel ecosystems. I summarise research carried out by myself and the wider team on eco-engineering and I outline guidelines and recommendations to provide multiple ecosystem services while maintaining engineering efficacy. This work demonstrates that simple enhancement methods can be cost-effective measures to manage local biodiversity. Care is required, however, in the wholesale implementation of these recommendations without full consideration of the desired effects and overall management goals.

Pax perniciosa – The deceptive dynamics of biodiversity loss

John M. Halley

Professor of Ecology, Department of Biological Applications and Technology, University of Ioannina, Greece
*E-mail: jhalley@cc.uoi.gr
Telephone: +30-6944-328099 (Mb)

It is often argued that since most of the expected extinctions due to habitat loss have not happened, then the dangers of habitat loss have been inflated. But if habitats contract or get fragmented, these reduced habitats cannot continue to support the same biodiversity as they did before – you simply cannot sustain the diversity of a rainforest on a postage stamp - so they must lose species. While some species may be lost immediately, others can persist for a long time. Indeed, areas recently protected may continue to lose species long after habitat loss has been halted. So, just because we don't observe extinctions right away does not mean that everything is going to be OK. A major scientific challenge is to understand the dynamics of this effect: how long before the extinctions are complete? Which parameters drive the process? Answering these questions requires not only good empirical data but also a sound theoretical model of the community. I will be reviewing our current state of knowledge in this area: what have theory, case studies and larger meta-analyses revealed so far? I will also show how the phenomenon of delayed extinction has plenty to say about how we interpret the future of ecosystems subject to climate change and ecological invasion.

Dark diversity of ecological communities: Theory and applications

Meelis Pärtel

Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia
E-mail: meelis.partel@ut.ee

Keywords: biodiversity, functional diversity, consrvation, species pool

Dark diversity of a site is the set of species which potentially can inhabit the site and are present in the surrounding region, but are still locally absent (Pärtel et al. 2011). In other words, dark diversity is the absent portion of the site-specific species pool.

A major question is how to calculate dark diversity for a study site. We cannot sample absent species but we can estimate these by using information on regional distribution and habitat requirements of taxa. One option is to use species co-occurrences within the region to identify absent taxa which often co-occur with present taxa in the region (Lewis et al. 2016).

By comparing observed and dark diversity, we can find how complete local communities are, i.e. how much of the theoretical biodiversity potential (site-specific species pool) is realized (Pärtel et al. 2013). This information allows comparisons of different regions, ecosystems and taxonomic groups. Dark diversity can be applied in understanding and protecting ecological communities at various spatial scales (Lewis et al. 2017). This task is especially important when considering time-delayed biodiversity dynamcs in global climate and land-use changes.

With dark diversity we can disentangle local and regional effects on biodiversity (Bennett et al. 2016). When combined with functional traits, we might be able to understand why some species are locally absent and currently in dark diversity (Pärtel et al. 2016). This requires that we compare functional traits of observed and dark diversity species. Often the dispersal potential of dark diversity species is lower, or they are less tolerant to stress.

Active research is ongoing to advance theory and applications of dark diversity. For example, a global research collaboration DarkDivNet currently samples plant communities both locally and regionally. With this highly standardised dataset we can refine dark diversity methods. We elaborate probabilistic measures and integrate information from large vegetation databases. We also aim to expand the concept to functional and phylogenetic aspects of diversity, and suggest ways how to use dark diversity in nature conservation.

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Being smaller in summer, larger in winter: A general pattern in freshwater phytoplankton?

Tamar Zohary

Kinneret Limnological Laboratory, Israel Oceanographic & Limnological Research
Haifa, Israel
E-mail: tamarz@ocean.org.il

Size is an important feature of all organisms across diverse taxa, with widespread ecological and economic implications. The phenomenon of shrinking body size with increasing temperature is well-known from large animals, as expressed already 170 years ago by Bergmann's Rule (Bergmann 1847), stating that warmer regions tend to be inhabited by smaller species of the same genus. Does this rule apply also to microscopic organisms, such as freshwater phytoplankton? Size influences all aspects of the life of a phytoplankton cell: nutrient uptake kinetics, photosynthesis, respiration, growth rates, sinking rates, avoidance of grazers. Phytoplankton cell size was shown experimentally to decline with declining illumination and nutrients and with increasing water temperature, but field studies to confirm that are sparse, especially in freshwater systems. Using PlanktoMetrix, a proprietary software for sizing phytoplankton, we found that many of the phytoplankton species in Lake Kinneret showed a typical annual pattern in which cell diameter or colony size were largest in winter and smallest in summer. This pattern was shared by species of cyanobacteria, diatoms, chlorophytes and dinoflagellates. It is now a challenge to explore whether the seasonality of cell size so common in Lake Kinneret is universal in freshwater phytoplankton, and to unveil the physiological and cellular processes involved. Its significance is in the context of climate change, by generating field data to test the hypothesis that with global warming freshwater phytoplankton will shrink in size.

Oral Presentations

Community ecology

Aggregations of native laurophylls in Italy to study ancient *refugia* and their non-equilibrium with present-day climate

Nicola Alessi[1], Jakub Tešitel[2], Stefan Zerbe[1], Francesco Spada[3,4], Emiliano Agrillo[3], Camilla Wellstein[1]*

[1]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bozen-Bolzano, Italy
[2]Department of Botany, Masaryk University, Brno, Czech Republic
[3]Department of Environmental Biology, Sapienza University of Roma, Roma, Italy
[4]Department of Plant Ecology and Evolution, Uppsala University, Uppsala, Sweden
[*]E-mail: Nicola.Alessi@natec.unibz.it

Keywords: Beal's index, evergreen broadleaved species, laurophyllisation, laurophyllous, species aggregations, species potential distribution, vegetation databases

European native laurophyllous species were traditionally studied in biogeography and evolutionary history as footprints of relic species of the Late Neogene laurophyllous biome. Recently, they were also studied for their responses to global changes. To understand whether these species are in equilibrium with the present-day climate, we identified Italian native laurophylls on the basis of morphology, biogeographical history and ecological niche. Furthermore, we localized Quaternary *refugia* and areas of potential spread of native laurophylls using distribution patterns of realized and potential aggregations of native laurophylls, respectively.

We extracted 17,087 forest plots from a phytosociological database in Italy. For each plot, we calculated means of species indicator values and selected significant climatic variables. An ordination (DCA) of forest plots with overlay of selected variables was performed to identify native laurophylls, i.e. evergreen broadleaved species of late Tertiary radiation, occupying a warm and wet niche. Potential ranges of laurophylls were calculated using Beals' index of sociological favourability. The realized and potential range-size ratio, respectively, was calculated for each single laurophyll to understand whether it is in equilibrium with the present-day climate. Distribution patterns of realized and potential aggregations of laurophylls were mapped.

We selected 11 species as Italian native laurophylls. Most of them occupied less than half of their estimated potential range. Realized aggregations richest in native laurophylls were localized in the central Apennines. However, the Italian forests showed high potential for native laurophylls with the richest potential aggregations in the whole Apennines and in the Southern Alps.

Non-equilibrium with the current climate occurred for most of the Italian native laurophylls, suggesting that the late-Quaternary biogeographical history could better explain the present-day distribution of native laurophylls than the ongoing climate change. Furthermore, their *refugia* in Central Italy suggest the persistence in sites with temperate climate during Quaternary environmental changes. The high suitability of Italian forests for laurophylls suggests possible future spreading along global changes. In light of these findings, the abandonment of agricultural areas and the decline of traditional forest management, inducing the increase and ageing of forests, could have led to increas suitable sites in numbers for the spread of late-successional species as the native laurophyllous are.

Fish associations in temporal and nichthemeral scales in Los Petenes Biosphere Reserve, Campeche, Mexico

Luis Amado Ayala-Pérez[1], Brenda Iliana Vega-Rodríguez[1], Esli Yazmín Rodríguez-Díaz[1], Julia Ramos-Miranda[2]*

[1]Departamento El Hombre y su Ambiente, Universidad Autónoma Metropolitana Xochimilco, Ciudad de México, México
[2]Instituto de Ecología, Pesquerías y Oceanografía del Golfo de México, Universidad Autónoma de Campeche, Campeche, México
[*]E-mail: luayala@correo.xoc.uam.mx

Keywords: Los Petenes biosphere reserve, seasonal scales, nichthemeral scales, dominant fish

Los Petenes Biosphere Reserve (RBLP), Campeche, Mexico is a wetland of international importance. Among the main structural components of this ecosystem are fish and their study allow us to understand different ecological interactions at different scales. The objective was to analyze the temporal and nictemeral behavior of the abundance and diversity of fish at the site known as El Cuyo located in the southern zone of the RBLP. Five sampling campaigns were carried out in February and May 2013, May 2015 and February and May 2016. In each campaign, samples were taken with a frequency of two hours in a cycle of 24 hours. In each sampling, environmental variables were recorded, and experimental collects of fish were taken. The water temperature ranged between 20.9 and 32oC, salinity between 36.1 and 47.7, dissolved oxygen between 1.4 and 7.9 mg/l and pH between 7.3 and 10.8 H+. A total of 3767 fish were caught with a weight of 65.2 kg. 37 species from 20 families and 27 genera were classified and 16 dominant species were identified for daytime hours and 11 for nighttime hours. *Lagodon rhomboides* and *Haemulon plumierii* were the most abundant species. In the temporal and nictemeral scales, changes in abundance (density, biomass and average weight) as well as diversity (species richness, equity and uniformity) are analyzed. The cluster analysis identifies four groups of species for daytime hours and two for nighttime hours (Fig. 1) and the canonical correspondence analysis highlights the salinity and dissolved oxygen vectors associated with the abundance of *Lutjanus analis*, *Nicholsina usta*, *Archosargus probatocephalus* and *Sphoeroides testudineus* for hours at daytime. For nighttime hours the vectors of greater magnitude are the temperature and the pH that are associated with *Calamus penna*, *Nicholsina usta*, *Eucinostomus gula* and *Lagodon rhomboides* (Fig. 2 and 3).

Figures

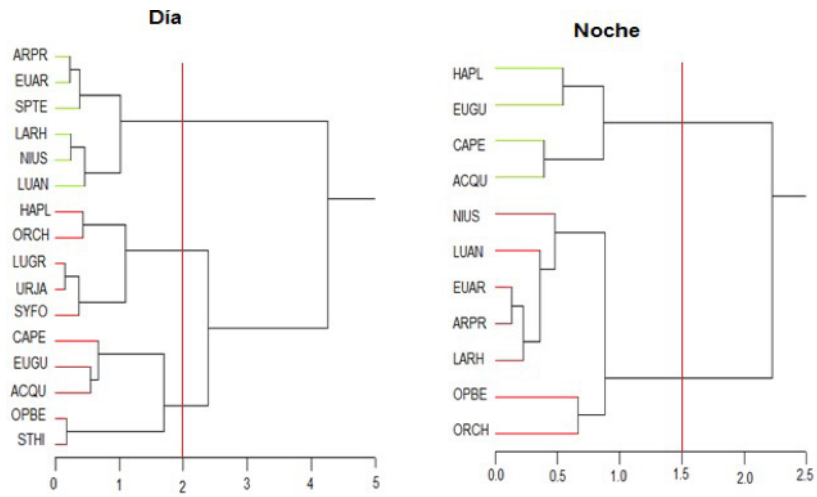

Figure 1. Cluster of association of dominant species by day (left) and night (right) hours of the fish of RBLP.

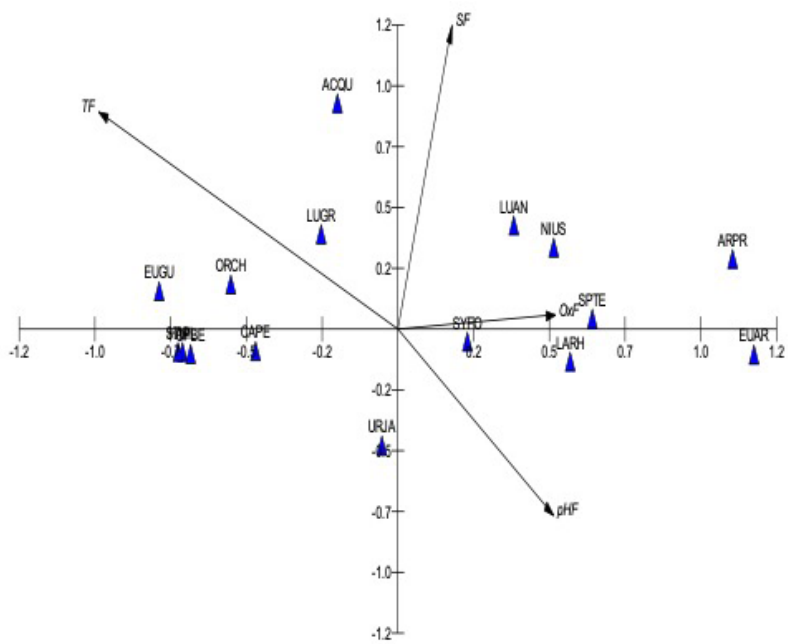

Figure 2. Analysis of canonical correspondence between the abundance of dominant species and the environmental variables corresponding to daytime hours.

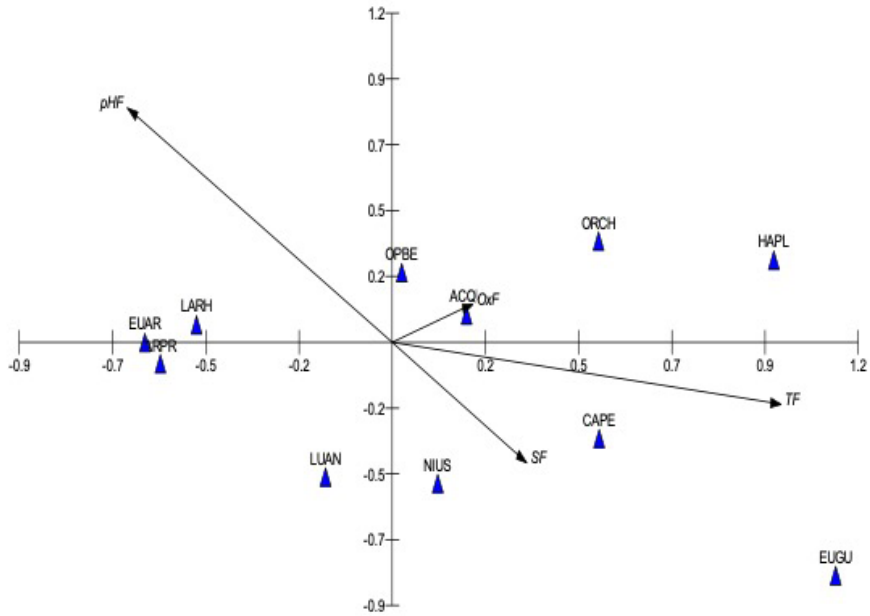

Figure 3. Analysis of canonical correspondence between the abundance of dominant species and the environmental variables corresponding to nighttime hours.

Acknowledgments

To Metropolitan Autonomous University Xochimilco.

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Are there invariant and specific characteristic spatial scales of diversity patterns in grasslands?

Sándor Bartha[1,2], Sándor Csete[3], Giandiego Campetella[4], Roberto Canullo[4], Andraž Čarni[5], Stefano Chelli[4], András I. Csathó[6], Judit Házi[7], András Kun[8], Róbert Kun[9], Zsolt Molnár[1,2], Dragica Purger[10], Eszter Ruprecht[11], Anna Szabó[12], Gábor Szabó[1,2], Szilárd Szentes[13], Klára Virágh[2], Camilla Wellstein[14], Zita Zimmermann[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
[3]Institute of Environmental Sciences and Nature Conservation, Faculty of Agricultural and Environmental Sciences, Kaposvár University, Kaposvár, Hungary
[4]School of Biosciences and Veterinary Medicine, Plant Diversity and Ecosystems Management Unit, University of Camerino, Camerino, MC, Italy
[5]Institute of Biology, Scientific Research Center of the Slovenian Academy of Sciences and Arts Ljubljana, Slovenia
[6]Battonya, Hungary
[7]University of Veterinary Medicine, Department of Botany, Budapest, Hungary
[8]Somogyvámos, Hungary
[9]Szent István University, Doctoral School of Environmental Sciences, Gödöllő, Hungary
[10]Institute of Pharmacognosy, Faculty of Pharmacy, University of Pécs, Hungary
[11]Hungarian Department of Biology and Ecology, Babeş-Bolyai University, Cluj Napoca, Romania
[12]Romanian Ornithological Society, Bucharest, Romania
[13]Rezi, Hungary
[14]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bozen, Italy
[*]E-mail: bartha.sandor@okologia.mta.hu

Keywords: community organization, maximum scale, minimum scale, spatial statistics

The concept of characteristic scales (e.g. minimum area) is fundamental in community ecology. Scales where community state-variables such as diversity measures show maximum or minimum variability are optimal for detecting patterns in plant coexistence and plant-environmental relationships. While there is a consensus among field ecologists about the approximate magnitude of the related optimum scales, few systematic studies exist for assessing the variability/invariance of these characteristics.

The spatial variance of selected vegetation state variables (diversity measures) was determined in contrasting grasslands. More than 60 vegetation stands representing four dry grassland types were studied with minimum of 10 replicates per types, applying a standardized sampling protocol. Meadows steppes (dry and semi-dry grasslands on loess), open sand steppes of humus-poor sand dunes, short grass salt steppes on solonetz soils and rock grasslands on dolomite and limestone hills were sampled at various locations in Hungary, Italy, Romania and Slovenia.

A list of species present in 5 × 5 cm contiguous micro-quadrats was sampled along 52 m long transects of 1040 units arranged within uniform (homogenous) vegetation patches in each grassland stand. From each transect, diversity measures (variance of species richness, number and diversity of species combinations) were estimated at increasing plot sizes from

5 cm × 5 cm to 5 cm × 10 cm … to 5 cm × 2500 cm. Spatial scales where vegetation characteristics reached maximum and minimum values were assessed in each transect.

Spatial scale of maximum variability ranged between 5cm and 500 cm. Maximum scales of different diversity measures were close to each other. The smallest maximum scales were found in meadow steppes and maximum scales increased gradually from dolomite to sand grasslands with the largest values in salt steppes. However, estimated maximum scales varied from stand to stand within a grassland type. No significant differences were found in medians, however, the variability of estimates within a grassland type increased from meadow steppe to salt steppe. Within a certain type, medians were significantly larger in disturbed stands and they tended to decrease in recovering stands. Estimates of maximum scales were robust while estimates of minimum scales were highly variable without apparent trends. Minimum scales were strongly influenced by the effect of rare species. In contrast, maximum scales showed clear trends reflecting types of the spatial organization rather than some syntaxonomic features.

Acknowledgments
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Taxonomical, coenological and functional approach to analyse the effect of multi-year mowing on sub-Mediterranean invaded grasslands

Alessandro Bricca[1*], *Federico Maria Tardella*[2], *Andrea Catorci*[2]

[1]Department of Science, University RomaTre, Rome, Italy
[2]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy
[*]E-mail: ale.bricca@gmail.com

Keywords: grassland invasion, grassland restoration, traits, species diversity, mowing

The cessation of semi-extensive farming or underutilization of grasslands is leading to vegetation changes throughout Europe, as well as in semi-natural sub-Mediterranean mountains. At the community level, these changes foster the invasion of unpalatable tall grasses, mostly with competitive stress-tolerant strategies, affecting species diversity and decreasing the nutrient value of pastures ecosystem. In the Italian peninsula, two perennial species of *Brachypodium* are fostered by grazing cessation or by a livestock pressure below the theoretical carrying capacity of pasture: *B. rupestre* (Host) Roem. *et* Schult. in the sub-Mediterranean hills and low mountains, and *B. genuense* (DC.) Roem. *et* Schult. over 1300–1400 m a.s.l. These species can spread over a wide range of abiotic conditions, shifting their strategy thanks to their high intraspecific trait plasticity. Consequently, finding proper management practices to restore invaded grasslands is an important issue to preserve their biodiversity and economic value.

This research was aimed to understand the effect of multi-annual mowing events on the recovery of a grassland community invaded by *Brachypodium rupestre*. In particular, we analysed the effects on taxonomic diversity, coenological composition, and trait composition (space occupation strategies, vegetative propagation, presence of storage organs, and flowering phenology) at the plant community level, and changes in *B. rupestre* traits.

The study site was located next to the "Montagna di Torricchio" Natural Reserve (central Apennines) undergrazed since at least 30 years. We fenced one homogeneous area of 2 ha invaded by *B. rupestre*: half of the surface was mown twice a year since 2010, and hay and litter were removed after each mowing event; the other half was unmown and used as a control. Species cover (%) was recorded in 30 random plots (0.5 m × 0.5 m) in late June, before the start of the experiment and in the following six years. We collected also data on *B. rupestre* traits in mown and unmown areas (plant height, leaf area, leaf dry mass, seed mass, hypogeogenous rhizome dry matter content, and aboveground phytomass), and calculated Specific Leaf Area.

B. rupestre cover and aboveground phytomass strongly decreased over time; species richness and transformed Shannon and Gini-Simpson indices increased, while Shannon's evenness showed fluctuations.

Fringe habitat and successional species, indicators of ongoing dynamic processes, decreased in cover, along with caespitose species, grasses, and species with rhizomes and runners as vegetative propagation modes. The cover of species that are typical of managed grasslands increased, as well as that of rosulate species, species with compact shoots with

innovation buds at the axil of basal leaves, and species flowering in mid-late summer. The resulting species composition was consistent with that of central Apennines' managed pastures.

B. rupestre Specific Leaf Area did not show a significant trend, while both leaf area and leaf dry mass, as well as plant height and seed mass, decreased. These results suggest that *B. rupestre* reduces the amount of dry matter (e.g. structural and storage carbohydrates) inside the rhizomes and the investment in growth (horizontally and vertically) and in sexual reproduction.

In summary, recurring mowing twice a year could represent the proper management practice to restore invaded grasslands, enhancing species diversity.

Communities in high definition: Spatial and environmental factors affecting small scale distribution of aquatic invertebrates

Gemma Burgazzi[1*], *Alex Laini*[1], *Mattia Saccò*[2], *Pierluigi Viaroli*[1]

[1]Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Parco Area delle Scienze 33/A, 43124, Parma, Italy
[2]Department of Applied Geology, Curtin University, Kent Street, 6102, Bentley Perth, Western Australia
[*]E-mail: gemma.burgazzi@unipr.it

Keywords: macroinvertebrates, small scale distribution, variance partitioning, community drivers

Macroinvertebrate communities exhibit high variability in diversity, abundance and structure at different spatial scales (Mykrä et al. 2007). Space is currently used as an explicit predictor to discriminate between environmental forcing and biotic processes at large and medium sized scales, but it is generally neglected at smaller scales, to which macroinvertebrate community organization is generally studied only within the environmental filtering framework, disregarding processes other than those based on abiotic factors (Tolonen et al. 2017). To fill this gap we considered environmental as well as spatial variables with the aim of explaining metrics and community patterns of macroinvertebrate community at small scale. We worked in three rhithral sections of perennial streams (Nure, Parma and Enza Streams) located in the Po River Basin (Northern Italy) by means of specific *in situ* 50-points random sampling grids. For each system one sampling station was selected and sampled twice, once during summer 2016 and once during winter 2017, for a total of six sampling campaigns. Benthic Organic Matter (BOM), flow velocity, water depth and dominant substrate were collected, as environmental factors, together with relative spatial coordinates (inside the grids) for each sample. The relationship among metrics (taxa richness, abundance and biomass) and environmental and spatial variables was checked by means of Generalized Additive Models (GAMs). Regarding the analysis of communities, coordinates were used to produce Principal Coordinates of Neighbour Matrices (PCNM) in order to detect additional spatial structures. Data were then analysed by means of variance partitioning methods, considering spatial coordinates, PCNM and environmental factors as groups of explanatory variables. Environmental factors (primarily BOM) resulted the main drivers affecting community metrics and composition. On the other hand, coordinates and PCNM accounted for a minor fraction of explained variance. Nevertheless, we found that in systems with a greater riverbed structuration, PCNMs variables had higher explanatory power, highlighting also the importance of space, as a proxy of small-scale community processes. These results suggest that trophic factors are powerful predictors of macroinvertebrate community organisation in rhithral sections of perennial streams. Such findings gain more importance especially if considered in the context of biomonitoring, for which small scale variability and the effect of BOM as driving variable are totally omitted. Restoration ecology, habitat suitability modelling and biomonitoring sampling methods could benefit from this approach.

Acknowledgments

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Diversity patterns of tropical freshwater fish communities through disturbance gradients

Isabel Cantera[1], Kévin Cilleros[1], Céline Jezequel[1], Alice Valentini[2], Amaia Iribar[1], Sébastien Brosse[1]*

[1]Laboratoire Evolution et Diversité Biologique (EDB UMR5174), Université Paul Sabatier-Toulouse3, CNRS, IRD, UPS, 118 route de Narbonne, 31062 Toulouce Cedex, France
[2]SPYGEN, 17 rue du Lac Saint-André Savoit Technolac – BP 274, Le Bourget-du-Lac 73375, France.
[*]E-mail: isa_cantera@hotmail.com

Keywords: Amazonia, taxonomic diversity, functional diversity, environamental DNA, metabarcoding

Amazonian freshwater ecosystems are facing intense human-induced pressures due to population's growth and economic activities. Those pressures were shown to affect more the species identity and the functional diversity of fish assemblages than species richness. Thus, disturbance effects should be assessed in a community based approach.
In this study, the freshwater fish diversity was considered through two diversity facets: taxonomic and functional diversity. The relationships between these facets can provide insights on the ecological processes shaping the structure of communities.

The taxonomic diversity was assessed using environmental DNA sampling and the functional diversity was measured using morphological measures and ecological traits of tropical fishes. We filtered 68L of water in 34 river and 23 stream sites in French Guiana in order to collect fish DNA. Then, the DNA was assigned to fish species using metabarcoding techniques. Disturbance gradients of increasing gold-mining, deforestation and urbanization were defined using GIS data layers.
For river sites, we observed a significant decrease of taxonomic and functional diversity through deforestation, gold mining and urbanization gradients. For streams sites, we only observed a decrease of the diversity thorough gold-mining gradients. Despite the erosion of fish diversity observed through disturbance gradients, the effect of disturbance gradients on ecological processes was not significant.

Modelling three-dimensional growth and competition of a community of corals under different disturbance scenarios

Anna K. Cresswell[1,2,3*], *Damian P. Thomson*[2], *Michael Renton*[1,4]

[1]School of Biological Sciences, The University of Western Australia, Perth, Australia
[2]CSIRO Oceans & Atmosphere, Perth, Australia
[3]The UWA Oceans Institute, Perth, Australia
[4]School of Agriculture and Environment, The University of Western Australia, Crawley, WA, Australia
[*]E-mail: anna.cresswell@research.uwa.edu.au

Keywords: cellular automaton, community ecology, coral reef, ecological strategy, functional diversity, functional–structural model, simulation, structural complexity, individual-based model

Scleractinian corals, which grow solid living structures via the secretion of calcium carbonate, create complex three-dimensional communities that provide habitats and support diverse ecosystems. There are a variety of growth forms of corals, which contributes to the structural complexity on reefs. Different growth forms have different advantages and disadvantages when corals compete for space and light and when they are exposed to hydrodynamic disturbances. We developed a three-dimensional functional-structural model, *Coralcraft*, to investigate how competition for space and light interacts with perturbations from a range of hydrodynamic disturbance regimes to drive the dynamics of a simulated community of corals. Using *Coralcraft* we first investigate the temporal dynamics of a community with five common growth forms of corals: encrusting, hemispherical, tabular, corymbose and branching (Fig. 1). *Coralcraft* captures the temporal dynamics of the community using four metrics: number of colonies, percentage cover and volume of each growth form, and the topographical complexity (rugosity) of the community. We show how these metrics capture the dynamics of impact and recovery from disturbance in different but complementary ways. Our findings illustrate the trade-off between being a fast growing marine sessile organism and occupying space quickly but being hydrodynamically vulnerable as a result. We then expand the model to investigate a greater diversity of growth forms to investigate the resilience of diverse communities versus less diverse communities, a key concept in community ecology. While there are already several models of coral growth, *Coralcraft* is the first to our knowledge to model the temporal dynamics of three-dimensional growth and competition of a community of multiple coral growth forms under different disturbance scenarios.

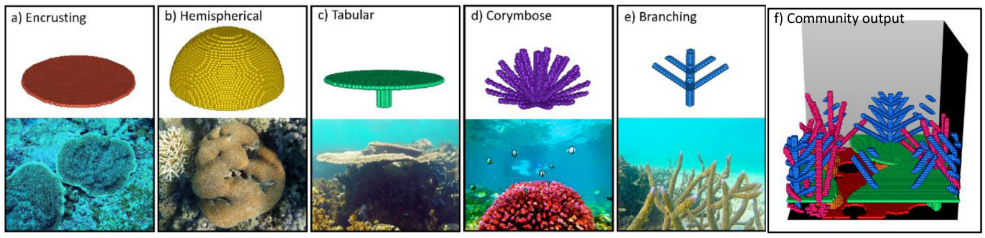

Figure 1. The five main coral growth forms (a–e) used in community simulations and f) an example of a resulting community

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On the importance of time-series data when making inferences on species interactions

Christian Damgaard

Aarhus University, Aarhus, Denmark
E-mail: cfd@bios.au.dk

The space-for-time substitution assumption is often used implicitly for studying species interactions in static spatial data sets. Ecological processes occur in time and are best studied when the effect of time is taken into account. This is also the case when studying interspecific interactions, but it is common to make inferences on the nature of species interactions based on observed correlations between the abundance of two species in large static datasets. This practice is problematic, especially in non-stationary environments. More processes might lead to the same spatial pattern, and instead of testing hypotheses on ecological processes by analyzing spatial variation in static data, it is more judicious to report the observed spatial patterns and only discuss which ecological processes are in concordance with the observed spatial pattern. Alternatively, it might be feasible to combine relatively sparse time-series data or experimental data with spatial variation data and analyze such data types in a common statistical framework.

Niche partitioning amongst river shark species is driven by seasonal fluctuations in environmental salinity

Ross Dwyer

The University of Queensland, Brisbane, Australia
E-mail: ross.dwyer@uq.edu.au

Tropical rivers are important nursery areas for euryhaline elasmobranchs; however, how these predators partition resources in these highly dynamic environments remains unclear. Using a combination of occurrence surveys, biotelemetry, plasma osmolyte analyses and multi-tissue stable isotope analysis (SIA), we investigated how interspecific competition and physiological tolerances influence the seasonal movements and distribution of two euryhaline carcharhinid sharks within a riverine nursery habitat.

Juvenile bull sharks *Carcharhinus leucas* (mean = 96.38 cm, s.d. = 16.19) and juvenile speartooth sharks *Glyphis glyphis* (mean = 89.04 cm, s.d. = 23.04) were captured in the Wenlock River, a tropical river system in northern Australia and implanted with coded acoustic transmitters. Their movements and salinity preferences were tracked between September 2014 and August 2018 using an array of 50 fixed underwater hydrophones and 10 conductivity loggers. To check for interspecific differences in blood chemistry and prey selection, tissue samples were also collected at capture and analysed for species differences in osmolarity, urea, electrolyte (Na^+ and K^+), and the stable isotopes δ13C and δ15N.

We found that juvenile *G. glyphis* typically inhabited an estuarine zone between 20 and 70 km from the mouth of the river, within a preferential salinity range between 2.9 and 24.7 ppt. Juvenile *C. leucas*, in contrast, occupied areas between 50 and 95 km upstream within a salinity range of 0 to 10 ppt, but undertook regular trips to the lower estuary, where they were detected at higher salnities (10 – 30 ppt). However, at the onset of the wet season, both species undertook a coordinated downstream migration to the lower estuary, where significant specifies mixing occurred between 0 km and 40 km upstream. Temporal segregation of species was evident through Bayesian niche overlap analysis which documented greater dietary mixing during the wet season.

This study supports the hypothesis that interspecific competition influences the distribution of carcharhinid sharks in river systems, where higher environmental salinities offer foraging advantages to juvenile *G. glyphis* over *C. leucas*. We discuss the importance of long-term investigative studies into resource competition between sympatric species and highlight the importance of these discrete brackish habitats for highly threatened riverine shark species such as *G. glyphis*.

The power of long-term observation: What can reveal 19 years of grassland monitoring without experimental manipulation?

Luciana Ghermandi[1*], *Sofia Gonzalez*[1], *Jorgelina Franzese*[1], *Facundo Oddi*[2]

[1]Institute of Biodiversity and Environment. INIBIOMA (CONICET-National University of Comahue), Bariloche, Argentina
[2] National University of Río Negro, Bariloche, Argentina
[*]E-mail: lghermandi@yahoo.it

Keywords: long-term monitoring, grasslands, disturbances, drought, fire, volcanism

Introduction

Long-term ecological monitoring is required for understanding population dynamics. Vegetation changes in arid and semi-arid ecosystems generally occur in the short- term in response to rainfalls and in the long-term in response to rare events (fires, volcanic eruptions). For developing management strategies for sustainable animal production and species conservation it is necessary to know how resilient arid and semi-arid ecosystems are.

Methods

We acquired three long-term plant community data sets for three sites in grasslands of the northwestern Patagonia region (San Ramon ranch, 41º 03' S, 71º 01' W; Argentina) (Fig. 1). The grasslands are co-dominated by *Pappostipa speciosa* (Trin. & Rupr.) Romasch and Festuca *pallescens* (St. Yves) Parodi tussock grasses with presence of *Mulinum* spinosum (Cav.) Persoon and *Senecio* bracteolatus Hook. & Arn. scattered shrubs and *Fabiana* imbricata Ruiz & Pav. shrublands.

Two of these sites were postfire (North and South sites) and the third (Control site) was an unburned grassland similar in vegetation, soil, and topography to the postfire sites. The South site is influenced by the nearness of a road, which constitutes a corridor for exotic species.

The peak-season foliar cover was measured by species in individual plots (18 by site) located in fixed transects (3 by site) from 1999 to 2007 (9 years) in the postfire sites and from 1999 to 2017 (18 years) in the control site. From these data we calculated richness, diversity and evenness of the three communities.

Natural disturbances: drought, fire and volcanic eruption

Before the 1999 first vegetation measuring a severe drought affected the region. Then a severe wildfire occurred in 1999 January affecting a big area (21477 ha, see Ghermandi *et al.* 2004) and in 2011 a volcanic eruption deposited between 30 and 0,2 mm of tephra on a very huge area (19700000 ha in Río Negro Province; Gaitán 2011, Ghermandi& Gonzalez 2012, Ghermandi *et al.,* 2015).

Climate and soil

The climate is Mediterranean and temperate with the 60% of precipitations concentrated in autumn and winter. The mean annual precipitation is 578 mm, and the mean annual temperature is 8.7º C. Strong W-NW winds blow frequently throughout the year, accentuating water

stress in summer (meteorological station of the San Ramón ranch, unpublished data). Soils are Haploxerolls with sandy-loam texture and superficial horizons containing organic matter (Gaitán *et al.,* 2004).

Weather data sets

We calculated seasonal weather from the data base of San Ramon meteorological station because we assumed that population dynamics of individual plant species, which underlie richness and diversity fluctuations, are affected by weather on a finer temporal scale than captured by annual values (Adler and HilleRisLambers 2008).

Data analysis

Vegetation monitoring began in 1999. Two recently burned sites and an unburned site were evaluated. Burned sites (North and South sites) were monitored until 2007 and unburned (Control) until the year 2017. In July 2011 a volcanic eruption occurred and from that year the unburned site represents a post-eruption site. Therefore, the data collection allowed to monitor the dynamics of the vegetation in three situations, control, post-fire (two sites), and post-eruption, where the Control and post-eruption sites are the same site in different periods.

The experimental design generated data with a hierarchical structure: observations nested in points (repeated measures) nested in sites. Thus, both the cover and the richness were analyzed with linear mixed-effects models considering the point as a random effect (random intercept model). The models included variance functions and the temporal correlation was modeled with an auto-regressive structure of mobile windows (ARMA). The fixed-effects of the models included time, disturbance condition, precipitation and temperature occurred during winter and spring, and interactions. Interactions analyzed were disturbance x time (to evaluate if temporal patterns differ among disturbance conditions) and the double-interactions between precipitation and temperature (to evaluate, for example, if the effect of spring temperature depends on whether winter was rainy).

Results

Cover

– Control

  The study began (1999) with an average coverage of 55%, which, on average and discounting the effects of climate, grew at an annual rate of 1.5% until 2010.

– Post fire

  After the fire both sites burned had a cover of ≈ 33% (between 20 and 25% less than the control), which, discounting the effect of the climate, increased in both sites at average rates close to 2% per year. However, the trends of temporal change were not significantly different from that of control.

– Post eruption

  Immediately after the eruption the control site had 57% cover. This represented a reduction of 10%, since the previous year the cover was 67%. Unlike control and burned sites, coverage remained almost constant after the eruption (0.3% / year increase).

– Weather
The winter and spring rains had a positive effect on vegetation cover (0.04 and 0.07% per mm, respectively). Positive interaction between spring and winter temperatures was found. This means that the coverage was higher in warm springs preceded by warm winters. In particular, when the winters were cold the spring temperature affected the cover. The spring temperature also benefited the cover when it was preceded by wet winters.

Richness
– Control
The study began (1999) with an average richness of 8 species. Eleven years later (year 2010), that is, before the eruption, it was 10 species. This implied that, discounting the effects of the weather, richness increased significantly during this period at an average annual rate of 0.3 species.
– Post fire
After the fire, the number of species of the burned sites was significantly higher than that of the control (9 and 11 species in each site). In addition, unlike the control, between 1999 and 2007 both sites decreased their richness at an average rate of between 0.05 and 0.25 species per year.
– Post eruption
After the eruption, the control site had, on average, 6 species. This means that the disturbance eliminated almost 3 species (the previous year the average richness was almost 9 species). After the volcanic event, the richness increased to an average rim of 0.7, differentiating significantly from the pre-eruption trend and from the post-fire sites.
– Weather
Precipitation benefited richness. In the winter, on average, richness increased by 0.01 species per mm of rain, and in the spring by 0.03 species per mm. The temperature of spring increased the richness and this effect was higher when the temperatures of winters were higher (positive interaction).

Preliminary conclusions
The climate affected similarly the cover and richness. Both the rains and the temperature had a positive effect, and the effect of the spring temperature depended on the winter temperature. In contrast, the cover and richness were affected differently by the type of disturbance. After the fire the cover was increasing in time and the richness was decreasing. In contrast, while the cover remained relatively constant post-eruption, the richness increased.

Flood pulsesand phytoplankton diversity in lakes of the Pantanal of Nhecolandia (Brazil)

Deborah C.L. Kufner[1], Pedro V. Eisenlohr[2], Alessandra Giani[1]*

[1]Department of Botany, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil
[2]Universidade do Estado de Mato Grosso, Alta Floresta, MT, Brazil
[*]E-mail: agiani@ufmg.br

Keywords: alfa diversity, beta diversity, wetland, inundation

The Pantanal is one of the largest continuous wetland on the planet, a mosaic of aquatic ecosystems with a rich biodiversity, characterized by a flood pulse followed by a period of flow and drought that occur every year at varying intensities. Although it is an ecosystem of worldwide ecological importance, just few studies were performed to date on to the ecology of phytoplankton in the thousands of lakes that make up the plain. The purpose of the present study was to measure alpha and beta diversity of the phytoplankton community as a function of inundation pulses and to evaluate species distribution according to 31 measured limnological variables. Our hypotheses were that less distant lakes would show higher similarity of species composition and that the hydrological level would have an effect of the similarity patterns. Samples were taken in 14 lakes located in the sub-region Nhecolândia, in the Pantanal of Mato Grosso do Sul (Brazil), in three distinct periods: flood, transition period and low water. The environmental variables demonstrated strong seasonality. Shannon and Simpson indexes revealed high alfa diversity, but the diversity profiles showed that no lake was consistently more diverse than other. Discriminant correspondence analysis attested the high beta diversity of the phytoplankton community of these ponds, and the dry period had the highest turnover of species when most recorded species changed. Redundancy analysis revealed that the distance between the ponds was not a predictor of species distribution, and accounted for only 1% of the distribution during the flood period. Among the physical and chemical variables, total phosphorus and chloride gave the best response of species distribution during the flood period (33% of explanation), phosphorus was the only significant predictor during the transition period (4%) and, finally, water temperature and nitrite were the main predictors during the dry season (12%). Even though many variables were assessed in this work, our results suggest that particular environmental or biological factors not considered in this study may have played a major role in the distribution of the phytoplankton species in the Pantanal of Nhecolândia. Further investigations are needed to better explain the changes observed in the phytoplankton community in this rapid changing environment.

Effects of habitat-forming species on meiofauna assemblages in harbour areas

Ferrante Grasselli[1*], *Costantini Federica*[1,2,3], *Mancuso Francesco Paolo*[1], *Bartolini Giada*[1], *Colangelo Marina Antonia*[1,2,3]

[1]Dipartimento di Scienze Biologiche, Geologiche e Ambientali (BiGeA), University of Bologna, Ravenna, Italy
[2]Centro Interdipartimentale di Ricerca per le Scienze Ambientali (CIRSA), University of Bologna, Ravenna, Italy
[3]Consorzio Nazionale Interuniversitario per le Scienze del Mare (CoNISMa), Roma, Italy
[*]E-mail: ferrante.grasselli2@unibo.it

Keywords: benthic community, mussel beds, green-engineering, artificial substrate, intertidal

As a consequence of coastal urbanisation, the sprawl of artificial structures is increasing. These structures replace the natural habitats modifying the ecosystem. Green engineering – that aim to include ecological principles in the design of infrastructures – can help to enhance the ecological value of these "novel" coastal ecosystems creating habitat more suitable to a wider number of organisms. However, such approach could be successfully applied only after an in-depth knowledge of the associated benthic communities.

Ravenna harbour is a clear example of coastal urbanisation, and it is characterised by a variety of artificial substrates. These substrates are almost entirely covered by mussels that represent the main habitat-forming species. Moreover, mussel beds provide a secondary substrate for associated communities including rich meiofauna assemblages. Despite the functional and ecological importance of meiofauna (Schratzberger and Ingels 2018), few studies have focused on the influence of artificial structures on the diversity of these assemblages. This work aims to understand how the features of the artificial structures (primary substrate) affect the spatial-temporal aggregation of mussels (secondary substrate) and, consequently, their associated meiofauna to obtain the knowledges necessary to implement the green engineering solutions in harbour environment.

We sampled the mussel beds and associated meiofauna in the intertidal zone from two types of artificial substrata (rock boulders *vs.* concrete seawalls) at the two jetties of the harbour (North *vs.* South) in three different times. The analysis of the structural complexity of the mussel beds (*e.g.* abundance, mean length of valve, bio-volume) and the taxonomic assessment of the meiofauna showed: 1) mussels more abundant and forming a thicker bed on concrete seawalls and, reversely, meiofauna assemblages more diverse and richer on rock boulders; 2) between the two jetties, mussel beds more different, particularly in terms of mean length of valves, while the associated meiofauna resulted more similar; and 3) a negative effect of bio-volume of the mussels on meiofauna assemblages that resulted poorer and simpler at higher values of bio-volume. Finally, we observed a temporal variability related to the biological life cycle of both meiofauna organisms and mussels.

This study highlighted that mussels, as habitat-forming species, and meiofauna, as associated assemblages, respond differently at spatial and temporal scales to the type of artificial structures. Moreover, the reversed pattern observed between meiofauna and mussels – imput-

able to food and space competitions, suspension-feeding of these bivalves on infauna larvae and anoxic periods provided by the mussels – probably outclasses the positive effects of increasing in niches availability and refugia provided by this habitat-forming species. Considering that nowadays most common green engineering solutions aim to increase habitat complexity incorporating topographic microhabitats or seeding habitat-forming taxa (Firth et al. 2014, Strain et al. 2018), such procedures should take into account the complexity of the substrate carefully and consider the biological characteristics of all the taxa involved.

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Hidden Biodiversity in freshwater bodies: Trichoptera

Bruna Gumiero[1*], *Serena Perego*[2], *Marco Valle*[2], *Oscar Ludovici*[2]

[1]Department of BIGEA, University of Bologna, Bologna, Italy
[2]Museo Civico di Scienze Naturali "E. Caffi" sezione Zoologia
[*]E-mail: bruna.gumiero@unibo.it

Keywords: aquatic macroivertebrate communities, marginal ecosystems, HDWS

Aquatic macroinvertebrate communities perform a variety of functions in freshwater food webs and provide essential ecosystem services by accelerating organic matter decomposition. Benthic invertebrates are estimated to process 20–73% of riparian leaf-litter inputs to headwater streams. Moreover they supply food for both aquatic and terrestrial vertebrate consumers.

On the other hand watercourses are intensively managed than human-driven water stress (HDWS), that differs from naturally-occurring water stress, causing strong alteration both in structure and function of the community. However the community of freshwater macroinvertebrates, even if they are interested by an increasing effort of sampling in the bio-monitoring activities, their knowledge at the species level is decreasing, at least in Italy. The main reasons are: first because often the determination at family level is sufficient in bio-monitoring and the genus or groups of species are rarely required, than because the morphological approach in taxonomy was losing interest in the past two decades. This leads to the paradox that the most sampled invertebrate community is probably the least known as species composition.

As the trichoptera is one of the most important order of freshwater insects, the aim of this work is to increase the knowledge of this biocoenosis starting from one case study in the High Apennines of Modena. The study area has been chosen because it is not very much investigated and because of the high diversity of freshwater ecosystems. In this study one stream, one spring, one peat bog and one high altitude pond were investigated. To determine species level, adults sampled with light traps were used. 5790 individuals were collected and 14 families, 32 genera and 72 species were identified. Of which 17 are new reports for Emilia Romagna and 23 are on the Swiss red list. The ecosystem with the largest number of new reports (9 species) and species belonging to the red list (12) is the Ospitale stream included all those belonging to the critical risk category (4 species) and 4 of 6 species considered threatened. These results underscore the important role of high mountain stream ecosystems for this insect order protection with such a functional key role within the whole community. Moreover this study underline the high value in terms of biodiversity of marginal and apparently irrilevant small water bodies like igropetric spring where we collected 31 species of Thricoptera. From this emerges the urgency of protecting such ecosystems.

Ecological and evolutionary changes shape future phytoplankton communities

Giannina S.I. Hattich[1], Luisa Listmann[2], Christian Pansch[3], Thorsten B.H. Reusch[2], Birte Matthiessen[1]*

[1]GEOMAR Helmholtz Centre for Ocean Research Kiel, Evolutionary Ecology of Marine Fishes, Kiel, Germany
[2]GEOMAR Helmholtz Centre for Ocean Research Kiel, Experimental Ecology (Foodwebs), Kiel, Germany
[3]GEOMAR Helmholtz Centre for Ocean Research Kiel, Experimental Ecology (Benthic Ecology), Kiel, Germany
[*]E-mail: ghattich@geomar.de

Keywords: adaptation, biodiversity ecosystem functioning, community change, community property, eco-evolutionary processes, environmental change, relative importance, ocean acidification

Evolutionry and ecological processes, occur on similar time scale. Consequently, predictions of total phytoplankton community change in response to ongoing climate change require quantifying the relative importance of ecological and evolutionary contributions. Evolutionary changes are reflected in altered genotype or allele frequencies within species, ecological changes are manifested in altered species composition respectively. In phytoplankton, the assessment of the relative importance of ecological and evolutionary change is methodologically limited, because existing numerical partitioning metrics are constrained by the impracticable requirement to measure frequency shifts and/or trait changes of genotypes in a community.

As an alternative we developed an experimental protocol, which does not require to determine genotype frequency and genotype trait changes. Rather the relative contributions of ecological and evolutionary changes to total community changes are quantified experimentally. Specifically, exposing a phytoplankton community consisting of each nine genotypes of a coccolithophore and a diatom over 185 asexual generations to ambient and high CO_2 concentrations allowed for changes in species and genotype frequency. The relative importance of these ecological vs. evolutionary changes for total community changes was assessed after short-, mid- and longer-term (until 50, 105 and >105 generations, respectively) by excluding either the species or genotype sorting, and measuring the resulting difference in community response.

We found that mid- and short-term total changes significantly depended on the CO_2 concentration and could be largely attributed to ecological changes. However, at mid- compared to short-term, the relative contribution of evolution increased. Over longer-terms community abundance increased while mean cell size decreased, irrespective of the CO_2 environment.

In conclusion, future phytoplankton communities and the therein arising functional changes depend on both, ecology and evolution. Our example also shows that the particular contributions of ecology and evolution vary temporally.

Are there signatures of microbial community compositions in historical and prehistorical soils? – 16s-rna soil profilings from prehistoric hill settlements and selected archeological excavation sites of Thuringia (Germany)

J. Michael Köhler[1], Franziska Kalensee[1], P. Mike Günther[1], Tim Schüler[2], Jialan Cao[1]*

[1]Techn. Univ. Ilmenau, Institute for Micro- und Nanotechnologies / Institute for Chemistry and Microreaction Technology, Dept. Phys. Chem. and Microreaction Technology, Ilmenau, Germany
[2]Thüringer Landesamt für Denkmalpflege und Archäologie, Weimar, Germany
[*]E-Mail: michael.koehler@tu-ilmenau.de

Recent investigations have shown that the composition of soil bacterial communities can be influenced by the historical or prehistorical use of an area [1]. Significant differences in the ratios of abundant types as well as the appearance of less-abundant types have been found inside and outside urns from iron-age burials [2]. These observations suggest the question, if early anthropogenic activities of places might be reflected by the formation of signatures in the composition of soil bacterial communities.

Here, the frequencies of less-abundant soil bacteria types of 30 surface soil samples from six prehistoric hill settlements and from four archeological excavation sites have been investigated. The selection of places included settlement areas on lime stone hills of northern and eastern Thuringia, a basalt hill settlement of South Thuringia and excavation samples from two medieval cities and from ancient open area burial places.

Beside the fact that some types and type combinations have been found in one area only, it was observed that other types appear in two or several places, but are absent in the other places. The coincidence of detection of low-abundant types can not only be explained by the geological situation or soil type. It is possible to distinguish between rare-type combinations which are related to similar soil character and combinations related to places with different soil character. Thus, the appearance of certain low-abundant types on a few places suggests the existence of signatures in the soil bacteria composition which could be caused by the historical use of a place. These can be interpreted as an ecological "long-term memory effect" of early local anthropogenic activities.

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How mountain forests are changing: Resurvey of historical vegetation data in the Northern Apennines (Italy)

Chiara Lelli[1], Juri Nascimbene[1], Davide Alberti[2], Nevio Agostini[2], Alessandro Chiarucci[1]*

[1]Department of Biological, Geological and Environmental Sciences, Alma Mater Studiorum University of Bologna, Via Irnerio 42, 40126 Bologna, Italy
[2]Parco Nazionale Foreste Casentinesi, Monte Falterona e Campigna, via Guido Brocchi 7, 52015 Pratovecchio, Arezzo, Italy
[*]E-mail: chiara.lelli7@unibo.it

Keywords: beta diversity partitioning, chestnut forests, European beech forests, forest abandonment, mountain forests, oak forests, Pietro Zangheri, species composition, species richness

Question: To what extent have the plant species assemblages of mountain forests changed during the past 60-80 years?

Location: Northern Apennines, Italy

Methods: In 2018, we resampled 22 historical vegetation plots recorded between 1934 and 1961 in three main forest types: i) European beech forests, ii) chestnut forests, and iii) oak forests. At present, these data are among the oldest vegetation plots available at European level for resurvey studies. Three replicates for each original plot were compared with the original data, in terms of forest structure, plant species richness and composition. To assess changes in species composition we ran PERMANOVA, NMDS ordination based on Bray-Curtis distance and beta diversity partitioning. Ellenberg indicator values were associated to each species to explore ecological changes in the assemblages.

Results: The final data set consisted of 88 plots (22 original and 66 resampled plots) and 366 plant species. All the sampled forests were originally managed, while currently almost all the sites are under abandonment. Species richness decreased in the herb and shrub layer, while increased in the tree layer. Species composition significantly differed between original and newly recorded plots, with changes mostly due to the replacement of light-demanding species with more shade-tolerant ones. Overall, forests are getting taller and darker. Chestnut and oak forests reached a more mixed composition as compared to the original plots, including several tree species typical of mixed-broadleaved forests.

Conclusions: Abandonment of mountain forests resulted in structural and compositional changes that would imply in a relatively short period the loss of cultural habitats, like chestnut orchards, as indicated by the increasing mixture in species composition of chestnut and oak forests, which are converging into mixed-broadleaved forests. However, these changes may be also the base for the recovery of natural dynamics and biodiversity in a broader spatio-temporal perspective.

Dynamics of environmental DNA explain community biodiversity in terrestrial ecosystems

Stefano Mazzoleni

Dept. Agricultural Sciences – University of Napoli Federico II, Laboratory of Applied Ecology and System Dynamics Modelling, Portici, Italy
www.ecoap.unina.it
E-mail: stefano.mazzoleni@unina.it

Biodiversity may be related to either accumulation or removal of DNA in the soil. In terrestrial ecosystems, high biodiversity levels are found in all environments where fragments of DNA produced by litter decomposition may accumulate in the soil, whereas mono-specific stands occur in all conditions of either limited accumulation or efficient removal.

This new concept has been demonstrated by both theoretical mathematical modelling and experimental work.

Species-specific inhibition is demonstrated on seedling root growth of several species by their own decomposed litter, while both mixed and heterologous litter materials produce humus which is fertile for all plants. The mechanism beyond such observations is the effect of extracellular DNA released by the decomposition process.

The general occurrence of plant-soil negative feedback both in natural conditions and agricultural crops can be explained by this new functional role of environmental DNA.

Metacommunities in dynamic landscapes

Gian Marco Palamara[1,2*], *Charles Novaes de Santana*[2,3,4], *Alejandro Rozenfeld*[2,5], *Carlos Melián*[2]

[1]Department of System Analysis, Integrated Assessment and Modeling, EAWAG, Dübendorf, CH
[2]Department of Fish Ecology and Evolution, EAWAG, Kastanienbaum, CH
[3]Department of Landscape Ecology, WSL, Birmensdorf, CH
[4]Group of Landscape Ecology, Department of Environmental Systems Science, ETHZ, Zurich, CH
[5]CONICET-CIFICEN-INTELYMEC, University of the Center of Buenos Aires, Argentina
[*]E-mail: gianmarco.palamara@eawag.ch

Keywords: landscape ecology, seasonality, migration, speciation, biodiversity

Habitat change, due to both human and non-human factors, is one of the main drivers of biodiversity changes at different spatiotemporal scales. Experiments, theory and field data have shown how landscape connectivity, measured as the maximum distance among connected sites in a static landscape, affects local (alpha) and regional (gamma) diversity. Whether species richness increases or decreases with the connectivity of a static landscape, the effect of landscape dynamics on biodiversity remains poorly explored and yet, a unified theoretical framework to describe such dynamical changes is lacking. In this talk, I will show how to extend metacommunity theory, classically used to describe biodiversity in static landscapes, to include dynamical changes in landscape connectivity. I will show how including periodic fluctuations in landscape connectivity allow alternate processes of migration and speciation driving patterns of biodiversity that consistently differ from the patterns predicted by metacommunity theory in static landscapes. This novel theoretical framework improves our mechanistic understanding of biodiversity dynamics and provides new testable predictions about species diversity in rapidly changing landscapes.

Using modelling to investigate how below-ground interactions drive diversity, resilience and evolution of plant communities

Michael Renton[1,2*], *Elizabeth Trevenen*[1]

[1]School of Biological Sciences, The University of Western Australia, Perth, Australia
[2]School of Agriculture and Environment, The University of Western Australia, Crawley, WA, Australia
[*]E-mail: michael.renton@uwa.edu.au

Keywords: cellular automaton, community ecology, ecological strategy, functional diversity, functional–structural model, simulation, plant-soil feedback, plant interactions, individual-based model

Different plant species grow together in communities with varying levels of diversity. Some highly diverse plant communities, such as the heathland communities in Mediterranean ecosystems around the world, exhibit relatively high levels of species diversity, but relatively low apparent levels of diversity in above-ground functional traits. The main ecological constraints in these communities operate below-ground, with limited water and soil nutrients acting as the main stressors. Plants in these communities have evolved a range of specialised strategies for coping with these below-ground constraints, including a variety of root structures, mycorrhizal associations, and nutrient mining mechanisms based on organic acid exudation. These communities are threatened by changing climates, increasing drought, and anthropogenic disturbance due to mining, agriculture and urban expansion. To help predict, manage, conserve and restore these plant communities, we need to understand how these below-ground factors might result in interactions that drive and maintain community diversity and resilience. As the ecological and evolutionary processes involved play out over long time frames that cannot be fully addressed with empirical methods, simulation modelling can play a valuable role. We used cellular automata simulation (Fig. 1) to explore how below-ground plant interactions would influence long-term community diversity, based on growth data obtained from glass-house experiments on plants from the hyper-diverse Kwongan heathlands of Western Australia. We then extended this work to investigate how different network architectures of hetero- and homo-specific plant interactions would influence long-term diversity, resilience and the success of different post-mining restoration strategies. We also combined a functional-structural model (Fig. 2) with evolutionary algorithms to predict how different root architectural development strategies and levels of phenotypic plasticity evolve in different environmental conditions. This approach is now being extended to look at plant community diversity, species co-existence and speciation.

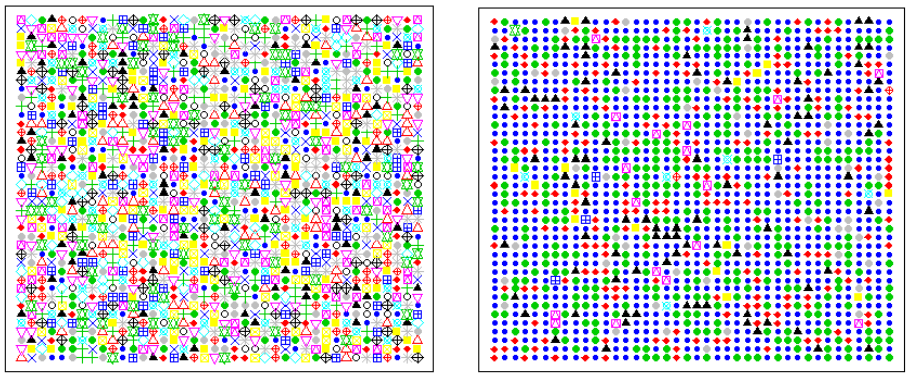

Figure 1. Cellular automata simulations of plant communities with varying levels of diversity

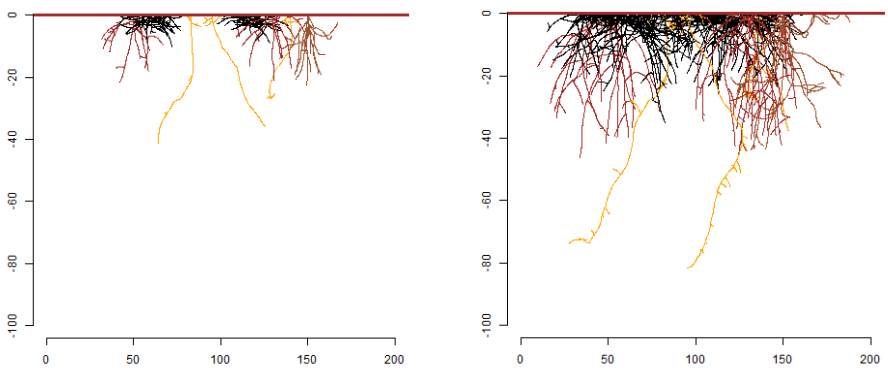

Figure 2. Functional-structural model of root structures in plant community developing over time

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Context-dependent response of the trait-related flowering pattern in sub-Mediterranean grasslands

Federico Maria Tardella[1*], *Andrea Catorci*[1]

[1]School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy
[*]E-mail: dtfederico.tardella@unicam.it

Keywords: phenology, resource acquisition, productivity gradient, temporal niche fluctuation

The timing of flowering is a key component of community assembly, being critical to competition for resources or avoidance of stress. In grasslands, the functional differentiation of species inside the community drives the flowering pattern, so that each phenological phase relates to a specific set of functional traits. Although the temporal dimension is an important factor in determining species assemblages, how plant traits respond to the heterogeneity of resource availability has been identified mostly through observations of spatial variations. To understand the role of temporal variation of resources in the species assemblage processes, we performed a trait-based phenological study in sub-Mediterranean grasslands (central Apennines). We counted flowering shoots of species of three plant communities along a productivity gradient in 1 m × 1 m plots, during the growing season. We calculated the mean proportions of flowering shoots of species sharing traits related to resource acquisition and stress tolerance and analysed their relations with soil temperature, soil humidity, and canopy height, comparing their temporal patterns using indicator species analysis, redundancy analysis, variation partitioning, and generalized linear modeling.

Our results highlighted that the temporal gradient, which synthesizes the variation trend of the environmental conditions and vegetation structure of the grassland communities during the growing season, is a major factor in determining the trait-based flowering pattern. In the early flowering phases, there is a predominance of species with strategies of slow resource acquisition and storage but rapid growth rate, while in the periods with optimal environmental conditions, the blooming species are the ones with strategies of slow growth rate and more efficient resource acquisition, conservation, and use. No common patterns emerged among plant communities for the late flowering species from mid-summer to autumn.

We also observed that the shift in soil temperature, soil relative humidity and canopy height among communities reflected a modification over time of the flowering expression of some traits, such as leaf anatomy and persistence, type of storage organ, and vertical space occupation. Harsh conditions filter species with resource-retaining strategies, drought resistance, and avoidance ability, whereas in productive conditions, competition for light promotes the coexistence of species with dissimilar resource acquisition strategies on a fine spatial scale. This seems to substantiate the hypothesis that the functional response to the seasonal variation in environmental conditions largely retraces the modifications, at the community level, of the functional composition across spatial resource gradients.

Our results show that the amplitude of the environmental fluctuations influences the type and number of strategies positively filtered by the system. Environmental fluctuations in time influenced the trait-related flowering pattern more in highly productive conditions (having the

highest differences in soil relative humidity and canopy height between spring and summer) than in less productive ones. In fact, in productive conditions, the phenological responses to environmental fluctuations are mostly related to traits that limit competition with dominant species by spatial niche segregation (vegetative propagation, vertical space occupation, and plant height) and to species that fit their life cycle to the variation of environmental conditions, through different life and leaf span. Conversely, such traits showed weaker trends in the driest community, where the flowering pattern was less dependent on temporal fluctuations of environmental conditions. These findings are consistent with the fluctuation niche theory, based on the different growth/phenological response of species to the variation of resource availability over time.

Plant strategies and functional diversity along communities successional gradients in alpine environment

Magda Zanzottera[1,2*], *Marco Caccianiga*[2], *Michele Dalle Fratte*[1], *Bruno E.L. Cerabolini*[1]

[1]Department of Theoretical and Applied Sciences (DiSTA), University of Insubria, via Dunant 3, 21100 Varese
[2]Department di Biosciences (DBS), University of Milano, via Celoria 26, 20133 Milano
[*]E-mail: magda.zanzottera@gmail.com

Keywords: CSR, plant functional traits, Natura 2000, habitat

Plant traits are currently widely applied to many research fields, as they provide information about multiple aspects of ecosystem functioning and services. Among plant traits, leaf area (LA), specific leaf area (SLA) and leaf dry matter content (LDMC) are the most widely available for all species. Different methods can represent traits variation within plant communities but it is still not clear which one is preferable. Functional diversity (FD), for instance, can be expressed by many components such as functional richness (FRich), evenness (FEve) and divergence (FDiv) (Mason et al. 2005). Also CSR plant strategies represent the trade-offs between LA, SLA and LDMC, through which they are computed (Pierce et al. 2017). Our goal was to test the discriminating capacity of these multi-traits FD indices and CSR plant strategies along a successional gradient of alpine plant communities included in habitats protected by the European Directive 92/43/EEC: alpine heaths, grasslands, screes and snow-patch communities. Indeed, alpine ecosystems are an ideal testing-ground for functional characterization of plant communities, having a high species diversity and a simple vertical structure (they are mainly characterized by a single herbaceous-shrubby layer). We based our analysis on 654 phytosociological *relevés* corresponding to 12 alpine sub-habitats (Brusa et al. 2017) and measured the values of LA, SLA and LDMC for the species detected. For each *relevé* we calculated FRich, FEve and FDiv, as well as the community weighted mean (CWM) of plant strategies C-, S-, and R- scores (following the mass-ratio hypothesis; Grime 1998). For each plant strategy score and FD index, we applied the Rosner test to identify and remove outliers *relevés* and the Shapiro-Wilk normality test to find the best transformation that normalized data, then we used ANOVA with *post-hoc* comparison to identify differences among sub-habitats. Plant strategies showed more recognizable patterns compared to components of FD, especially along the S- and R- selection gradients, providing relevance to the importance of the leaf economics spectrum in high elevation environments. In details, snow-patches as well as screes communities had higher values of R- scores, respectively attributable to climatic and mechanical disturbance, whereas heaths and grasslands communities had higher S- scores values according to their successional stage (i.e. climax communities characterized by woody species). C- selection gradient was less discriminative, even if a clear segregation between sub-habitats at the extremes of the successional gradient were still present. The pattern previously discussed was only partially reflected by FRich, indeed it was lower for screes but also for heaths communities, and higher for grasslands. FEve was similar among all sub-habitats confirming the high suitability of alpine vegetation to investigate plant traits variation. FDiv, instead, was the less discriminative index. Further analyses are necessary

to gain a better understanding of relations between plant strategies and FD; specifically our findings suggest that it could be considered the application of FD indices on plant functional types or even on plant strategies.

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One ring to rule them all: A killer fungus fosters plant and microbial diversity in grassland

Maurizio Zotti[1], Francesca De Filippis[1,3], Gaspare cesarano[1], Danilo Ercolini[1,3], Stefano Mazzoleni[1,3], Marina Allegrezza[2], Francesco Giannino[1], Giuliano Bonanomi[1,3]*

[1]Department of Agricultural Science, Federico II university of Naples, Portici (NA), Italy
[2]Department of Environmental sciences and plant production, Marche Polytechnic University, Ancona (AN), Italy
[3]Task Force on Microbiome Studies, University of Naples Federico II, Naples, Italy
[*]E-mail: maurizio.zotti@unina.it

Keywords: plant–soil interaction, fairy rings, *Agaricus campestris*, Basidiomycota, next generation sequencing

Several ecological models explained pattern of species coexistence in grasslands plant communities. Actually, is acknowledged that plants species coexistence largely depends by the interactions with soil microbial community. The variations of soil microbiome modulate plant competitive relations resulting in pattern of monodominance or, alternatively, in diversity enhancement. In our work we studied the development of a dominant killer fungus and how it affects species richness and composition in plant and microbiological communities of a Mediterranean calcareous grassland. We examined the effect of the fungal saprotrophs *Agaricus campestris* L. in soil and its legacy in soil experienced its passage. This pattern is commonly known as "Fairy rings" given the characteristic ring-shaped changes of plant coloration in grasslands. In our surveys we monitored plant species composition in six zones across fairy rings. We identified zones across fairy rings as: (OUT) in external grassland previously to the development of the fairy ring; (FF) in area experiencing the passage of fungus that is well recognized by the presence of dead or poor vegetation, (BELT) an internal area with increased flush of vegetation, and three consecutive areas at a distance on one, two and five meters from the BELT zone (1 m, 2 m and 5 m). In each of the six zones we performed next generation sequencing analysis to assess bacterial and fungal communities structure and composition.

The results of the surveys showed that, both, plants, bacterial and fungal communities dramatically change in species abundances and equitability after the passage of *A. campestris*. Furtherly, multivariate analysis showed a marked change in species composition in the communities analysed. Specifically, in plant community is assessed a sudden increase of opportunistic species in BELT zones followed by gradual plant species shift in the internal zones. Finally, a restoration of plant community condition similar to that of OUT zones was recorded in the 5 m zone. Species composition changes are also well appreciable in bacterial community with a shift-restoration process similar to that of plant community. On the other side, is less appreciable a similar pattern for fungal communities with a segregation of FF zones with respect to the other zones. Heat plot analysis showed specific response of species abundance in correspondence of each fairy rings zones. Particularly is well appreciable an association between the plant *Knautia collina*, the bacterial genus *Bulkolderia* and the fungal genus *Trichoderma* in the FF zones. In the other zones is well assessed the rise of mycophagous species of the genera *Chitinophagacea* and *Actinoallomurus* among bacteria. Taken together the results indicate that *A. campestris* act as an ecosystem engineer, promoting plant and microbial species coexistence.

Island biogeography

Microclimate variability significantly affects low altitude plant species composition in an oceanic island

Md Lokman Hossain[1,4,5], Carl Beierkuhnlein[2,4], Anke Jentsch[3], Varela Fernández de Arcaya J.N.[4], Mst. Umme Salma Nila[4], Jianfeng Li[1]*

[1]Department of Geography, Hong Kong Baptist University, Kowloon Tong, Hong Kong
[2]Department of Biogeography, University of Bayreuth, Bayreuth, Germany
[3]Department of Disturbance Ecology, University of Bayreuth, Bayreuth, Germany
[4]Global Change Ecology, International Elite Study Programme, University of Bayreuth, Bayreuth, Germany
[5]Department of Environmental Protection Technology, Germany University Bangladesh, Gazipur, Bangladesh
[*]E-mail: lokmanbbd@gmail.com; 18481191@life.hkbu.edu.hk

Keywords: altitudinal gradient, climate change, island biogeography, La Palma, species distribution

Plant species distribution on oceanic islands has been a subject of considerable interest to ecologists and is gaining increased importance in the face of climate change (Beierkuhnlein and Irl 2017). Species distribution at high altitude are primarily regulated by series of environmental and ecological factors (Irl et al. 2017). However, environmental changes may drive the low altitude species to upward shift or cause species extinction (Harter et al. 2015). Little is known about the influence of micro-climate variability on plant species composition at low altitude of oceanic islands. In attempting to understand which environmental drivers significantly affect low altitude species composition, we considered five altitudinal gradients from two contrasting climate zones (northeast and northwest) of La Palma Island. La Palma is an oceanic-volcanic island located off the coast of southern Morocco. This island is 47 km long and 29 km wide with substantial elevation (2426 m a.s.l.). We used the hiking track and collected data at every 100 m altitude between 50 m and 450 m from both the macro-climate zones. We recorded perennial plant species within the 5 m X 5 m plot, scored the species and measured soil salinity of 121 plots. We used redundancy analysis in order to understand the relationship of sampled species composition with their environmental variables. We used boxplots to display the occurence of species in relation to salinity. In order to identify differences in the variation of the species composition, we used beta diversity, which showed the dissimilarities between different studied variables, macroclimate and salinity level. We found that precipitation and altitudes have highly significant ($p=0.001$) effects on species composition. Temperature has also significant ($p=0.007$) influence on species composition, however, slope and aspect have no effect. The relationships of species composition with soil salinity were also significant ($p=0.039$). We found that species composition in the northwestern zone are more explained by altitude and precipitation, whereas, species in the northeastern zone are influened by salinity, aspect and temperature (*Fig. 1*). The study revealed that species composition above the saline zone in the northeastern part are more variable (higher tercile shows higher variation) compared with northwestern part (no variation among all terciles)

(*Fig. 2*). Our study suggests that global climate change (temerature and precipitation variability) would have considerable threat to low altitude species composition in La Palma island and therefore, intensive future researches are required.

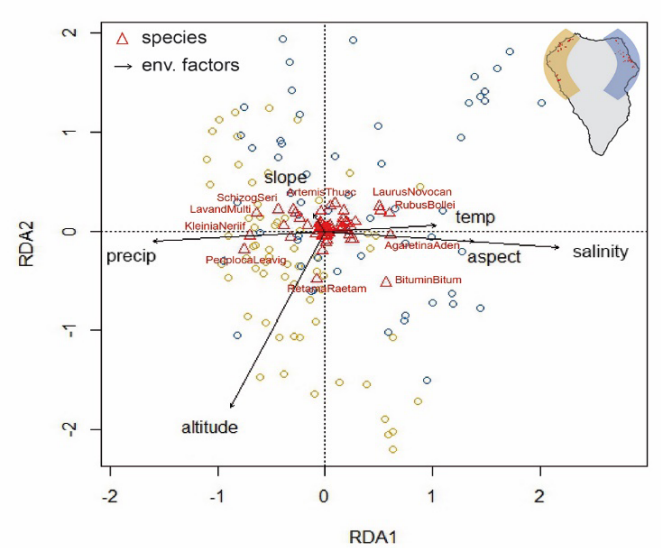

Figure 1. Redundancy analysis on species composition. Points show sites, triangles species and arrows environmental factors.

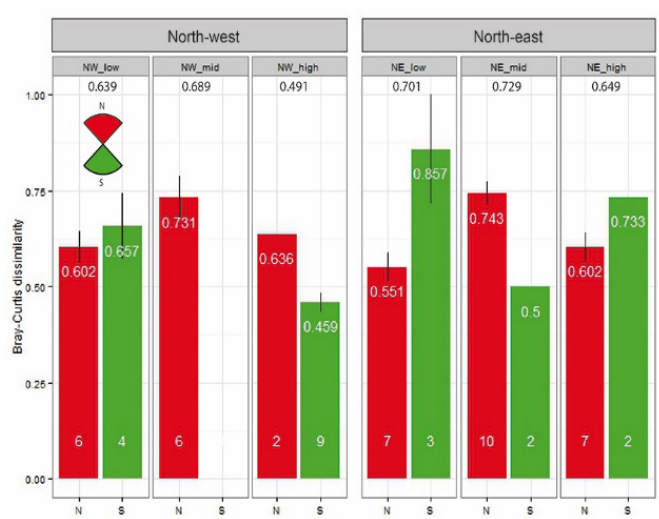

Figure 2. Beta diversity of species composition for the northwestern and northeastern climate, divided into the terciles of "low", "middle", "high" salinity, shown for the macro-climatic aspects and with their respectively mean beta diversity values.

Acknowledgments
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Ecological and cultural characteristics of coastal forest in Namhae-Gun, Korea

Dabin Kim[1], Hyunhee Kim[2], Wooseok, Kong[3]*

[1]NatureGraphy (Research Institute of Biogeographical Distribution and Diversity), 02447, Seoul, Korea
[2]University-Industry Cooperation Foundation, Kyung Hee University, Seoul, Korea
[3]Department of Geography, Kyung Hee University, Seoul, Korea University
[*]E-mail: duro900@gmail.com

Keywords: coast forest, fish shelter forest, ecological, cultural characteristics

Surrounded by the sea on three sides, the Korean Peninsula has many coastal forests along the coast. Most of these coastal forests consist of *Pinus thunbergii*, and they reduce the damage caused by coastal winds (sea breeze) or monsoon winds during winter. Namhae-gun, a research area, is an island in the southern part of the Korean Peninsula, unlike ordinary coastal forests, here consist of a variety of species, such as evergreen broadleaf, deciduous leaf, and coniferous trees, and have a multilayer forest structure. This Namhae-gun's coastal forest is called the Fish Shelter Forest (魚付林) as a traditional village forest of coast villages. Namhae-gun's Fish Shelter Forest is known to have various functions such as windbreak function of the general coastal forest mentioned above, as well as the function of preventing natural disasters such as tide and breakwater, the function that collects fish by making shade, and ecological transition zone between land, coastal and marine ecosystems. these areas have been used as a cultural space in the village, and have many values, and scenic beauty. These Namhae-gun Fish Shelter Forests appear along the coast of more than 16 places within this island, most of which were created about 300 years ago, and are the traditional way of life of our ancestors who lived together using natural environment instead of artificially harming the natural environment.

Fish Shelter Forests in Namhae-Gun can be classified into four types according to their shape, function, and the species conditions in which they are composed, and the distribution and function of each type are characterized. In particular, the distribution by type varies depending on the coast. On the east coast of Namhae-Gun, there are curve shaped coastal forest, which are composed of evergreen broadleaf and deciduous leaf trees, and along the coast of the southern adjacent coasts, the coastal forests of the common coniferous forest tend to be many. The reason why various types and forms of coastal forests are located in Namhae-gun is because of direct and indirect influences on natural and human factors such as the amount of annual Precipitation in the Namhae-gun, the average temperature, the wind direction, the status of major vegetation in nearby areas, and cultural and historical background.

The most representative of the coastal forests of Namhae-gun is Mulgeun Fish Shelter Forest, which measures about 1.6 kilometers and is shaped like a crescent moon along the coast. The created time, identified through the oldest tree is estimated at about 300 years ago. This forest is composed of 180 classification plants, and is dominated mainly by *Aphananthe aspera, Zelkova serrata* and *Celtis sinensis*. Also, rare endangered plants such as the *Celtis choseniana, Koelreuteria paniculata,* and *Chionanthus retusa* are growing. Culturally, the

forest space is currently used as a community workshop in nearby villages, and in the past, rituals were held to pray for the safety of the village and the full load of fish. Further research into the coastal forests of Namhae-gun, which have such ecologically high species diversity, environmental values and cultural and historical values, is needed and under way.

Acknowledgments
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Plant distribution and diversity in the islands area in the Korea Peninsula

Hyunhee Kim[1*], *Dabin Kim*[2], *Wooseok Kong*[3]

[1]University-Industry Cooperation Foundation, Kyung Hee University, Seoul, Korea
[2]NatureGraphy (Research Institute of Biogeographical Distribution and Diversity), Seoul, Korea
[3]Department of Geography, Kyung Hee University, Seoul, Korea
[*]E-mail: hhkim24@khu.ac.kr

Keywords: island biogeography, species diversity, plant refugia, indicator space

Isolated island areas surrounded by the sea are difficult to predict, with extreme natural environments (e.g. weather, topography, hydrology, etc.), which have very poor environmental conditions for plants to grow naturally. Nevertheless, plants that now grow native to the islands are a kind of environmental indicator species adapted to such extreme natural environments. In addition, the islands area itself is an environmental indicator space.

Located east of the Eurasian continent on the Korean Peninsula around about 3,500 islands scattered in the East Sea, South Sea and West Sea (Yellow Sea). The Korean Peninsula's islands area has some of the physical geographical features that are noticed. First, the islands of the Korean Peninsula are largely divided into islands that have been isolated from land due to rising sea levels since Pleistocene, and islands formed by volcanic activity in the Cenozoic, which has a diverse geologic historical background. Second, the Korean Peninsula Island Area is the Northern Limit Line of Southern Plants (*Camellia japonica* in Daechung Island) and the Southern Limit Line of Northern Plants (*Vaccinium uliginosum* in Jeju Island), which has great biogeographical meaningful. Third, a variety of plants are distributed as ecotone, where the climate zone changes from the temperate climate region to the cold climate region.

MacArthur and Wilson (1967) argued through their Island-Biogeography theories that the island is large and the closer it is to land, the higher the variety of species. In Korea, there are not many studies on the theory of Island-Biogeography yet. However, a recent study by Kim et al (2017). reported that Korea's islands has a high correlation between island size and sea level elevation and plant species diversity, while there is little distance effect from land. This is thought to be the result of Korean islands located on the continental shelf, not on the ocean, and the physical distance from the land is relatively not far away.

There are 4,518 species of native plants on the Korean Peninsula (Ministry of Environment, 2018) and approximately half of them are thought to be distributed in the islands. Currently, South Korea has six UNESCO biosphere reserves, two of which are islands. Islands areas are very vulnerable to environmental changes (climate change) and development pressures because of their limited plant habitate. On the contrary, the islands are isolated from land, so that there can escape a certain part of the tree disease (such as pine wilt disease) and human activity. This is very interesting in that the area of the islands can be used as a plant refugia. Therefore, the preservation of the plant in the islands area should take precedence over the land. In this study, we will discuss the diversity of species and biogeographical characteristics with raw-data of plant life in the Korean Peninsula.

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Biodiversity and ecosystem functioning

Paleoreconstruction and current state of the forest cover of Northern Eurasia

Olga Smirnova[1], Anna Geraskina[1], Alexey Aleynikov[1], Vladimir Korotkov[2]*

[1]Centre for Forest Ecology and Productivity of Russian Academy of Sciences, Moscow, Russia
[2]Yu.A. Izrael Institute of Global Climate and Ecology, Moscow, Russia
[*]E-mail: korotkovv@list.ru

Keywords: paleoreconstruction, potential vegetation, tall herb forests, key species

Detailed studies of forest vegetation, soils and the ontogenetic structure of tree populations were conducted in the large intact areas of the northern taiga (Smirnova et al., 2017). Historical and archival data on the types of nature management in the north taiga forests, as well as paleontological data on the taxonomic composition of paleo-ecosystems in the studied areas were summarized.

According paleontological data at the Late Pleistocene pasture ecosystems with forest patches of coniferous and broadleaved tree species prevailed in the area of the present-time forest regions of North Eurasia. High species diversity is maintained by key species – mega-herbivores of the mammoth complex (*Mammuthus primigenius, Coelodonta antiquitatis, Bison priscus, Equus spp., Megaloceros giganteus*, and others). Eradication of the mammoth complex to the beginning of the Holocene led to an increase in the role of tree species. Anthropogenic impacts associated with different methods of economic activity (burning, logging, slash-and-burn agriculture, and other) led to a decrease in soil fertility and diversity of tree and herb species.

Together with widespread green moss spruce(-fir) forests (association *Linnaeo borealis-Piceetum abietis* Caj., 1921) investigated in detail in this zone, a unique type of boreal tall herb forest dominated by Picea spp. and Abies sibirica and tall herb spruce-fir forests with Pinus sibirica (association *Aconito septentrionalis-Piceetum obovatae* Zaugolnova et al., 2009) was distinguished and described.

A comparison of the two types showed that old-growth tall herb forests have a full set of features characterizing long-existing and self-sustaining forests. Tall herb forests are characterized by clearly expressed gap-mosaics, full-scale ontogenetic spectra of tree populations, treefall pit-and-mound topography, high soil fertility, high species richness and species density, and a significant variety of functional groups of vascular plants and mosses. Productivity of ground vegetation of tall herb forests is 8 times higher in comparison with green moss forests. Species composition and biomass of earthworms in the soil and in the deadwood of tall herb forests are very high in comparison with poor green moss forests. Analysis of the obtained data in combination with paleontological and historical data made it possible to conclude that (1) boreal tall herb forests were spread over a significant part of European Russia and Western Siberia in prehistoric times, and 2) widespread modern green moss forests are secondary and formed as a result of anthropogenic fires and felling. The obtained data on the

composition, structure, and distribution of boreal tall herb forests allow us to consider them as an etalon of prehistoric taiga forests.

During the research, forest areas with a stable structure of tree populations, a unique species composition of ground vegetation and soil biota, fertile soils were identified. These fragments of prehistoric forests, analysis, maintenance and restoration of which in most of the boreal forests of Northern Eurasia, we consider as one of the global tasks of mankind.

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Exploring topological similarity and phylogenetic relatedness between species in food webs

Shu-mei Lai[1], Wei-chung Liu[1], Hsuan-wien Chen[2]*

[1]Institute of Statistical Science, Academia Sinica, Taiwan
[2]Department of Biological Resources, National Chiayi University, Taiwan
[*]E-mail: wliu56@gate.sinica.edu.tw

Understanding the mechanism shaping species assemblage is a fundamental goal in ecology. In the past two hypotheses have been suggested. One is the filtering hypothesis where environmental factors select for species of similar traits such that they co-occurring in similar niches. The other is the competitive exclusion hypothesis where related species are driven far part by competition such that they over-disperse across different niches. Here, we investigate the relationship between species assemblage and their phylogenetic relatedness from the network perspective by using five different ecosystems ranging from oceans to inland lakes. We quantified the similarity in species' positions in a food web and cluster them into functional groups; and from on-line databases we quantified their phylogenetic distances. We then investigated whether related species tend to under or over-disperse across different functional groups. In general, our result suggests a lack of overdispersion and therefore competition is unlikely to shape the assemblage of all five ecosystems. Such a pattern is more significant for open ecosystems than closed or isolated ones.

Consequences of intraspecific diversity shifts for phytoplankton community properties

Birte Matthiessen[1], Luisa Listmann[2], Thorsten B.H. Reusch[2], Giannina S.I. Hattich[1]*

[1]GEOMAR Helmholtz Centre for Ocean Research Kiel, Experimental ecology (Foodwebs), Kiel, Germany
[2]GEOMAR Helmholtz Centre for Ocean Research Kiel, Evolutionary Ecology of Marine Fishes, Kiel, Germany
[*]E-mail: bmatthiessen@geomar.de

Keywords: adaptation, biodiversity ecosystem functioning, intraspecific diversity, community change, community property, eco-evolutionary processes, environmental change

Selection on standing intraspecific diversity can be the starting point of evolutionary adaptation as has been demonstrated in species monocultures. Such rapid evolutionary adaptation occurs at similar time scales as ecological dynamics and thus is considered a potential important factor for species to keep pace with global environmental change. This applies in particular to microbial systems characterized by short generation times such as phytoplankton. The ecological meaning of rapid evolutionary adaptation on community functioning remains, however, open. In a collaborative effort we experimentally tested (i) whether evolutionary adaptation to increased seawater CO_2 concentration depends on the presence of other species; and (ii) couples back to the ecological level affecting the abundance of species and thus community composition. Based on the findings we investigated (iii) if changes in both intraspecific and interspecific composition propagate to altered community properties. To test these objectives we used a long-term experimental model system (~180 generations) consisting of two globally important, functionally distinct (a calcifier and a silicifier) and stably coexisting marine phytoplankton species. Each of the two species initially comprised of nine genotypes to allow for intraspecific selection and thus potential diversity shifts of genotypes.

In the short to mid-term CO_2 affected community composition by constraining the calcifier as expected. This effect resulted in a significantly declined total abundance and increased mean cell size. However, the CO2 effect disappeared after 100 generations. We found that species in this community did not adapt to increased seawater CO_2 concentration, no matter if they occurred alone or in the presence of the respective other species. Instead genotype sorting of both species was the same in all treatments. In parallel to genotype sorting the abundance of the calcifier significantly increased in the long term translating to a ten times higher total cell abundance and four fold reduced mean cell size compared to the onset.

Our results suggest that interspecifically the predominant selection factor was CO_2. Intraspecifically selection was likely driven by the experimental conditions in the first place. These were characterized by periodically recurring nutrient limitation. Genotype sorting towards a competitively superior genotype coupled to the population abundance hence to altered community composition which significantly changed community properties. Our results emphasize that intraspecific diversity shifts can have significant impacts on community properties by changing the composition of species.

Which functional traits promote dark diversity among Southeast European hoverflies (Diptera: Syrphidae)?

Marija Miličić[1,3*], *Snežana Popov*[2], *Ante Vujić*[2], *Pedro Cardoso*[3]

[1]BioSense Institute-Research Institute for Information Technologies in Biosystems, University of Novi Sad, Serbia
[2]Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia
[3]LIBRe – Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland
[*]E-mail: marija.milicic@biosense.rs

Keywords: absent species, conservation, environmental perturbations, functional characteristics, insects, Syrphids, vegetation classes

In order to better understand and try to alleviate the negative consequences of biodiversity loss, it is important to comprehend different aspects of biodiversity. Therefore, beside using the information about observed diversity, so called dark diversity could bring to light new biodiversity patterns, which were not evident when only observed diversity was investigated. Dark diversity represents portion of species that are not recorded at a particular site, but belong to its species pool, i.e. those species that are currently 'missing' from a site, but have potential to occur there (Pärtel et al. 2011).

In our study, we examine dark diversity of hoverflies, important insect pollinator group, across different vegetation types in Southeast Europe and assess which functional traits promote the absence of species from apparently suitable sites (missing species), hence promoting higher levels of hoverfly dark diversity. Dark diversity was calculated as the difference between the species pool (all species available that could potentially colonize and inhabit certain habitat) and observed diversity of each vegetation type. To establish the unique contribution of each trait to the probability of being part of dark diversity, we used Random forest (RF) regression model. Findings show that dark diversity was the lowest in Mediterranean mixed forests (33 species, 11.9%), while the highest value was in Southwest Balkan submediterranean mixed oak forests (162 species, 62.8%). Traits found to have the greatest importance in shaping the patterns of dark diversity were connected with larval food type (saproxylic larvae, phytophagous developing in bulbs and in roots), indicating that specialist species are more susceptible to contribute to the dark diversity.

Knowing which functional traits are responsible for dark diversity can help in identifying the processes causing species to be absent from their original species pool. Overall, the assessment of dark diversity enables more precise conservation prioritization, but also can contribute in identification of sites for potential restoration.

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Exploring the distribution and underlying drivers of native and non-native mussel and oyster species in harbour environment

Francesco Mugnai[1*], *Francesco Paolo Mancuso*[2], *Federica Costantini*[1,2], *Laura Airoldi*[1,2]

[1]Centro Interdipartimentale di Ricerca sulle Scienze Ambientali (CIRSA), University of Bologna, Ravenna, Italy
[2]Dipartimento di Scienze Biologiche, Geologiche e Ambientali (BIGEA), University of Bologna, Ravenna, Italy
[*]E-mail: francesco.mugnai3@unibo.it

Keywords: invasive, mytilidae, ostreidae, Ravenna, artificial structures, community

Human pressure on marine system is exponentially increasing, leading to natural habitat loss and massive sprawl of artificial structures along seafronts and offshore developments [1]. Commercial ports, dock, seawalls and marinas are examples of marine artificial habitats. Despite their artificial nature, these artificial habitats can support significant biodiversity. At the same time, current knowledge suggests that many artificial habitats tend to be characterized by low species richness and prevalence of non-native species [2,3]. The opposite trend can be found on natural rocky reefs [2,3]. The underlying drivers of these differences are not clear [4], and little is known about the distribution and dynamics of the marine native and non-native species inhabiting ports. In this study, we assessed the distribution and abundance of two native (*Mytilus galloprovincialis*, *Ostrea edulis*) and two non-native (*Xenostrobus securis*, *Crassostrea gigas*) bivalves growing on artificial seawalls along the canal port of Ravenna, and quantified the spatial-temporal distribution of their settlers. We further explored whether the distribution of adults and the spatial-temporal variability of settlers were related to variable environmental parameters along the canal port. Our results showed an increase of non-native species as the canal-port goes inland, related to higher temperatures, lower oxygen, and higher nitrate seawater concentrations. Settler abundances were correlated to the spawning windows of the different species, but not to adult abundances retrieved on the seawalls, suggesting a dominant role of post-settlement processes. Future work, using a metabarcoding approach, will be useful to identify species during the settlement stage and to explore the settlement and post-settlement colonization dynamics.

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Population sizes, life-history traits and ecological stoichiometry determine energy conversion efficiencies and material flow rates

Christian Mulder[1*], *Erminia Conti*[1]

[1]Department of Biological, Geological and Environmental Sciences, University of Catania, Catania, Italy
[*]E-mail: christian.mulder@unict.it

Keywords: ecological networks, soil food webs, invertebrates, agroecosystems, allometry, biodiversity and ecosystem functioning

Ecosystems provide habitats for species and biological communities, but are also pivotal for delivering food, fibre and biofuels, clean air and drinking water and carbon storage. The demand of goods and the restricted area available to produce such goods is basic to the conflict of using land for food production versus nature conservation. Moreover, the intensification of agricultural production has profound adverse effects on above- and belowground biodiversity with consequences for such as the provision of clean water, control of greenhouse gasses and control of pests and invasive weeds. Therefore, it is urgent to understand how land should be managed in order to achieve sustainable agricultural and natural ecosystems. Worldwide research programs have been developed that look for ways how land use may conserve or even restore biodiversity and ecosystem functioning. These strategies include sustainable transitions towards more environmentally friendly agricultural systems as well as land-use conversion from agricultural to natural ecosystems. Detrital energy and elemental flow rates are the key.

Soils and soil biodiversity are the basis of each terrestrial production system, as well as of many ecological processes and (supporting and provisioning) ecosystem services. The relationships between biodiversity and ecosystem functioning have been widely explored, but mostly these studies have focused on the effects of biodiversity change within single trophic levels. Understanding the relationship between soil biodiversity and ecosystem functioning asks for a different approach. The food-web approach is seen as suitable to analyse the biodiversity-ecosystem functioning relationship. First, because food-web descriptions embrace all trophic levels in one single framework. Second, because food-web interactions represent transfer rates of energy and matter. Therefore, as soon we are able to characterize and quantify the population dynamics of species in soil food webs, we can explicitly link these population dynamics to the transfers of materials, energy and nutrients and the resulting ecological processes. In turn, because the acquisition and processing of energy and nutrients are critical to the growth, dynamics and persistence of most populations, the way in which materials, energy and nutrients are processed in detrital soil food webs may impose a dynamic constraint on the food-web topology, structure and stability. Hence, the effect of diversity and composition on ecological processes links back to the analysis of the way in which the food-web structure of soil biota responds to human-induced changes like cattle pressure, acidification and eutrophication.

We use information of the consequences of various kinds of land use for the structure of the belowground ecological networks. These detrital soil food webs have been quantified *in*

situ in terms of population sizes and traits in combination with information regarding feeding and life-history. Our dataset includes physical, chemical and biological information of 500 sites, mostly from The Netherlands, organized over different categories regarding soil and land use. Especially the biological information is highly valuable (covering bacteria, fungi, nematodes, arthropods and oligochaetes), as it consists of complete descriptions and quantifications of the structure of these detrital soil food webs. Moreover, all the ecological networks and trait distributions are established with the same experimental techniques and computational approaches which enable clear and straightforward comparisons between land managements.

The ecology of Mediterranean gorgonian forests

Massimo Ponti[1*], *Eva Turicchia*[2], *Marco Abbiati*[2], *Carlo Cerrano*[3]

[1]Department of Biological, Geological and Environmental Sciences, University of Bologna, Ravenna, Italy
[2]Department of Cultural Heritage, University of Bologna, Ravenna, Italy
[3]Department of Life and Environmental Sciences, Polytechnic University of Marche, Ancona, Italy
[*]E-mail: massimo.ponti@unibo.it

Keywords: species interaction, suspension feeders, habitat complexity, biodiversity, coralligenous habitat

Healthy coralligenous habitats (i.e. biogenic reefs growing in dim light condition, Ballesteros, 2006) may host dense populations of gorgonians that build marine animal forests (Rossi et al., 2017). According to recent studies, these forests may increase the resilience of coralligenous habitats and to enhance the structural complexity and bioconstruction processes by favouring the settlement and development of encrusting calcareous algae and by limiting the growth of erect algae under different study conditions and in many investigated sites down to 40 m depth (Ponti et al., 2014; Ponti et al., 2018). They are also able to increase species diversity and limit the invasion of alien species (Ponti et al., 2018). Moreover, by entrapping benthic mucilaginous aggregates with their branches, gorgonians risk topical necrotic lesions but may reduce the suffocation risks for understorey organisms (Piazzi et al., 2018; Ponti et al., 2018).

Integrity of gorgonian forests, however, is threatened by fishing lines and nets, anchors and recreational divers causing mechanical damage (Bavestrello et al., 1997; Linares and Doak, 2010; Tsounis et al., 2012), suffocation by mucilaginous benthic aggregates (Mistri and Ceccherelli, 1996; Giuliani et al., 2005), invasion from non-indigenous species (Cebrian et al., 2012), and increase in water turbidity and sedimentation rates due to run-off as a result of bad land management (Mateos-Molina et al., 2015). At the same time, gorgonian forests are also heavily threatened by global climate change-related disturbances such as increased frequency of exceptional storms (Teixidó et al., 2013) and thermal anomalies (Cerrano et al., 2000; Cerrano and Bavestrello, 2008; Garrabou et al., 2009) that may induce physiological stress and increase their susceptibility to pathogens (Calvo et al., 2011; Rivetti et al., 2014). The latter, coupled with reduced food availability due to the stratification of the water column in summer, seem to lie at the basis of the gorgonian mass mortality events recorded in recent decades in the north-western Mediterranean Sea (Cerrano et al., 2000; Martin et al., 2002; Linares et al., 2005; Garrabou et al., 2009; Calvo et al., 2011; Crisci et al., 2011; Huete-Stauffer et al., 2011; Rivetti et al., 2014; Marbà et al., 2015). The crises have not spared even the most remote gorgonian forests, far from direct anthropic disturbances (Turicchia et al., 2018).

Currently, as a result of both local and global disturbances, many gorgonian forests are fragmented and considered in strong regression. Concerns for gorgonian forests loss and the related consequences (e.g. impairment of fertilisation and larval connectivity, shifts in the structure of benthic assemblages and the related ecosystem functioning) are rising. The major limitation in the conservation of these forests is the lack of knowledge on their distribution patterns and the extents of their ecological roles.

Recently, by applying a multi-source approach that combines information from scientific literature, marine citizen science projects and the so-called Web Ecological Knowledge (Di Camillo et al., 2018), a baseline on the spatial and depth distribution of the three main species that form extensive gorgonian forests in the Mediterranean Sea (*Eunicella cavolini* (Koch, 1887), *Eunicella singularis* (Esper, 1791) and *Paramuricea clavata* (Risso, 1826) was built-up (Ponti et al., 2019). That may lay the basis to implementing ecosystem-based conservation strategies and restoration projects.

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Marine Phytoplankton under control: Abiotic and biotic drivers

Elena Stanca[1*], *Alberto Basset*[1]

[1]Department of Biological and Environmental Sciences and Technologies, University of Salento, Lecce, Italy
[*]E-mail: elena.stanca@unisalento.it

Keywords: phytoplankton, drivers, biovolume, shape, zooplankton

Marine phytoplankton are a taxonomically and functionally diverse group of organisms that are key players in the most important biogeochemical cycles. Abiotic and biotic drivers can strongly influence phytoplankton biomass and the interactive effects of these parameters can affect phytoplankton structure. Phytoplankton community composition varies along a template of covarying factors, including gradients of nutrients, light, temperature, based on the physiology and life-history strategies of taxa. In addition to these bottom-up factors, there is a top-down control of zooplankton on phytoplankton. How changes of these drivers could alter the phytoplankton taxonomic and morpho-functional diversity? We hypothesize that abiotic control of phytoplankton would be more important, whereas biotic control would be less important, in this typology of water systems.

We investigate how phytoplankton taxonomic and morpho-functional compositions, e.g biomass (biovolume/L), size and shape, change across gradients of abiotic parameters, as nutrient concentrations, pH, Salinity, and biotic parameters, as zooplankton density. We analyzed temporal and spatial variation of phytoplankton features in 2 stations located in Brindisi (Adriatic Sea) and Porto Cesareo (Ionian Sea), along the coastal-marine waters of the Salento peninsula (Southern coast of Puglia, Italy). Samples were collected from 2003 to 2006, fortnightly. Phytoplankton analysis was performed using an inverted microscope (Nikon Eclipse Ti-S) following Utermöhl's method (Utermöhl, 1958) on a sub-sample of 200 cells at 400× magnification. Phytoplankton counts and morphometric measurements were carried out using a video-interactive image analysis system (L.U.C.I.A Version 4.71, Laboratory Imaging) connected to the microscope.

The relationship among abiotic and biotic parameters and phytoplankton taxonomic and morphological (biomass and shape) diversity were determined. Analysis of variance (ANOVA) was used to determine differences at spatial and temporal scales and Canonical correspondence analysis (CCA) to select the most useful abiotic and biotic factors explaining the variability of phytoplankton characteristics and the relationships among them.

Phytoplankton taxonomic and morpho-functional diversity, as well as water physical and chemical conditions and zooplankton density significant differed at spatial (Brindisi vs Porto Cesareo) and temporal scales, showing annual and seasonal patterns. At temporal scale, the phytoplankton change due to changes in the availability of nutrients, along with seasonal variations in temperature and predatory pressures. Changing environmental conditions influence the biological interactions among species characterized by different biovolume, sizes and shapes, e.g. increased stratification will enable rounded dinoflagellates to outcompete elongated diatoms. Change in dominance taxa, characterized by specific shape and size, is an indicator of adaptation to increasing temperature changes and selection by zooplankton. Pre-

dation by zooplankton is also dependent on size and shape, as well as nutritional and toxicity characteristics of their prey.

Understanding the factors that control phytoplankton dynamics in coastal seas is of increasing importance, particularly in the context of climate change. The knowledge of phytoplankton variability at spatial and temporal scales and interactive effects of abiotic and biotic factors will have major impacts on biodiversity and ecosystem function and thus need to be considered in environmental management plans.

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Ecosystem impacts of outbreaks by a native defoliating insect pest on forest soil carbon sequestration and dynamics

Stephen Heard[1], Louis-Pierre Comeau[2], Cameron Wagg[2], Michael Stastny[3]*

[1]Department of Biology, University of New Brunswick, Fredericton, Canada
[2]Agriculture and Agri-food Canada, Fredericton, Canada
[3]Atlantic Forestry Centre, Fredericton, Canada
[*]E-mail: michael.stastny@canada.ca

Keywords: insect-tree interactions, forest pest management, carbon sequestration, ecosystem functioning, mycorrhizal community

Multi-year outbreaks of spruce budworm (*Choristoneura fumiferana*), a Lepidopteran defoliator of fir and spruce, are the most important natural forest disturbance in the mixed and conifer forests of eastern Canada. Periodic canopy loss and tree morality over millions of hectares cause a significant reduction in photosynthesis and future growth of surviving trees, and changes to the microclimate of forest soils and the associated biota. Defoliation also alters carbon inputs into the soil, in the form of insect frass and litterfall in the short term. The magnitudes of these contributions to carbon cycling in the boreal and sub-boreal forest, and their interplay via shifts in the composition and functioning of mycorrhizal communities, are poorly understood. Because spruce budworm is managed regionally through aerial application of biological insecticides, comparisons of control (outbreak) and sprayed (protected) forests can elucidate the impacts of large-scale forest disturbances through defoliating insects, or their prevention through pest management, on short-term dynamics of soil carbon and mycorrhizal communities.

In one study, we compared soil carbon in spruce-fir stands in south-eastern Quebec where a severe budworm outbreak is currently active. In replicate pairs of forest plots with similar composition but differing in their history of defoliation due to pest management decisions, we quantified tree defoliation, and collected soil cores to analyze physical, chemical, and biological properties of the soil, including carbon and nitrogen concentrations and soil respiration. While organic litter residues at the soil surface (LFH) were similar, belowground plant residues were higher in defoliated than in protected stands, possibly due to LFH incorporation or to an increase in fine root mortality under outbreak. While our analyses are still being completed, total soil organic carbon also responded to the history of defoliation.

In parallel, in an ongoing, multi-year experiment in the Gaspésie region of eastern Quebec, we have begun a novel study to quantify these processes in forest watersheds at the onset of spruce budworm outbreak by experimentally manipulating defoliation in half of the watersheds through spraying. In addition to soil sampling for litter, carbon and nitrogen, we are also measuring frass and litter inputs, and soil temperature, to study short-term dynamics of soil carbon due to canopy and microclimate changes during the spruce budworm outbreak. In addition, we are characterizing ectomycorrhizal colonization and diversity through microscopy and DNA sequencing to assess how forest defoliation influences soil biota and their role in carbon flux and storage.

Collectively, improved understanding of differences in carbon cycling between forest stands impacted by spruce budworm outbreaks and those protected through spray application presents an opportunity to inform forest pest management decisions as well as carbon budget policies in one of the Earth's most extensive forest biomes.

Ecological networks

Trait-based understanding of topological importance in marine food webs

Anett Endrédi[1*], *Katalin Patonai*[1,2], *Ferenc Jordán*[1,3]

[1]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[2]Eötvös Loránd University, Budapest, Hungary
[3]GINOP Evolutionary Systems Research Group, MTA Centre for Ecological Research, Tihany, Hungary
[*]E-mail: endredi.anett@okologia.mta.hu

Keywords: food web, keystone groups, topological importance, trait

Trophic interactions are considered to be among the most important factors determining the functioning of ecological communities. Thus, food web models can be useful tools to understand the functioning and to predict future changes of the community. One of the main questions which can be studied with these models is: Which trophic group has the largest impact on others in the community and why?

An increasing number of food web models have been developed to answer this, but these models are usually case-specific, focusing on different questions and they contain trophic groups of heterogeneous nature. However, there is an increasing need to find general patterns, and trait-based approaches probably can help in this: characterizing trophic groups by their functional traits can make them more standardizable, food webs more comparable and models more predictive.

According to some previous studies, some traits (e.g., biomass, mobility or habitat) can be good proxies in predicting the importance of a trophic group, but these studies mainly focused on just one/few food webs; thus the generalization of their results or their predictive power is still uncertain.

We examine the usability of functional traits in predicting the importance of trophic groups (measured by different topological centrality indices) in a large database of marine food web models (containing a total of 2218 groups for 93 food webs).

16 structural indices were computed and biological (size, mobility, habitat) and habitat-related (maximum depth, proximity to shore and ecotype) trait data were collected for as many trophic groups as possible. At first, the predictive power and redundancy of the different indices were tested, then the habitat-dependent relationship of the estimated importance and the biological traits were examined.

The results show large differences in the predictive power and redundancy of different structural indices. However, the relationship between the traits and the structural importance also highly depends on the index used to quantify the importance, most of the examined traits (e.g., habitat, like water column/benthic) shows a significant relationship with some indices. However there is a massive lack of data for some traits, our analysis can be a first step towards the trait-based understanding of structural importance in food webs.

Keystone species complexes in food webs

Ferenc Jordán[1,2*], *Juliana Pereira*[3]

[1]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[2]GINOP Evolutionary Systems Research Group, MTA Centre for Ecological Research, Tihany, Hungary
[3]Central European University, Budapest, Hungary
[*]E-mail: jordan.ferenc@gmail.com

Keywords: keystone species, food web, multi-species

Central food web positions may indicate key species with rich direct or indirect interactions. Their strutural importance can be quantified and different species can be ranked by their relative importance. A recently emerged question is how to quanitfy the centrality of small sets of graph nodes and how does the composition of these „KeyPlayer sets" differ from the identity of the most central individual nodes. This new approach suggests that the „core" of food webs consists of a few species that are linked to each other and occupy different trophic levels [1,2,3]. This would mean that generally there is a food chain that acts like a central backbone in the community and, to some extent, other organisms and interactions ensure redundancy and robustness in the system. We present the methodology and illustrate our approach on big real databases.

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Keystone features of flower-visitation networks in a traditional low-intensity agricultural system and their vulnerability to honeybee loss

Anikó Kovács-Hostyánszki[1,2*], *Ferenc Jordán*[2,3], *Rita Földesi*[4], *Anett Endrédi*[3], *András Báldi*[1]

[1]Lendület Ecosystem Services Research Group, Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary
[2]GINOP Evolutionary Systems Research Group, MTA Centre for Ecological Research, Tihany, Hungary
[3]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[4]University of Bonn, Institute of Crop Science and Resource Conservation, Agroecology/Organic Farming, Bonn, Germany
[*]E-mail: kovacs.aniko@okologia.mta.hu

Keywords: arable fields, body size, centrality, connectedness, diet breadth, grassland, wild bee

Declining populations of several wild bee species and honeybees worldwide heavily affects and risks the pollination of both crop and wild plants. This poses major threats to agriculture and raises conservation issues. We studied bee communities and conducted the first large scale field study of flower visitation networks between pollinators and wild plants in a low-intensity traditional farming system in Transylvania, Romania. We were interested, how the structure of flower-visitation networks in different habitat types may influence the vulnerability of pollinator communities to the potential loss of honeybees. Furthermore, we studied the relationship between the ecological and morphological characteristics of wild bees such as relative abundance, body size and diet breadth and their positional importance in the network. We questioned what extent are wild plant species visited by just a few, dominant bee species, as opposed to requiring many different ones. The data were collected in 38 arable fields and 38 grasslands, which varied along different crop and/or management types. First, we performed network analysis based on flower visitation data and quantified the structural vulnerability (i.e. the effect of the loss of honeybee) of the plant-pollinator networks by a topological index (distance-based fragmentation). According to our results very different plant-pollinator communities inhabited the studied different agricultural habitat types. In general, an intermediate plant/pollinator ratio was associated with high vulnerability in the absence of honeybees. The pastures in mid-summer had the less, early summer arable fields had the most vulnerable structure. Second, three different centrality indices (connectedness, centrality and keystoneness) were used to quantify the importance of a species by the position it holds within the weighted plant-pollinator networks of arable and grassland systems. While honey bee was the most abundant species that contributed almost one-third of flower visitations, it visited less than half of the plant species. Whereas 63% of flower visitation was delivered by wild bees. The dominant species (relative abundance > 5%) visited the highest number of plant species (highest connectedness) and had the richest interaction structure and the strongest community effects (highest centrality). Rare species (relative abundance < 1%) were among the species of highest keystoneness, and visited one-sixth of the plant species

exclusively. Third, based on the relationship between body size, diet breadth and the values of centrality indices, the body size of wild bee species showed a positive correlation with keystoneness in the total and arable networks, while polylectic species had higher connectedness and centrality values in the grassland network than oligolectic species. Based on our results we suggest that increased plant species richness can ensure higher wild bee diversity and more stable plant-pollinator networks without honeybee, where flower-visitation can rely more on wild bees. Keystone feature of large-sized wild bees in arable fields highlights the importance of landscape scale conservation. Whereas, maintenance of extensive grassland management and diverse flower resources is crucial for the most central and most connected wild bee species in the grassland networks. The high proportion of rare species raise also conservation concerns, since these are suggested to be more vulnerable in general to habitat loss and adverse management effects.

Statistical ecology

Does Community Assembly by Trait Selection (CATS) algorithm estimate the role of mass effect correctly?

Zoltán Botta-Dukát

MTA Centre for Ecological Research, Thany, Hungary
E-mail: botta-dukat.zoltan@okologia.mta.hu

It is widely accepted that assembly of local plant communities is neither a fully deterministic nor a 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. Modeling observed abundances by the maximum entropy approach (Community Assembly by Trait Selection; CATS; Shipley et al. 2012) allows statistical decomposition of total information content that are attributable to environmental trait filtering, mass effect and demographic stochasticity. The aim of the present work to check the reliability of the estimates. For this purpose, artificial meta-communities were simulated in an individual-based simulation framework. The simulation procedure can be subdivided into five steps. (1) A species pool is created and two trait values are simulated for each species; the first trait defines the survival of a species in a given environmental condition. The second trait describes the resource use. (2) Death of individuals: In each community one random individual dies. (3) Seed production: Each community produces seeds where the number of seeds per individuals is determined by resource competition. (4) Dispersal: Each seed has a probability to remain in its community of origin or to disperse to any of the other communities. (5) Establishment: The dead individual is replaced by one new individual from the seeds choosing the winner seed regarding the survival probability in the given community. Steps 2–5 are applied to each community until there is a 100-fold complete turnover in individual identity. Setting parameter values allows changing relative importance of dispersal, demographic stochasticity, habitat filtering and competition. The simulated landscape contains two habitats whose proportion and the difference between them differs among scenarios, but 10 plots from both habitats were analyzed in each scenario. The main findings are the following: (1) CATS approach estimated lower importance of habitat filtering if the habitat is more common in the landscape; (2) estimated importance of mass effect decreases, when the difference between habitats increases; (3) estimated importance of demographic stochasticity is lower, when probability of seed dispersing into other local community is higher. The main conclusion is that interpreting results without considering the possible confounding effects of landscape structure results in misleading conclusions on the importance of assembly processes.

Acknowledgments
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A multi-phase monitoring program for assessing Natura 2000 habitat conditions

Cervellini, M.[1], Chiarucci, A.[1], Nascimbene, J. [1], Angelini, P.[2], Casella, L.[2], Maccherini, S.[3], Angiolini, C.[3], Cerabolini, B.[4], Dalle Fratte, M.[4], Fattorini, L.[5]

[1]Department of Biological, Geological, and Environmental Sciences, Alma Mater Studiorum, University of Bologna, Bologna, Italy. Presenting author: alessandro.chiarucci@unibo.it
[2]ISPRA – Italian National Institute for Environmental Protection and Research, via V. Brancati, 60, 00144 ROMA Italy
[3]Department of Life Sciences, University of Siena, Via Mattioli 4, 53100 Siena, Italy
[4]Department of Theoretical and Applied Sciences, University of Insubria, via J.H. Dunant, 3, I-21100 Varese, Italy
[5]Department of Economics and Statistics, University of Siena, P.za S.Francesco, 8, 53100 Siena, Italy

Improving the conservation status of species and habitats targeted by the "Directive 92/43/EEC" means to achieve an effective and standardized monitoring program of Natura 2000 sites, this approach fits well with aims of European 2020 Biodiversity Strategy. This goal has to be accomplished by each EU member state. We present a sampling strategy we are developing for monitoring all the habitat types on the Italian territory, based on a multi-phase monitoring programme. General aim of this sampling scheme is to generate a standardised, reliable and comparable approach for the quantitative assessment of the habitat amount and conservation status. Monitoring is based on three sampling phases: 1) for each habitat type, presence absence data on the geographical grid of 10km×10km cells (Dir. Art. 17) are used to select a spatially balanced sample of cells containing the habitat by means of one-per-stratum sampling, with sampling fractions ranging from 100%, for rare habitat types to 10%, for common habitat types; 2) Each cell selected in the first phase is partitioned into sub-quadrats exploited as sampling units to select habitat patches by means of network sampling in order to estimate the habitat cover and/or the number of patches; 3) for some habitat types, point, plot or transect sampling are performed in a third phase to estimate some vegetation attributes. This monitoring program allows achieving statistically sound estimates of habitat cover and status based on a sampling scheme that can be easily standardised and repeated over time. After the validation of this multi-phase habitats monitoring on the Italian territory, the possibility to maintain at European scale, a favourable conservation status of the Nature 2000 habitats network, could be a reliable, applicative and shareable achievement by all member States.

Bird-habitat relationships in riparian forests in North-eastern Algeria (Medjerda River)

Mohcen Menaa[1*], *Kaouther Guellati*[1], *Abderraouf Chouaib Rebbah*[2], *Salah Telailia*[3], *Lamia Boutabia*[3], *Haithem Khedhiri*[1], *Mohamed Cherif Maazi*[1]

[1]LEAT Laboratory, Department of Biology, Faculty of Natural and Life Sciences, Souk Ahras University, Souk Ahras, Algeria
[2]Department of Natural and Life Sciences, Faculty of Sciences, Oum El Bouaghi University, Oum El Bouaghi, Algeria
[3]Faculty of Sciences, El Tarf University, El Tarf, Algeria
[*]E-mail: m.menaa@univ-soukahras.dz

Keywords: birds, riparian forests, large timber, tree layer, shrub layer

This study was set in riparian forest habitats of Medjerda River within the province of Souk Ahras (North-eastern Algeria). We conducted the first bird survey in this area using the point count method to describe the composition of breeding riparian birds and to analyze the spatial distribution among habitats with respect to habitat variables, summarising habitat structure, tree and shrub layers. A total of 89 species were observed where the avian species richness at each point-count ranged between six and 17 species. The most dominant families in number of pairs are Muscicapidae, Sylviidae, Turdidae, Paridae and Picidae. They occupy more than 70% of the total abundance of the entire community. We noted 22 protected species, only three endangered species, and five endemic species to the Maghreb and/or to North Africa. The presence of these species with patrimonial value reinforces the importance of the conservation of Medjerda avifauna. Using multivariate analysis methods (PCA, CCA, RDA and MRT), we determined that two major patterns of relationships among bird and habitat were traced: the first involved changes in tree structure during their growth (height of tree layer and large timber), the second was related to characteristics associated with shrub layer. According to GLM analysis with a Poisson distribution, bird diversity, abundance was related to diameter of the largest timber.

Census timing alters stage duration distributions in matrix population models

Toshinori Okuyama

Department of Entomology, National Taiwan University, Taipei 106, Taiwan
E-mail: okuyama@ntu.edu.tw

Keywords: stage-structure, demography, elasticity, population growth

Matrix population models are widely used to study the dynamics of stage-structured populations. A census in these models is an event monitoring the number of individuals in each stage. Pre-breeding census and post-breeding census, two of the most commonly used methods, assume that breeding occurs immediately before or immediately after the censuses, respectively. In some models such as age-structured models, the two methods give the identical results. However, in stage-structured models, where the duration of the first life stage varies among newborns, a choice between the two methods may result in different conclusions. This difference is attributed to the different first-stage duration distributions assumed by the two methods. Inappropriate uses of these methods are common in published studies, which suggests the detail is not widely known to ecologists. This presentation describes the unintended consequence of the pre-breeding and post-breeding censuses.

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Diversity change in space and time: Measuring Rao's Q from space

Duccio Rocchini

University of Trento – Fondazione Edmund Mach, San Michele all'Adige – Trenti, Italy
E-mail: duccio.rocchini@unitn.it

Understanding biodiversity changes in time is crucial to promptly provide management practices against diversity loss. This is overall true when considering global scales, since human-induced global change is expected to make significant changes on the Earth's biota.

Biodiversity management and planning is mainly based on field observations related to community diversity, considering different taxa. However, such methods are time and cost demanding and does not allow in most cases to get temporal replicates. In this view, remote sensing can provide for a wide data coverage in a short period of time. Recently, the use of Rao's Q diversity as a measure of spectral diversity has been proposed in order to explicitly taking into account differences in a neighborhood considering abundance and relative distance among pixels.

The aim of this talk is to extend such a measure over the temporal dimension and to present an innovative approach to calculate remotely sensed temporal diversity. We demonstrated that temporal beta-diversity (spectral turnover) can be calculated pixel-wise in terms of both slope and coefficient of variation and further plotted over the whole matrix / image.

From an ecological and operational point of view, for prioritisation practices in biodiversity protection, temporal variability could be beneficial in order to plan more efficient conservation practices starting from space-time diversity hotspots. In this paper we delivered a highly reproducible approach to calculate spatio-temporal diversity in a robust and straightforward manner. Since it is based on open source code, we expect that our method will be further used by several researchers and landscape managers.

Enough is enough: searching for the optimal sample size to characterize and monitoring sand dune Natura 2000 habitats

Enrico Tordoni[1], Claudia Angiolini[2], Giovanni Bacaro[1], Andrea Bertacchi[3], Daniela Ciccarelli[4], Bruno Foggi[5], Matilde Gennai[5], Simona Sarmati[2], Daniele Viciani[5], Simona Maccherini[2]*

[1]Department of Life Sciences, University of Trieste, via L. Giorgieri 10, 34127 Trieste, Italy
[2]Department of Life Sciences, University of Siena, via P.A. Mattioli 4, 53100 Siena, Italy
[3]Department of Agriculture, Food and Environment, University of Pisa, via del Borghetto 80, 56124 Pisa, Italy
[4]Department of Biology, University of Pisa, via Luca Ghini 13, 56126 Pisa, Italy
[5]Department of Biology, University of Florence, via G. La Pira 4, 50121 Firenze, Italy
[*]E-mail: etordoni@units.it

Keywords: multivariate pseudo standard error, precision, sampling effort, spatial variation, species assemblage

Coastal dune systems are among the most threatened and investigated environment worldwide. Sand dune are characterized by a marked vegetation zonation which often host rare or exclusive species. Due to their particular characteristics, most of the habitats occurring in these environments are considered of community interest (Directive 92/43/EEC) and protected within the Natura 2000 Network; therefore, continuous monitoring actions are needed in order to assess habitat changes or biodiversity loss. However, multifaced monitoring of community composition is usually considered a problematic task for three main reasons: inadequacy of a single monitoring design for all species occurring in a community (e.g., rare vs. common species), unpredictable and often unquantifiable variability of the multivariate dataset, high costs. Recently, Anderson and Santana-Garcon (2015) proposed a measure of variability defined "pseudomultivariate dissimilarity-based standard error" (*MultSE*) for assessing the sample-size adequacy in studies of ecological communities. This measure can be interpreted as a multivariate precision estimate for multivariate assemblage data in the space of the chosen dissimilarity measure. In this study, we aimed at: 1) using the *MultSE* to determine the adequate number of replicates needed to characterize the species composition of sand dune habitat within a given precision level; 2) understanding how the observed compositional variation is partitioned among the spatial levels of the sampling design adopted. Combining these two types of information could be vital to design efficient and optimized future sampling campaign for monitoring purposes. Accordingly, we sampled psammophilous vegetation by using a simple random sampling in three EUNIS habitat types (shifting coastal dunes - B1.3; coastal stable dune grassland - B1.4, and coastal dune scrub - B1.6) belonging to three Special Areas of Conservation (SACs) in Tuscany ("Parco dell'Uccellina", "Dune Litoranee di Torre del Lago", "Selva Pisana"). Plant species composition and abundance were sampled in a total of 206 squared plots (size 4 m^2) during spring-summer 2018. Analyses were performed both on abundance and incidence matrices using Bray-Curtis and Jaccard distances, respectively. The study of the *MultiSE* profiles revealed that an approximated number of 10 plots was able to grasp the overall variation in plant composition for B1.3 and B1.6

habitats, while a sampling effort of about 25 plots was needed for habitat B1.4. A two-way PERMANOVA confirmed that plant community composition is significantly explained by the interaction between habitat type and SAC. The analysis of diversity components for the studied communities (namely α and β diversity) pointed further out that the three sampling sites actually protect different dune vegetation and plant communities, especially among habitats. To the best of our knowledge, this is one of the first attempt made to characterize sampling adequacy in plant communities using *MultSE*. Our results, that evaluated different aspects of the multivariate variability in plant communities, will be useful for plant ecologists and nature managers to plan optimal sampling design for habitat monitoring activities.

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Effects of global change

Saltmarsh responses to escalating local and global stressors and implications for coastal protection

Laura Airoldi[1*], *Veronica B. Lo*[1], *Elisabeth M. Strain*[1], *Joanne X.W. Wong*[1]

[1]Dipartimento di Scienze Biologiche, Geologiche ed Ambientali, *Alma Mater Studiorum*-University of Bologna
[*]E-mail: laura.airoldi@unibo.it

Keywords: saltmarsh, heat waves, climate change, sea-level rise, coastal protection

Saltmarshes play a crucial role in coastal protection by attenuating waves or flood risk. Integrating their conservation and/or rehabilitation as part of coastal defence practices is increasingly valued as a sustainable, cost-effective and ecologically sound approach. At the same time saltmarshes face growing pressures from escalating local anthropogenic impacts and global climate-related stressors. Identifying the factors that sustain these ecosystems and their functional role is crucial to enable their large-scale application in coastal protection. We examine these problems in saltmarsh ecosystems along the highly urbanised coastal regions of the North Adriatic Sea. We analyse: 1) the status of saltmarshes in the region; 2) the effects of multiple interacting local and global climatic stressors; 3) the potential functional consequences of predicted changes; 4) which conditions can facilitate or hamper the future persistence of these systems. We report an extensive and overlooked degradation of the systems, increasingly shaped by non-indigenous species invasion and heat wave events, which are triggering shifts from *Spartina* meadows to the annual succulent *Salicornia veneta*. The increasing spread of this succulent could reduce the future capability of the system to respond to projected increasing sea levels, particularly in nutrient rich regions. Yet, there will be conditions under which saltmarshes will still be resilient to climate-related disturbances. This knowledge is used to predict changes at the foreshore of saltmarshes related to sea level rise, and to identify conditions that would offer the most reliable conditions for the use of saltmarshes in coastal protection.

Responses of forest tree community to climate change in the eastern United States

*Jonathan Knott, Songlin Fei**

Department of Forestry and Nautral Resources, Purdue University, West Lafayette, Indiana, USA
*E-mail: sfei@purdue.edu

Keywords: climate change, forest ecosystems, topic model

Forests across the eastern U.S. have been altered over recent decades due to a variety of factors, including climate change, invasive species, and management practices. While many studies have analyzed species-level changes, much less attention has been paid to forest communities, especially at a large spatial scale. Identifying and quantifying shifts in forest tree communities can reveal how climate change will impact forest ecosystem functioning and services. Utilizing an extensive dataset with repeated measures on over 40,000 plots from the Forest Inventory and Analysis Program (FIA), we identified forest communities with the Latent Dirichlet Allocation (LDA) topic model in the eastern U.S. In addition, we tracked the geographic shifts of these communities over the last three decades by calculating the shifts in community centroid and community area. In total, LDA identified 38 communities in the eastern U.S. The mixed pine-oak-hickory community of the Southern Pine-Hardwood Region had the largest area, and the oak-hickory community of the Central Hardwoods Region had the largest overall abundance. In total, 16 out of the 38 communities (42%) have changed significantly. Ten communities have had significant shifts in the centroid of their distributions (6 northward, 3 southward, and 1 westward shift). Additionally, 6 communities have significantly expanded or contracted their total area (2 expansions and 4 contractions). Factors related to climate change (changes in temperature, precipitation, and drought severity) were poor predictors of community change. While this might indicate resilience of forest communities to climate change, it might also indicate a lag between climate change and forest community responses and the importance of other stressors on forest communities.

The impact of land-use change and species invasion on biodiversity and ecosystem functioning

Gianalberto Losapio[*], *Mark C. Mescher, Consuelo M. De Moraes*

Department of Environmental Systems Science, ETH Zurich, Universitätstrasse 16, 8006 Zurich, Switzerland
[*]E-mail: gianalberto.losapio@usys.ethz.ch

Human impact on the environment is causing accelerated changes in Earth's ecosystems, resulting in unprecedented biodiversity loss. Global change drivers such as land-use change and species invasion are threatening to disrupt key ecosystem functioning on which humans rely on. However, we have only limited understanding of the combined effects of multiple global change drivers on ecological communities. Here, we studied the impact of overgrazing disturbance and species invasion on plant diversity and ecosystem functioning by combining large-scale natural experiment with local-scale field experiment. We found that the resilience of biodiversity to overgrazing disturbance was inhibited by species invasion. Under overgrazing pressure, the prickly invader species protected and supported otherwise vulnerable biodiversity. Meanwhile, species invasion inhibited the recovery of biodiversity once overgrazing pressure ceased. Notably, the combination of overgrazing disturbance and species invasion disrupted ecosystem functioning, eroding the positive effects of biodiversity on biomass productivity. This result indicates the fundamental role of biodiversity in mediating the effects of global change on ecosystem functioning. Our study highlights that complex interactions among species invasion, biodiversity and overgrazing disturbance drive the resilience and recovery of ecological communities to human activity.

Conservation biology

A multi-site and multi-taxon assessment of edge effect in grassland arthropods

András Báldi[1*], *Péter Batáry*[2]

[1]MTA ÖK Centre for Ecological Research, Tihany, Hungary
[2]MTA ÖK Lendület Landscape and Conservation Ecology Research Group, Vácrátót, Hungary
[*]E-mail: baldi.andras@okologia.mta.hu

Keywords: grazing, Hungary

Assemblages of arthropods may respond to habitat heterogeneity, for example via the the change of presence and abundance of species near habitat edges. To understand this pattern is a key to understand landscape scale patterns, like the effects of habitat fragmentation on biodiversity and on ecosystem services these species provide. There are many publications on edge effect, but not easy to find a general pattern because of the restricted spatial and taxonomical scales included into a study. In the present study we investigated the presence and abundance of 569 species and 42193 individuals of arthropods (Homoptera, Orthoptera, Aranea, Carabidae, Curculionidea, Apoidea), in interior and edge of 48 grazed semi-natural grasslands in Hungary (Báldi et al. 2013). Simply comparison of edge versus interior species numbers and abundances did not revealed significant differences. Using more advanced GLM analysis, we showed that edge effect had significant interactions with management (extensive versus intensive grazing), and/or region (three distinct region of the Hungarian Plain) in three of the six groups (Homptera, Orthoptera and Carabidae). Therefore, habitat edges may influence arthropod assemblages, but this effect is taxon specific, and is influenced by local factors like management and vegetation characteristics.

Acknowledgements
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Fire and grazing management shape ground beetle and dung beetle community structure and function in restored grasslands

Nicholas A. Barber[1], Sheryl C. Hosler[2], Melissa Nelson[2], Holly P. Jones[2,3]*

[1]Department of Biology, San Diego State University, San Diego, USA
[2]Department of Biological Sciences, Northern Illinois University, DeKalb, USA
[3]Institute for the Study of the Environment, Sustainability, and Energy, Northern Illinois University, DeKalb, USA
[*]E-mail: nbarber@sdsu.edu

Keywords: functional traits, ecosystem restoration, insect community, prescribed fire

Disturbances shape the diversity and composition of ecological communities[1,2], and these changes have consequences for ecosystem functions[3]. Disturbances can also be used as habitat management tools to benefit the establishment and maintenance of desirable species[4,5]. Understanding how these activities influence other community members, and the effects of community variation on ecosystem functions, can help determine how best to restore and manage habitats. Community–function relationships are well-studied for producer communities[6], but there is less knowledge of how differences in consumer communities change the functions to which they contribute. We studied the impacts of prescribed fire and re-introduced native grazers (American bison) on the structure and function of ground beetle and dung beetle communities in a chronosequence of restored and remnant grassland. We determined taxonomic and functional diversity of communities and measured relevant consumer functions (seed and arthropod predation[7], dung decomposition[8]) to determine if habitat management affected consumer communities and if community changes translated to differences in predation and decomposition rates.

Ground beetles tended to increase in abundance but decrease in richness in older sites, and these changes were associated with more carnivorous and flightless beetles that resulted in reductions in functional dispersion and functional evenness. Fire and bison had little impact on ground beetle communities, but fire significantly decreased seed predation rates and increased arthropod predation rates. Dung beetles were significantly more abundant in sites with re-introduced bison, but this largely was driven by just two species, so bison sites generally had lower functional diversity. Nonetheless, dung decomposition rate was not related to fire or bison management and was highest in young sites. Prescribed fire and grazing, as well as site age, may shape the taxonomic and functional diversity of these beetle communities, but these community changes do not seem to be directly related to predation and decomposition rates.

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Individual decisions drive the changes in movement patterns of ground beetles between forestry management types in Hungary

Zoltán Elek[1*], *Jana Růžičková*[1], *Péter Ódor*[2,3]

[1]MTA-ELTE-MTM Ecology Research Group, Budapest, Hungary
[2]MTA Centre for Ecological Research, Institute of Ecology and Botany, Vácrátót, Hungary
[3]MTA Centre for Ecological Research, GINOP Sustainable Ecosystem Research Group, Tihany, Hungary
[*]E-mail: zoltan.elek2@gmail.com

Keywords: ground beetles, movement trajectories, hidden Markov models, radio-tracking

Moving from a habitat to another, the individual's dispersal has consequences for individual condition, population dynamics and gene flow. This is important to predict how populations will respond to habitat alteration. Our major motivation was to explore the effects of different forestry treatments such as preparation (partial) cuts and clear cuts on the selected population of the forest specialist ground beetle, *Carabus coriaceus*. We hypothesized that the detected animal trajectories will be different in the forestry treatments compared to their edges toward the adjacent control forest stand. We tagged six individuals (three males and three females) with small radio-transmitters and each were released in the treatment habitat core and the edges and in the core of control forests. We tracked their movement every four hours for five days in autumn, 2018. The recorded trajectories were divided into two major movement phases such as random walk (a proxy for foraging) and directional movement (a proxy for migration) using hidden Markov models. Our results revealed that the detected trajectories were specific for all individuals without any gender or time constrains. The proportion of the random walk and directional movement in the individual trajectories were related with the habitat type where they moved. In the core zone of preparation cuts, the trajectory was equally included the random walk and directional movement. A clear directional movement was observed in the clear cuts suggesting the beetles moved directly toward the adjacent (control) forest interior. The trajectories at the edges of both treatments were dominated by random walk. In addition, we identified a consistent time lag in the movement in a 6-15 hour interval, when beetles were inactive. This pattern may considered as a predator avoiding behavior. Although the recorded trajectories were specific for all individuals, the beetles released in both treatment types were able to abandon these habitats within a few days. These results suggest that forest specialist ground beetles avoid the forestry treatments especially clear cuts, however edge habitats and the studied preparation cuts can mitigate the migration constrains due to their more favorable environmental conditions compared to clear cuts. This research was supported by Hungarian Research Found (OTKA 111887, K_18 128441) and by the National Research Development and Innovation Office (GINOP-2.3.2-15-2016-0001).

Defining the native and naturalised flora for the Australian continent

Roderick J. Fensham[1,2,*], *B. Laffineur*[1,2]

[1]Queensland Herbarium, Mt Coot-tha Road, Toowong, Qld, Australia 4066
[2]Department of Biological Sciences, University of Queensland, St Lucia, Qld, Australia 4072
[*]E-mail: rod.fensham@qld.gov.au

Keywords: alien plants, exotic plants, flora, indigenous plants, naturalised, native

The value of distinguishing between plant species regarded as 'native' and 'alien' has special relevance in the island continent of Australia where European settlement was a springboard for human-assisted plant dispersal. The year of European settlement is proposed here as providing a distinction between a 'native' and 'naturalised' flora and is applied for the entire Australian flora of vascular plants. Herbarium collections and ecological criteria were employed to determine the status of 168 species of ambiguous origin. The date of 1788 proved to be a relatively straightforward criterion to assign native and naturalised status and the origin of only 27 plant species remains ambiguous. The dispersal of plants between continents is an ongoing process but European settlement of the Australian continent represents a very sharp biogeographic event for the Australian flora and provides a straightforward criterion for determining the 'naturalised' species.

Conservation of terricolous cryptogams in continental lowlands: the role of open dry habitats

Gabriele Gheza[1], Silvia Assini[1], Chiara Lelli[2], Lorenzo Marini[3], Helmut Mayrhofer[4], Juri Nascimbene[2]*

[1]Department of Earth and Environmental Sciences, University of Pavia, Via S. Epifanio 14, 27100 Pavia, Italy
[2]Department of Biological, Geological and Environmental Sciences, University of Bologna, Via Irnerio 42, 40126 Bologna, Italy
[3]DAFNAE Department, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
[4]Institute of Biology, Division of Plant Sciences, Karl-Franzens University of Graz, Holteigasse 6, 8010 Graz, Austria
[*]E-mail: gheza.gabriele@gmail.com

Keywords: bryophytes, dry grasslands, dry heaths, lichens, Natura 2000 Network, vegetation management

Open dry habitats are of focal importance for the conservation of terricolous cryptogams in human-impacted lowlands. However, these organisms are often not enough considered in the management of these habitats.

To demonstrate this important role, we investigated richness and diversity of lichen and bryophyte communities in the three main dry habitats occurring in temperate lowlands of Europe, i.e. acidic dry grasslands, calcareous dry grasslands, *Calluna vulgaris* heathlands. Lichen and bryophyte species were recorded in 287 circular plots (radius = 3 m) placed in 76 sites of the central-western Po Plain (N Italy), together with the main environmental variables, i.e. vegetation structure, % cover of vascular plant biological forms within the plots, habitat type, soil pH and texture, annual temperature and rainfall.

Species assemblages were analyzed by means of a non-parametric MANOVA and a non-metric Multidimensional Scaling. Character species of habitat types were detected by means of an Indicator Species Analysis. The role of the enviromental variables in shaping species assemblages was tested by means of a PERMANOVA, while their effect on species richness was tested by means of mixed-effect generalized models.

Overall, 55 species (33 lichens and 22 bryophytes) were recorded. Species assemblages differed significantly between the habitat types for both lichens and bryophytes. The ISA showed the presence of both exclusive and indicator species – including rare and/or protected species – for each habitat type: 14 (2 significant, 13 exclusive) for heathlands, 25 (17 significant, 10 exclusive) for acidic grasslands, 16 (14 significant, 11 exclusive) for calcareous grasslands. Habitat type, cover of therophytes, hemicryptophytes and phanerophytes, substrate texture, annual precipitation and cover of the shrub layer had a significant effect in shaping both lichen and bryophyte assemblages; substrate pH and cover of the herb layer had an effect on lichens and the interaction between substrate pH and texture had an effect on bryophytes. Heathland habitat and hemicryptophyte cover had a significant negative effect on lichen richness, whereas increasing precipitation and therophyte cover had a significant positive effect on bryophytes; the acidic grassland habitat had a positive effect on both the taxa.

The three considered habitats host habitat-specific terricolous cryptogam assemblages rich in total and rare species: therefore, their management should include actions aimed at the conservation of lichens and bryophytes. The negative effects against lichen richness disclosed in this study are related mainly to the encroachment of *Molinia arundinacea* (a hemicryptophyte) in heathlands: this should be carefully taken in account when planning management actions.

Patterns of plant communities in Sacred Natural Sites across Italy

Piero Zannini[1], Juri Nascimbene[1], Fabrizio Frascaroli[1], Sara Landi[1], Riccardo Guarino[2], Alessandro Chiarucci[1]*

[1]Department of Biological, Geological and Environmental Sciences, University of Bologna, Via Irnerio 42, 40126 Bologna, Italy
[2]Section of Botany and Plant Ecology, Department of Biological, Chemical and Pharmaceutical Sciences and Technologies, University of Palermo, Via Archirafi 20, 90123 Palermo, Italy
[*]E-mail: piero.zannini2@unibo.it

Keywords: biodiversity conservation, species richness, species composition, alien species

Sacred Natural Sites (SNSs) are regarded as the oldest protected areas in human history. Knowledge of their history and spatial location in Europe can be considered exhaustive, although only few studies have tried to quantify their contribution to conserve local biodiversity. To fill this gap we sampled 25 SNSs in Italy by stratifying our sampling sites along two orthogonal gradients of landscape hetereogeneity and naturality. For each site, habitats were mapped in a 250m buffer as well as in the surrounding landscape in 3 reference sites (RS). In each habitat we collected data on vascular plants using 10m x 10m quadrats. We compared several parameters between SNS and RS, as species richness, Shannon's diversity, percentages of alien species and plant traits. Preliminary results indicate contrasting situations. From one hand they suggest that SNSs have peculiar features and greatly contribute to local diversity as compared with the surrounding landscape. From the other hand, they indicate that SNSs may be impacted by human activities.

Poster Presentations

Community ecology

Two-year survey of ground-dwelling spider assemblages of artificial forest gaps

László Bali[1], Dániel Andrési[1,2], 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: *Araneae*, pitfall trapping, deadwood, soil humidity, openness, undergrowth cover

Our current study is part of a complex research, where we analyze the effects of gap openings on ground-dwelling spider communities in different forest stands. We have already published some of our findings regarding a homogenous turkey oak stand in Vép 32/D and now we would like to present the results of another survey, which took place in a mixed oak-hornbeam stand during two consecutive years. Our previous results show for example, that the gap opening had a positive effect on both the species and specimen numbers and also on the diversity of the local spider assemblages (Bali et al. 2016, 2017; Andrési et al. 2018).

The aims of our current study were to assess the effects of artificial gap opening on ground-dwelling spider assemblages in context with several environmental variables in a mixed forest stand.

To this end, the spider communities of two artificial gaps and their surrounding oak-hornbeam stand were surveyed in the Bejcgyertyános 13/A forest sub-compartment, located in Alsó-Kemeneshát, West-Hungary. For the data collection, we used Barber-type pitfall traps (Barber 1931). The traps were planted in two 70 m long transects, 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 for 2 years (for 414 days). In each year, we collected the samples fortnightly, during 8 months.

Several environmental variables were also measured, such as the soil humidity, the canopy openness, the luminance, and the undergrowth cover (contribution of NAIK ERTI). The quantity and quality of the lying deadwood in the 2.5 m vicinity of the traps were also measured, using the Ódor method (Ódor 2005).

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Dynamics, abundance, trends of green roof communities under limiting factors

Francesca Bretzel[1*], *Francesca Vannucchi*[2]

[1]Institute of Research on Terrestrial Ecosystems, CNR, Pisa, Italy
[2]Institute of Life Science, Scuola Superiore Sant'Anna, Pisa, Italy
[*]E-mail: francesca.bretzel@cnr.it

Keywords: species richness, pin intercept, functional groups, nitrogen

Roofs are harsh condition environment, where it is possible to grow plants with the aim of implementing ecosystem services, only if they can adapt to extreme conditions of climate and nutrient availability due to the thin substrate layer (Oberndorfer et al. 2007). In many cases, the most successful attempts are the ones that provided to plant different species with different functionality and life forms, inspired by ecological models, to constitute a self-sustainable community (MacIvor et al. 2013). In addition, the establishment of diversified plant communities allows coping with extreme conditions (limited nutrients and drought) through the variation in plant composition and recovery. Particularly, the limited availability of nitrogen in the green roof growing media promotes species richness and the hardiness of the plant community (Vannucchi et al. 2018). Aim of this study is to evaluate the structure and dynamics of a green roof community in limited nutrient condition, especially during the summer drought. We planted and seeded forbs, geophytes, CAM and *graminae* species on a roof in Mediterranean climate, in boxes with 3 substrates with similar pH, electrical conductibility, C_{org} and different N_{tot} content. No inputs of cultivation were given. We monitored the effects of the substrate on the plant community in terms of species abundance, variations related to limited factors and trends over two years. For this purpose, we analysed the total canopy cover and the community composition (species and functional groups), using respectively the digital image analysis (Rasmussen et al. 2007) and the pin intercept method (Glatzle et al. 1993). CAM species showed higher cover (45%) in nitrogen-rich substrate reducing to 9% in nitrogen-poor substrate. Instead, forbs increased up to 35% in cover, in presence of low nitrogen content. During the summer drought, the number of species drastically fell, and CAM was the dominant functional group in the three substrates, showing differences in percentage of cover. In September a vegetation recovery was observed. These results suggest the role of substrate properties in affecting the community structure (species composition and richness), particularly after the summer drought.

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Scrutinizing functional patterns and assembly rules estimated from transect data

Sándor Bartha[1,2], Sándor Csete[3], Giandiego Campetella[4], Roberto Canullo[4], Stefano Chelli[4], Andrea Mojzes[2], András Kun[5], Róbert Kun[6], Zsolt Molnár[1,2], Gábor Szabó[1,2], Szilárd Szentes[7], Tsvetelina Terziyska[8], Camilla Wellstein[9], Zita Zimmermann[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
[3]Institute of Environmental Sciences and Nature Conservation, Faculty of Agricultural and Environmental Sciences, Kaposvár University, Kaposvár, Hungary
[4]School of Biosciences and Veterinary Medicine, Plant Diversity and Ecosystems Management Unit, University of Camerino, Camerino, MC, Italy
[5]Somogyvámos, Hungary
[6]Szent István University, Doctoral School of Environmental Sciences, Gödöllő, Hungary
[7]Rezi, Hungary
[8]Bulgarian Academy of Sciences, Institute of Biodiversity and Ecosystem Research, Sofia, Bulgaria
[9]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bozen, Italy
[*]E-mail: diego.campetella@unicam.it

Keywords: plant community organization, functional diversity, grid, sampling design, spatial statistics, transect

Transect sampling is routinely used in vegetation science. Yet, the reliability of this type of sampling for assessing community assembly rules has not been scrutinized. Local interactions and limited dispersal have essential role in the organization of plant communities. Information about vegetation patterns in the neighbourhood is probably crucial for assessing and understanding community assembly rules. The "one-dimensional" transect sampling does not provide information about adjacent vegetation patterns in the neighbourhood, therefore vegetation characteristics and assembly rules might be incorrectly estimated from transect data.

In this study, alkaline, loess and sand grasslands were sampled. Presence of plant species was recorded in large elongated grids of 10 x 1040 units of 5x5cm resolution, which corresponded to a spatial extent of 50 cm x 5200 cm. Vegetation characteristics (taxon-based alpha and beta diversity and trait-based functional diversity) derived from the central 1x1040 units long transect were compared to characteristics derived from the full grid data. In the second analysis the central transect was analyzed by variography and then the patterns in the neighbouring transects were approximated by kriging. These simulated patterns were compared to the original patterns of the neighbouring transects. Community assembly rules were assessed by comparing realized patterns of functional diversity to null models.

The main vegetation characteristics were similar between sampling types. Abundances and patterns of abundant species were reliably estimated from transects while the patterns of rare species varied between sampling types. Functional diversity (expressed by Rao index) was also properly estimated from transects. Local vegetation characteristics were autocorrelated within 50cm in each grasslands. Consequently, the patterns of adjacent transects, running in the close neighbourhood, could be well approximated by geostatistics. The strongest

spatial dependence appeared in alkaline grasslands. Due to differences in the abundance estimates of rare species, null models derived from grids and transect were slightly different with more power in the case of grid-based data. However, the spatial structure of the dominant species and the related assembly rules did not differ between sampling types. Due to strong autocorrelations at fine spatial scales, transect sampling proved to be effective for estimating functional patterns and assembly rules.

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Helminth infracommunity of grass snake *Natrix natrix* (Reptilia, Colubridae) in differently transformed ecosystems

Serhii Yermolenko[1], Viktor Gasso[1], Anna Hahut[1], Valeriia Spirina[1]*

[1]Department of Zoology and Ecology, Oles Honchar Dnipro National Univeristry, Dnipro, Ukraine
[*]E-mail: viktor.gasso@gmail.com

Keywords: parasites, semiaquatc snake, central Ukraine, diversity indices

Habitat as a factor for the helminth communities' construction forms the necessary conditions for the development of all stages of the life cycle of parasites. Grass snake is an ecologically flexible species tied to ponds, where it feeds mainly amphibians. The helminth infracommunities of *N. natrix* were selected as an object of the study.

The studies were carried out in two ecosystems of the Samara River basin (Dnipropetrovsk region, Ukraine), which differ in the rate of anthropogenic load: natural floodplain forest (48.76° N, 35.43° E; n = 8) and sedimentation basin of coalmines sewage (48.36° N, 36.41° E; n = 7). The Brillouin's diversity index and the Berger-Parker domination index were used to evaluate the helminth infracommunities. Statistical analysis was performed using the Mann-Whitney test.

We identified six helminth species in *N. natrix* inhabited the studied areas: one species of nematodes (*Serpentirhabdias fuscovenosa*, Railliet, 1899), two species of cestodes (*Ophiotaenia europeaea*, Odening, 1963; *Spirometra erinaceieuropaei* (Rudolphi, 1819)) and 3 species of trematodes (*Encyclometra colubrimurorum* (Rudolphi, 1819), *Telorchis assula*, Dujardin, 1845, and *Macrodera longicollis* (Abildgaard, 1788)). Five species of them need to go through the developmental stages in amphibians and invertebrates before the invasion into grass snake.

An average of 3.25 parasite species was found in infracommunities of helminths in the snakes from natural forest ecosystems, which is 2.5 times higher than in the communities of the anthropogenically transformed ecosystems, where 85.7% of the surveyed snakes are infected with only one species of *S. fuscovenosa.*

The Brillouin's ($p = 0.009$) and Berger-Parker ($p = 0.005$) indices revealed statistically significant differences between the ecosystems. That is because the *N. natrix*'s helminth infracommunities from the natural ecosystems are much more varied and balanced in their species composition.

Comparison of the results suggests that with an increase in the anthropogenic load, the helminths' infracommunities of the grass snakes simplifies due to considerably higher diversity of possible intermediate hosts in natural ecosystems. Thus, an infracommunity of parasites of complex life cycles may be an indicator of aquatic and semi-aquatic ecosystems state that requires further research.

The influence of disturbance on functional traits and invader establishment

Gabrielle Lebbink[1*], *Rod Fensham*[2], *John Dwyer*[1]

[1]University of Queensland, St Lucia, Queensland, Australia
[2]Queensland Herbarium, Mount Coot-tha, Queensland Australia
[*]E-mail: gabrielle.lebbink@outlook.com

Keywords: *Bothriochloa pertusa*, grazing, fire, competition

Invasive plants are a leading cause of biodiversity decline worldwide. Understanding the mechanisms which facilitate the dominance of invasive flora is important for informing and prioritising management strategies. There is considerable evidence to suggest disturbances, such as changed grazing or fire regimes increase establishment opportunities for potential invaders. Depending on the characteristics of the disturbance and the trait composition of the resident community, disturbance can favour the growth and persistence of some species more than others leading to changes in the community's functional composition. By investigating the relationship between the post-disturbance functional composition and the likelihood of invasion by exotic species we can enhance our understanding of the factors determining invader success under different disturbance regimes. By implementing novel disturbance regimes (grazing and fire) in an Australian rangeland ecosystem, we explore these relationships in determining the invasion success of the invasive perennial grass species *Bothriochloa pertusa*. Specifically, we will address the following questions; 1) How does disturbance influence species and trait composition? and 2) Does the post-disturbance functional composition of the native "recipient community" influence the likelihood of invasion by B. pertusa?

Aquatic macroinvertebrate community as indicator to assess a Neotropical river through an Index of biotic integrity

Eugenia López-López[1*], *Ricardo A. Ruiz-Picos*[1], *J. E. Sedeño-Díaz*[2]

[1]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México
[2]Coordinación Politécnica para la Sustentabilidad, Instituto Politécnico Nacional, CDMX, México
[*]E-mail: eulopez@ipn.mx

Keywords: macroinvertebrate traits, land cover and land use, landscape

Rivers are among the most threatened habitats in the world due to their high degree of connectivity with their environment and are considered as integrative systems of their watershed. Modification in land use exert strong effects in these aquatic ecosystems. Indices of Biotic Integrity are a usefulness tool to assess human impacts on rivers. However, there is a need to develop a methodology that allow the detection of the metrics that recognize the impacts exerted by human on the river, particularly in Neotropical rivers. The goal of this study is to develop an IBI based on macroinvertebrate metrics, land uses coverage and water quality and to assess the combination of metrics that best recognize the biotic integrity of streams. We used the sub-basins of the Apatlaco and Chalma-Tembembe rivers (Balsas Basin, México) as study case, which pose a mosaic of land uses (agriculture, urban, and natural vegetation). The study includes 20 study sites in four season (rainy and wet periods). We used 51 descriptive metrics including land use, Physicochemical Water Quality Index, metrics of aquatic macroinvertebrates and ecological indices, BMWP index, functional feeding groups and respiratory modalities. Five IBI modalities were tested with different number and types of attributes, which were previously selected by a Factor Analysis. The IBI that best recognize the impacts of human activities and was capable to detect spatial and seasonal differences included 25 of the 51 metrics: 4 of land use, 5 of metrics and 5 of diversity indices, 7 of feeding functional groups, 2 of respiratory modalities, the BMWP and Physicochemical Water Quality Index. The IBI developed in this study, as validated through all the tests conducted, is a reliable, sensitive and has a great discriminatory capacity being a usefulness tool to evaluate the water quality of the Apatlaco and Chalma-Tembembe rivers. The IBI designed was suitable for detecting the areas to be preserved with the best conditions, identified the sites that should be included in restoration programs (the urban river zone of the Apatlaco River); and also detected sites that should be protected, as was the case of the agriculture zone of both rivers.

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Trophic levels: Differences and modifications for the fishing activity in Campeche, Mexico

Julia Ramos[1], Domingo Flores[2], Silvia Salas[2], Miguel Cabrera[2], Jorge A. Lopez[3], Francisco Gomez[1], Luis Ayala[4], Misael Sosa[1]*

[1]Instituto Epomex, Univerisidad Autonoma de Campeche, Campeche, Mexico
[2]Centro de Investigacion y Estudios Avanzados (CINVESTAV), Merida, Mexico
[3]Universidad Nacional Autonoma de Mexico (UMDI-Sisal), Sisal, Mexico
[4]Universidad Autonoma Metropolitana Xochimilco, Ciudad de Mexico, Mexico
[*]E-mail: julramos@uacam.mx

Keywords: trophic level, fishing activity, Campeche, Mexico

One of the principal characteristics of the marine, estuaries and lagoon ecosystem, is their trophic composition because the depredation is a central process for the wild. Nevertheless, the fishing activity can inside by means of species trophic level of the trophic network, because normally fishing activity is focused in the depredators because are the biggest species or in the species with the higher market price. In Campeche, at the south of the Gulf of Mexico there are 10,907 peoples that work in artisanal fisheries. This activity is registered in 13 landing fishing sites, the most important in accord with landings are Champoton and Cd. Carmen. For several years the artisanal fisheries have increased, generated problems such as decreasing catches. Nerveless in spite of this, has not been assessed, how the trophic structure of the fish community of the catch is composed himself, and if this is variable with the time and space. In this work, the trophic structure of fisheries resources community that are captured under the artisanal fleet was assessed in two fishing ports (Champoton and Cd. Carmen). The information of species catch was obtained directly of each fishing boat in each port (May 2017 to May 2018). We registered also the landing (kg) and price. The trophic level (TL) of each species was obtained directly by FishBase. First, we determined the Index of landing important (IIPC) using the percentage of weight (C), of market price (V) and of the frequency (F), (IIPC= %C + % V + % F) of the species caught for select the most important species (Ojeda y Ramirez, 2012). Each one was assigned with the TL, and we compared the TL of community between both ports. Champoton and Carmen are different TL structure community (Kruskal Walli test, $p<0.05$) and this are variable in the time in accord with species seasonality. In Carmen port fish activity are focused at shrimp, , and fish; so, the TL 2-2.49 and 4.5-4.99 are the most representative a difference of Champoton where the TL > 4 are representing because the fishing activity is over fish key species, while if the average TL are similar for both ports (TL 3.9 and 3.8 for Champoton and Carmen respectively. The impact in the TL > 4 in Carmen is important and show that in the future the trophic level can be demised for the overfishing effort. Arreguín-Sánchez and Arcos-Huitrón (2011) realized a study about the TL in different fishing ports of Mexico and signaled for the Campeche Bank that 20% of species are collapsed, 35.5% are over-exploited, 38.2% are harnessing. The future of the fish communities are a high spot, we need to be addressed and to develop strategies for the fishing control.

Acknowledgments

The authors appreciate to CONACYT-Mexico, by the economic support through the project: 000000000252215, Caracterizacion de la pesca artesanal en la peninsula de Yucatan: identificando unidades de manejo (Characterization of the artisanal fisheries in Yucatan Peninsula: identifying management units).

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Parasitic plant creates ephemeral belting pattern in a reservoir banks

Nicole Salvatori[1,2], Francesco Giannino[3,4], Fabrizio Carteni[3,4], Maurizio Zotti[3], Gaspare Casarano[3], Stefano Mazzoleni[3,4,5], Giuliano Bonanomi[3,5]*

[1]DI4A, Department of Agri-Food, Environmental and Animal Sciences, University of Udine, via delle Scienze 206, 33100 Udine, Italy
[2]Life Science Departement, University of Trieste
[3]Department of Agricultural Sciences, University of Naples Federico II, via Università 100, 80055 Portici, Italy
[4]Laboratorio di ecologia applicata e sistemi dinamici, University of Naples, Federico II
[5]Task Force on Microbiome Studies, University of Naples Federico II, Naples, Italy
[*]E-mail: nicole.salvatori@phd.units.it

Keywords: vegetation pattern, plant-plant interaction, mathematical modelling, soil water content, *Cuscuta* spp., *Xanthium italicum*

In nature regular vegetation patterns occur due to several environmental conditions and interactions among organisms with biotic or abiotic factors (Bonanomi et al. 2014). Furthermore, these factors can also produce transient patterns which, in the long time, would lead to homogeneous states (Hasting et al. 2018).

Recently, we have observed a newly emerged transient vegetation pattern in a reservoirs banks in Alento lake (40.315503 N, 15.106814 E). A plant-plant interaction between *Xanthium italicum* and *Cuscuta* spp., a known parasitic plant, has created an interesting vegetation belting pattern due to the seasonal decrease of the water level of the reservoir. In particular, each year in November the lake submerges the organisms switching off the dynamic. Furthermore, when the water level of the reservoir goes down (about 11 meters from May to November 2018) creates open space for the germination of *X. italicum*. Then, about a month later, also *Cuscuta* germinates, attacking and killing *X. italicum*. When all *X. italcum* plants are dead, *Cuscuta* proceeds downward the banks of the reservoir, since on the upper level there are no hosts for the parasitic plant. Measurements of the water content carried out in September and October 2018 have shown that desiccation of plants was not dependent on soil water depletion.

The data collected in this area have shown some interesting results. In fact, while in the previous years *Cuscuta* had created rings by attacking *X. italicum*, this year (2018) the interaction among the two species has generated well defined belting patterns. Within the pattern, three stripes can be identified: the belt closest to the lake is represented by healthy plants (green belt), this is then followed by a stripe of *Cuscuta* attacking *X. italicum* (yellow belt) and, finally, in the last stripe only dead plants occur, both *X. italicum* and the parasitic species (brown belt). Furthermore it has been observed that the width of the belts depend on the slope of the area (Figure 1).

The dynamic has been also modelled with a simple Lotka-Volterra ODE with the addition of the dynamic of the water of the lake; the model has been then validated with different sloped levels. The model could be then used to test some hypothesis about the emergence of this phenomenon according to slope, water dynamic and different initial conditions of X. italicum and Cuscuta.

Finally, it would be interesting to use the combination of the mathematical model and the data collection in the same area in the following years, in order to reveal the dynamic underlying this process.

Figure 1. Pictures of the study site with clear vegetation belting pattern.

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Ants shape functional diversity and community assemblage of epiphytic lichens in montane *Abies alba* forests

*Renato Benesperi, Paride Balzani, Elisabetta Bianchi, Maria Beatrice Castellani, Luca Di Nuzzo, Filippo Frizzi, Alberto Masoni, Federica Morandi, Giacomo Santini**

Department of Biology,University of Florence, Florence, Italy
*E-mail: giacomo.santini@unifi.it

Keywords: red wood ants, lichens, impact, imported species

The Formica rufa group comprises several ant species which are collectively referred to as 'red wood ants' – RWA (Stockan and Robinson 2016). These ants are usually numerically and ecologically dominant and may influence the structure and dynamics of the habitats they colonise. Owing to these features, several RWA species have been used as biological control agents. In Italy, nests collected from the Alps were transplanted to various sites along the peninsula where they were formerly absent. However, the same features that made these species interesting as control agents make them potentially dangerous for other organisms, as is suggested by the literature on the ecological interactions of RWA within their native range of distribution. A recent investigation (Frizzi et al. 2018) on the fate and ecological impact of the populations of one of these species (*Formica paralugubris*) clearly showed that this species has non-negligible detrimental effects on the local invertebrate fauna, but no information exists on the possible effects on epiphytic communities. This study aimed to fill this gap, evaluating whether the presence of this species could affect the structure of lichen communities.

Three *F. paralugubris* nests were randomly selected from the population introduced in the Campigna Biogenetic Nature Reserve (Italy). Six trees *Abies alba* (Mill), located at increasing distances (three within 10 m, and three within 20 m) from the nest were chosen to sample lichen communities. As a control, we randomly picked three points from nearby non-occupied areas and repeated the same sampling design. Lichens were sampled using four standard frames of 10×50 cm as sampling grids, subdivided into five 10×10 cm quadrats, which were verically attached to the tree trunk at three different heights above the soil (with the low side at 0, 50 e 100 cm). At 0 and 100 cm the frames were attached at the cardinal points, whereas at 50cm were rotated 45°. All lichen species inside the frames were listed, and their frequency was computed as the number of the quadrats in which the species occurred. The results allowed to detect subtle effects of ants on the structure of lichen community. Although there was no detectable impact on species richness, a significant difference between impacted and control sites was detected by multivariate analysis. Furthermore, a difference in functional diversity among sites emerged as well, probably as the consequence of a selective action of ants on some species.

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A multimetric index based on aquatic macroinvertebrate community to assess the biological condition in neotropical rivers of Mexico

J. E. Sedeño-Díaz[1*], *Eugenia López-López*[2]

[1]Coordinación Politécnica para la Sustentabilidad, Instituto Politécnico Nacional, CDMX, México
[2]Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, CDMX, México
[*]E-mail: jsedeno@ipn.mx

Keywords: macroinvertebrate assemblage, aquatic ecosystem assessment, biotic index

Multimetric indices are combinations of individual measurements such as richness and composition of taxa, tolerance values, abundance or functional groups that, together, are supposed to represent the response of an assemblage or community to human disturbances. In the case of aquatic macroinvertebrates, multimetric indices are among the most widely used approach, and have become standard tools for bioassessment. In Mexico, biomonitoring is unusual for assess the water quality. However, in this study a multimetric index was implemented using family level macroinvetebrate data from Tuxpan and Tecolutla rivers of Mexico (which drain to the Gulf of México) in order to assess the ecological status of these water bodies. Five study sites in homologous sections (upper, middle and lower portions) of each river were chosen. Samples of macroinvertebrates were collected using a kick net from riverbed covering a large diversity of habitats. Seventeen metrics of macroinvertebrate community were incorporated in this index of biotic integrity (IBI), which falls into six general categories: a) Richness (total number of taxa), b) Composition (%EPT, % Odonata, % Diptera), c) Tolerance/intolerance (% Dominant taxon, EPT/Chironomidae, Baetidae/Ephemeroptera), d) Abundance (Abundance of Chironomidae), e) Diversity (Shannon-Wiener Diversity index and Pielou Evenness index), and f) Biological traits (respiratory modes). Selection of metrics was carried out taking into account metrics whose predicted response increase (v.g. % odonata, abundance of chironomidae) or decrease (v.g. total number of taxa, evenness) with human impact. Each metric was standardized considering the 95th percentile; then, the range of each metric was divided in a scale of four values (score from 1 to 4) such that the maximum value of IBI is 40, and a minimum value of 10. When the metric increased with human disturbance, the score was assigned in reverse. In order to establish critical values to classify the study sites according to state of their biological condition, the reference site was considered as one whose difference was not greater than 5% of maximum value of IBI. The final score for rivers Tuxpan and Tecolutla fluctuated from 31 to 49 units; from these, only three samples reached the category of Excellent, 29 were classified as Good, and 8 as Regular. This a first attempt to include respiratory modes in an index of Biotic Integrity, because the currently condition of rivers in Mexico. This IBI allowed assess the ecological condition of Tecolutla and Tuxpan rivers based on macroinvertebrate fauna.

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Neutral effect of common milkweed (*Asclepias syriaca*), an invasive plant species on wild bee (Hymenoptera: Apiformes) communities

Viktor Szigeti[1], Boglárka Berki[2], Márton Vörös[3], Annamária Fenesi[4], Anikó Kovács-Hostyánszki[1]*

[1]Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary
[2]University of Veterinary Medicine, Budapest, Hungary
[3]University of Szeged, Szeged, Hungary
[4]Hungarian Department of Biology and Ecology, Babeş-Bolyai University, Cluj-Napoca, Romania
[*]E-mail: szigeti.viktor@gmail.com

Keywords: plant-pollinator interaction, introduced species, floral resources

Invasive plant species often become dominant after establishment and decrease the diversity of native vegetation. It might affect the related insect communities such as pollinator insects too, through e.g. altered flower resources. The effect of invasive plants on pollinators can be negative, positive or neutral, depending on various circumstances. The expansion of common milkweed (*Asclepias syriaca* L., Apocynaceae) is a serious conservation and agricultural problem in Hungary, central Europe, however, its effects on pollinators have not been studied so far. We focused on plant and pollinator communities in ten pairs of invaded (>25% of milkweed coverage) and control (<3%) sandy old field sites. We sampled floral resources and wild bees (Hymenoptera: Apiformes) along two 100m transects per site, before, during, and two times after the flowering of milkweed. We used p-value adjusted paired Brunner–Munzel tests to analyse the difference in abundance, species richness and diversity of flowers and bees between invasive and control sites and non-metric multidimensional scaling (NMDS) to analyse species compositions. We found that the flower abundance was higher in control than in invaded sites before flowering of milkweed, while there were more flowers in the invaded sites during flowering of milkweed. In contrast the diversity of flowers was lower in invaded sites during flowering of milkweed. We found no difference between the invaded and control sites in flower abundance and diversity after the flowering of milkweed, and no differences in the number of flowering plant species at all during the whole season. The number of bee species was higher in control sites shortly after the flowering of milkweed, while the opposite pattern was found later in the season. We found no difference between the invaded and control sites in the abundance and diversity of wild bees in any sampling periods. The invasion of milkweed had no effect on the species composition of wild bees and flowering plant species. However, species composition of flowering plants, as well as the abundance, species richness and diversity of flowering plant and wild bee species varied among the sampling periods. Our results suggest that the common milkweed had basically a neutral effect and did not affect importantly the flowering plant and wild bee communities in sandy old fields. These results can be explained by 1. the spatial scale of our study: milkweed is abundant in the studied region of Mid–Hungary for decades, therefore it has probably a persistent effect on the wild bee communities at a large spatial scale. 2. In contrast to several other invasive plant species in various habitats, milkweed does not cover more than 20-60% in dry sandy vegetation, does not replace all native species, still any shadow that milkweed offers can have

a positive micro-climatic effect on the underneath vegetation. Besides, milkweed may offer extra foraging resource for wild bees for several weeks. Despite the lack of negative effects of milkweed in the studied highly degraded sandy old fields, its invasion may cause serious conservation problems in the more natural sites, as well as in agriculture. Nevertheless our results suggest that the effect of invasive plant species on plant and pollinator communities can be various at different temporal and spatial scales, and might be neutral or even beneficial to a certain extent.

Functional response of alpine grassland species in the recolonization process of eroded areas

Rita Tonin[1*], *Stefan Zerbe*[1], *Michael T. Löbmann*[1], *Camilla Wellstein*[1]

[1]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bolzano, Italy
[*]E-mail: rita.tonin@unibz.it

Keywords: shallow erosion, functional traits, recolonization

Shallow erosion on steep grasslands occurs frequently in mountain areas. It results in the removal of vegetation cover and degradation of soil with a consequent loss of related ecosystem services. During the last decades, an increase of this phenomenon has been detected on pastures and meadows in the Alps. The role of vegetation in contrasting erosion process has been examined, however, mostly in forests and shrublands. With our study in South Tyrol (N Italy), we aim to investigate the recolonization process of eroded areas by grassland species. We made a preliminary investigation of the ecological strategies adopted by plant species in the process of recolonization. Therefore, we analysed intraspecific functional traits' differences between individuals growing inside the eroded spots and in the surrounding meadow. A first field campaign was carried out during summer 2018 on two study sites interested by shallow erosion in South Tyrol within the Puez-Geisler Nature Park. At each site, we selected three eroded areas. Leaf functional traits were determined for seven vascular species growing within the three eroded areas and three controls in the surrounding meadow. We chose traits well-known in scientific literature to be important in defining plant ecological strategies, i.e. leaf area (LA), specific leaf area (SLA) and leaf dry matter content (LDMC). The species were chosen based on their presence both in the eroded areas and the meadow.

Results show a clear trend for SLA that is always significantly lower in the eroded areas compared to the meadow. Regarding LDMC, three from seven species show significantly higher values of the trait in the eroded areas. LA yielded no significant results. Lower SLA and higher LDMC are most likely indicative of reduced growth rate and leaf turnover in individuals that are recolonizing the spots interested by shallow erosion. These tendencies could represent a reaction to drought stress experienced by plants in eroded areas. Indeed, water loss through leaves can be regulated by decreasing SLA and increasing LDMC.

This research has been conducted within the international project "Shallow erosion dynamics in mountain grasslands of South Tyrol: Monitoring, process analysis and mitigation measures (EroDyn)". Our intention is to extend the analysis to more functional traits and eroded areas to identify those characteristics that would increase the probability of a future restoration experiment to succeed. Our results can contribute to appropriate restoration management of mountain grassland.

Biodiversity and ecosystem functioning

Ecology of tropical temporary ponds at the University of the West Indies, Mona, Jamaica

Gavin Campbell[1*] *and Eric Hyslop*[1]

[1]University of the West Indies, Kingston, Jamaica
[*]E-mail: gavinrcampbell@outlook.com

Unlike a permanent body of water, a temporary body of water has a recurrent dry phase. As a unique and ubiquitous habitat, temporary bodies of water may harbor rare species found in no other habitat. The project aims to identify the successional series of species of fauna of tropical temporary ponds.

The two temporary ponds being examined are located at the University of the West Indies, Mona. The first pond lies behind the Mona Information Technology System (MITS) building (18.00339181, -76.74462356), while the second lies near Mary Seacole Hall (18.0049006, -76.74409247). Data were collected weekly from November 2017 to January 2019, including pond characteristics, biological samples and environmental data. Biological samples were collected by kick nets by 1-3 large sweeps of the ponds, frozen for nutrient analyses then stored in jars of 10% formalin.

Throughout the course of data collection particular patterns have been noted. Immediately after a rain shower in a dry pond area, adult dytiscid beetles, veliids and notonectids are found to inhabit the MITS pond. As the hydroperiod is lengthened, dragonfly nymphs, ostracods and chiromonid midge larvae become established. As the pond is kept inundated, tadpoles are able to develop, giving preliminary insight into the ecological succession of tropical temporary ponds. Data thus far have shown these two temporary ponds supporting 29 different aquatic species throughout their hydroperiods. The research is essential in identifying the responses to rapid environmental change at the community level, and the corresponding changes in ecosystem functions.

Examining natural and artificial renewals in red oak stands in relation to their effects on regrowth and natural vegetation

Tamás Marcsisin[1*], *Gergely Király*[1]

[1]Institute of Sylviculture and Forest Protection, Faculty of Forestry, University of Sopron, Sopron, Hungary
[*]E-mail: Marcsisin.Tamas.Mate@phd.uni-sopron.hu

Keywords: *Quercus rubra,* regrowth, natural vegetation, seedlings, diserve

The share of red oak (*Quercus rubra* L), originated from Atlantic North America, is approximately 1% in the Hungarian forest. Its expansion may be considered minimal country wise; it can be still significant in some regions (Koloszár 2010). This species mostly viable on acidic sand soil (Nyírség and Somogy) and sparsely in mountainous regions with acidic soil. The scope of its timber utilization is expanding (Vancsura 1960). Its plentiful and regular acorn yield (Lámfalussy 1950) offer unexploited opportunities for natural renewal. For this reason, it is considered an alternative in forestations, and in stand replacements of both native and not native tree species. Since it is not a native species in Hungary, its usage is prohibited or limited in many regions for conservation reasons. Several phytocoenologial research have shown that red oak stands tend to be less diverse.

Our goals were to asses the possibilities of the red oak's natural regeneration and its effects on the native vegetation.

The field surveys were conducted between October 2016 and January 2017, in the naturally renewed forest-subcompartments of Encsencs 8F and 11B, in the Nyírlugos Forestry. To ascertain the growth ratio and timber volume of the maternal stand, we used individual surveys. We measured the height dimensions with 1 m accuracy. To assess the sapling count of the regrowth per hectare in 2016, we used 40 cm wide (0,5m^2 area) sample circles with random distribution. We used 30 sample circle in Encsencs 8F and 20 in Encsencs 11B. In 2017, the circle method was no more viable, because of the growth of the sampling. For this reason, we switched to parcel method with dimensions of 6x8 m. Also this method was used in Nyírbéltek 39B, where a 1.1 hectare artificial renewal was designated.

During the first surveys, we counted 1047 samplings in total in Encsencs 8F, which means an average of 700,000 samplings/hectare. In Encsencs 11B, we counted 511 samplings in total, which means an average of 520,000 samplings/hectare. In the second year, we found a small decline in sampling numbers: 5870,000 samplings/hectare in Encsencs 8F and 470,000 samplings/hectare in Encsencs 11B. In Nyírbéltek 39B, we counted 483 samplings in the survey area, which means an average of 483,000 samplings/hectare.

In our opinion, the variants of natural renewal technologies applicable in red oak stands must be adjusted for the main used cutting methods and for the adjacent naturel renewal options. As the examples previously showed, not only the gradual renewal cutting, but the clear cut like renewal cutting has a reality, if there is an adequate regrowth beneath the maternal stand. The vegetation of the undergrowth had low diversity, even the phytocoenologialy com-

mon species (*Urtica dioica, Stenactis annua, Asclepias syriaca, Mycelis muralis*) occurred only in small numbers. From conservation perspective, red oak has a clear negative effect on the native vegetation.

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Context-dependent responses of alpine grasslands communities along elevation

Gabriele Midolo[1*], *Patrick Kuss*[2], *Camilla Wellstein*[1]

[1]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bolzano, Italy
[2]Institute of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland
[*]E-mail: gabriele.midolo@natec.unibz.it

Keywords: functional diversity, altitudinal gradient, land-use disturbances, L-H-S strategy

Composition and function of alpine plant communities along elevational gradients strongly depend on temperature conditions. However, little is known about whether the direction of such relationship is shaped by other environmental conditions along the gradients. Here, we tested whether temperature change along elevation interacts with precipitation, soil properties and land use disturbances, determining context-dependent patterns of species diversity and functional composition in alpine plant grassland communities. We combined climatic and soil data with 236 vegetation releves conducted in oligotrophic alpine grasslands of the Swiss Alps along a 1900 m elevational range. We used species richness, the cover of plant functional groups (forbs and graminoids), and the community weighted mean (CWM) of specific leaf area (SLA), plant height and seed mass, as response variables in our analysis. We found that the patterns of species diversity and functional traits response to temperature depend on environmental and land-use disturbance conditions. Species richness decreased with mean summer temperature (MST) only along sites with low precipitation. The abundance of forbs along the temperature gradient followed an opposite pattern depending on soil pH, with forbs cover increasing with temperature only along more acidic soil (pH ~ 5) compared to neutral (pH ~ 7). The abundance of graminoids increased significantly with temperature only in pastures, while fallows and meadows showed a non-significant trend. Finally, land use disturbances of the grasslands also played a relevant role affecting plant functional traits at the community level. We found CWM_{SLA} and CWM_{Height} to increase with increasing temperature in meadows and pastures, while in fallows CWM_{SLA} and CWM_{Height} followed a weak opposite trend. Our results shows that precipitation, soil pH and land use play a key role to shape herbaceous plant assemblages along elevational gradients in alpine environments. Moreover, the different sensitivity of various response variables to different environmental factors and land-uses underline the importance of integrating multiple dimensions of plant communities into large-scale assessments.

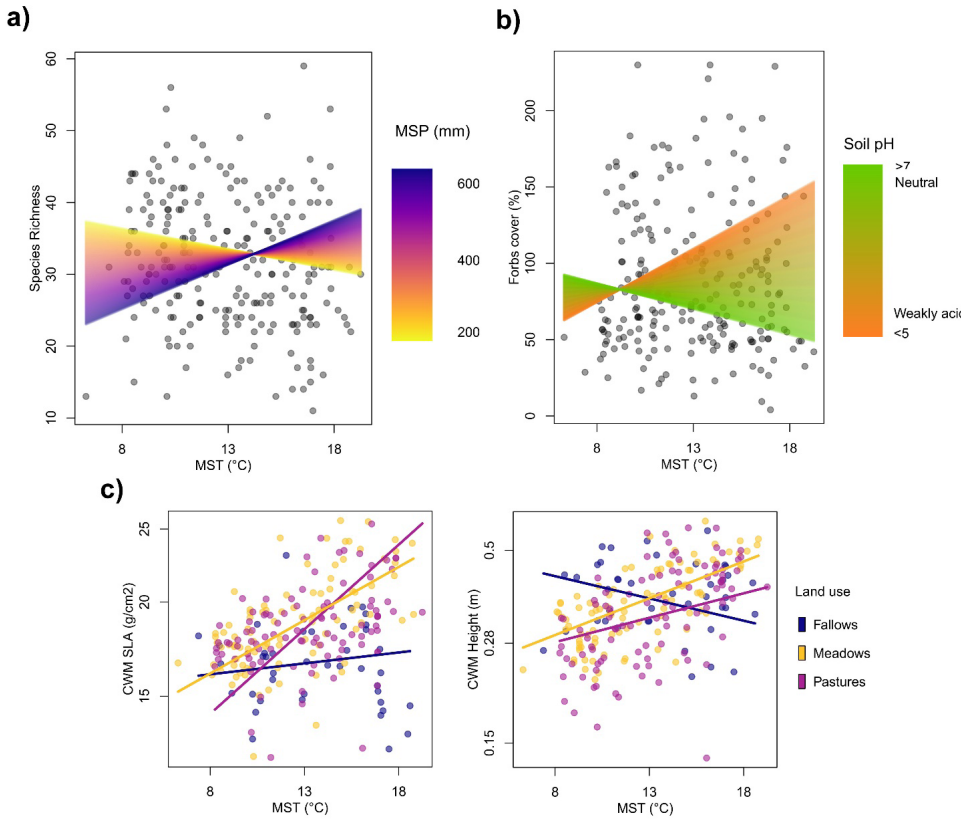

Figure 1. Graphical representation of the most parsimonious linear regression models capturing context-dependent responses of alpine grasslands communities along the temperature gradient analysed. The relationship with mean summer temperature (MST) is affected by mean summer precipitation (MSP) for species richness (a), by soil pH for total forbs cover (b), and land-use disturbances regimes for the community weighted mean (CWM) values of specific leaf area (SLA) and plant height (c).

Dredging disturbance imprinted in the structure of benthic communities: The case of the Port of Cervia

Barbara Mikac[1], Massimo Ponti[1,2], Marina Antonia Colangelo[1,2], Marco Abbiati[1,3]*

[1]Interdepartmental Research Centre for Environmental Sciences, University of Bologna, Ravenna, Italy
[2]Department of Biological, Geological and Environmental Sciences, University of Bologna, Ravenna, Italy
[3]Department of Cultural Heritage, University of Bologna, Ravenna, Italy
[*]E-mail: mikacbarbara@gmail.com

Keywords: dredging, benthos, impact, Adriatic

Dredging activities are regularly performed in front the entrance of most of the ports worldwide in order to remove subtidal sandbars, continuously accumulated due to coastal sediment dynamics, and assure minimum depth needed for access. These operations may have severe negative chemical, physical and biological impacts on marine environment (Manap & Voulvoulis, 2015) as well as high economic costs. As possible environmentally and economically friendly alternative, a new technology for seabed maintenance based on "ejectors", intended to prevent sediment accumulation, is under development. The goal of this research was to analyse macrobenthic communities exposed to dredging activities in front of the Port of Cervia (northern Adriatic Sea) and in the nearby not affected areas, that would serve as a baseline for the evaluation of impacts of new technology that is going to be experimentally deployed in front of this port.

Samples were taken in Spring 2018 in the dredged location in front of the Port of Cervia just couple of weeks after the operations and in four control locations, placed 600 m and 1200 m north and south of the impact, at 2-3 m depth range. Two sampling areas were defined in each location and at each area 4 replicated samples of sediment and fauna were taken by SCUBA diving using an aluminium frame (23.5×13.5 cm). In each sample analyses encompassed sediment grain size, percentage of organic matter, dry weight of shell debris and benthic macrofauna (after sieving on 0.5 mm mesh sieve) determination to the lowest possible taxonomic level. Univariate and multivariate analyses were done using software Primer v 6 and PERMANOVA+.

Altogether 80 macrofaunal taxa were recorded. Structure of benthic communities was significantly different among sampling locations but not between areas within each location. Dredged location indicated clearly different structure of benthic communities from control ones and showed much higher variation among samples (Figure 1). Impacted communities were characterised by drastically lower species diversity and abundance (Figure 2a, 2b). SIMPER analyses (90% cut off) showed that average similarity in species composition and abundance between samples in control locations was very high (81% to 85%) and due to only three most abundant bivalve species: *Lentidium mediterraneum, Donax semistriatus* and *Chamellea gallina*. On the other hand similarity between samples in impacted location was only 37% (characterised by *L. mediterraneum* and *C. gallina*). Very high dissimilarity (75% to 80%) in species composition and abundance between impacted and control locations

was due to a drastic decrease of abundance of the same three bivalve species on impacted location. Amount of shell debris and the percentage of medium sand (>250 μm) in the sediment were the parameters that had the highest correlation (Rho = 0.716) with the structure of benthic assemblages.

Our results indicate that dredging activities had negative impacts both on species richness and abundance, however the settlement of opportunistic species on impacted location was not reported. The three bivalve species mostly characterising benthic assemblages on all locations belong to species sensitive to disturbance, which are characterised by relatively long life, slow growth and high biomass (Simboura and Zenetos, 2002). Communities that are characterized by sensitive species in general show strong effects and slow recoveries of dredging (Kotta et al., 2009). Moreover *Chamelea gallina* is edible mollusc thus negative impact of dredging on this species, might have economic implications. Several tens of taxa present in control samples weren't recorded in impacted ones. Although these species weren't very abundant their ecological importance in benthic communities cannot be neglected. Careful analyses of life traits of these species will have to be performed in order to understand eventual shifts in the functioning of benthic communities.

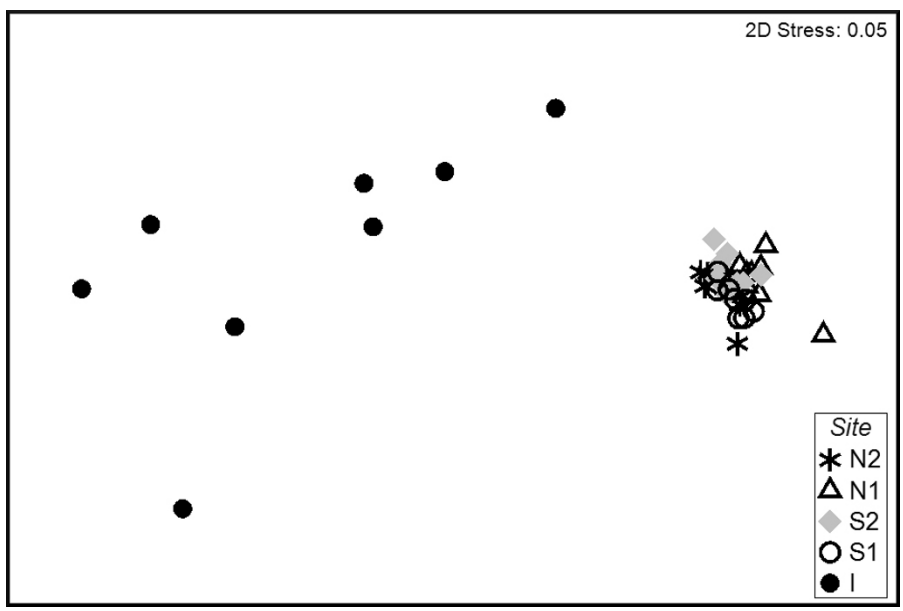

Figure 1. Non-metric MDS ordination plot (Bray-Curtis Similarity; square root transformation) comparing structure of benthic communities between impacted and control sites. N1, North 600 m; N2, North 1200 m; S1, South 600 m; S2, South 1200 m; I, impact.

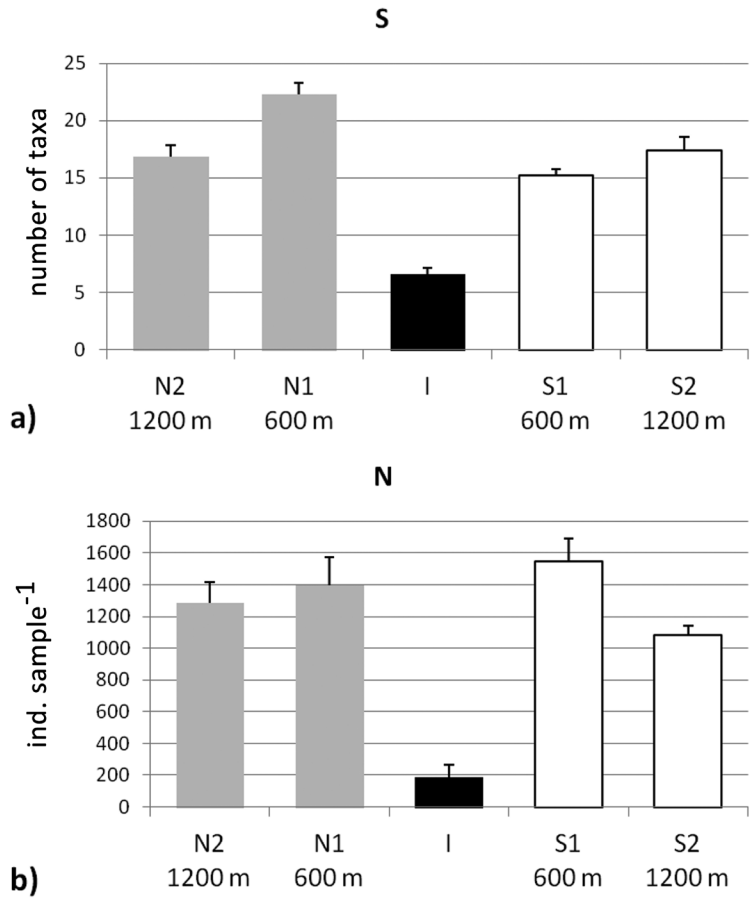

Figure 2. Mean (± SE) number of taxa (a) and abundance (b) at control (N1, N2, S1 and S2) and impact (I) locations.

Acknowledgments

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Tell me what you eat and I will tell you what you are: Trophic variety of hoverflies (Diptera: Syrphidae) in Southeast Europe

Snežana Popov[1*], *Marija Miličić*[2,3], *Ante Vujić*[1]

[1]Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia
[2]BioSense Institute-Research Institute for Information Technologies in Biosystems, University of Novi Sad, Serbia
[3]LIBRe – Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland
[*]E-mail: snezana.jovicic@dbe.uns.ac.rs

Keywords: forests, insects, larvae, phytophagous, pollinators, saproxylic, vegetation, zoophagous

Biodiversity continues to decline all over the world, significantly affecting ecosystem structures and processes. Recent decline in wild pollinators clearly threatens pollination services, which can lead to serious consequences in terms of disruptions of plant-pollinator interactions. Hoverflies play a significant role in the pollination in agricultural and natural systems, and their associations with vegetation has been well documented. While adult mostly feed on nectar and/or pollen, larvae exhibit various spectrum of feeding resources, such as decaying vegetation, bulbs, aquatic detritus, wet wood, etc. The objective of the present study was to assess hoverfly species richness within different vegetation classes in Southeast Europe (SE Europe) and to evaluate representation of specific larval trophic groups in the sample. Additionally, spatial variation of larval trophic groups across different vegetation classes was addressed. All documented species in SE Europe (N=564) were each assigned to one of five larval trophic groups: saproxylic, phytophagous developing in bulbs, phytophagous developing in roots, saprophagous and zoophagous. Results have shown that relative frequency of the different feeding groups varied significantly across Southeast Europe (χ^2 (4) = 76.46, p = .00), as well as across different vegetation classes. Not surprisingly, species with zoophagous larvae dominated among Southeast European hoverflies. These species can be considered generalist species, not directly dependent on specific vegetation. Thus, suitable environment for the development of these species can be found across different vegetation classes.

Acknowledgments
This work was supported by the Ministry of Education, Science and Technological Development, Republic of Serbia, under Grant No. 4300, the Provincial Secretariat for Science and Technological Development under Grant No. 114–457– 2173/2011–01 and H2020 Project "ANTARES" (664387).

Diversity partitioning

Temporal and spatial changes in composition have stronger relationships at species and phylogenetic levels than for traits β-diversity

Oscar Peláez[1*], *Carla S. Pavanelli*[1,2]

[1]Programa de Pós Graduação em Ecologia de Ambientes Aquáticos Continentais, Universidade Estadual de Maringá, Maringá, Brazil
[2]Núcleo de Pesquisas em Limnologia, Ictiologia e Aquicultura (NUPÉLIA), Maringá, Brazil
[*]E-mail: oscar.pelaez06@gmail.com

Keywords: temporal turnover, nestedness, environmental heterogeneity, Neotropical fishes, freshwater

In a rapidly changing world, it is necessary to determine which components of diversity undergoes changes over space and time. Variation in composition, more than the number of species, seems to respond to anthropogenic impacts on biodiversity, for instance resulting in biotic homogenization. Although, it is expected that changes at the species level lead to changes in the phylogenetic composition, it is less clear whether taxonomic compositional shifts result in compositional changes in traits. Hence, we aimed to investigate two main questions: i) whether changes in traits composition were related with changes at the taxonomic and phylogenetic levels; and ii) whether temporal patterns of species and functional β-diversity responds in similar ways to environment. We used a dataset of freshwater fish assemblages sampled quaterly between 2000-2016 in the upper Paraná River basin, in Brazil. For the 136 species captured during the surveyed period, we constructed a set of 16 traits measurements, from laboratory and bibliography. The correlations between compositional shifts at the taxonomic, phylogenetic and trait levels were tested using the partition of β-diversity in a turnover and nestedness component. In addition, partial redundancy analyses (pRDA) were carried out to determine the contribution of enviromental, spatial and temporal factors to each component of diversity. Our results show that changes in composition are positively and strongly correlated across space. However, weaker relatioships were observed for temporal β-diversity. Also, that enviroment is a stronger driver of phylogenetic and trait β-diversity, than for species β-diversity. Thus, species β-diversity might have a higher influence of stochastic processes (e.g. ecological drift, random colonization-extiction), whereas trait and phylogenetic composition appeared as more deterministic and less divergent through time, although are influenced by changes at taxonomic level.

Ecological networks

Quantifying interaction strength and sign in food webs: Linking network analysis and simulation

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

[1]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary
[2]GINOP Evolutionary Systems Research Group, MTA Centre for Ecological Research, Tihany, Hungary
[*]E-mail: sandor.piross@gmail.com

Keywords: food web, simulation, perturbation

Food web models serve as a basis for understanding the trophic interactions of ecological communities. Dynamic simulations are useful in investigating and predicting community responses to perturbations, but the efforts and knowledge required to build these models make them available only to a handful of ecosystems. The aim of our study was to investigate how well simple analyses — based on food web structure — can identify key species and important direct and indirect interactions in the trophic dynamics of communities. We used topological network analysis on signed graphs to estimate magnitude and sign of the trophic effects of each species to every other member of the community both in simulated and real food webs. We compared these net trophic impacts with species level responses to perturbations.

Effects of global change

How defoliation frequency affects community and ecosystem stability in native grassland under rainfall manipulation

Felícia M. Fischer[1,2*], *Bruna S. Jorge*[1], *Daniela Hoss*[1], *Bruna R. Winck*[1], *Valério D. Pillar*[1]

[1]Quantitative Ecology Lab, Graduate Program in Ecology, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil
[2]Vegetation Science Group, Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
[*]E-mail: feliciafischer@yahoo.com.br

Keywords: rainout shelters, primary productivity, grazing simulation, plant community, detritivory

Climate change can threaten grassland ecosystem services by altering vegetation functional structure and mediated ecological processes. Such threats can risk the sustainable use of natural rangelands for cattle production. Here we investigate how changes in rainfall alter functional traits and diversity and ecosystem processes of a native grassland under different defoliation frequencies. For this, we run a field experiment adopting a complete randomized block, split-plot factorial design with two factors (rainfall manipulation and defoliation frequency, Fig1). In five blocks, 17 1.1 × 1.1 m main plots in total were submitted to different levels of rainfall manipulation using rainout shelters (decrease) and irrigation (increase) plus controls. In each main plot, three 0.5 m x 0.5 m subplots were submitted to different frequencies of defoliation by clipping. Preliminary results show that though none of the experimental factors changed species composition, rainfall manipulation significantly altered community weighted means and diversity of some functional traits. Also, primary productivity was higher in the low defoliation frequencies, and in plots under rainout shelters (rainfall decrease and control). Invertebrate detritivore activity was only affected by rain treatments, being reduced under rain decrease. Rainfall manipulation treatments affected functional structure, although with different species shifting at each plot. Rainfall decrease did not represent a drought stress for the plant community; on the contrary, rainout shelters acted by boosting plant growth.

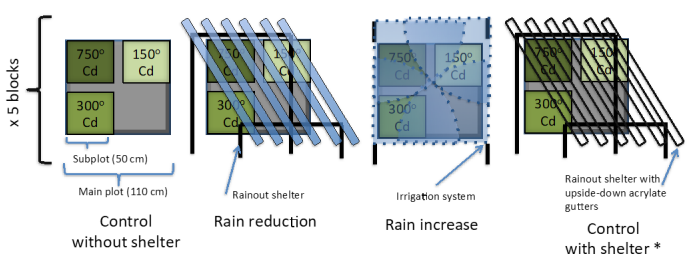

Figure 1. Scheme of the experimental design. Treatments of the main plots are representad by the rain manipulation system; while in the subplots grazing intensity simulation treatments are indicated by the clipping frequency determined by 150, 300 and 750oCd (degree-day sum). * The "control with shelter" treatment was included in only two of the five blocks.

The impact of climate change on stenoendemic alpine plant species in the southern Alps: A research proposal

Francesco Rota[1*], *Camilla Wellstein*[1]

[1]Department of Science and Technology, Free University of Bozen/Libera Università di Bolzano
[*]E-mail: francesco.rota@natec.unibz.it

Keywords: alpine endemic plants, climate change, functional traits, ecotypes

Alpine plant communities are globally endangered by climate change. Endemic alpine species are high threatened due to their eco-evolutionary history having a narrow geographical and altitudinal distribution range.

To assess the functional response of alpine endemic to climate change in the Alps detailed ecological studies are needed. We want to carry out a comparative study that investigate the functional response of different ecotypes of several endemic and stenoendemic alpine species in the southern eastern Alps, an area of high endemism. The functional traits allow to show possible divergent selection pressures across plant populations, the local adaptation and thus to understand the species plasticity against environmental change.

Several species will be selected by analyzing the available floristic data for the Orobie Alps and the Dolomites, looking for endemic and stenoendemic species. After that, the field sampling sites will be choosen. Leaf traits (specific leaf area [SLA]; leaf dry matter content [LDMC]), whole plant traits (height, horizontal stem length), seed traits (i.e. seed mass and seed germination) as well as further below ground and clonal traits will be measured. Microclimate data will be collected with data loggers put in the field. A common garden experiment will allow to deepen the ecotypes responses to environmental change.

We expect to find out how and how much climate change is affecting that species unravelling also biogeographical questions, buffering against uncertainty of future climate scenarios and fostering future conservation actions to preserve these high-threatened species.

Plant and cryptogam communities along elevational gradients on the Majella massif (Italy)

Chiara Vallese[1*], *Alessandro Chiarucci*[1], *Valter Di Cecco*[2], *Luciano Di Martino*[2], *Paolo Giordani*[3], *Chiara Lelli*[1], *Juri Nascimbene*[1]

[1]Department of Biological Geological and Enviromental Sciences, University of Bologna, Via Irnerio 42, 40126 Bologna, Italy
[2]Majella National Park, Botanical Office, Via Badia 28, 67039 - Sulmona (L'Aquila), Italy
[3]DIFAR, University of Genoa, Viale Benedetto XV 3, 16132 Genova, Italy
[*]E-mail: chiara.vallese2@unibo.it

Keywords: bryophytes, global change, lichens, Majella National Park, vascular plants

Among the drivers of Global Change, temperature warming is one of the most impacting on biodiversity. There is growing evidence that the rate of warming is amplified with elevation, thus implying that mountain regions of the world will experiences dramatic effects in terms of species range shifts, lost, and community composition change (e.g thermophilization). The upward shift of species could restrict the habitat for endemic species living in the high elevation environments. Majella massif, located in the central Apennine with a north-south orientation spanning about 20 Km in latitude, is characterized by a high climatic and orographic variation and hosts several endemic and arctic-alpine species. Those characteristics make it a perfect case study in order to evaluate the risks and the dynamics that are threatening plant and cryptogam biodiversity in high elevation environments of Italy. The aim of this study is to evaluate the variation of plant and cryptogam (bryophytes and lichens) communities along a latitudinal and an elevational gradient. We designed a transect across the summit of the massif with a north-south direction and we performed a random sampling of the communities along the elevational gradient. Our preliminary results suggest that there is an effect of the elevational as well as latitudinal gradient in determining community patterns. Moreover, some artic-alpine species seems to be restricted to the highest part of the gradient, tracking the coldest microclimatic niches. This is for example the case of the arctic-alpine lichens *Allocetraria madreporiformis* and *Megaspora verrucosa*, the former being also at the southern border of its European distribution.

Surface trade-off between the largest Italian glacier and vegetation: A thirty-year time-series of remote-sensed imageries

Camilla Wellstein[1*], *Nicola Alessi*[1,2], *Duccio Rocchini*[3,4], *Klaus Oeggl*[2], *Stefan Zerbe*[1]

[1]Faculty of Science and Technology, Free University of Bozen-Bolzano, Bozen-Bolzano, Italy
[2]Department of Botany, University of Innsbruck, Innsbruck, Austria
[3]Department of Biodiversity and Molecular Ecology, Fondazione Edmund Mach, Research and Innovation Centre, San Michele all' Adige, Italy
[4]Centre for Integrative Biology, University of Trento, Trento, Italy
[*]E-mail: Camilla.Wellstein@unibz.it

Keywords: fuzzy clustering, global warming, normalized difference indices

The current retreat of glaciers due to global warming is increasing the extension of new ice-free areas. Thus, a colonization process with pioneer plants is initiating the establishment of alpine plant communities on these emerging sites. An evaluation of the time-lag between the ice retreat and the plant colonization process as well as changes in terms of occupied surface by ice and vegetation could help to make inferences on the developing landscape. Furthermore, these evaluations specified for different vegetation types, increase the understanding of the alpine communities dynamics in times of global warming.

We applied a remote-sensing approach to analyse land-cover changes of the landscape surrounding the Adamello glacier (Province of Trentino, N. Italy) over the last three decades. In fact, remote sensing allows analysing the complete studied area using repeated measures over long time span. Accordingly, we built a time-series of circular Landsat (TM, ETM+) imageries centred at the glacier. We pre-processed the imageries excluding unreliable pixels values of topographically shaded areas, the clouds and their shadows. A fuzzy approach was used to distinguish different land-cover types. The fuzzy clustering calculates the probability for each pixel to belong to different land-cover types, which can be assumed as the proportion of the diverse components of the pixel. Furthermore, to distinguish between different vegetation types, we converted original imageries using normalized difference indices, and thus, increasing the dissimilarity between land-cover types, and in particular, vegetation types. In order to do so, we used the normalized difference indices for vegetation (NDVI), soil (NDSI), water (NDWI) and the modified version for water (MNDWI).

We found a decrease of 25% in the extension of the glacier during the last three decades. Additionally, vegetation cover increased by 13% colonizing the newly evolved ice-free areas. However, we found a time-lag between the retreat of the glacier and the vegetation expansion of about 5 years. The use of normalized difference indices in the fuzzy classification improved the interpretation of the land-cover types, and thus, of the vegetation types. In fact, different vegetation types characterising different altitudinal ranges were detected on the basis of the proportions of NDVI and NDSI. This last finding will allow us to exactly determine temporal and spatial changes among different vegetation types. Our results contribute to the multi-disciplinary project "Calibrating Plant Biodiversity in Glacier Ice (CALICE)" funded by the Euregio (Tyrol Südtirol Trentino) initiative. The project aims to understand plant biodiversity in recent pollen deposition and to reconstruct plant biodiversity changes by means of pollen and eDNA sedimentation in the Adamello glacier.

Conservation biology

Diversity and status of avifauna in Souk Ahras region, North-eastern Algeria

Kaouther Guellati[1*], *Mohcen Menaa*[1], *Ilhem Hemaidia*[1], *Mouna Benradia*[1], *Haithem Khedhiri*[1], *Mohamed Cherif Maazi*[1]

[1]LEAT Laboratory, Department of Biology, Faculty of Natural and Life Sciences, Souk Ahras University, Souk Ahras, Algeria
[*]E-mail: kaouther.guellati@hotmail.fr

Keywords: avifauna, the wetland eco-complexes of Souk Ahras, the Forest of Boumezrane, the city of Souk Ahras, the Medjerda River, conservation

An investigation was done to determine the pattern of distribution and diversity of avian fauna community in the region of Souk Ahras (North-eastern Algeria) and in order to identify the conservation priorities of bird species, we conducted bird counts September 2011 to August 2018 in four habitat types (The wetland eco-complexes of Souk Ahras, the Forest of Boumezrane, the city of Souk Ahras and the Medjerda River). This study area is exploited by winter birds, breeding birds or Migratory birds which need to stop during migrations due to the richness of its habitats associated with an exceptional climatic conditions. A total of 195 species were observed. 80 species were recorded in riparian forests of Medjerda River, 70 were found in the forest of Boumezrane, 57species were found in the wetland eco-complexes of Souk Ahras and 45 species were recorded in the city of Souk Ahras. Overall, 65 of 195 species were resident breeding species. We noted 52 rare and protected species, only four endangered species, and nine endemic species to the Maghreb and/or to North Africa. The presence of these species with patrimonial value reinforces the importance of the conservation of Souk Ahras avifauna. Some species have become so vulnerable that in the absence of a real national policy of management and conservation, where one would reach their final loss in the coming decades. We consider our work as a complementary basic tool for the management of wildlife species and natural environments, in order to limit the rate of loss of this significant center for biodiversity.

Vegetation comparison between nature conservation area of Deogyusan National Park, Korea and its periphery and the implications

Jeong, Sung Chan[1], *Kim, Kee Dae*[1*]

[1]Department of Environmental Education, Korea National University of Education, the Republic of Korea
[*]E-mail: kdkim@knue.ac.kr

Keywords Deogyusan, national park, vegetation, *Pinus densiflora – Quercus variabilis* community, conservation

The purpose of this study is to conduct the vegetation survey on the small scale area of Mt. JukSang, Mt. JoHang and Mt. Bonghwa near Deogyusan National Park and Deogyusan National Park for enlisting all plant communities and investigate into the conservation meanings of surrounding ecosystems of nature conservation area. We compared diversities of plant associations and plant species. As results, we concluded that total 19 plant associations appeared from the classifications and analysis of plant communities at the periphery area of Deogyusan National Park. Of plant associations, *Pinus densiflora – Quercus variabilis* community were regarded as the highest class among vegetation conservation ranks. The *Pinus densiflora – Quercus variabilis* commmunity were recorded along the edges of Mt. JukSang which belong to Deogyusan National Park. The destructed area within forests of the periphery area produced from clear cutting, plantation after clear cutting and use of cultivated lands. Specifically, the private forests continue to cut clearly, plant horticultural tree species such as *Pinus densiflora*, *Pinus rigida*, *Liriodendron tulipifera*, *Thuja orientalis* and so on and grow forestry products under permissions by Korea Forest Service. We suggest that the studies related with forest conservation near national parks are urgently needed to preserve and manage transition zones for protecting the whole national park areas.

Conservation status of Natura 2000 habitats in Portugal assessed with National Forest Inventory data: The outcomes of an european harmonisation criteria

Leónia Nunes[1,2*], *Inês Marques Duarte*[1], *Francisco Castro Rego*[1], *Iciar Alberdi*[1], *Susana Dias*[1]

[1]Centre for Applied Ecology "Professor Baeta Neves" (CEABN), InBIO, School of Agriculture, University of Lisbon, Lisbon, Portugal
[2]CITAB - Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal
[3]INIA-CIFOR, Dpto. Selvicultura y Gestión de Sistemas Forestales, Madrid, Spain
[*]E-mail: lnunes@isa.ulisboa.pt

Keywords: cork oak, holm oak, biodiversity indicators, stand variables

Natura 2000 habitats have a wide distribution on Europe. Member states are obliging under EU Directives to undertake surveys and inventories for the assessment of the conservation status of those habitats. Currently across Europe, assessments can be based on a complete survey, estimated based on partial data with some extrapolation and/or modelling, or they can be estimated based on expert opinion with minimum sampling or none at all (EC, 2013).

Forest habitats are one of the most relevant component of Natura 2000 network (Duarte et al. 2016), although their conservation status is sometimes considered not good or unassessed. In order to consistently improve their conservation status, progresses in the assessing methods are needed, as also in its harmonisation through Europe.

Several authors highlighted the potential of European National Forest Inventories (NFIs) to addressed harmonised estimates for the assessment of the conservation status of forest habitat at different scale (e.g. Alberdi et al. 2016). NFIs are a large scale source of information on forest resources allowing the integration of stand dynamics. Thus, under the project H2020 DIABOLO - Distributed, Integrated and Harmonised Forest Information for Bioeconomy Outlooks (http://diabolo-project.eu/), an approach was developed to analyse the use and suitability of NFIs in this conservation status assessment (Alberdi et al. in press) and also developed the harmonisation of methods for data collection in inventories and monitory schemes. In this study, we present the outcomes of this approach for Portugal and provided recommendations for improving forest conservation assessment using NFIs. In Portugal the assessment of conservation status has been made so far based on expert opinion what brings a particular opportunity to apply and test the potential of the assessment methods developed. In the wide spectrum of potential indicators and within the forest habitat types (FHTs) represented in Europe, we selected the habitats dominated by sclerophyllous oaks (Figure 1), *Quercus suber* L. and *Quercus ilex* s.l. Structural and functional criteria for evaluation of habitat type are not yet available though in development. Forty-two common indicators can be determined for all FHTs in Portugal. We could use eleven of the those common indicators in this first study case for sclerophyllous oaks using Portuguese NFI, as such: tree species richness, non-native species, regeneration, diameter distribution, large trees, vertical structural diversity, deadwood, browsing damage, forest disturbances, soil treatment, tree pests

and diseases. Indicator thresholds were established according to literature. The results made evident a variety of conservation status in each FHT and among them. Discussion will account the observed dynamics in the habitats in which the human factor plays a significant role (e.g. wildfires, pastures and land abandonment) and how to overcome challenges such as a robust mapping of FHT in an appropriate resolution and the inclusion of new NFI variables in the quality assessment process.

Figure 1. Location of NFI plot used in tis study.

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