

INTERNATIONAL WORKSHOP

BIODIVERSITY
IN THE MEDITERRANEAN BASIN

BOOK OF ABSTRACTS



University of Primorska
Faculty of Mathematics, Natural Sciences
and Information Technologies
Department of Biodiversity

Koper, 11 - 13 March 2015

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International workshop Biodiversity in the Mediterranean basin

Koper, 11-13 March 2015

Book of abstracts

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Naložba v vašo prihodnost
OPERACIJO DELNO FINANCIRA EVROPSKA UNIJA
Evropski socialni sklad

UP IN SVET - Mednarodna vpetost Univerze na Primorskem: operacijo delno financira Evropska unija iz Evropskega socialnega sklada ter Ministrstvo za izobraževanje, znanost in šport. Operacija se izvaja v okviru Operativnega programa razvoja človeških virov za obdobje 2007–2013, 3. razvojne prioritete Razvoj človeških virov in vseživljenjskega učenja; Prednostne usmeritve 3.3.: Kakovost, konkurenčnost in odzivnost visokega šolstva.

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PROGRAMME

Wednesday, 11 March 2015

- 8.00-9.00 Registration
- 9.00-9.30 Opening session: Elena BUŽAN

SESSION: FRESHWATER BIODIVERSITY

- 9.30-10.30 Plenary talk 1 - Ivana MAGUIRE
- 10.30-11.30 Plenary talk 2 - Magdalini CHRISTODOLOU
- 11.30-11.45 Coffee break
- 11.45-12.00 Chiara MANFRIN
- 12.00-12.15 Victoria BERTUCCI MARESCA
- 12.15-12.30 Anja PALANDAČIĆ
- 12.30-12.45 David STANKOVIĆ
- 12.45-13.45 POSTER SESSION / lunch break

SESSION: TERRESTRIAL BIODIVERSITY

- 13.45-14.45 Plenary talk 3 - Silvia CASTRO
- 14.45-15.45 Plenary talk 4 - João LOUREIRO
- 15.45-16.00 Boštjan SURINA
- 16.00-16.15 Blanka RAVNJAK
- 16.15-16.30 Sandra HASIĆ
- 16.30-16.45 Coffee break
- 16.45-17.00 Jure JUGOVIC
- 17.00-17.15 Josip SKEJO
- 17.15-17.30 Lucija ČESNIK
- 17.30-17.45 Tjaša ZAGORŠEK
- 17.45-18.00 Jasna MLADENOVIĆ
- 18.00-18.15 Miha KROFEL
- 18.15-18.30 Closing session

Thursday, 12 March 2015

8.00-9.00 Registration

SESSION: MARINE BIODIVERSITY

9.00-10.00 Plenary talk 5 – Ante ŽULJEVIĆ

10.00-10.15 Manja ROGELJA

10.15-10.30 Andrej JAKLIN

10.30-10.45 Sergio STEFANNI

10.45-11.00 Rocco AURIEMMA

11.00-11.15 Coffee break

11.15-12.15 Plenary talk 6 - Andrew J. WRIGHT

12.15-12.30 Hrvoje ČIŽMEK

12.30-12.45 Bojan HAMER

12.45-13.00 Tilen GENOV

13.00-13.15 Lovrenc LIPEJ

13.15-13.45 Discussion

13.45-15.00 POSTER SESSION / lunch break

WORKSHOP: SCIENCE - HOW TO TALK AND WRITE IT?

15.00-16.30 Andrew J. WRIGHT

16.30-18.00 Matjaž KLJUN

18.00-18.30 Closing session

Friday, 13 March 2015

Excursion to Škocjan Caves Park

Biodiversity in the Mediterranean Basin

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The Mediterranean region represents only 2% of the world's surface but it is one of the major reservoirs of marine and terrestrial biodiversity. The location at the intersection of two major landmasses, Eurasia and Africa, characterises this area of high landscape diversity, enhanced also by the long-term human presence. In the mosaic of natural and cultural landscapes human civilization and wildlife have coexisted for centuries. Although the Mediterranean Sea makes up less than 1% of the global ocean surface, it is extremely rich in biodiversity for such a small area. Mediterranean wetlands and other habitats are very important for millions of migratory birds which stopover or breed on their way to Europe or Africa. The Mediterranean flora consists of a broad mixture of species with disparate evolutionary histories and biogeographic origins, which results in high species-level endemism. Due to its rich biodiversity and growing pressures of unsustainable human activities, the organization Conservation International identified the region as a biodiversity hotspot. Urbanization, coastal development, pollution, and unsustainable exploitation of natural resources are just some of the many human activities that are leading to an ever-increasing number of Mediterranean species to be facing a high risk of extinction. The main aim of the present workshop is to assemble a scientific community from the Mediterranean region working on different aspects of biodiversity, to present new insights into terrestrial, freshwater and marine biodiversity and to transfer the knowledge on early stage researchers and students.



SESSION 1:

FRESHWATER BIODIVERSITY

Freshwater crayfish diversity in Europe – what do we know about it?

Ivana MAGUIRE¹

¹ University of Zagreb, Faculty of Science, Department of Biology, Zagreb, Croatia

Freshwater crayfish are the biggest macroinvertebrates within freshwater habitats. They have an important ecological role in the functioning and biodiversity of freshwater ecosystems. Indigenous European crayfish species (ICS) belong to the family Astacidae and comprise two genera, *Astacus* and *Austropotamobius*. Due to anthropogenic influence onto their habitats, water quality decline, climate change and the introduction of American crayfish species, ICS have dramatically decreased in both their distribution and number. Observed declines instigated an increased awareness and interest in the freshwater crayfish research and concern for their conservation. The first requirement of conservation management is a sound knowledge about distribution, biology, ecological needs and the diversity of a species. Therefore, this lecture will give an overview of the current state of knowledge about freshwater crayfish, with a special emphasis on the crayfish from the genus *Austropotamobius*.

Freshwater shrimps (Atyidae, Palaemonidae, Typhlocarididae) in the broader Mediterranean region

Magdalini CHRISTODOULOU¹

¹ Aristotle University of Thessaloniki, School of Biology, Department of Zoology, Thessaloniki, Greece

Looking at a world map, one can see that the Mediterranean is not just a landlocked sea, but rather a region where continents meet. The turbulent and intricate geology of the Mediterranean has been responsible for connections, redirections, and interruptions of freshwater systems, that have been instrumental in the speciation and distribution of many organisms in freshwaters. Typical inhabitants of these ecosystems are the freshwater shrimps of the families Atyidae, Palaemonidae, Typhlocarididae. Atyidae is one of the most diverse shrimp families found in freshwater habitats world-wide. Currently, 43 atyid genera have been described numbering more than 469 species. In the wider Mediterranean region (Mediterranean and adjacent countries) three epigeal genera are found: *Atyaephyra* de Brito Capello, 1867; *Caridina* H. Milne Edwards, 1837; *Dugastella* Bouvier, 1912 and four subterranean genera: *Gallocaris* Sket and Zakšek 2009; *Troglocaris* Dormitzer, 1853; *Typhlatya* Creaser, 1936; *Puteonator* Gurney, 1987. The family Palaemonidae in contrary to Atyidae has representatives in freshwater, brackish and marine waters. Specifically, in freshwaters the family numbers more than 13 genera and 276 species world-wide, while in the Mediterranean region only one (*Palaemon* Weber, 1795) is found which includes 9 species. This high number of species, observed both on Atyidae and Palaemonidae, is probably an underestimate of the families' true richness. New morphologically distinct species are described every year, while molecular studies reveal morphologically hidden species fostered within widespread species. Finally, the family Typhlocarididae includes only one cave dwelling genus, *Typhlocaris* Calman, 1909, with four species distributed in North African and Middle East. Although members of these families can be found to co-exist in the Mediterranean region their phylogenetic history, life strategies as well as their distributional patterns are far from being the same, as it will be shown in the presentation. A special emphasis will be given to the most widespread genus in the region, *Atyaephyra*.

Biomonitoring invasive species: the case study of the red swamp crayfish in Friuli Venezia Giulia

Chiara MANFRIN¹, Federica PIAZZA¹, Piero GIULIANINI¹, Alberto PALLAVICINI¹,

¹ *University of Trieste, Department of Life Sciences, Trieste, Italy*

The impact of introduced species on ecosystems has been widely recognized as one of the factors causing loss of biodiversity. This is the case of the red swamp crayfish (*Procambarus clarkii*) which has been introduced in the Friuli Venezia Giulia (FVG) in 2007, and that represents a threat to the native white-clawed crayfish. This study presents the findings obtained from a massive sampling campaign conducted from 2012 to 2013 within the FVG. Nine out of 216 stations sampled resulted positive to the presence of *P. clarkii* and most of them were located in the southern part of the region. The genetic variation among these nine populations was examined using partial sequences of the mitochondrial COI gene. A phylogenetic reconstruction showed that the majority of introduced populations remain very similar to each other, with the exception of the one from Casette locality, which was the most divergent one. From an analysis of population size changes, Casette, resulted characterized by populations in expanding phase and statistical analyses highlighted as the population did not stem from a neutral model of constant size. Casette is therefore the locality presenting higher variability of *P. clarkii* populations and could be the point of introduction in FVG of this species. For an early warning and a better management of this invasive species we have set up a web site for public reports (<http://gamberialieni.divulgando.eu/>). We also demonstrated that the red swamp crayfish in FVG is able to live and reproduce in water 12°C colder than the alleged optimum (Peruzza et al., 2015). Monitoring actions on *P. clarkii*'s populations are due in order to define the state of the invasion, to collect information about the vectors and the number of introductions and, as a consequence, we may attempt to halt or to slow down the invasion process.

Conservation genetics of the crayfish *Austropotamobius pallipes* complex in Friuli Venezia Giulia (NE Italy)

Victoria BERTUCCI MARESCA¹, Piero Giulio GIULIANINI¹, Alberto PALLAVICINI¹

¹ University of Trieste, Department of Life sciences, Trieste, Italy

The white-clawed crayfish *A. pallipes* has suffered in recent decades a strong decline throughout its entire distributional range, mainly due to the growing number of threats coming from anthropic influence, including habitat loss and degradation, overfishing, infectious diseases, and the introduction of non-indigenous crayfish species (NICS). The species is included in the red list of the IUCN (International Union for Conservation of Nature) as a species at risk of extinction. An important goal in conservation biology is to assess the genetic variability and thus the “genetic health” of populations and to identify any evolutionarily significant unit (ESU) within endangered species, before management decisions are taken. Within RARITY (<http://www.life-rarity.eu>), a LIFE+ project for the eradication of the invasive Louisiana red swamp and for the preservation of the native white-clawed crayfish in Friuli Venezia Giulia (FVG, NE Italy), we were responsible for the genetic characterization of *A. pallipes* complex in this area. The analysis of two mitochondrial genes (COI and 16 rDNA) of about 500 individuals from 58 monitored sites showed that the FVG crayfish belong to the *A. italicus* species, with two different subspecies present: *A.i. carsicus* and *A.i. meridionalis*. The analysis of six microsatellite loci revealed generally low levels of genetic diversity within population ($0,0 < H_o < 0,5$) with overall high inbreeding coefficients (average $F=0,422$), likely as a result of genetic drift in small sized populations. FVG populations appeared significantly differentiated among the different river drainages and were highly structured within rivers, suggesting significant habitat fragmentation of stream ecosystems. The combination of mitochondrial and microsatellite markers allowed us to clearly identify two ESUs, corresponding to the two subspecies in northern and southern FVG. Our data also support the maintenance of separate of separate demographic management strategies for crayfish inhabiting different river systems. This study provided new knowledge on white-clawed crayfish populations to create “genetic maps” that can be used as valuable data for restocking practices and conservation programs in FVG.

Resolving phylogeny of the genus *Phoxinus* in the Western Balkan Peninsula with the help of museum specimens

Anja PALANDAČIĆ¹, David RAMLER², Jernej BRAVNIČAR³, Aleš SNOJ³, Harald AHNELT²

¹ *Natural History Museum Vienna, First Zoological Department, Vienna, Austria*

² *University of Vienna, Faculty of Life Sciences, Department of Theoretical Biology, Vienna, Austria*

³ *University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Ljubljana, Slovenia*

Using museum biological collections in phylogeographic studies is gaining gravity, since they offer insights into the recent history of a species with respect to changes of faunal assemblages and the existence of cryptic species or species complexes. However; the use of museum specimens is not without difficulties, and the condition of the museum specimens is highly variable. We performed a molecular phylogeny study of the genus *Phoxinus* in the Balkan Peninsula, but morphological data for those samples is missing. Thus, we use 200 individuals from our museum collection, and perform genetic, morphometric and classical morphological analysis to help us resolve phylogeny of *Phoxinus* in this area. Our preliminary results support our hypothesis based on molecular data, which point to a multispecies complex of *Phoxinus* in the Western Balkans. There is an ongoing debate on how the collecting of endemic species for scientific purpose can be harmful to already impoverished populations. Even though this considerations are not very realistic (Rocha et al. 2014), it would be helpful to assess, how much can be done from already collected samples held at museum collection. We encountered many problems working with the museum material, concerning all methods used. In this preliminary study, they will be explored and possible solutions discussed.

Origin of self-sustaining rainbow trout (*Oncorhynchus mykiss* Walbaum, 1792) populations in western Slovenia

David STANKOVIĆ¹, Aleš SNOJ¹

¹ *University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Ljubljana, Slovenia*

The rainbow trout is the most widely introduced salmonid in Europe. For decades, large numbers of fry, juveniles and adults (10^5 – 10^7 annually) were introduced into open waters. Even though this species has successfully invaded large freshwater systems in various climates of South and North America, Australasia, South Africa and Japan, continuous introductions in Europe have not led to general naturalisation. In Europe, only a limited number of rivers host self-sustaining populations, with the highest abundance in the Prealpine regions. Mediterranean watershed of western Slovenia is one of such areas and at least fifteen self-sustaining populations exist in the river systems of the Soča, Idrijca and Nadiža. These populations are of significant importance for the study of rainbow trout invasion biology as they inhabit pristine and near-natural waters, while this species is in general considered to be more susceptible to naturalisation in highly modified waters, where native salmonids struggle to survive. To get an insight into invasion history and origin of translocated rainbow trout we examined variation in mitochondrial D-loop, Y chromosome-linked OmY1 marker and eleven microsatellite loci in nine self-sustaining populations from western Slovenia and various native populations from North America (27 from California for microsatellites, and over 70 across the entire Pacific coast for the mitochondrial and Y-chromosome sequences). High genetic diversity and low inter-population genetic variation of the rainbow trout in western Slovenia was observed indicating that these populations probably derived from multiple sources, with a great majority of parental populations belonging to steelhead and coastal rainbow trout from Central and Northern California. Comparing to the native populations the translocated ones showed much lower genetic diversity and specific microsatellite DNA signatures that they apparently developed via genetic drift, recombination and artificial selection in 120 years of their isolation.

Molecular phylogeny of the branchiobdellidans (Annelida: Clitellata) living on Croatian populations of *Austropotamobius torrentium* and *Austropotamobius pallipes*

Ivana ŠARIĆ¹, Ivana MAGUIRE¹, Goran KLOBUČAR¹, Martina PODNAR², Anamaria ŠTAMBUK¹

¹ University of Zagreb, Faculty of Science, Zagreb, Croatia

² Croatian Natural History Museum, Zagreb, Croatia

Branchiobdellidans are ectosymbiotic annelids that are primarily associated with freshwater crayfish. Previous studies of branchiobdellidans in Croatia have been focused mainly on the distribution and diversity of the genus *Branchiobdella*. The objective of this research was to infer the phylogenetic relationships of the branchiobdellidan species living on the Croatian populations of crayfish from the genus *Austropotamobius*, in order to examine potential coevolution of branchiobdellidan and crayfish species in Croatia. Results of the phylogenetic analysis of both genera were compared. The examination of freshwater crayfish from 74 sites confirmed the existence of five branchiobdellidan species: *Branchiobdella astaci*, *B. hexodonta*, *B. parasita*, *B. pentadonta* and *B. italica*. Nucleotide sequences of two mitochondrial genes (cytochrome c oxidase subunit I and 16S rRNA) have been used to estimate the phylogenetic relationships between the Croatian species from the genus *Branchiobdella*. The results of the phylogenetic analysis, based on the examination of the constructed phylogenetic trees and values of p-distances, indicate that the speciation pattern observed within the genus *Austropotamobius* in Croatia might be similar in studied branchiobdellidans.

Geometric morphometrics as a tool to discover phenotypical divergence

David RAMLER¹, Giovanni B. DELMASTRO², Anja PALANDACIC¹, Harald AHNELT¹, Ernst MIKSCHI¹

¹ Natural History Museum Vienna, Vienna, Austria

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Phoxinus is a genus of freshwater fish, which currently consists of seven species in Europe. Kottelat & Freyhof (2007) consider *P. phoxinus* as a species complex and used the name *P. lumaireul* for the cis-Alpine populations. The discrimination is primarily based on meristic features and distance ratios. We used geometric morphometric methods (GMM) to assess shape differences among different populations of minnows. By comparing trans-Alpine *P. phoxinus* with cis-Alpine *P. lumaireul*, we aim to review the separation of the species from a morphometric point of view.



SESSION 2:

TERRESTRIAL BIODIVERSITY

Polyploidy as a mechanism of rapid sympatric speciation: understanding the ecological processes in the initial stages after polyploid formation

Sílvia CASTRO¹, Mariana CASTRO¹, Miguel SERRANO², João LOUREIRO¹

¹ *University of Coimbra, Centre for Functional Ecology and Department of Life Sciences, Coimbra, Portugal*

² *University of Santiago de Compostela, Faculty of Pharmacy, Department of Botany, Santiago de Compostela, Spain*

Polyploidy has long been recognized as a major mechanism in plant speciation, and is widespread in the evolutionary history of Angiosperms. As new polyploids can arise in a single step, polyploidy has been proposed as a mechanism of rapid sympatric speciation. Yet, under random mating, the establishment of neopolyploids is subjected to strong frequency-dependent selection. Thus, their successful establishment and spread will only occur when a set of ecological features increases the probability of persistence, otherwise neopolyploids will be selectively eliminated from the population. However, genome duplications have broad-scale impacts on gene dosage, cell size, and developmental processes, potentially leading to immediate shifts in morphology, breeding system and ecological tolerances. These changes have been linked with increased competitive ability, niche differentiation and/or wider geographic ranges, which can enhance the ability of new polyploids to establish and spread within or beyond their diploid progenitor populations. Despite the importance of rapid ecological effects of polyploidy, there is still little comprehensive research available to test its adaptive significance. Although many Mediterranean plant lineages include polyploidy species, few is known about the evolutionary significance of polyploidy in the Mediterranean flora, in particular the contribution of genome duplications *per se* to ecological differentiation and, consequently, to the establishment and persistence of new polyploid lineages, the first step for polyploid speciation. In this presentation, we examine several polyploidy complexes from the Iberian Peninsula such *Blackstonia*, *Gladiolus* and *Jasione*, in particular the distribution patterns of cytotypes to disentangle the nature of contact zones and occurrence of niche differentiation, as well as the morphological, reproductive and ecological traits of each cytotype both in natural populations and in plants growing in a common garden. I conclude by discussing how our results will provide significant insights into the immediate effects of genome duplication and their contribution for plant speciation.

Causes and consequences of biological invasions: the case study of *Oxalis pes-caprae* invasive in Mediterranean climatic regions of the world

João LOUREIRO¹, Sílvia CASTRO¹, Victoria FERRERO², Susana RODRÍGUEZ-ECHEVERRÍA¹, Joana COSTA¹, Mariana CASTRO¹, Patrícia CALDEIRINHA¹, Daniela TAVARES¹, Rodríguez Arós IVÁN², Sérgio ROILÓA³, Helena FREITAS¹, Spencer BARRETT⁴, Luis NAVARRO²

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² University of Vigo, Faculty of Science, Department of Plant Biology, Vigo, Spain

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⁴ University of Toronto, Department of Ecology and Evolutionary Biology, Toronto, Canada

Biological invasions have significant ecological and evolutionary consequences, both for the communities invaded, as well as for the invasive species themselves. The establishment and spread of invasive species in new areas depends on diverse evolutionary and ecological factors, with traits governing the production, dispersal and genetic composition of propagules playing a special role. Because reproductive strategies determine demographic and genetic characters of invasive populations, variation in reproductive characters has the potential to influence evolutionary processes during invasion. Therefore, comparative studies of reproductive systems in native vs. introduced ranges are crucial for understanding the mechanisms of plant invasion, for predicting microevolutionary change in anthropogenic environments, and ultimately, for designing control measures for invasive species. However, the roles played by reproductive modes in the successful invasion of exotic species are poorly understood. Here, we evaluate evolutionary shifts in reproductive systems and genetic variation in native and introduced populations of the clonal plant *Oxalis pes-caprae* L. (Oxalidaceae). This species is a tristylous geophyte native to South Africa. Invasive populations throughout much of the introduced range are almost exclusively composed of a sterile clonal pentaploid short-styled form. In this presentation I examine: (1) the contribution of asexual and sexual reproduction to invasion dynamics in the Western Mediterranean, in comparison with the native area; (2) the expression of self- and morph-incompatibility across this invaded area, and comparison with the native range; (3) the influence of *O. pes-caprae* on native plant-pollinator networks; (4) the effect of reproductive mode and ploidy on genetic diversity in native and introduced populations. I conclude by discussing how our results are important for understanding the evolutionary dynamics of plant invasions.

Biogeography of the Balkan Peninsula in light of phylogeographical patterns of vascular plants

Boštjan SURINA¹

¹ University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Department of Biodiversity, Koper, Slovenia

Phylogeographic studies in Europe have repeatedly revealed that the Iberian, Apennine and Balkan peninsulas have acted as major glacial refugia of temperate plant and animal species and provided sources for post-glacial northward range expansion. With the accumulation of phylogeographic studies, it became evident that, within these peninsulas, many lineages show strong genetic subdivisions indicative of population isolation in separate refugia, a concept termed 'refugia within refugia'. To that end, some results suggest that phylogeographic patterns of low- and high-elevation species may differ, while differences among the taxa investigated in traits of potential importance for range shifts, such as dispersal capability, render generalization of the observed patterns difficult. We will try to interpret the biogeography of the Balkan Peninsula in light of the results of recent phylogeographic studies on vascular plants with recommendations and suggestions for future research.

Population occurrence of white flowered varieties of some plant species in the submediterranean area of Slovenia

Jože BAVCON¹, Blanka RAVNJAK¹

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Plant biodiversity in Slovenian Mediterranean area is really rich. The causes for this richness are the area heterogeneity, various micro localities and impact of neighboring phytogeographical regions. However the appearance probability of white flowered varieties of individual plant species is higher in submediterranean region. This can be seen as higher number of white flowered specimens within local populations. Until now white populations of species *Iris pallida* subsp. *illyrica*, *Muscari botryoides*, *Globularia punctata*, *Antylis jacquinii*, *Veronica barrelierii*, *Verbascum phoenicum*, *Aster amellus*, *Aster tripolium*, *Centranthus ruber* and *Allium senescens*, have been found only in submediterranean region. The occurrence of white population of a single species is a consequence of various factors. Among them mostly extreme conditions on growing site such as include shallow ground, high temperatures connected with drought, extreme exposure to sunlight, number of sunny days etc. are to be considered. In some species combination of these factors interrupts the synthesis of antocyanins and other plant pigments, which causes white coloration of the flowers. Examples which most clearly demonstrate the effect of abovementioned factors on white coloration of flowers are the species *Primula vulgaris* and *Peonia mascula* subsp. *rusii*. For the first species in Sicily there are mostly white populations present while the yellow ones are rather an exception. The closer we are to the center of species distribution in central part of Europe, the more white specimens are an exception. In Slovenia the white specimens are mostly present in warm areas of submediterranean region. Quite the same is true for the other species. While white population of *P. mascula* subsp. *rusii* can be found only in Sardinia, the pink-violet populations are present in the center of its distribution.

A survey of selected alien plant species in Koper

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Urban ecosystems represent a suitable environment for invasive plant species. Due to the presence of the port and its related logistic activities coupled with the mild sub-Mediterranean climate, Koper can be considered a potential threat for the spread of alien species inland. In our research we aimed to identify 1) which invasive species are present in the old town of Koper and its surroundings, 2) what is their abundance and 3) which species' pose a threat to local biodiversity. The study area was divided into 116 quadrants (200 x 200 m) covering the area of the old town of Koper and the surrounding ruderal area. For the purpose of the study, we dividend this area into three parts: the old town area, the ruderal surrounding area and the transitional part. We conducted a monitoring of 15 alien species which have been recognized to pose a threat on a national level. Each species was marked as present or absent in each quadrant. Distribution analysis and maps were made using Esri ARCGIS version 10 and later a correspondence statistical analysis was performed using PAST statistical tool. The highest number of invasive species (7-8) was found only in two quadrants near the port and the railway station. In most quadrants (43) only 1-2 invasive species were found, while 22 quadrants were free of invasive species. Correspondence analysis showed that most invasive species were found across the whole monitored area. Two species (*Lonicera japonica* and *Amorpha fructosia*) prefer ruderal areas, while three species were found only in the town centre (*Alianthus altissima*, *Broussonetia papyrifera* and *Phytolacca americana*). The results of our study showed that invasive species in Koper are abundant; however, the composition of invasive species is quite different than in other parts of Slovenia. Close monitoring, raising public awareness and even eradication of some species should be taken into account.

Seasonal segregation between and within the guilds of dung beetles (Coleoptera: Scarabaeoidea)

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We have investigated the biodiversity of the dung beetles at a local scale on two sites (Hrastovlje, Zazid) on Karst Edge (southwestern Slovenia). At each site, biodiversity of the dung beetles from three habitats (open pasture, pasture with overgrowth, and habitat in later successional stage outside the pasture) were investigated in order to inspect for the dung beetles preferences towards a specific habitat and freshness of a dung, and assess their seasonal activity and segregation among and within the guilds (rollers, tunnelers, dwellers). During 30 sampling occasions in a period from March until the beginning of November 2012, 3773 specimens belonging to three families and 29 species (Scarabaeidae – rollers: 1 species; Scarabaeidae – tunnelers: 14 species, Geotrupidae – tunnelers: 2 species, Aphodiidae – dwellers: 12 species) were trapped in four pitfall traps per each habitat. Three species (Scarabaeidae – roller *Sisyphus schaefferi*, Geotrupidae – tunneler *Trypocopris vernalis* and Scarabaeidae – tunneler *Onthophagus grossepunctatus* with 2378 (63.0 %), 659 (17.4 %) and 507 (13.4 %) specimens, respectively) were by far most abundant. Beetles show preferences (in species number and in abundances) towards traps with fresh dung bait at both sites and in Hrastovlje they were significantly more abundant in pasture with overgrowth than in other two habitat types. Aphodiidae – dwellers were mostly active in spring or autumn, while Scarabaeidae – tunnelers were active also during the summer. The only roller was abundant throughout the whole season however with three obvious peaks in April, June and September. Clear temporal segregation among the two major guilds (Aphodiidae – dwellers and Scarabaeidae – tunnelers) as well as between the taxa within the Aphodiidae – dwellers and Geotrupidae – tunnelers suggest that their syntopic occurrence is mainly correlated to different phenologies of the investigated taxa, and/or habitat preferences that lower the interspecies competition for the resources.

An insight into Croatian Caeliferan fauna (Insecta: Orthoptera)

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The fauna of short-horned grasshoppers (Orthoptera: Caelifera) has never been systematically investigated in Croatia. In a last few years a lot of new species for the country has been recorded, while some species reported in old papers have been omitted from the list of Croatian grasshoppers. The aim of this lecture is to present the preliminary results of four year research of Croatian Caelifera with special emphasis on diversity of taxa in the Mediterranean and Submediterranean part of the country - number of species, their diversity, endemism, as well as to present ideas for further research and to call students and young scientist to become a part of the systematic research of Croatian Orthoptera - their taxonomy, nomenclature, phylogeny, ecology, bioacoustics, distribution and conservation.

Composition of the ant fauna (Hymenoptera: Formicidae) in meadow and forest habitats on Karst Edge

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We studied the composition of the ant fauna (Hymenoptera: Formicidae) at three localities on the Karst Edge: Socerb, Kastelec and Osp. We also determined how environmental parameters affect ant diversity and distribution. Sampling took place from early June to mid-July 2013. For sampling in meadows we used three methods, i.e. baits, pitfall traps and direct sampling, while for sampling in forests, in addition to the above mentioned methods, litter sifting was also applied. We determined twelve environmental parameters. In total, we recorded 33 ant species, 25 of which were found in forest habitats and 22 in meadow habitats. The most effective sampling methods were direct sampling and litter sifting. Species diversity expressed with the Shannon Wiener index was highest in Kastelec ($H' = 1,76$) and lowest in Socerb ($H' = 1,18$). Cluster analysis (CA; Jaccard and Bray – Curtis index) showed a separation into a three communities: forest, meadow and in meadow in succession state. Non – metric multidimensional scaling analysis (NMDS) showed that forest ant communities are influenced by a high percentage of dead wood and shrub coverage and high level of shading, while meadow ant communities are affected by a high percentage and high number of stones. Canonic correspondence analysis (CCA) showed that the Mediterranean species are related to habitats with higher temperatures and higher inclination, Southern European – Anatolian species are related to habitats with a high percentage of shrub coverage and higher inclination as well, Euro – Caucasian species are related to habitats with higher level of shading, higher humidity and high percentage of shrub coverage and dead wood and that Tethyan species are related to habitats with higher temperatures and high number and percentage of stones.

Can Barn Owl, *Tyto alba* (Aves, Tytonidae) accurately sample local fauna of small mammals?

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The barn owl diet has been studied in more detail than of any other bird of prey. We have examined the pellets of barn owl (*Tyto alba*) that were collected in Pisa (Italy) in 2012. Altogether 221 individual specimens of small mammals were found in 85 pellets. The barn owl's diet was composed of ten species of small mammals, representing three different families (Muridae, Cricetidae, Soricidae). Muridae made up of 55.2% of specimens of total prey intake (TPI). The main prey species was the wood mouse *Apodemus sylvaticus* (24.8% TPI), followed by the house mouse *Mus musculus* (16.7 % TPI) and the Savi's pine vole *Microtus savii* (14.9% TPI). The remains of insects were scarce. Barn owl pellets could also be a way we learn about the prey community that provides the predator diet, caused by the different feeding strategies of the predator. The feeding strategy may vary from an opportunistic (predator hunts a variety of prey species) to selective (predator focuses on one or a few prey species). We rather confirm that in our case barn owl most probably prey selectively, with special focus towards European water vole *Arvicola terrestris* (9.5% TPI) and avoidance of house mouse, despite the presumably high density of the latter. While smallest of the small mammals from the area, Etruscan shrew, *Suncus etruscus* (average body mass, BM = 3 g) was well represented in pellets (3.6% TPI), some larger species of small mammals were not represented at all. The reason for such result may be an upper limit for the barn owl's prey size. Our results suggest that optimal prey weight for barn owl may be between 26–75 g of BM, however the prey can be occasionally as heavy as almost 100 g, represented by adult *Rattus* spp. (only 0.9% TPI). Nevertheless, our data and results from this study may not reflect the true hunting strategy of the barn owl, but the availability of a certain food item at one point in time.

Population densities and habitat use of the golden Jackal (*Canis aureus*) in selected areas of Croatia and Slovenia

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Golden jackal (*Canis aureus*) is a widespread canid species ranging from central, eastern and southern Europe to northern Africa, Middle East and Southeastern Asia. Since the beginning of the 20th century the species' range is expanding. Today it is widespread throughout many lowlands of eastern Mediterranean, including Adriatic coast and neighbouring areas. However, population densities and habitat use of golden jackals in this region have so far been poorly understood. During 2007-2013 we performed several jackal surveys in Croatia and Slovenia with the use of acoustic («play-back») method to estimate population densities and study habitat use in four selected lowland regions in Croatia (Ravni Kotari and neighbouring islands, Pelješac peninsula, Lonjsko polje and Kopački rit) and six regions in Slovenia (Ljubljana Marshland, Cerkniško polje, Planinsko polje, Kras, Upper Soča Valley, Prekmurje). The surveys were conducted from 374 calling stations (monitoring sites), covering an area of 2130 km² in Croatia and 670 km² in Slovenia. In total, we recorded 232 territorial jackal groups in Croatia. In Slovenia, presence of 7 territorial groups was confirmed, 5 of them for the first time. We estimated population densities in Croatia and they ranged between 0.69-0.79 territorial groups/10 km² in Ravni Kotari to 2.27-2.43 territorial groups/10 km² in Pelješac peninsula. We analysed jackal habitat use in the study areas. Certain parameters, e.g. habitat type and distances from settlements, water sources and main roads were tested with the aim to find correlation between these parameters and jackal occurrence and number of jackal groups. We tested the common belief that mine fields represent a refuge for jackals in Croatia. The comparison with surrounding areas did not support the assumption that mine fields are populated by higher densities of jackals, therefore this assumption appears to be erroneous.

Diversity and importance of interspecific interactions involving Eurasian lynx in Dinaric Mountains

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Biodiversity studies often focus on species richness, while other aspects of biodiversity are neglected. Here I will present the diversity and importance of interspecific interactions involving an apex predator in Dinaric forest ecosystems – the Eurasian lynx (*Lynx lynx*). Interspecific interactions, especially those involving apex predators, were recognized as one of the key factors affecting structure of animal communities. Firstly, I will focus on diversity and effects of direct predation by lynx. In Dinaric Mountains, lynx is specialized in hunting European roe deer (*Capreolus capreolus*), but in total eight taxa were recorded in lynx diet. Annually, average lynx kill rate was estimated to 48 roe deer and on average each lynx killed 8% of local roe deer population. In contrast to other regions of Europe, we observed frequent predation of the edible dormice (*Glis glis*). This interaction appears to be under strong indirect effect of beech (*Fagus sylvatica*) masting. When hunting ungulates, we observed that lynx did not kill prey randomly. For example, compared to the human harvest, lynx more often killed roe deer in poor nutritional condition and adult females. Even stronger demographic selection was observed in predation of larger ungulate species. In the second part I will focus on interspecific interactions among the large carnivore guild. The strongest interaction observed was kleptoparasitism by brown bears (*Ursus arctos*) on lynx kills. Bears usurped 32% of lynx prey remains and in total, 15% of all biomass of large prey killed by lynx was lost to scavenging by bears. In response, lynx increased their kill rate by 23% but were able to compensate for only 59% of the losses. The frequency of interactions with bears was strongly connected with bear activity patterns. On the other hand, data indicate relatively low level of competition between Eurasian lynx and gray wolves (*Canis lupus*).

Plant species richness and environmental heterogeneity in an agricultural landscape of the Central Greece

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The Mediterranean basin maintains high biodiversity with a large portion of endemic species and is considered to be a biological “hotspot”. Ecological factors in the agricultural landscape include the capacity to support a variety of habitats and species. Changes in the agricultural landscape have an important influence on ecology and biodiversity. Plant species richness is frequently used to measure biodiversity, ecosystem recovery and ecological restoration. Hence, this study aims to test the relative predictive importance of several agricultural and environmental factors (Shannon diversity index and density of herbaceous plants, winter birds and earthworms, farm size, altitude, yield, slope, air temperature and humidity, soil temperature and moisture, farm exhibition, manure application, herbicides, insecticides and fungicides, inorganic fertilizer of K-Mg, N and K, soil physicochemical properties and presence of litterfall) for herbaceous plant species richness in organic and conventional olive groves. The study was conducted in the rural area of western Magnesia Prefecture of Central Greece. Herbaceous plant species richness were measured during the winter of 2009-2010, using the line point method. The resultant GLM model for herbaceous plant species richness in organic olive groves comprised three variables (Shannon diversity index of herbaceous plant, farm size and manure application—all positively varying with species richness), and explained a fairly high percentage (77%) of variance ($F=11.23$, $P<0.05$). In conventional olive groves, the model built for herbaceous plant species richness accounts for 85% of the variability of the depended variable ($F=19.11$, $P<0.05$). The model consists of three variables (Shannon diversity index of herbaceous plant, soil nitrogen and inorganic fertilizer-K) and shows that herbaceous plant species richness increases significantly with increasing Shannon diversity index of herbaceous plant and soil nitrogen and decreases significantly with increasing inorganic fertilizer-K application. In conclusion, agricultural and environmental factors are key determinants of the winter flora composition in the agroecosystems.

Biodiversity conservation and sustainable forest management in Greece: a study of past and future views under continuing stress factors

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The geographical position of Greece, its geomorphology, the presence of flora of past geological eras and the coexistence and interplay of biotic and abiotic factors have defined Greece as a country of high plant diversity and endemism, especially regarding forest ecosystems. The degree of underestimation of sustainable management is particularly high in southern and eastern Mediterranean countries. The current state of the country's forests includes many degraded ecosystems while the efficiency of the current management regime retains an ambiguous character. Considering the stress of climate change, the growing economic crisis and the vague character of Greece's legal framework, efficient and innovative forest management strategies are needed to consider future forest dynamics in view of biodiversity conservation, in one of Europe's biodiversity hotspots. On the event horizon of the changing political scenery in Greece at the dawn of 2015, possibly new outtakes and perspectives on sustainable forest management remain to be seen. This paper aims at documenting past management strategies, demonstrating their faults and proposing new tactics for managing forests to achieve biodiversity conservation in Greece.

Effects of intercropping systems on diversity of herbaceous plants and arthropods in the Mediterranean Region

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Intercropping is a crop management system involving two or more crop species grown together for at least portion of their respective productive cycle and planted sufficiently close to each other. Many ecologists advocate intercropping increases the crop yield, reduces soil erosion and improves nitrogen fixation. However, good documentation is lacking on the effects of intercropping on the herbaceous plant and arthropod diversity in fields. Hence, a number of field experiments have been carried out in Thessaly plain (Experimental Farm of the University of Thessaly, Velestino), Central Greece during May-June 2014. The samplings of herbaceous plants and soil arthropods were carried out in 30 randomly selected plots of 0.25 m² and 30 pitfall traps, respectively, within the each following type of intercropping: Pea-Oats (P-O), Pea-Barley (P-B), Winter vetch-Oats (WV-O), Winter vetch-Barley (WV-B), Grass pea-Oats (GP-O) and Grass pea-Barley (GP-B). A total number of eight species of herbaceous plants and six taxa of arthropods were recorded in all types of intercropping. The highest mean density of herbaceous plants (21.80 ± 13.68 individuals/m², $p < 0.05$) and arthropods taxa (39.01 ± 1.00 individuals/10 trap-days, $p < 0.05$) were recorded in the Grass pea-Barley. As regards the herbaceous plants and arthropod taxa diversity, the highest values of Shannon diversity index were estimated in the Pea-Barley (1.33-herbaceous plants, 1.45-arthropod taxa) and the lowest were in the Grass pea-Barley (0.00-herbaceous plants, 0.00-arthropod taxa) ($p < 0.05$). Similarly, Pea-Barley exhibited the highest values (1.00-herbaceous plants and arthropods taxa) of evenness index. Conclusively, the intercropping type Pea-Barley favours the herbaceous plant and arthropod taxa diversity making it the intercropping type that will favours biodiversity parameters both in Greek and the wider Mediterranean area.

The conservation of *Apis mellifera* (Linnaeus, 1758) in the Karst and Istria

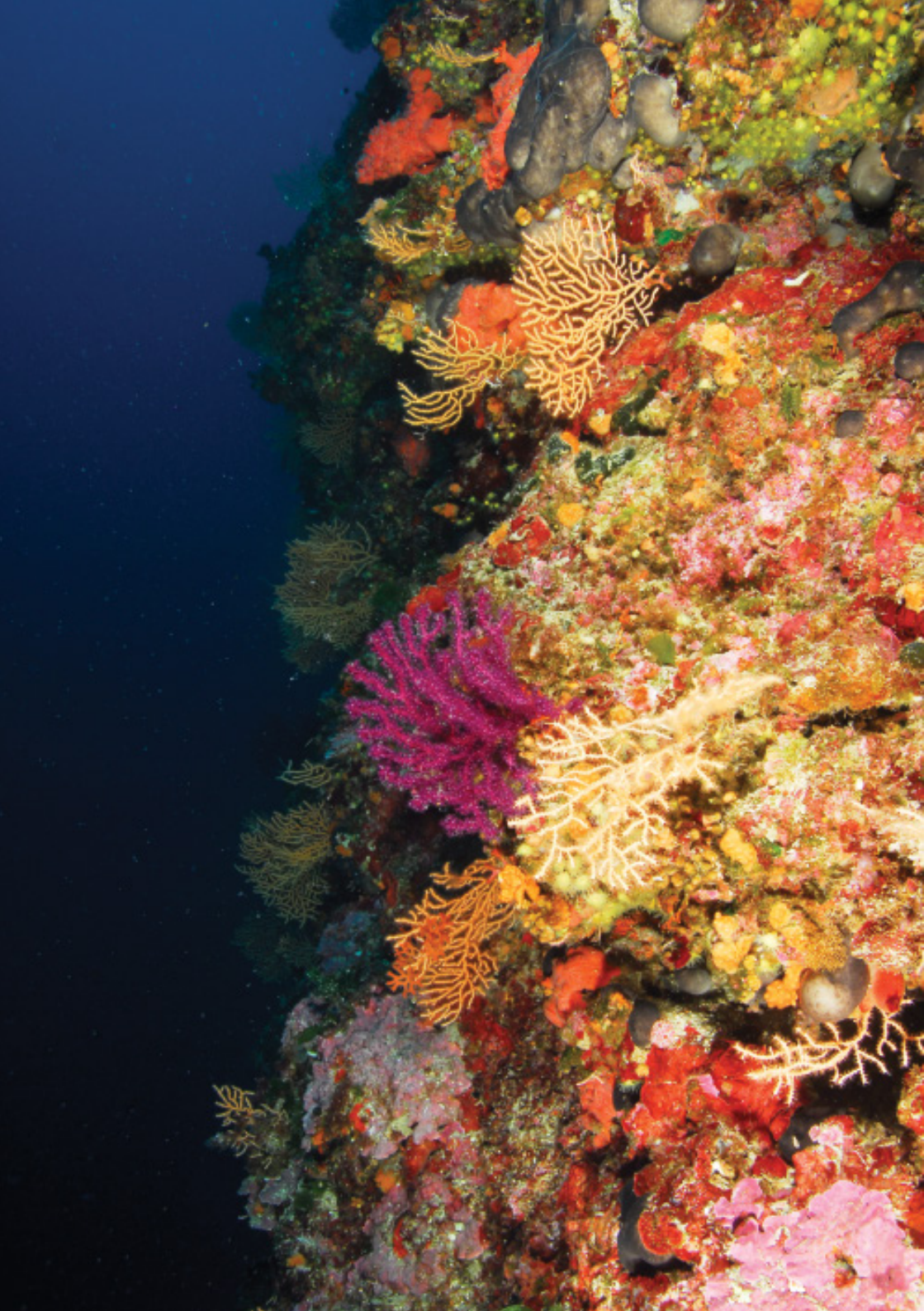
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Genetic analyses conducted on bee samples from Istrian Karst have revealed the presence of a high degree of genetic reshuffling of local populations due to repeated imports of non-native bees for commercial purposes. Nevertheless, genetic traces of two presumably native ecotypes are still present. The first is a hybrid between the yellow Italian bee and the grey Carniolan bee and was found mainly in the area of the Karst above Trieste, the natural boundary between the two subspecies. The second, more abundant in Istria, could be the Istrian-Dalmatian ecotype, which is described in the literature as a coastal form of the Carniolan bee adapted to the warmer drier climate of the coastal Karst. These two ecotypes are morphologically very similar, but distinct from a genetic perspective. The identification and characterization of these local strains is a first step to implementing targeted programmes for the conservation and the restoration of their rearing. It then becomes of primary importance to create regulations that prohibit the introduction of non-native bees in the area to curb the risk of extinction of local varieties. This work was conducted in the frame of BioDiNet, an Italia-Slovenia Crossborder Interregg project 2007-2013 for the conservation of biodiversity and cultural heritage.



SESSION 3:

MARINE BIODIVERSITY

Natural history of the Adriatic marine life

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The Adriatic Sea has one of the longest histories of marine biological research. This has resulted in well documented biodiversity at species level. Nevertheless, new taxa still can be found, especially in deep sea habitats, neglected lineages and through the use of molecular approaches to distinguish cryptic species. But what do we currently know about the natural history of marine species? The proof of our superficial knowledge is presented in the form of a broad selection of different marine life guidebooks. For the majority of common marine species, aside from morphological description, habitat preference, reproductive timing and commercial interest, there is almost no information on their natural history. The main obstacle to the expansion of our knowledge is that observations have to be made underwater. Marine biological research, in contrast to its terrestrial counterpart, is more demanding logistically, more expensive and critically time and depth limited. Many of the interesting natural histories of marine species are discovered accidentally and therefore any additional observations cannot be predicted. As such natural history chronicles, which lack experimental approach and are rarely observed, are difficult to validate statistically. As a result they are tricky to publish and many remain in the field-notebook of the researcher. Conversely, one can ask what else we can discover in marine organisms that could be evaluated as attractive for natural history. Some examples of the research of marine algae, invertebrates and fishes in the Adriatic Sea will be presented to demonstrate how even now unexpected and fascinating biological events can be discovered often based on accidental observations. Such as natural history records, besides their scientific values, are immeasurably important in public awareness of biodiversity and are therefore an essential tool in nature protection.

Hidden impacts of noise: stress, distraction and cumulative impacts

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The mitigation and (to a lesser extent) management of human impacts on marine mammals traditionally focuses on lethal “takes”, while behavioural responses are often downplayed as short-term and insignificant. However, an increasing body of research is revealing that there is likely a range of other non-lethal (or not immediately lethal) impacts of human disturbance on marine mammals and other wildlife, indicating that impact assessments are underestimating the total effect. While acoustic masking – the obscuring of signal of interest by noise – has long been acknowledged to exist, it has been largely ignored by managers as it remains extremely hard to quantify and even harder to determine the extent of the consequences. More recently, there has been growing acceptance that prolonged or repeated activation of the stress response, can lead to “chronic stress”, which comes with a range of associated conditions that can also have serious conservation implications. While the physiological stress response is a life-saving combination of systems and events that maximises the ability of an animal to kill or avoid being killed, chronic stress is linked to numerous conditions in humans, including coronary disease and infertility. More insidious still is the potential for noise exposure to divert attention from danger, prey or potential mates: each of which carries further costs to the animal concerned. Finally, behavioural responses to disturbances may be mal-adaptive and lead to energetic and opportunity costs, or even death. Further complicating the matter is the fact that many of these impacts can interact with each other, or other threats, leading to emergent cumulative impacts. Lack of consideration for all of these hidden impacts by managers is likely to have troubling implications for efforts to conserve marine mammals and other species, with associated problems for attempts to maintain a certain level of biodiversity in a region.

Microphytobenthic response to high CO₂ concentration and temperature in the Aeolian Islands (Tyrrhenian Sea, Italy)

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Aeolian Islands are of volcanic origin. In November 2002, a great gas emission event occurred and since then the interest for scientific research toward this area increased. In order to get an insight into the ecosystem changes and benthic community adaptations to higher CO₂ concentrations and temperature we conducted four sampling campaigns in 2012-2014 at Panarea and Basiluzzo Islands. We sampled sediments at two vents (B1, B3) and one reference site without emissions (B2) near Basiluzzo Island and at two stations (CB-HOT, CB-COLD) close to Panarea Island characterised by different CO₂ concentration and sea bottom temperature. We aimed to investigate potential changes in the microphytobenthic community abundance and composition and relate them to the presence/absence of the hydrothermal vent. The highest microphytobenthic densities were consistently recorded at St. B1, with its absolute maximum in October 2012 (20045 ± 2344 cells cm⁻²). Differences in the microalgal densities between St. B2 and St. B3 were not so marked. Even greater differences were observed between St. CB-COLD and St. CB HOT where at the latter microphytobenthic abundance in June 2012 reached ~ 243000 cells cm⁻² vs ~ 2500 cells cm⁻², respectively. Diatom genera like *Amphora* spp., *Diploneis* spp. and *Navicula* spp. and the species *Ceratoneis closterium* were present at all stations regardless of the season. *Amphora limbata*, *Entomoneis* spp. and *Cocconeis* spp. were always absent at the station CB-HOT that has also proven to be the station with lowest biodiversity. *Nitzschia longissima* and *Ceratoneis closterium*, that were abundant at St. CB-COLD and B2, showed deformities in their morphology probably induced by the effect of the thermal vent. The microphytobenthic abundance and species composition were remarkably different between stations indicating a significant influence of the CO₂ concentration and temperature on this phototrophic community. On the other hand, differences between seasons were less distinctive.

Metagenetic analysis of zooplankton at large spatial scale

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Zooplankton plays a major role in the sea and with this study we provide a comprehensive biodiversity survey from 45 sampling stations distributed in the Adriatic Sea. This survey is part of the monitoring programme within the Ritmare project and all samples were collected during the period August-September 2014. We used a metagenetic analysis of the mtDNA COI using the PGM Ion Torrent technology. In total, we obtained 86,114 high quality reads that clustered into more than 400 operational taxonomic units distributed in about 25 phyla. Limits of this metagenetic approach were due to the fact that several known species from the Mediterranean are not yet barcoded. Within the Cnidaria, the class Hydrozoa resulted to have very few sequences deposited in the NCBI repository. The taxonomical assignment did not find any match for 1.4% of the sequences under the term of Eukariota. Global analysis at the taxonomic level of Family clustered the sampling sites by depth profiles. The search for presence of alien species detected a few Crustacea, Polychaeta, Macrophyta and Cnidaria that might be new for the Mediterranean / Adriatic Sea. The potential applicative implementation of this large dataset is also provided.

Macrozoobenthic response to fishing cessation: a case study from the gulf of Trieste (Northern Adriatic)

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Changes in the macrozoobenthic community composition before and after the establishment of a marine protected area (Dosso di S. Croce) were examined in this study. The marine protected area is a submarine elevation (350 m in length and 220 m in width) with an average grade (slope) of 15%, located 5 km from the coastline. This elevation rises, slowly changing into pelitic sands (with abundant biogenic remains), 5 m above muddy flats (sandy pelites) at 16 m depth, with a surface of about 71,000 m². Before the protection came into force, this area was interested by an intense fishing effort due to trawling and dredging. Benthic organisms were collected before and after the protection of the area in order to detect fishing cessation effects by long time changing in biodiversity and communities composition. A high resolution spatial design was used to collect the benthic fauna. Species were collected at 25 different sampling stations (18 stations located on the elevation and 7 stations located around the elevation) through 5 van-Veen grabs each, during 5 non-consecutive years from 1994 to 2005. The significance of changes was assessed using ANOVA for the diversity indices (H' Shannon, d Margalef and J' Pielou) while a multivariate qualitative approach was used to detect differences in community composition and structure (Bray-Curtis dissimilarities and MDS ordination). Significant differences in community composition between sampled years and stations were determined using ANOSIM tests. The benthic fauna shows a remarkable increase in biodiversity and communities' complexity, also by modification in trophic guilds. Some epibenthic species increased in abundance (e.g., polychaetes *Pomatoceros triqueter* and *Serpula vermicularis*) especially in the upper part of the submerged hill, the most interested by the previous fishing activities. The protection of the area appeared to give rise to persistent changes in communities structure that were also detectable by a remarkable increase in species numbers and related biodiversity.

Baseline research for developing monitoring protocol for no-take zones in MPA Telascica, Croatia

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There are 5 MPAs in Croatia, 3 National and 2 Nature parks but only in Telascica MPA, for now, really no-take and no-entry zones will be established. NGO Marine Explorers Society “20000 leagues” from Zadar was hired to make baseline research and to develop protocol for monitoring no-take zones in Telascica MPA. The goal of this research was to survey every part of proposed no-take zones and define the best sites for monitoring inside and referent sites outside no-take zones. During our survey we examined entire no-take zones with scuba diving down to 40 meters of depth. During dives divers made 20x5 meters transect where they collected data about fish species and abundance. Depth ranges were 37-40m, 27-32m, 17-22m and 7-10m. Data was collected by two divers, one was on 40 and 10 meters and another was on 30 and 20 meters depth range. Seven 20x5 meters transects were surveyed (40m-1 replicate, 30m-1 replicate, 20m-2 replicates, 10m-3 replicates) per dive. After surveying of whole no-take zones we defined 14 sites for future monitoring, 7 inside no-take and 7 referent inside and outside MPA. On few sites we made preliminary benthic photographic sampling of algal cover and survey of urchin barrens which will all be integrated in monitoring protocol. The plan is to do improved research this year inside Lastovsko otocje MPA. They have plans for 12 small no-take zones. We will make uniform protocol for monitoring no-take zones in Croatian Nature parks. If we succeed, this will be the first attempt at merging Croatian MPAs into a national network for the specific purposes of standardizing scientific research.

Complex social structure in northern Adriatic bottlenose dolphins

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Complex social structure is a prominent feature in several species of mammals, and plays an important role in population dynamics and behavioural patterns. But understanding social structure is not only interesting biologically – it may also help conservation and management efforts. This is important because although conservation actions usually target populations, not all segments of a population necessarily interact with human activities in same way, or at the same time. Social network analysis allows groups of social animals to be studied as a network of nodes and ties. When coupled with information on behaviour and interactions with human activities, it can be a powerful tool in the study and conservation of social animals. In this study, we examined the social structure of common bottlenose dolphins (*Tursiops truncatus*) in the northern Adriatic Sea, using social network metrics and association indices. We used nine years of photo-identification data (2003 – 2011) of 38 individuals sighted ≥ 4 times and in ≥ 2 different years. We calculated association patterns and standard lagged association rates, using the half-weight index of associations and permutation tests within the program SOCPROG 2.4. Network analyses and visualisations were done in program NetDraw 2.123. We show that 1) the local bottlenose dolphin population is structured into distinct social clusters or communities; 2) that the two largest clusters overlap spatially, but not temporally (segregation being based on time of day rather than season); and 3) that the two clusters differ in ways they interact with fisheries (“trawler” vs. “non-trawler” dolphins). This study demonstrates how different segments of animal populations can have different effects on human activities and in turn respond differently to anthropogenic impacts.

Population analyses (cox1 gene) and bile PAH metabolites content in several commercial fishes along Adriatic coast

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Bile PAH metabolite content in selected commercial species *Mugil cephalus*, *Sarpa salpa* and *Mullus barbatus* purchased from local fish markets: Ploče (F2-Pl), Split (F4-St), Šibenik (F5-Ši), Rijeka (F8-Ri) and Rovinj (F9-Ro) were analysed as a biomarker of exposure to oil and possible indicator of marine environment quality. Local fish markets were used because chosen species were not possible to catch at selected sites during SW and mussel sampling in the frame of our national biomonitoring pilot project “Project Adriatic II”, Descriptor 8 and 9: Biological effects. Fishes are selected according food web positions: *Mugil* (water column, omnivore), *Sarpa* (water column, herbivore) and *Mullus* (benthic, detritofag). PAH metabolites were analyzed in bile by means of fixed wavelength fluorescence (FF) measurement using fluorimeter excitation/emission wavelength pairs 290/335, 341/383, and 380/430 nm. By FF290/335, mainly naphthalene type of metabolites, typically associated with petroleum products are detected, benzo[a]pyrene type of metabolites are best detected by FF380/430 and by FF341/383 mainly pyrene-derived metabolites. The population analysis of cox1 gene was applied as tool for fish specimens’ identification (barcoding) and determination of abundance of possible haplotypes. The Red Mullet (*Mullus barbatus*) and Salema (*Sarpa salpa*) were proved as single species with few haplotype at whole investigated area, but fishes purchased as *Mugil cephalus* were identified by sequencing and DNA analyses (blastn, NCBI) as 4 species (*Liza aurata*, *L. ramado*, *Cheon labrosus* and *Mugil cephalus*). The morphometric characteristics of family Mugilidae species settled in Mediterranean (8) are minimal and only 6 of them inhabited the Adriatic Sea.

Contribution to the ecology of the sponge *Suberites domuncula* (Olivi, 1792): Cox1 gene population and colour analyses

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Focusing on the Adriatic Sea, past research of sponge diversity provided illustrative descriptions decisive for a systematic compilation. *Suberites domuncula* (Olivi, 1792) (Porifera, Demospongiae, Tetractinomorpha, Hadromerida, Suberitidae) was originally described from the Adriatic Sea, but subsequently was widely recorded from all over the world. Due to a small amount of discriminatory morphological characteristics it was suggested that this widespread occurrence is an artefact. Consequently, worldwide known *S. domuncula* should be a complex of similar but different sponge species. *Suberites domuncula* is generally found on muddy sand bottoms between 5-40 m in the northern Adriatic Sea, but can occur down to 200 m of depth in the Mediterranean Sea. As *S. domuncula* is in an almost obligatory symbiosis with a hermit crab, the sponge obtains certain mobility and unknown seasonal migration which can affect gene population analyses. During collection of biological material by means of bottom trawls and SCUBA diving, we observed *S. domuncula* specimens of different colour patterns living at the same time and site together. The red-orange coloured specimens were dominant (cca 85% abundance), with unpredictable appearance of differently colored specimens (blue, yellow, brown, white, as well as combinations of them). Therefore, the present research was directed towards the study of sponge colour source and pigment origin, followed by specimen identification and barcoding population analysis using mitochondrial cox gene. Specimens of *S. domuncula* were collected at two distinct areas: 2 km off Rovinj westwards and at site in front of Umag (7 km, open sea), northern Adriatic, Croatia. By solvent extraction (water/chloroform) we separate blue and red colour. The red chloroform fraction was identified as β -carotene by spectrometry analyses comparing spectra (300-700 nm), and blue colour was separated by acetone precipitation, and SDS PAGE. The protein analyses and sequencing (MALDI) are underway. Beside sponge reversible contraction, different colours probably also have an adaptive, stress-protective function with far-reaching consequences on the life of *S. domuncula* specimens *in situ*. *Ex situ*, in aquaria with artificial seawater, after certain time (several months) sponges lose their colour and body mass, (food restriction, absence of phytoplankton and carotene, adequate lightening). The population analysis of cox1 gene was applied as tool for sponge specimens' identification (barcoding) and determination of possible haplotypes abundance. The red and blue *S. domuncula* morphs were proved as single species by sequencing and DNA analyses (blastn, NCBI), with few haplotypes at both sampling sites.

Feeding habits of the Mediterranean Shag *Phalacrocorax aristotelis desmarestii* in the Gulf of Trieste (northern Adriatic Sea)

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The Mediterranean Shag (*Phalacrocorax aristotelis desmarestii*) is an endemic subspecies, present only in the Mediterranean and the Black Sea (Annex I of the Birds Directive 79/409). In the framework of the project SIMARINE-NATURA a special part was dedicated to the study of feeding habits of this endangered species, present in Slovenia. The diet was assessed by analysing 500 pellets, gathered at shag roosts in summer of three different years (2011-2013). Otoliths were used to obtain data on abundance and species identification of preyed fish. Beaks and chelae were counted to assess the number of cephalopods and crabs. Otoliths were determined by using specific identification keys such as Tusset et al. (2008) and AFORO (<http://www.cmima.csic.es/aforo/>). Altogether 20430 prey items were isolated from 500 shag pellets. Almost all preyed animals were fish (>99%), while decapods and cephalopods were present in negligible percentages. Mediterranean shag preyed 30 different coastal fish species. The great majority of all specimens preyed were black gobies (*Gobius niger*) with 49.41%. Other goby species together with undetermined juveniles or specimens represented additional 25% in the diet. Other species with more than 1% in the diet were the brown comber (*Serranus hepatus*) with 13.4%, the red bandfish (*Cepola macrophthalma*) with 3.05% and sand smelt (*Atherina boyeri*) with 2.34%. Similar data were obtained also by using the index of relative importance (IRI). The diet analysis of Mediterranean shag in Slovenia showed that the bulk of the diet is constituted by typical sand and mud dwelling species. The black goby, the brown comber, the red bandfish and many other species are in fact very common in such environment. The black goby seems to be an optimal prey. It is a dominant species on sediment bottom, rather inactive and of appropriate size, which make it an ideal target for the Mediterranean shag.

Phytoplankton diversity in the Port of Koper, Slovenia

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The introduction of harmful aquatic organisms is seen as one of the greatest threats to world's oceans and ballast waters are a major vector for their transport. The countries of the Adriatic region have recognized that the major weakness in the control and management of ships' ballast water is the lack of knowledge about the biodiversity of marine organisms in the ports. Therefore, one of the objectives of the on-going BALMAS (Ballast Water Management System for Adriatic Sea Protection) project is the realization of port baseline survey in the 12 ports of the Adriatic Sea. This work presents the list of phytoplankton, including harmful species in the Port of Koper, which will be used as a baseline for the tracking of new introductions. Sampling was carried out at four stations using phytoplankton net with mesh size of 20 µm and a hose-sampler accommodated to different depths. Three stations are located in port's basins with active berths and the fourth is at the anchorage area. Campaigns were performed in May, July and November 2014 and in February 2015 to cover all seasons. Phytoplankton was determined and counted under an inverted microscope. The phytoplankton community structure and abundance within the samples was described and compared by means of different diversity indices. Phytoplankton species belonged to dinoflagellates, diatoms, silicoflagellates, coccolithophores and ebridian flagellates. 13 dinoflagellates (most belonging to *Dinophysis* and *Alexandrium* genera) and one diatom genus (*Pseudo-nitzschia*) were recognized as potentially harmful. All identified harmful species were already known from the Gulf of Trieste and were associated with past harmful events. The present study confirms the presence of harmful phytoplankton in the Port of Koper and indicates the need for ballast water management to prevent introductions of alien harmful phytoplankton species and the spread of the present harmful species with ballast waters.

Marine Important Bird Areas (IBA) in Slovenia

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Conservation of marine biodiversity is essentially supported through the BirdLife International Important Bird and Biodiversity Area (IBA) Programme. Its aim is to identify, protect and manage a network of sites that are significant for the long-term viability of naturally occurring bird populations. Part of the Programme specifically addresses marine birds and their habitats. Compared to the terrestrial sites, marine areas have been underevaluated until recently and few sites have been identified due to lack of hardly accessible population data. The identification of marine IBAs in Slovenia is an ongoing process. In 2011 two near-shore sites (Debeli rtič, Strunjan) were added to the existing network and one site (Sečoveljske soline) was extended into marine environment. The entire delineated marine area covered six species of marine birds. This inclusion of marine environment to the network, however, was based solely on limited land observations. Important progress has been made in the past three years within the scope of the project SIMARINE-NATURA (LIFE10NAT/SI/141). Marine IBA candidates have been identified based on systematic boat censuses and GPS telemetry methods. The Mediterranean Shag (*Phalacrocorax aristotelis desmarestii*) was estimated to be the most likely qualifying species for the off-shore areas and was thus chosen as a target species in this research. Moreover, random observations of large foraging congregations of Mediterranean Shags made by land observers were used as an important additional data layer for the delineation of the areas. One new area (Central Gulf of Trieste, CGT) and extension of one existing marine IBAs (Debeli rtič, DR) have been identified and proposed as marine IBAs based on regular use by threshold numbers (1% of biogeographic population) of foraging Mediterranean Shags. The newly delineated areas cover 8146 ha of the Slovenian sea. The numbers of Mediterranean Shags which use the new areas were 350-480 in CGT (estimated) and up to 310 in DR (observed). Once confirmed by BirdLife International, the new marine IBAs will be proposed to be included into Natura 2000 network.



WORKHOP:

SCIENCE – HOW TO TALK AND WRITE IT?

Communication with non-scientists

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Communicating with scientists is crucial to a scientific career. However, preserving biodiversity also requires that scientists also reach out to policy makers and the general public. Non-native English speakers are acutely aware of the difficulties are communicating science across a language barrier. However few scientists appreciate that the language barrier between science and policy can be just as large and difficult to navigate as the differences between British and American English. Many words carry different meanings to different audiences, such as “theory” and “significant”. The subtleties of different interpretations of phraseology and the writing conventions used by scientists can also cause trouble when released into the world through the soundbite-driven mass media. However, accurate understanding is not the biggest issue facing efforts to reach the public. Newer technologies have devalued typical outreach tools, such as print advertisement, public service announcement (PSAs) on the radio, and celebrity PSAs on television (the previous gold standard). The demand for the attention of the public is much greater than ever before, making it much harder to get your message across. Well-crafted pieces detailing your particular conservation problem are no longer sufficient. Instead, engaging and entertaining items are needed to gather the social media Likes and Shares that the modern world requires for messages to get through. However, achieving this requires that the detail is dropped in favour of a more stylised presentation, which can be extremely difficult for scientists to accept. Despite this, we must accept that we are addressing another sector of the population and rethink approaches to engage people on a new, much more basic level.

Management of research papers

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Research involves, among other things, management of research papers that form the basis for our work. Management of papers can be facilitated by various resource managers software such as Mendeley, Zotero, OneNote and JabRef. At the lecture we will cover the basis of each of these programs and take a closer look at Mendeley.

ABOUT INVITED SPEAKERS

Silvia CASTRO, University of Coimbra, Portugal

She is employed at the Department of Life Sciences, Faculty of Sciences and Technology, University of Coimbra as Assistant Researcher. Her main interests are plant-animal interactions, plant reproductive biology, phenotypic selection of floral traits, evolutionary dynamics of diploid-polyloid plant groups and conservation of endemic and endangered plants.

Magdalini CHRISTODOULOU, Aristotle University of Thessaloniki, Greece

Magdalini Christodoulou, PhD, is interested in biodiversity and taxonomy, especially of caridean shrimps (Crustacea: Decapoda: Caridea). She currently works on revision of the genus Atyaephira from Europe and Middle East, using phylogenetic analyses and morphometrics to resolve the taxonomy of the genus.

João LOUREIRO, University of Coimbra, Portugal

He is an Assistant Professor at Faculty of Sciences and Technology, University of Coimbra, doing his research at the Centre for Functional Ecology where he is the PI of the research line Biodiversity and Evolution. His main interests are the evolution of plant traits, mainly genome traits and reproductive strategies, in particular the evolutionary dynamics of diploid-polyloid complexes, the ecological impacts of hybridization in plant diversity, the evolution of genome size and chromosome numbers in plants using phylogenetic approaches and in the advancement of the application of flow cytometry to plant systems.

Ivana MAGUIRE, University of Zagreb, Croatia

Ivana Maguire (PhD in Biology in 2002) is Associate Professor at the University of Zagreb, Faculty of Science, Department of Biology. Her research includes applied ecology, demography, phylogeny, phylogeography and conservation of freshwater crayfish (Decapoda).

Andrew J. WRIGHT, George Mason University, USA

Andrew J. Wright obtained his PhD in 2013 at Aarhus University, Denmark. He is self-employed but has an affiliate position at George Mason University, USA. He provides science-policy advice regarding marine mammals and the effects of noise on them. He is also specialized in data handling and processing, including acoustical data.

Ante ŽULJEVIĆ, Institute of Oceanography and Fisheries, Croatia

Ante Žuljević, PhD, is Senior research associate at the Institute of Oceanography and Fisheries in Split. His main interests are phytobenthos, invasive species, marine Natura 2000 sites and marine conservation education.

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