Journal of Wildlife and Biodiversity

International Conference on Wildlife Ecology and Biodiversity Conservation (ICWEB 2021)

Abstract Book

17-18 JUNE 2021

Online Conference

ORGANIZING COMMITTEE

SYMPOSIUM CHAIR

Prof. Dr. Ahmet KARATAŞ, Turkeyü

VICE CHAIRS

Assoc. Prof. Dr. Morteza Naderi, Iran – Turkey

Assoc. Prof. Dr. Fethi Bengil, North Cyprus

SCIENTIFIC COMMITTEE (alphabetic order)

Alexey Yanchukov - Turkey - Ukraine

Aliasghar Abdoli – Iran

Ayşegül Karataş - Turkey

Can Bilgin - Turkey

Cemal Varol Tok - Turkey

Çağan Şekercioğlu - USA - Turkey

Damla Beton, North Cyprus

David Tarkhnishvili - Georgia

David Waters – United Kingdom

Elena Buzan – Slovenia

Elizabeth Grace Tunka Bengil - North Cyprus

Elshad Askerov - Azerbaijan

Erika Cuellar Soto – Oman

Fatih Hüseyinoğlu - North Cyprus

Hisham al-Hennawy - Egypt

Indra R. Gadhvi – India

Ismail K. Sağlam - Turkey

İbrahim Raşit Bilgin - Turkey

İrfan Kandemir - Turkey

Katarzyna Bojarska - Poland

Kerim Çiçek - Turkey

Kurtuluş Olgun - Turkey

Marios Papageorgiou - Cyprus

Maurizio Sara – Italy

Mehrdad Hadipour – Iran

Mert Elvirici - Turkey

Morteza Naderi – Turkey- Iran

Mustafa Sözen – Turkey

Oğuz Türkozan - Turkey

Oleksandr Zinenko - Ukraine

Paraskavi Karachle - Greece

Petr Benda - Czechia

Roberta Bencini – Australia

S. Saeed Hosseinian Yousefkhani - Iran

Shahrbano Oryan –Iran

Sonia Saeed – France

Yordan Keshov - Bulgaria

Zuhair Sami Amr – Jordan

SYMPOSIUM ORGANIZING COMMITTEE MEMBERS

Fethi Bengil, Girne American University, North Cyprus

Mehmet Kürşat Şahin, Karamanoğlu Mehmetbey University, Turkey

Morteza Naderi, Koç University, Turkey – Arak University, Iran

Elizabeth Grace Tunka Bengil, Girne American University, North Cyprus

LIST OF PRESENTATIONS

WELCOMING

INVITED PRESENTATION

Journal of Wildlife and Biodiversity

Welcoming by Prof. Dr. Ahmet Karataş

Dear Participants,

Welcome to International Conference on Wildlife Ecology and Biodiversity Conservation

The number of living species classified and considered valid so far is more than 2,200,000. For example, about 74 thousand species of Chordata are known. There are thousands of living species still waiting to be discovered. For example, an average of 300-400 fish species per year are added to the above number. If we look specifically at Turkey, apart from about 12.000 plant taxa, about 35.000 insects, 1760 vertebrate species and more than 70.000 living species are known. While we are proud of this wealth; On the other hand, thousands of species are extinct or threatened with extinction, mainly due to habitat loss, invasive species, global climate change, hunting, overfishing, genetic pollution, etc. A forest the size of 37 football fields is cut down and destroyed every minute. One-third of the world's climate regulators, coral reefs, are bleached.

Through evolution, species arise through the process of speciation—where new varieties of organisms arise and thrive when they are able to find and exploit an ecological niche—and species become extinct when they are no longer able to survive in changing conditions or against superior competition. The relationship between animals and their ecological niches has been firmly established (Sahney et al., 2010). A typical species becomes extinct within 10 million years of its first appearance, although some species, called living fossils, survive with little to no morphological change for hundreds of millions of years (Newman, 1997). As long as species have been evolving, species have been going extinct. It is estimated that over 99.9% of all species that ever lived are extinct. The average lifespan of a typical species is 1–10 million years, although this varies widely between taxa (Mills, 2009).

There have been at least five mass extinctions in the history of life on earth, and four in the last 350 million years in which many species have disappeared in a relatively short period of geological time. The largest extinction is considered as the "Permian–Triassic extinction event" about 250 million years ago, which is estimated to have killed 90% of species then existing (Benton, 2005; Sahney & Benton, 2008). However, bigger extinction event is in process and this sixth mass extinction is called the Holocene extinction or Anthropocene extinction, as a result of human activity (Dirzo et al., 2014; Ripple et al., 2017; Ceballos & Ehrlich, 2018).

The current rate of extinction of species is estimated at 100 to 1,000 times higher than natural background extinction rates (Lawton & May, 1995; Pimm et al., 1995, 2014; De Vos et al., 2014; Ceballos & Ehrlich, 2018). More than 190 bird species have gone extinct over the past 500 years, while 103 mammal species have gone extinct, according to the ASM's database. When other groups such as reptiles, amphibians, fish, butterflies and plants are added to these, it is seen that thousands of living species have become extinct since 1500. In only Turkey, at least five freshwater fish species have become extinct in the last century (Karataş, 2020).

I would like to say welcome you all and wish you a successful presentation and opportunity for exchanging of knowledge by interaction during the sessions.

References

Benton, M.J. (2005). When Life Nearly Died: The Greatest Mass Extinction of All Time. Thames & Hudson.

Ceballos, G. & Ehrlich, P. R. (2018). The misunderstood sixth mass extinction". Science. 360 (6393): 1080-1081.

De Vos, J. M., Joppa, L. N., Gittleman, J. L., Stephens, P. R., Pimm, S. L. (2014). Estimating the normal background rate of species extinction. Conservation Biology, 29 (2): 452–462 [in Spanish]. doi:10.1111/cobi.12380.

Dirzo, R., Young, H. S., Galetti, M., Ceballos, G., Isaac, N. J. B., Collen, B. (2014). Defaunation in the Anthropocene, Science. 345 (6195): 401–406. doi:10.1126/science.1251817.

Karataş, A. 2020, Türkiye'nin Kırmızı Listesi, National Geographic-Türkiye.

Lawton, J. H. & May, R. M. (1995). Extinction Rates, Journal of Evolutionary Biology. 9: 124–126. doi:10.1046/j.1420-9101.1996.t01-1-9010124.x.

Mills, L. S. (2009). Conservation of Wildlife Populations: Demography, Genetics and Management. John Wiley & Sons. p. 13. ISBN 978-1-4443-0893-8.

Newman, M. (1997). "A model of mass extinction". Journal of Theoretical Biology. 189 (3): 235–252. doi:10.1006/jtbi.1997.0508.

Pimm, S. L., Russell, G. J., Gittleman, J. L., Brooks, T. M. (1995). The Future of Biodiversity. Science. 269 (5222): 347–350. doi:10.1126/science.269.5222.347.

Pimm, S. L., Jenkins, C. N., Abell, R., Brooks, T. M., Gittleman, J. L., Joppa, L. N., Raven, P. H., Roberts, C. M. & Sexton, J. O. (2014). The biodiversity of species and their rates of extinction, distribution, and protection, Science. 344 (6187): 1246752. doi:10.1126/science.1246752.

Ripple, W.J., Wolf, C., Newsome, T.M., Galetti, M., Alamgir, M., Crist, E., Mahmoud, M.I., & Laurance, W.F. (2017). World Scientists' Warning to Humanity: A Second Notice, BioScience, 67 (12): 1026–1028. doi:10.1093/biosci/bix125.

Sahney, S. & Benton, M. J. (2008). Recovery from the most profound mass extinction of all time. Proceedings of the Royal Society B: Biological Sciences. 275 (1636): 759–765. doi:10.1098/rspb.2007.1370.

Sahney, S., Benton, M. J. & Ferry, P. A. (2010). Links between global taxonomic diversity, ecological diversity and the expansion of vertebrates on land. Biology Letters. 6 (4): 544–547. doi:10.1098/rsbl.2009.1024

Teyssèdre, A. (2004). Biodiversity and Global Change. Towards a sixth mass extinction crisis?. Paris: ADPF.

Journal of Wildlife and Biodiversity

Use of Ichthyoplankton Surveys in the Conservation of Marine Fishes

Sinan Mavruk

Department of Marine Biology, Çukurova University, Fisheries Faculty. Adana/Turkey

smavruk@cu.edu.tr

Abstract

Marine teleost fishes usually have planktonic egg and/or larval stages in their early life, which are called ichthyoplankton. Not only morphology, but also functions change during the ichthyoplanktonic phase. The active movement ability and the perception capacity of fish gradually increases with the growth and development. These changes increase the ability of larvae to find food and avoid predators. Life risks therefore decrease as the fish grow and develop. Ichthyoplankton data has many applications in the management and conservation of fish populations. For example, ichthyoplankton samplings can provide information on the local fish biodiversity, along with their spawning periods and areas. Moreover, this data can directly be adopted to the stock management models as an indicator of the size of the spawning stock biomass. Ichthyoplankton based approaches provide important advantages over the classical monitoring or sampling methods. Firstly, collecting ichthyoplankton is non-invasive method that minimizes the sampling damage on fish populations, since, fishes produce vast amount of eggs, most of which die under natural process. In addition, sampling ichthyoplankton does not harm sensitive habitats unlike most fishing operations. Ichthyoplankton based approaches also has economical and logistical advantages, as fish eggs and larvae are easy and cheap to collect compare to sampling adult fishes. On the other hand, there are some challenges to using ichthyoplankton based approaches. To begin with, identifying ichthyoplankton requires advanced specialization as well as strong literature support. Because fishes have different spawning seasons, a yearlong sampling is necessary to provide a full biodiversity inventory. Advection is another problem since fish eggs and larvae can drift long distances, and this can cause important misinterpretations. Despite several challenges, ichthyoplankton based approaches can provide key information in the monitoring, conservation, and management applications.

Keywords: Biodiversity, fish egg, fish larvae, fishery management, monitoring

Journal of Wildlife and Biodiversity

Understanding stakeholders' perceptions on threats and adapting conservation strategies a case study from the Gediz Delta, Turkey

Dilara Arslan[1, 2], Anis Guelmami[1] and Lisa Ernoul[1]

[1] *Tour du Valat, Institut de Recherche pour la Conservation des Zones Humides Méditerranéennes, Le Sambuc – 13 200 Arles – France,*

[2] *Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale 3(IMBE), Avignon Université, UMR CNRS IRD Aix Marseille Université, IUT Site Agroparc, BP 61207, 84911 Avignon Cedex 09, France.*

kizildilara@gmail.com

Abstract

Wetlands face important anthropogenic pressures resulting in continued degradation and destruction. Mediterranean wetlands are particularly impacted due to the increasing human population and needs, with more than 45% of wetlands transformed into agricultural, urban, and industrial areas since 1970. In order to combat these negative trends, it is necessary to make a systematic identification of existing and potential threats in order to develop effective conservation strategies. In this case study from the Gediz Delta, Turkey, we first produced land use/land cover change (LULC) maps covering 1984, 1990, 2000, 2010 and 2019 annual time periods using Landsat TM, Landsat ETM and Sentinel-2 time series satellite images. We then conducted key informant interviews with stakeholders in the delta to identify the perceived threats facing the wetlands and its associated biodiversity. A total of 30 participants were interviewed in 22 different governmental and non-governmental organizations. Each interview lasted between 30-40 minutes using 3 open-ended survey questions. The qualitative results were analyzed using coding and clustering techniques and then classified according to the IUCN threat classification. Each threat was localized on the LULC maps using two-kilometer grids. Additional threats obtained from urban planning documents and local news sources were added for the period from 1980 to 2020. A total of 141 responses were collected through the interviews and pollution (agricultural and industrial) was identified as the most cited threat (28% of the responses). Despite the fact that urbanization has increased by 147 percent in the area, this was not identified as a threat by the stakeholders. Our results suggest that several different strategies are important to undertake to combat the threats (both perceived and real) in the Gediz Delta in order to ensure the sustainability of the wetlands in the future.

Keywords: conservation planning, conservation strategies, Gediz Delta, land use/land change, threats perceptions

Journal of Wildlife and Biodiversity

Preliminary results on Cyprus elasmobranch bycatch

Elizabeth Grace Tunka Bengil[1], Louis Hadjioannou[2], Marios Papageorgiou[2], Robin Snape[1,3]

[1]*SPOT - Society for Protection of Turtles, Levent Apt 2, Ulus sokak, Gönyeli, Cyprus,*

[2]*Enalia Physis Environmental Research Centre, Acropoleos 2, Aglantzia 2101, Nicosia, Cyprus,*

[3]*Centre for Ecology and Conservation, University of Exeter, Cornwall Campus, Penryn TR10 9EZ, UK.*

tunkaeronat@hotmail.com

Abstract

Cyprus Elasmobranch Research and Conservation Network (CERECON) was launched in 2019 to increase the understanding of elasmobranch species biodiversity, biology, fishery threats, and to develop conservation measures. Detailed data on bycaught elasmobranchs were collected as part of the project by onboard observers, by self-reporting participatory fishers and by reports in press or social media that were followed up by the research team with the fishers. Individuals or information on bycaught individuals were collected from 11 locations, between January 2018 and February 2021. Data on the species, number of individuals, location and date were recorded. Where possible, fishing gear, set and haul times, and depth were also recorded. A total of 511 individuals were recorded (39% batoid and 61 % shark species), 496 were identified to the species level (27 species) and 14 to lowest possible taxon. The results of this project are the most comprehensive study on elasmobranchs in Cyprus and will make an important base line for future studies in the eastern Mediterranean Sea.

Keywords: Sharks, Batoids, Cyprus, Biodiversity, Fisheries interaction

Some Biological Aspects of *Saurida lesepsianus* inhabiting Northern Cyprus

Elizabeth Grace Tunka Bengil

SPOT - Society for Protection of Turtles, Levent Apt 2, Ulus sokak, Gönyeli, Cyprus,

tunkaeronat@hotmail.com

Abstract

Saurida lesepsianus Russell, Golani & Tikochinski, 2015 specimens were collected in winter of 2018 from a fisherman at Gazimağusa. A total of 100 individuals; 59 male, 38 female and 3 unidentified were examined. Length and weight relationships were found to be $W= 0.0029x^{3.2622}$, $W= 0.0021x^{3.3807}$, and $W= 0.0031x^{3.2353}$ for all, male and females, respectively. As it is shown the species show positive allometry for all, female, and males. Only half of the individuals (53 individual) had stomach content, all composed of teleost fish. The preliminary results show that the species show similar biological features in Northern Cyprus as previously conducted other studies from the eastern Mediterranean.

Keywords: Lessepsian fish, biological features, positive allometry, teleost, Levantine Sea

Journal of Wildlife and Biodiversity

Some Population Dynamical Parameters of Bogue (*Boops boops* (L,1758)) in Mersin and Iskenderun Bay, the Eastern Mediterranean

Liban Isse Farah, Sinan Mavruk, Hacer Yeldan, Dursun Avşar

Department of Marine Biology, Cukurova University, Fisheries Faculty, Balcalı/Adana/Turkey

libaanisse2019@gmail.com

Abstract

Bogue, *Boops boops* (Linnaeus 1758), is among the important commercial species in marine fisheries of Turkey. This study was performed to document feeding, growth, mortality, and exploitation rate of bogue population in the Gulf of Mersin and Iskenderun, the Eastern Mediterranean Sea. Between September 2019 and August 2020, a total of 967 specimens were collected from commercial fishers operating in the area. Total length (TL) ranged from 11.1 to 28.4 cm, and total weight (W) ranged from 12.1 to 281 g. The exponential coefficient of the TL–W relationship (LWR) was significantly different between sexes ($p<0.05$). The LWR for juveniles, females, males and combined sexes were estimated as $W=0.011TL^{2.90}$ ($R^2=0.947$), $W=0.002TL^{3.52}$ ($R^2=0.947$), $W=0.004TL^{3.29}$ ($R^2=0.912$), $W=0.003TL^{3.38}$ ($R^2=0.941$), respectively. The growth profile was found to be positive allometric except for juveniles. The von Bertalanffy growth parameters were calculated as L=32.991, $k=0.181 years^{-1}$ and $t_0=-1.928$ years for combined sexes. The growth performance index was Ø'=5.286. The total, fishing and the natural mortality rates were estimated as M=0.520, F=0.882, Z=1.402, respectively. The exploitation ratio was E=0.629, indicating that the bogue stock inhabits the study area was overexploited. Therefore, the fishing pressure should be reduced to sustain its population. Out of examined 190 specimens stomach content, 46 (24%) were found containing undigested food. The diet composition consisted of larval and juvenile fish, copepods, shrimps, and squids. Larval and juvenile stages of invasive *Bregmaceros nectabanus* were the most dominant prey items occurring, corresponding to 94.89% of the full stomachs. This provided a good example of how an invasive species became an important food item for a native species and can restructure the marine food web.

Keywords: Exploitation, diet, feeding, length-weight relationship, Sparidae, Von- Bertalanffy growth parameters

Acknowledgement: This study is a part of MSc thesis of Liban Isse Farah and performed with the financial support of Cukurova University, Scientific Projects Coordination Unit with project number FYL-2020-13301

Journal of Wildlife and Biodiversity

Potential residency behaviour of Atlantic bluefin tuna in the Eastern Mediterranean by using local fishermen's knowledge

İsmet Saygu

Fisheries Faculty, Cukurova University, Adana, Turkey.

ismetsaygu@gmail.com

Abstract

Atlantic bluefin tuna, *Thunnus thynnus*, is highly migratory large pelagic fish species. Stocks from the eastern and western Mediterranean Sea are separately conserved and managed by the International Commission for the Conservation of Atlantic Tunas. The eastern stock resides throughout the Mediterranean and eastern Atlantic Ocean, breeds in well-defined areas in the Mediterranean including the Northeastern Mediterranean between May and July. Its fishery depends on spawning migration to these areas and occurs from 25 May to 25 June in the eastern Mediterranean. Fishing strategy of the bluefin tuna is capture-based aquaculture by way of catching, farming and fattening. However, a little is known about the migration behaviour of the bluefin tuna. Tagging studies indicate that while some bluefin tuna individuals have homing behaviour, others reveal complex migration patterns or stay around the spawning areas. In this context, the aim of the study was to detect the potential residency behaviour of bluefin tuna in the Eastern Mediterranean by applying local fishers' knowledge. The interviews were conducted with 73 fishers from 23 fishing ports along the Mediterranean coast of Turkey. Findings from this study show that fishers can come across with bluefin tuna at any month of the year along the study area with peaks from May to August covering the breeding season. In addition, median of the mostly encountered individuals' weight was larger than the weight of first sexual maturity (30 kg) in the Mediterranean. These results provide support for the idea that some individuals of bluefin tuna reside in the eastern Mediterranean all along the year or migrate this area for feeding in out of the spawning season as well.

Key Words: Local Ecological Knowledge, *Thunnus thynnus*, Eastern Mediterranean, Fisheries

Journal of Wildlife and Biodiversity

Efficacy of non-invasive genetic sampling in studies on wildlife

Miriam A. Zemanova

Centre for Compassionate Conservation, University of Technology Sydney, Australia.

zemanova.miriam@gmail.com

Abstract

We are currently experiencing rapid biodiversity loss worldwide, resulting in many species facing the risk of extinction. More than ever before, it is imperative that animal and plant populations are being monitored so that efficient conservation measures can be designed and implemented. Traditionally, wildlife been monitored through field survey methods such as counting of individuals encountered within a transect, observations of traces left behind by animals, capture-mark-recapture techniques, or genetic assessment. With new technologies and improved methods being developed and implemented during the last decades, genetic assessment, in particular, is increasingly being used for biodiversity monitoring. Typically, DNA for genetic analysis would be collected through invasive or lethal sampling from blood or tissues. But concerns about animal welfare, as well as strive for efficiency, have led to the development of techniques allowing genetic assessment from non-invasively obtained material, such as faeces, hair, saliva, or the so-called environmental DNA. However, the scientific evidence on the efficacy, cost-, and time-effectiveness of non-invasive genetic assessment in wildlife research is currently limited, and the implementation rate of non-invasive genetics remains relatively low. Therefore, I conducted a systematic review and searched three scientific databases for relevant studies that compared the efficacy of non-invasive genetic assessment with another method (e.g., invasive genetic sampling, camera traps, or field visual or acoustic survey) in different types of studies. I identified 113 relevant studies, published between 1997 and the beginning of 2021, of which the majority (94%) reported that non-invasive genetic assessment has equivalent or superior efficacy when compared with another research method. It can perform better particularly in studies on population size estimation, species detection or species identification. Non-invasive genetic assessment might be also cheaper and more time-efficient than other methods. In summary, non-invasive genetic assessment is a highly effective research approach, and its implementation across different types of studies on wildlife can be highly recommended.

Keywords: 3Rs principles, DNA sampling, wildlife welfare

Journal of Wildlife and Biodiversity

The Plant Community and Floristic Diversity of Göknarlık Nature Protection Area (Beykoz, ISTANBUL-TURKEY) From The Perspective of Conservation Biology

Okan ÜRKER

Eldivan Vocational School of Health Service, Environmental Health Program, Çankırı Karatekin University, Çankırı/Turkey.

okanurker@karatekin.edu.tr

Abstract

Göknarlık Nature Protection Area (NPA) which is one of the 31 NPAs in Turkey, is located within the boundaries of the province of Istanbul, Beykoz District's Tokatköy Village. The protection area covers approximately 46 hectares. The protection status has been given on 02.12.1987 (Anonymous, 2020). It also has the status of a 1st Degree Natural Site. It is also a unique and interesting area, as it is the only locality where fir tree grows up, which is one of the 2200 plant species that spreads naturally in Istanbul (Akkemik, 2017).

In this study, the main goal is to observe the current plant community properties, dendrology, floristic diversity, vegetation, habitat and ecosystem characteristics of the study area. It is also aimed that the findings obtained will contribute to the long-term and sustainable conservation of the protected area in the form of an action plan.

Studies for determining floristic diversity were carried out by following the line-transect method at 10 different points in the study area in August and November 2020, and in January and April 2021. On the other hand, during April 2021 in 2 different forest habitats (fir forest and chestnut forest) in the study area the point intercept method (Canfield, 1941; Bonham, 1989) was used in this study because it provides various interpretations about the vegetation structure and plant community parameters.

According to the map of EUNIS habitat types which is produced using by forest stand map; there are three different habitat types inside the study area; G3-1I - *Abies sp.* reforestation (9,97 ha), G1.7D - *Castanea sativa* woodland (32,60 ha), J1.2 - Residential buildings of villages and urban peripheries (3,43 ha).

In the light of recent studies in the field, a total of 197 plant taxa have been identified, of which only 2 are endemic (*Abies bormuelleraina* subsp. *equi-trojani* and *Lathyrus undulatus)*. Although it has been determined that these endemic species are also under threat on a global scale (both of them are EN category in IUCN Red List ver.2021.1), it should be stated that the population densities in the study area have a relatively wide distribution.

Although it is understood that species belonging to families of Euphorbiaceae and Orchidaceae are included in the list of CITES Annex-II in the study area, it has been determined that only one taxon (*Cyclamen coum* Mill. subsp. *coum*) is included in the Bern Convention Annex-1 List.

A total of 54 species have been identified in point intercept studies carried out on both fir and chestnut forest vegetations, and 19 of these species have been found in both vegetations. While the species richness of fir forest vegetation is 27, it is 46 of chestnut forest vegetation. The highest species diversity (3.65) in the protected area was determined in chestnut forest vegetation. Considering the equation of Sorensen similarity coefficient; The similarity coefficient between chestnut forest vegetation and fir forest vegetation was calculated as 0.52, which indicates a moderate similarity ratio.

In order to ensure the gene flow of the protected area in terms of conservation biology in the future, it is of great importance to ensure wildlife mobility by designing ecological corridors from now on. These wildlife corridors can be implemented by using the data obtained in this study.

Keywords: Plant community, flora, habitat, conservation, nature protection area.

Journal of Wildlife and Biodiversity

Investigation of Gene Expression Changes in *Cymodocea nodosa* Depending on Environment Factors

Esra Ozturk Yigit

Department of Biology, Faculty of Science, Ege University, Izmir, Turkey.

esraozturktr@gmail.com

Abstract

Conservation and management of marine ecosystems is problematic in the Anthropocene. While ecosystems that offer direct uses for humans, such as seagrass meadows, have historically faced challenges of overfishing, habitat destruction, and eutrophication, most recent threats to marine ecosystems stem from global climate change. Climate change causes an increase in ocean temperatures and acidification, as well as regional changes in nearshore salinity in coastal habitats. These environmental alterations pose a grave threat to the physiology of marine organisms.

The aim of this research is to examine and compare gene expression changes in *Cymodocea nodosa* depending on time and location. *C. nodosa* leaves were collected in Urla and Aliaga provinces of Izmir for gene expression analysis at different daily periods during May 2021. Measures of the physical environment were also recorded. In this paper we will report the relationship of *C. nodosa* metabolic pathways with the environment. Results obtained through the comparison of gene expression data for target genes and reference genes will also be presented. Determining this link will inform future studies on remote monitoring of the environmental effects of climate change through gene expression.

Keywords: *C. nodosa*, climate change, gene expression

Acknowledgement: This study was supported by the grant Ege University BAP-FKB-2021-22244.

Journal of Wildlife and Biodiversity

Activity pattern of the European wildcat (*Felis silvestris silvestris*) in northern Greece using GPS telemetry and accelerometer logging data

Despina Migli [1], Christos Astaras[2], George Boutsis[1], Nikolaos Evangelos Karantanis[3], Anastasia Diakou[4], Dionisios Youlatos[1]

[1] *Department of Zoology, School of Biology, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece,*

[2] *Forest Research Institute, ELGO-DIMITRA, 57006 Thessaloniki, Greece*

[3] *Princess Royal College of Animal Management and Saddlery, Capel Manor College, EN7 5HR, London, UK,*

[4] *School of Veterinary Medicine, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece.*

despmigk@bio.auth.gr

Abstract

The European wildcat (*Felis silvestris silvestris*) is the only felid with confirmed presence in Greece. Due to its elusive nature, the species has received little scientific attention with most information about its distribution, status and ecology obtained opportunistically from studies of other species (e.g. by-catch detections in camera traps). For the first time in Greece, we designed a study focused on understanding the ecology and behavior of the wildcat in a wetland - agricultural mosaic landscape, where the species' estimated density is among the highest in the country. We present preliminary findings on the activity pattern of four adult individuals (three females, one male) using biotelemetry data (E-obs GPS collars with 3-axis accelerometer) collected over a four-month period (Nov. 2020 – Feb. 2021). We report the winter home range size of the study animals (range 1.4 - 6.8 km^2; 95% UD). Moreover, we examine intraspecific and temporal (diel, lunar phase) variations in wildcat activity patterns using the very high temporal resolution accelerometer data. Specifically, we discuss the influence of moonlight illumination on wildcat nocturnal behavior in light of the contrasting "Predation Risk Hypothesis" and the "Visual Acuity Hypothesis". According to the former hypothesis, small predators would be expected to decrease their activity in bright nights in order to reduce predation risk. On the contrary, the latter hypothesis suggests that species, such as felids, relying on visual detection of prey and danger, would be expected to increase their activity.

Keywords: European wildcat, temporal activity pattern, moonlight, accelerometer data, meso-predator behavior

Acknowledgements: This research is co-financed by Greece and the European Union (European Social Fund- ESF) through the Operational Programme «Human Resources Development, Education and Lifelong Learning 2014- 2020» (MIS 5047853).

Journal of Wildlife and Biodiversity

Effects of Wind Farms on Terrestrial Mammals: A Case Study in Turkey

Yasin İlemin

Department of Environmental Protection and Technologies, Fethiye Ali Sıtkı Mefharet Koçman Vocational School, Muğla Sıtkı Koçman University, Fethiye, Turkey.

yasinilemin@mu.edu.tr

Abstract

This study was carried out in an area where four wind turbines found in Tekirdağ province of Turkey. The survey was conducted in winter and summer time and 3 days in each season during 2018. Sampling methodology is based on using the feces-tracking method along 100 m linear transects. One transect is close to wind turbines the other is 2.5 km away from turbines. Both transects have same ecological conditions. In this study, it is aimed to reveal the effects of wind turbines on terrestrial mammals for the first time in our country. It is aimed to compare species composition and density of the species in the study area. Wolf (*Canis lupus*), red fox (*Vulpes vulpes*), Eurasian badger (*Meles meles*) and European hare (*Lepus europaeus*) were detected during the surveys. Wolf records are away from turbines (n = 2 and feeding record n = 1), badger records are close to turbine line (n = 3) and away from turbines (n = 1), hare records are close to turbine line (feces n = 4) and away from turbines (n = 11), red fox records are close to turbine line (n = 4) and away from turbines (n = 3). According to these results, wolfs avoid wind turbines. Hares show more intense activity away from the turbine line. On the other hand, badgers are more active close to wind turbines. Red foxes show neutral response to wind turbines. According to the results of this preliminary study, wolf and European hare less frequently visited wind farm areas and areas close to wind turbines, probably due to both the physiological effects of excessive noise and habitat loss around the turbines. Badgers follow the insect species which are coming to the turbine area because of the turbine illumination and heat.

Keywords: Wind turbine, terrestrial mammals, interaction, wolf, eurasian badger, european hare, the Marmara

Journal of Wildlife and Biodiversity

An analysis of wildlife road mortality in North of Portugal

Andreia Garcês[1,2], Justina Prada[3,4], Filipe Silva [3,4], Celso Santos[3], Isabel Pires[3,4]

[1]*Inno – Laboratory Veterinary, Microbiology Department, Braga, Portugal,*

[2]*CESPU - Cooperativa de Ensino Superior Politécnico e Universitário, Gandra Portugal,*

[3]*Department of Veterinary Science of the University of Trás-os-Montes and Alto Douro, Vila Real,*

[4]*CECAV - University of Trás-os-Montes and Alto Douro, Vila Real, Portugal.*

andreiamvg@gmail.com

Abstract

One of the major causes of death of wild animals worldwide is vehicle collisions. In Portugal, the number of animals killed in car collisions has increased in recent years. However, the data available in this area is still scarce. In order to characterize wildlife species that died in vehicle collisions, the necropsy records of 170 animals (mammals and birds) between January 2010 and June 2019 were evaluated. Most of the animals were mammals (73.5%), being Red Fox (*Vulpes vulpes*) (26.5%) the most common species. There were more collisions in adult animals (88.2%) than in young animals, with no difference between genders. This study provides important information on the animal species most affected by vehicle accidents in northern Portugal. Incorporating this information into animal behaviour can help establish measures to prevent collisions with wildlife.

Keywords: collision; Portugal; roadkill; road ecology, vehicles

Journal of Wildlife and Biodiversity

Modeling habitat suitability for small and medium sized felids in Maduru Oya National Park, Sri Lanka

Dulan Jayasekara[1,2]; Dharshani Mahaulpatha[1*]

[1]*Department of Zoology, Faculty of Applied Sciences, University of Sri Jayewardenepura, Sri Lanka,*

[2]*Faculty of Graduate Studies, University of Sri Jayewardenepura, Sri Lanka.*

mahaulpatha@sjp.ac.lk

Abstract

Small and medium sized felids of Sri Lanka include three cat species; fishing cat (*Prionailurus viverrinus*), jungle cat (*Felis chaus*) and, rusty-spotted cat (*Prionailurus rubiginosus*). These felids are hyper-carnivorous elusive predators that play important ecological roles in a variety of habitats. We conducted this study to identify the habitat associations and model the habitat suitability of Maduru Oya National Park (MONP), Sri Lanka for small and medium sized felids. Species occurrence data were obtained based on the camera trap capture events, direct observations and road kill records. Modeling was conducted based on the maximum entropy algorithm (MaxEnt) using the software package Maxent (version 3.4.3). After accounting for multicollinearity, we selected six bioclimatic variables from the WorldClim Global Climate data (www.worldclim.org), elevation, distance to water, vegetation parameters (NDVI) as continuous variables and habitat type as a categorical variable. The predictive accuracy (AUC) of the selected models were evaluated to be greater than 0.80. Distance to water resources (44.9%), bio1-mean annual temperature (33.6%) and habitat type (Dry-mixed forest; 79.8%) were identified as the most important variables contributing to habitat selection of fishing cat, jungle cat and rusty spotted cat respectively. Habitat suitability maps were generated to predict the distributions of the species. Suitable habitat area availability was 21.33% for fishing cat, 21.13% for jungle cat and 27.73% for rusty spotted cat. We further identified that spatial variation in habitat use facilitates these three species to coexist in the forest habitats of MONP. The outcome of this research will contribute towards future conservation and management. The findings will be useful in future comparative studies in Sri Lanka as well as elsewhere in the world.

Keywords: Habitat use, species distribution modeling, Felidae, meso-carnivores, MaxEnt modeling

Journal of Wildlife and Biodiversity

Climate niche modeling of *Scorpio kruglovi* (Scorpiones: Scorpionidae) in Iran

Taghi Ghassemi-Khademi[1], Rasoul Khosravi[2]

[1]*Department of Biology, Faculty of Sciences, Shiraz University, Shiraz, Iran,*

[2] *Department of Natural Resources and Environment Engineering, School of Agriculture, Shiraz University, Shiraz, Iran.*

ghasemi.taghi@gmail.com

Abstract:

Species distribution models (SDMs) are one of the most effective tools in conservation programs of biodiversity. These algorithms use occurrence points and environmental predictors to estimate the probability of occurrence of species across geographical areas. In this study, we predicted the climate niche of *Scorpio kruglovi* in Iran. This species was previously a subspecies of *S. maurus* which was introduced as an independent species in 2015. To build the models, we used MaxEnt distribution algorithm, 19 bioclimatic variables, and 21 occurrence localities. The AUC value for training dataset was 0.98 which indicated the excellent discriminative performance of the model. Precipitation of coldest quarter, precipitation seasonality, and minimum temperature of coldest month collectively had the highest percentage of contribution (52.4%) in building the model. Based on the Jackknife test, precipitation of coldest quarter had the highest percentage contribution and contained the most useful information in the model. Based on the response curves, *S. kruglovi* prefers some parts of Iran with precipitation of coldest quarter between 110-125 mm, precipitation seasonality less than 75, and minimum temperature of coldest month between -7 to -14 0C. Also, the southern half of the country is unsuitable for the species' occurrence. The results of this study which predicted some ecological features of *S. kruglovi*, for the first time, can be used in conservation programs of this species, as one of the valuable biological resources of Iran. Although the distribution range of this species is not limited to Iran, our results can complement future genetic/phylogenetic studies.

Keywords: *Scorpio kruglovi*, Habitat suitability, Maxent, Climate variables, Iran.

Journal of Wildlife and Biodiversity

Investigating the Urban trees' diversity in Tehran –Iran using i-Tree Eco model

Reihaneh Rasoolzadeh, Naghmeh Mobarghaee Dinan, Hassan Esmaeilzadeh, Yousef Rashidi

Environmental Sciences Research Institute of Shahid Behehshti University, Tehran,Iran.

r.rasoolzadeh@gmail.com

Abstract

Urban green spaces' structure and function can promote human health and environmental quality and also decrease some challenges that have been increased due to urbanization. So it is important to done some studies on the urban trees' diversity and urban green space structure because it can not only raise environmental awareness but also help policymakers for a better management to achieve the desirable environment. According to our knowledge, there has been no investigation on the urban trees' diversity of Tehran. Therefore, the research can be worthwhile.

The assessment of the trees' parameters and structure of Tehran urban forest, such as each tree species, DBH, crown width, total tree height and etc…, were conducted during 2020. Data from 316 field plots located throughout Tehran were collected during the growing season. It must be noted that the primary number of plots was 330, but some of them were not accessible. The plots were selected based on randomized cluster sampling and analyzed using i-Tree Eco model. The results showed that the overall tree density in Tehran is 30 trees/ acre and the number of trees is 7,127,933. The most common tree species are Afghan pine (13.0 percent), Black locust (10.0 percent) and, Arizona cypress (9.4 percent). In Tehran, about 28 percent of the trees are Asian endemic species and most trees have American origin (26 percent of the trees). So, Tehran urban trees are composed of endemic and exotic tree species. Therefore, Tehran urban forest often has a diversity that is higher than the surrounding native landscape. Increasing the tree diversity can minimize the overall impact or destruction by insects or disease, but it can also pose a risk to native plants if some of the exotic species are invasive plants that can potentially displace the native species.

Keywords: Urban green space, Tehran, I-tree model, biodiversity.

Journal of Wildlife and Biodiversity

Habitat preferences and land use dynamics of *Darevskia rudis* in Northeastern Anatolia, Turkey

Mehmet Kürşat Şahin

Department of Biology, Kamil Özdağ Faculty of Science, Karamanoğlu Mehmetbey University, Karaman, Turkey

yasambilimci.kursat@gmail.com

Abstract

The spiny tailed lizard, *Darevskia rudis* (Bedriaga, 1886) has been inhabiting in Central and Northern coastal region of Anatolia (Turkey), and also Georgia, Armenia, Russia and Azerbaijan. Despite its wide range of distribution, there has been only few studies on its ecological requirements and / or habitat preferences. The aim of this study about the spiny-tailed lizard habitat preferences and the impacts of climatological and vegetational conditions on its activity. Field excursions were carried out in Northeastern Anatolia, Turkey between 2017 and 2018. A total of 62 grids surveyed and 59 localities were detected as where the spiny-tailed lizard inhabits. Firstly, these occurrence data were processed in Geographic Information System (GIS) and the habitat preferences and utilization of the lizard were determined by European Nature Information System (EUNIS) and Copernicus Land Monitoring Service products. Secondly, multi-step general linear model (GLM) via 41 climatological and vegetation conditions (i.e. monthly temperature, precipitation, solar radiation dynamics, elevation, distance to river, canopy pattern of the area) was applied to assess the impacts on the land use of lizards. The results showed that, they inhabit ten different EUNIS habitat types in the study area. Moreover, the GLM demonstrated that, there is a significant difference between non-tree areas and trees predominantly used for agricultural practices (i.e. nut bushes as a broadleaved canopy pattern). However, the microhabitat requirements enlighten us to understand the land use of the lizards in detail. Due to the basking activity of the rock lizards, it is expected that solar radiation has an influence on habitat use. Further GLM analysis supported this hypothesis with a remarkable consequence that the solar radiation rates on May, June and August have significant impacts on the habitat use that perfectly matches with reproduction season and hatchlings. Adult and juvenile lizards have high activity pattern in these periods, because of their thermal regulations via environmental dynamics. Further studies depending on the local environments might provide the thermal patterns of structural habitat use.

Keywords: EUNIS, habitat use, canopy pattern, solar radiation, general linear model

Journal of Wildlife and Biodiversity

The introduction of sika deer in Poland and the Czech Republic - analysis of changes in abundance

Jagoda Czajkowska, Paweł Janiszewski

Department of Fur-Bearing Animal Breeding and Game Management, Oczapowskiego 5, University of Warmia and Mazury in Olsztyn,10-718 Olsztyn,

*Poland*czajkowskajagoda97@gmail.com

Abstract

Sika deer (*Cervus nippon*) is a representative of family *Cervidae*, which naturally lives in East Asia. Its introduction started the development of subpopulations in various regions of the world. Currently, the sika deer is considered both an invasive species and an animal causing many damages, especially in forest management in European countries. The aim of the study was to analyse the development of the sika deer population in Poland and the Czech Republic since introduction, to the present day. The study was based on a diverse statistical and literature sources containing data on the abundance and development of regional sika deer population in the analysed time period. The study covered two adjacent countries with similar geographical conditions. Based on the obtained data, 4 historical sub-periods were presented, which significantly influenced the current status of the both populations. Sika deer was introduced to Poland and the Czech Republic at the end of the 19th century, in amount of 7 and 4 individuals. Comparable living conditions in the both countries should generate similar increases in its numbers, but it was found that both subpopulations have been developed in a very different way. Probably, it was due to various climatic conditions, and the different breeding systems, and others. Current data show the number of sika deer in Czech Republic at over 16 000, and there are only 200 individuals in Poland. The diversified development of the two analysed populations may indicate the threats resulting from the introduction as well as the influence of many factors on their quantitative development.

Keywords: population development, introduction, alien species, *Cervus nippon*

Journal of Wildlife and Biodiversity

Occurrence and distribution of Philippine warty pig (*Sus philippensis* Nehring, 1886) in Mt. Banahaw de Tayabas, Philippines

Al John C. Cabanas[1,2], Judeline C. Dimalibot[2], Anna Pauline O. de Guia[2], Renato SA. Vega[2]

[1]*University of the Philippines Los Banos, Philippines,*

[2]*Southern Luzon State University, Philippines.*

accabanas@up.edu.ph

Abstract

This study addresses knowledge gaps relating to the occurrence and distribution of Philippine warty pig (*Sus philippensis*) in the Philippines, specifically in Mt. Banahaw. To confirm the presence of Philippine warty pig, ten camera trap stations were established with camera traps functioning 24 hours for 17 days, along different elevations in Mt. Banahaw de Tayabas. The habitat characteristics of different camera locations were determined, using the habitat description sheet from the Southeast Asian Mammal Project. Data gathered were then used to construct box plots that determined the occurrence of the Philippine warty pig in the area. Species distribution models (BIOCLIM, DOMAIN, MAXENT) were constructed to determine the potential distribution of the species in Mt. Banahaw. Results showed that Philippine warty pigs prefer to occupy secondary growth forest, as high probability of occurrence was observed at 600-800 m.a.s.l. Further, modelling predicts that Philippine warty pigs are occupying large portions of Mt. Banahaw de Tayabas, although sparsely in the extreme southern and northern sections of the mountain. The most reliable model which predicted the distribution of the species was MAXENT. This study confirms the presence of Philippine warty pig in Mt. Banahaw de Tayabas and its preferred habitat. More work is needed to be done in order to determine the remaining populations of *S. philippensis* in the wild.

Keywords: Camera traps, species distribution model, habitat

Journal of Wildlife and Biodiversity

Camera trap data reveals the habitat use and activity patterns of secretive forest bird: Sri Lanka Spurfowl *Galloperdix bicalcarata*

Chathuranga Dharmarathne[1], Dulan Jayasekara[1,2], Dharshani Mahaulpatha[1]

[1]*Department of Zoology, Faculty of Applied Sciences, University of Sri Jayewardenepura, Sri Lanka,*

[2]*Faculty of Graduate Studies, University of Sri Jayewardenepura, Sri Lanka.*

mahaulpatha@sjp.ac.lk

Abstract

Conservation of rare and secretive forest species depends on appropriate prediction of habitat variability effects on their distribution patterns. Use of remotely triggered cameras for studies of bird ecology is uncommon. We used camera trap bi-catch data, recorded during a meso-mammal survey conducted from January 2018 to January 2021, to analyze the habitat use and diurnal activity patterns of Sri Lanka Spurfowl *Galloperdix bicalcarata* which is known as a shy and secretive forest bird endemic to Sri Lanka. Study sites included three protected areas in Sri Lanka, situated respectively in dry zone, wet zone and montane zone of the island. Camera traps were placed representatively in all available habitat types following a random approach using a survey grid. Camera placement was in a height of 25cm above the ground level and recorded photographs were analyzed using Wild.ID™ software. We used camera trap capture rate as an index of relative abundance (RAI). The R packages "activity", "pscl", "MASS" and "AICcmodavg" were used to analyze the activity patterns and habitat covariates related to abundance based on zero-inflated negative binomial model (ZINB). A total of 108 independent captures of *G. bicalcarata* were recorded during the study. RAI of spurfowl was highest in the primary forests of Sinharaja National Heritage Wilderness Area (2.38) closely followed by dry-mixed dense forests of Maduru Oya (2.22) and cloud forests of Horton Plains national parks (1.54). The diurnal activity peaks of *G. bicalcarata* occurred during the periods 0600h–1000h and 1500h–1800h indicating a bimodal activity pattern. However, there were differences in activity within the study sites. We identified canopy cover, trees with higher DBH, litter cover and litter depth to be positively affecting the spurfowl abundance while thick undergrowth and rock availability in the habitat were reducing the abundance. Findings of this study will be useful for the conservation and management decisions on Sri Lanka spurfowl and habitats that are vital for its survival. The suitability of bi-catch data from motion-activated camera surveys as a tool of studying secretive forest bird species is also highlighted through our findings.

Keywords: Ground dwelling birds, phasianidae, habitat use, camera trapping technology, conservation

Journal of Wildlife and Biodiversity

Investigation of demographic structure and Sexual dimorphism in Lorestan toad (*Bufotes luristanicus*, Schmidt, 1952)

Sareh Okhovat[1], Alireza Pesarakloo[1], **Raziyeh Alaei[1]**

[1]*Department of Biology, Faculty of Science, Arak University, Arak, Iran*

alaeiraziye@gmail.com

Abstract

The Lorestan toad is endemic to Iran and inhabits in the western foothills of the Zagros Mountains, namely Lorestan, Khuzestan, Kohgiluyeh Va Boyer Ahmad and Fars Provinces. In order to investigate the morphological variation in this toad, 15 morphological characters in more than 22 specimens of three regions [Jahangirkhani (lat: 32 46 42 N, long: 48 15 48 E, 454m a.s.l); Tafab (32°46'42N, 48°15'49" E, 461m a.s.l); Paytakht golzar (32°48'18"N, 48°24'6"E; 553m) in the southwest of Iran, were studied. Sexual size dimorphism was computed according to the sexual dimorphism index, where SDI= (average length of larger sex/average length of smaller sex) ±1; the result is arbitrarily defined as positive (+1) if females are larger than males, and negative (-1) if males are the larger sex. The Shapiro-Wilk's test showed normality of snout-vent length (SVL) (W = 0.947, P = 0.053). So, we used the t-test to compare the SVL between sexes. Patterns of phenetic relationships between local populations was investigated by One-way ANOVA. The SDI was 0.06, indicating an intersexual difference in body length (female-biased SSD), and the SVL differs significantly among females and males according to the t- test (P≤ 0.05). In the intraspecific level, based on morphometric characters, our analysis showed that all populations belonged to a single population, because there was no statistically significant difference between them (ANOVA; $P \geq 0.05$).

Keywords: *Bufotes luristanicus*, Morphometric Characteristics, Sexual Dimorphism,

Journal of Wildlife and Biodiversity

Investigated Sexual dimorphism in two dimensions of shape and body size in the tree frog *Hyla savignyi* (Audouin, 1827) in Lorestan Province

Raziyeh Alaei[1], Alireza Pesarakloo[1]

[1]*Department of Biology, Faculty of Science, Arak University, Arak, Iran*

alaeiraziye@gmail.com

Abstract

Sexual dimorphism describes existence of phenotypic differences between males and females, and also involves a series of different traits such as coloration, size, shape and behavior within species. In the present study, we investigated sexual dimorphism in two dimensions of shape and body size in the tree frog, *Hyla savignyi* (Audouin, 1827) using 13 males and five females from Lorestan Province in western Iran. Three patterns have been proposed for sexual dimorphism in amphibians, according to body size (SSD): Female-biased (females larger than males), male-biased (males larger than females), and unbiased (males equal to females). Sexual size dimorphism (SSD) was computed according to the sexual dimorphism index (SDI), where SDI= (average length of larger sex/average length of smaller sex) and statistical significance for a hypothesis of SSD of the frogs were tested using independent t-test. As well, ANOVA was conducted to compare vectors of means of the two sexes. Although the SDI was 0.07 indicating an intersexual difference in body length (female-biased SSD), SVL did not differ significantly among females and males according to the t-test; $P \geq 0.05$. In the present study, the ANOVA analysis distinguished a significant difference ($P \leq 0.05$) in four traits (ND: Distance between nostrils; IMTL: Inner metatarsal tubercle length; WMT: Width of metatarsal tubercle and WUE: Width of upper eye lid). So, in this species, snout–vent length (SVL) is not significantly different between adult males and females, but there are significant shape differences between sexes.

Keywords: *Hyla savignyi*, Sexual dimorphism, Lorestan Province.

Journal of Wildlife and Biodiversity

Expanding to the North: Assessing Anatolian distribution of Genus *Acanthodactylus*

Muammer Kurnaz[1], **Mehmet Kürşat Şahin[2]**

Kelkit Vocational School of Health Services, Department of Medical Services and Techniques, Gümüşhane University 29600, Kelkit / Gümüşhane, Turkey,

[2]Department of Biology, Kamil Özdag Faculty of Science, Karamanoğlu Mehmetbey University, Karaman, Turkey.

yasambilimci.kursat@gmail.com

Abstract

About 45 species belonging to the genus *Acanthodactylus* show a very wide area in the Palearctic Realm, including Africa, southeast Asia and southeast Europe. Four of them inhabits in Anatolia with very limited distributions. While *A. boskianus* lives in Birecik, *A. harranensis* in the ruins of the university in Harran plateau. Adana-Hatay coastal region hosts *A. schreiberi* in a very narrow area, and *A. ilgazi* has recently been reported from a small area in Yazıhan-Malatya. As can be understood from the literature, these 4 species are known to spread from very few areas in Anatolia. The aim of this study was to determine the presences of distribution areas of the *Acanathodactylus* species in Turkey using the species distribution modelling (SDM). According to the results of the analysis, the possible distribution of species in southern Turkey is predicted to take place in larger areas than their current distribution. In the dissemination analysis made for *Acanthodactylus* species under the present climatic conditions, it has been revealed that the distribution of species is compatible with the habitat requirements. As a result of these analyzes, 3 out of 19 bio-climatic variables greatly affect distribution of the species. The most contributing variable affecting the distribution of these species is Bio 11 with a percentile of approximately 85%. The reason why the Bio 11 variable determined the distribution of this genus in particular is that this climatic variable has been well matched by the genus general tendency for both hot and arid environments. As a result of this study, it is possible for this genus to be found from different locations in other studies to be carried out in Anatolia. The best example of this case is that the first four *Acanthodactylus* species, which have been known to spread only on the southern region for many years, the recent expedition for *A. ilgazi* expands the distribution to north with its presence on the Anatolian Diagonal. Therefore, it is strongly suggested that new field surveys, supported by preliminary analysis of SDM, contribute to the Anatolian biodiversity with an enormous perspective while the occurrence records are limited.

Keywords: fringed fingered lizard, distribution area, bioclimatic variables, Lacertidae, Turkey

Journal of Wildlife and Biodiversity

To Study the Physico Chemical Parameters, Plankton Diversity of Shamirpet Lake, Telangana State, India

Sivalingam Pothula

NRM Department, Forest College and Research Institute, Telangana State, India

proffessordrpsivalingamnrmdept@gmail.com

Abstract

The aquatic ecosystem is the main important Natural resource in the World. More percentage of the earth occupied by water resources. In developing countries, most of the percentage economic development depends on water resources like Dam, lakes, projects, tanks, ponds. During the study period, 14 physicochemical parameters were estimated. All the parameters were compared seasonal-wise. Physico - Chemical characteristics were variations occurred depends on pollution levels of water body, seasonal wise high pollution levels were recorded in the rainy season. Planktons were minute organisms it's a transfer of energy from one habitat stage to another habitat stage. During the study period, 13 phytoplankton species were identified, high plankton productivity identifies in the rainy season. Zooplankton diversity depends on phytoplankton species productivity, in the study period 11 zooplankton species were identified. Plankton Diversity positive relationship between phytoplankton species and Zooplankton species with lake environment. All over my study period, Shamir pet Lake water characteristics were moderated pollution levels.

1) Two precautions should take compulsory to protect the lake environment.

2) Avoid sewage water consult to lake environment.

3) Domestic activities avoid the lake surrounding environment.

Keywords: Plankton diversity, habitat stage, positive relationship

Journal of Wildlife and Biodiversity

Survey of mites (subclass: Acari) in some caves of Fars Province, Iran

Mojgan Sadat Shojaei, Mohamad Javad Ghasempoor, Saber Sadeghi

Department of Biology, Faculty of Sciences, Shiraz University, Shiraz, Iran

ssadeghi@shirazu.ac.ir

Abstract

The subclass Acari belongs to the class Arachnida from the phylum Arthropoda. Acari are cosmopolitan organisms and are found in different habitats due to their various diets. Caves are interesting and unique habitats with different ecological conditions and animals than surface habitats. So far, no comprehensive research has been done on mite communities in the cave habitats of Iran. This study examines the presence of mites (subclass Acari exclude order Ixodida) in 10 caves in Fars Province, Iran. Sampling was done from October 2020 to May 2021 from Sahlak 1, Sahlak 2, Tadovan, Zakaria, Dalkhoon, Shafagh, Deh Ziarat, Shoparak, Bibi Ghar and Kavar caves. In each cave, the specimens were collected from three given parts of the cave: endogean (photic zone or entrance), parahypogean (twilight zone), and hypogean (aphotic zone). Sampling was done randomly from the soil or bat guano or both as a mixture on the bottom of each cave. The bags containing the samples were transported to entomology research lab at the Biology department of Shiraz University. The mite specimens were extracted using Berlese funnels. The abundance and the diversity of obtained mites from parahypogean part were more than that from endogean and hypogean parts of the caves. Also, no mite specimens were extracted from the soil of the caves with poor animal fauna. It seems that the more the biodiversity of the cave and the richer the fauna of other animals especially bats and invertebrates, the more the abundance and diversity of cave mites. In caves with rich biodiversity, more diverse micro-habitats will be available to the different groups of mites, and biological interaction with other cave-dwelling animals is more likely. Further studies are underway by the authors. It is recommended to study other biological aspects of caves in Iran.

Keywords: Biodiversity, Cave mites, Habitat, Biological interaction, Iran.

Journal of Wildlife and Biodiversity

Distribution and conservation gaps of Eurasian lynx in Iran

Raziyeh Shahsavarzadeh[1], Mahmoud-Reza Hemami[1], Sima Fakheran Esfahani[1], Mohammad Ali Adibi[2], Shima Malakoutikhah[1], Urs Breitenmoser[3]

[1]Department of Natural Resources Engineering, Isfahan University of Technology

[2]Iran Department of Environment, Semnan Provincial Office, Semnan, Iran)

[3]Universität Bern, Institute of Veterinary Virology

shahsavar.raziyeh@gmail.com

Abstract

Knowledge on environmental factors affecting the distribution of species is important for biodiversity conservation. Eurasian lynx (*Lynx lynx*) is widely distributed in northern and western Iran. However, there is a lack of spatially explicit understanding of lynx habitat across its range in Iran. We used a Maximum entropy approach to model suitable habitat of the species using 13 uncorrelated environmental variables. The predictions were used to estimate the proportion of the species suitable habitat covered by the protected areas and to identify conservation gaps. The model's ability to predict species distribution was excellent (AUC = 0.97 TSS = 0.75). Climatic variables Contains Precipitation of Coldest Quarter and Precipitation of Driest Quarter followed by prey availability were the most important variables affecting the species habitat's suitability. Our results show that lynx are distributed in the north and northwest of Iran. About 52,000 km^2 of the country were recognized suitable habitat for lynx, of which 47% overlapped with the extent of the protected network. Our results have management implications for the conservation of Eurasian lynx and its prey species in Iran.

Keywords: Habitat, prey, climate variable, protected network

Journal of Wildlife and Biodiversity

Genetic and morphological diversity in Halocnemum strobilaceum (Pall.) Beib. (Chenopodioideae) populations

Fatemeh Nasrollahi[1], Abolfazl Tahmasebi[2]

[1] *Department of Biology, Faculty of Science, Qom University, Qom, Iran*

[2]*Department of Agriculture and Natural Resources, Gonbad Kavous University, Iran*

nbotanist@yahoo.com

Abstract

Halophytes are remarkable plants which have the ability to complete their life cycle in a substrate rich in NaCl that normally found toxic to other species. Chenopodioideae is a cosmopolitan, eudicot lineage especially diverse in arid, semiarid, saline, and hypersaline ecosystems. The subfamily is extremely variable in its ecomorphological and anatomical types and modes of photosynthesis. Halocnemum strobilaceum of the subfamily Chenopodioideae is one of the key species of saline and alkaline rangelands in the north of Golestan province, which has an important protective role against desert development and soil degradation. In present study 13 geographical populations of *H. strobilaceum* were investigated based on the morphological and genetic (ISSR) data. ANOVA test revealed a significant morphological difference among the studied populations. Analysis of molecular variance revealed a significant genetic difference among date of the studied *H. strobilaceum*. Networking and STRUCTURE analyses, show a significant positive correlation between genetic and morphological distance and geographical distance of the studied populations. AMOVA test revealed two major groups with different geographic distribution. One group includes five examined populations restricted to northeastern Golestan province and the other group comprises a majority of the populations from northwestern Golestan province. Genetic analysis results revealed that along with genetic drift, low level of gene flow and migration, adaptive loci also helped populations diverge and adapt these populations to their local condition. Thus, we have two different groups which can be considered as two ecotypes for *H. strobilaceum* based on the morphological and genetic data.

Keywords: *Halocnemum strobilaceum*, ISSR, Morphometry, Golestan.

Journal of Wildlife and Biodiversity

Genetic diversity in Haloxylon aphyllum (Minkw.) L. (Chenopodioideae) populations

Fatemeh Nasrollahi[1], Abbas Pourmeidani[2] and Elham Amini[3]

[1] *Department of Biology, Faculty of Science, Qom University, Qom, Iran*

[2]*Research Division of Natural Resources, Qom Agricultural and Natural Resources Research and Education Center, AREEO, Qom, Iran*

[3]*Department of Biology, Faculty of Sciences, Gonbad Kavous University, Gonbad, Iran*

nbotanist@yahoo.com

Abstract

Halophytes are remarkable plants which have the ability to complete their life cycle in a substrate rich in NaCl that normally found toxic to other species. Chenopodioideae is a cosmopolitan, eudicot lineage especially diverse in arid, semiarid, saline, and hypersaline ecosystems. The subfamily is extremely variable in its ecomorphological and anatomical types and modes of photosynthesis. *Haloxylon aphyllum* of the subfamily Chenopodioideae is one of the key species of saline and alkaline rangelands in Iran, which has an important protective role against desert development and soil degradation. In present study 27 populations of *H. aphyllum* from 4 geographical regions in Iran were investigated based on the genetic (ISSR) data. ISSR markers could differentiate the studied populations, as AMOVA revealed significant genetic difference among the studied populations. Networking and STRUCTURE analyses indicated that the populations can be placed in two main genetic groups. Environmental disturbances causing disappearance and fragmentation of natural populations reduce the rate of gene flow among populations, which in turn increases the population genetic differentiation. In this situation, the genetic drift acts strongly and reduces within population genetic variability. However, we obtained a high degree of within population genetic variability in the studied populations of *H. aphyllum.* Genetic analysis results revealed that along with genetic drift, low level of gene flow and migration, adaptive loci also helped populations diverge and adapt these populations to their local condition. Data obtained can be used in future conservation and breeding studies of this important species.

Keywords: Chenopodioideae, *Haloxylon aphyllum*, Iran, ISSR.