Lack of population differentiation of common tern (Sterna hirundo) populations in Europe

Galov, Ana; Lončar, Veronika; Kralj, Jelena; Stronen, Astrid Vik; Pavlinec, Željko; Jurinović, Luka; Piro, Simon; Herrmann, Christof; Škornik, Iztok; Tome, Davorin; ...

Book of abstracts

eccb2024.eu

ECCB
2024
BOLOGNA

7th European Congress
of Conservation Biology

“Biodiversity positive by 2030”

17-21 June 2024 – Bologna, Italy

ECCB 2024
BOLOGNA
7th European Congress of Conservation Biology

“Biodiversity positive by 2030”

17-21 June 2024 – Bologna, Italy

Book of abstracts

With the partnership of

Society for Conservation Biology

Society for Conservation Biology
Italy Chapter

Society for Conservation Biology
Europe Section

With the endorsement of

ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

Edited by
Symposia S.r.l. S.U.

Graphics first page: Cactus di Pelissero Esteban Lucas and Symposia S.r.l. S.U.
Conference logo: Cactus di Pelissero Esteban Lucas

ISBN: 9788854971783
DOI: 10.6092/unibo/amsacta/7995 (link esteso:
https://doi.org/10.6092/unibo/amsacta/7995)
Year of publication: 2024

Book of abstracts

7th European Congress of Conservation Biology
“Biodiversity positive by 2030”

Published by:
Dipartimento di Scienze Biologiche, Geologiche ed Ambientali
Alma Mater Studiorum Università di Bologna

distribution of the selected tree species were extracted from the GBIF database.

Our models reveal differences in velocities among islands and pairs of species. We discuss our findings in the context of existing protected areas and propose targeted conservation and mitigation measures which should be island specific.

Bibliography

Serra-Diaz, J. M., Franklin, J., Ninyerola, M., Davis, F. W., Syphard, A. D., Regan, H. M., & Ikegami, M. (2014). Bioclimatic velocity: the pace of species exposure to climate change. Diversity and Distributions, 20(2), 169-180. https://doi.org/10.1111/ddi.12131

Médail, F. Plant Biogeography and Vegetation Patterns of the Mediterranean Islands. Bot. Rev. 88, 63–129 (2022). https://doi.org/10.1007/s12229-021-09245-3

Vogiatzakis, I.N., Mannion, A.M. & Sarris, D. Mediterranean island biodiversity and climate change: the last 10,000 years and the future. Biodivers Conserv 25, 2597–2627 (2016). https://doi.org/10.1007/s10531-016-1204-9

ID: 1159

Evaluating the effectiveness of a large scale campaign aimed at reducing demand for wild meat in the megacity of Kinshasa, DRC

Juliet Helen Wright[1,2], Divin Malekani[1,2], Lude Kinzonzi[1,2], Liliana Vanegas[1], Diogo Verissimo[2]

[1]Wildlife Conservation Society, DRC; [2]University of Oxford, UK

One of the main drivers of wildlife declines across Central Africa is the flow of wild meat to satisfy consumer demand in urban centres, yet few conservation projects have focused on addressing this demand. After conducting research into consumers, the Wildlife Conservation Society launched a large-scale multi-media campaign in the megacity of Kinshasa, Democratic Republic of Congo, in 2021. Targeting the campaign at three demographic groups with higher levels of education and wealth, the campaign aimed to demonstrate that it is possible to buy and prepare delicious Congolese food without using wild meat. The campaign ran for three years and was divided into two phases. The impact evaluation of the campaign involved the use of quantitative surveys before and after each phase, initially using interactive voice response mobile phone surveys and later face-to-face household interviews. Qualitative interviews were also conducted with key stakeholder groups. Responses to the campaign were generally positive but the impact evaluation has reinforced the fact that behaviour change takes time, particularly in large cities with busy media environments. To result in sustained behaviour change, messages must be disseminated on a multi-year basis with the establishment of local coalitions to maximise audience exposure and continue momentum.

ID: 1160

Lack of population differentiation of common tern (Sterna hirundo) populations in Europe

Ana Galov[1], Veronika Lončar[1], Jelena Kralj[2], Astrid Vik Stronen[3], Željko Pavlinec[2], Luka Jurinović[4], Simon Piro[5], Christof Herrmann[6], Iztok Škornik[7], Davorin Tome[8], Gyula Kovacs[9], Balint Preiszner[10], Peter Szinai[11,12], Stefano Volponi[13]

[1]University of Zagreb, Faculty of Science, Croatia; [2]Croatian Academy of Sciences and Arts, Croatia; [3]University of Ljubljana, Biotechnical Faculty, Slovenia; [4]Croatian Veterinary Institute, Poultry Centre, Croatia; [5]Vogelwarte, Zoological Institute and Museum, University of Greifswald, Germany; [6]Agency for Environment, Nature Conservation and Geology Mecklenburg- Vorpommern, Hiddensee Bird Ringing Scheme, Germany; [7]Sečovlje Salina Nature Park, Slovenia; [8]National Institute of Biology, Slovenia; [9]BirdLife Hungary South-Balaton Local Group, Hungary; [10]Balaton Limnological Research Institute, Hungary; [11]Balalton-felvidéki National Park Directorate, Hungary; [12]Bird Ringing and Migration Study Group of BirdLife Hungary, Hungary; [13]Italian Institute for Environmental Protection and Research, Italy

The common tern (Sterna hirundo) is a migratory seabird that breeds in temperate and subarctic regions and winters in tropical and subtropical coastal regions. European populations have declined due to various threats, including habitat destruction, human disturbance, and predation. In contrast to the marine colonies, those located inland are particularly at risk due to flooding of their breeding sites. Genetic markers can provide important information about the connectivity of populations. Because of philopatry, geographical distance, use of different habitats and migration routes, we expect European populations to show some level of genetic structure. Therefore, we used 18 microsatellite markers to infer the population genetic structure of 219 common terns from 12 breeding locations in Europe, which we grouped into three clusters: Northern (Germany), Southern Inland (Hungary, continental Slovenia and Croatia) and Southern Marine (Italy, coastal Slovenia and Croatia). We found a relatively high level of genetic diversity with an expected heterozygosity ranging from 0.67 to 0.71. Surprisingly, no population structuring was detected and the most likely number of identified subpopulations was one, suggesting a limited influence of factors promoting the isolation of breeding colonies.

Bibliography

BirdLife International (2023) Species factsheet: Sterna hirundo. Downloaded from http://datazone.birdlife.org/species/factsheet/common-tern-sterna-hirundo on 04/09/2023

Kralj, J., Martinović, M., Rubinić, T., Krnjeta, D., & Jurinović, L. (2019). Dynamics of Common Sterna hirundo and Little Tern Sternula albifrons populations along the Sava River in North-western Croatia between 2002 and 2019. Acrocephalus, 40(180–181), 49–54. https://doi.org/10.1515/acro-2019-0002

Kralj, J., Martinović, M., Jurinović, L., Szinai, P., Süto, S., & Preiszner, B. (2020). Geolocator study reveals east African migration route of Central European Common Terns. Avian Research, 11(1), 1–11. https://doi.org/10.1186/s40657-020-00191-z

ID: 1163

Preserving the Ground beneath the Paws: does the Biodiversity Hypothesis matter for Wildlife Health?

Toni Markus Jernfors[1], Esa Koskela[2], Giulio Galla[1], Heidi Hauffe[1], Eva Kallio[2], Tapio Mappes[2], Phillip C. Watts[2]

[1]Fondazione Edmund Mach, Italy; [2]University of Jyväskylä, Finland

Mounting evidence supports the biodiversity hypothesis stating that contact to immunoprotective factors in the environment is required for development of a balanced immune system, explaining the prevalence of allergies and other inflammatory disorders in humans inhabiting post-industrial societies. Yet, while urban areas are the most rapidly expanding ecosystems on Earth, little is known how the biodiversity hypothesis applies to wildlife.

We performed a soil exposure experiment using the ecological model bank vole (Myodes glareolus), where laboratory-born vole pups were exposed to different forest soil mixtures and sterile bedding in individually ventilated cages for four weeks and monitored metataxonomic changes in gut microbiota. Treatment soil was collected from urban forests and national parks, considering that soil microbiota can greatly differ between levels of human development index.

We found that soil treatment decreases species evenness and increases dispersal in beta diversity estimates in faecal samples compared to sterile control. This dataset will be further analyzed for inflammation markers such as Foxp3 and Il-17 using qPCR. These data can inform conservation of soil