

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

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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.

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

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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.

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

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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.

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ID: 1163

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

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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