

Advances in Diversity and Conservation of Terrestrial Small Mammals

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Rodents and insectivores are key components in terrestrial ecosystems. They participate in ecosystem services, disperse seeds and fungi, aerate and bioturbate the soil, prey on invertebrates, and are a food resource for most vertebrate predators. Small mammal communities are affected by climate [1], habitat, and landscape [2,3] changes. The intensification of anthropogenic habitat and climate alteration poses an increased threat to the diversity of small mammals at all scales, which calls for efficient conservation measures and strategies. In this Special Issue, we intended to collect papers covering studies of small mammals and various aspects of issues related to their diversity or conservation.

In their review of the monitoring of mammal fauna in the northern part of Australia, including small mammals, Preece and Fitzsimons [4] examined the causes of species decline. They found that these declines were related to multiple factors, such as climate warming, fires, invasive pest species, grazing by introduced herbivores, and unexpectedly, even the management actions aimed at ecosystem and species recovery. In response to the alarming prognosis that nine mammal species could become extinct within the next 20 years, the authors propose a strategic monitoring approach, prioritizing certain bioregions. They also emphasize the need for increased funding, requiring decisions at the political level to double the budget. The reporting system should be designed to accommodate the needs of Indigenous observers, supported by a network of scientists. This approach can be adapted to other countries with limited budgets for mammal monitoring, where the potential of citizen science results is not fully utilized, leading to an underestimation of mammalian diversity and threats.

Benedek et al. [5] analyzed the influence of the duration of protection regimes on small mammal communities in montane areas. The authors conducted a comprehensive five-year study, which involved comparing small mammal communities in non-protected sites with those in sites under long- and short-term protection. During the study, they also assessed the impact of elevation, habitat heterogeneity, and seasonal variations on these communities. The protection status had a significant impact on the abundance and species composition of the small mammal community. Two shrew species, the common shrew (*Sorex araneus*) and pygmy shrew (*S. minutus*), exhibited positive responses to protection, evident in both their increased abundance and higher proportion within the community. The authors pay attention to the positive impact of long-term protection on montane small mammal communities and emphasize the need for comprehensive and multifaceted research to assess the effects of protection. Furthermore, they underscore the importance of understanding the role of small mammals in ecosystems to design effective protection measures that support ecosystem services.

The diversity and abundance of small mammals inhabiting territories of the colonies of great cormorants were analyzed in [6]. The study revealed that small colonies with a low number of nests during their initial formation positively influence the small mammal community, leading to higher species richness, diversity, and relative abundance. Conversely, larger colony sizes with high breeding numbers have negative impacts on the small



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mammal community, such as lower species richness, diversity, and relative abundance, as well as poorer body condition index among individual small mammals. However, following the cormorants' abandonment of a portion of the colony and nesting site, all the previously impacted parameters in the area experienced recovery. Therefore, the authors concluded that, up to a certain colony size, cormorant pressure is a driver of natural habitat succession and has a similar effect on small mammal communities as other successions in disturbed habitats.

Despite thorough analyses of the phylogeography of the field vole (*Microtus agrestis*) in Eurasia using genetic methods, the genetic variability in the contact zone of eastern and western genetic lineages remains poorly understood. To address this, Prakas et al. [7] conducted a sequence analysis of the cytochrome b (*cytb*) gene and D-loop regions, examining individuals from eastern, northern, and western parts of Lithuania, where the contact zone spreads through the country. The investigation based on both genetic loci demonstrated the existence of two distinct genetic lineages, eastern and western. These lineages were found to be mixed in the country except for the western region, where only the western lineage was present. An absence of the eastern lineage was explained by the barrier effect, as the investigated location is separated from the mainland by the delta of Nemunas, the largest river in the country. However, the data from earlier research are too limited to allow for meaningful comparisons or to identify changes in the presence and proportion of genetic lineages of this species over the past two decades.

Two papers in this Special Issue focused on human-influenced habitats and small mammal communities. A country-wide study conducted in Lithuanian commercial orchards and berry plantations [8] aimed to determine whether the common vole (*Microtus arvalis*) should be considered the focal species in the risk assessment of plant protection products, rather than the field vole (*M. agrestis*). Materials from this study confirm that, despite Lithuania being considered part of the Northern Zone for selecting relevant small mammal species in higher tier risk assessments, the small mammal community structure is more closely related to that of central or eastern Europe. Field voles were found in only 30% of locations, accounting for a mere 2.1% of all trapped individuals. In contrast, the common vole was present in 75% of orchards and 80% of control habitats, comprising 30% of all trapped individuals. Consequently, in Lithuania, the common vole dominates in both orchards and natural habitats, making it the most relevant small mammal species for higher tier risk assessment.

The analysis of the trophic ecology and diversity of small mammals among syntopic species in commensal habitats (homesteads and gardens) in the northern part of the mid-latitudes was based on the first data presented in [9]. The authors aimed to determine whether the separation of species corresponds to specific trophic guilds, whether their diets are influenced by the availability of additional food from humans, and whether their diets exhibit seasonal trends. The highest small mammal species richness was observed in commensal habitats that provided additional food resources. In contrast, the kitchen garden, which experienced the highest human influence, exhibited low species richness among small mammals. The widest trophic niche according to the range of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values was that of the yellow-necked mouse (*Apodemus flavicollis*). Human influence in commensal habitats can lead to different effects on the diets of various small mammal species, and these effects are better observed and distinguished when considering the $\delta^{15}\text{N}$ isotopic values.

Andreychev and his colleagues [10] conducted an analysis of the role of terrestrial and subterranean small mammals in zoonotic anthropogenic diseases. The study focused on the Republic of Mordovia in Central Russia, which is known for having a foci of haemorrhagic fever with renal syndrome (HFRS) and tularemia. Through their research, the authors addressed an important gap in evaluations by considering the last group (subterranean small mammals) as significant reservoirs of zoonotic pathogens that contribute to human morbidity. This study sheds light on the previously overlooked role of subterranean species, providing valuable insights into zoonotic disease transmission dynamics. Among all the

analyzed samples of the greater mole rat (*Spalax microphthalmus*), 83% tested positive for tularemia antigens, and 17% tested positive for HFRS antigens. In contrast, none of the analyzed European moles (*Talpa europaea*) showed antigens for tularemia or HFRS. Subterranean mammals did not exhibit double infections with both tularemia and hantavirus; such co-infections were only detected in the bank vole (*Clethrionomys glareolus*) and the forest dormouse (*Dryomys nitedula*). Additionally, two other species, the yellow-necked mouse (*Apodemus flavicollis*) and the house mouse (*Mus musculus*), were identified as playing an important role in the transmission of zoonotic diseases in the region. Furthermore, a positive relationship was observed between the relative abundance of small mammals and the incidence of morbidity in the human population.

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