Benefits of mosquito surveillance programs in protected areas: two case reports from Eastern Austria

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Abstract

Mosquitoes (Diptera: Culicidae) are important vectors of pathogens, which raises conflicts between human interests and species conservation in protected areas. We will present two studies partly focusing on wetland areas in Eastern Austria (including e.g. the Nationalpark Donau-Auen) that demonstrate the comparatively little importance of protected wetland areas as vector sources for the spread of emerging human pathogens like West-Nile Virus and how protected areas can benefit from carefully designed mosquito monitoring to inform visitors, stakeholders and the local populace.

Keywords

Culicidae, non-native species, autecology, *Culex pipiens* complex, pathogens

Introduction

Mosquitoes (Culicidae: Diptera) are hematophagous insects of significant importance in human and veterinary medicine due to their ability to transmit several pathogens such as *Plasmodium* spp., Dengue and West Nile viruses, all of which can have a severe impact on human health. Despite their epidemiological importance, comparatively little is known about the extant mosquito species inventory, occurrence, distribution and dispersal in Austria. Furthermore, mosquito species and vector-borne diseases continuously spread outside their native range into new countries and continents as a consequence of climate change, global trade, and transcontinental movement. Moreover, recent human activities substantially changed the environment, and facilitated the displacement of mosquito species by creating new habitats. As mosquito species differ in their vector capacity and competence they also differ in their medical importance. Therefore, a better knowledge of the seasonal and spatial distribution of the Austrian mosquito species is essential to assess vector-pathogen dynamics (Zittra et al. 2017a). Particularly, mosquito monitoring in combination with pathogen screening allows estimating potential health risks for humans, their pets, and stock-rearing.

Nature reserves, especially wetlands, are frequently confronted with accusations to be sources of enormous amounts of mosquitoes. As frequently, there are insinuations that protected areas lead to increased health risks for the human population. Here we present results from a mosquito diversity assessment and screening for mosquito-borne pathogens conducted in Eastern Austria, including protected areas, especially the National Park Donau-Auen.

Methods

Female mosquitoes were sampled twice a month for a 24-h time period from April to October 2014 and 2015 at 35 permanent and 23 non-permanent trapping sites using carbon dioxide-baited traps. Collected mosquitoes were stored at -80 °C and morphologically identified using the key of Becker et al. (2010).

We assessed mosquito community responses to environmental parameters based on 14-day-average values that possibly affect mosquito ontogenesis. Furthermore we used canonical correspondence analysis to relate mosquito community fluctuation patterns based on abundance responses of single species to environmental parameters. Land use type as available in the CORINE Land Cover (CLC) database was included as a predictor variable. Furthermore, the analysis included scaled weather data (raw data provided by the Austrian official weather service, ZAMG), and Danube water levels (raw data provided by the viadonau GmbH). We used ontogenetically relevant 14-day-mean values prior to each single sampling date to assess effects of meteorological data (relative air humidity, sunshine duration, the amount of precipitation, air temperature and atmospheric pressure) as well as Danube water levels on mosquito communities (Zittra et al 2016; Zittra et al. 2017a).

Morphologically identified mosquitoes were pooled by species, collection site and date. Genomic DNA and RNA were extracted from single pools. Pools were then screened for flaviviruses, filarioid helminths, *Plasmodium* spp. (avian malaria), *Trypanosoma* spp. and *Francisella tularensis* using molecular methods. We used standardized protocols to amplify and sequence gene loci. If PCR gave positive results for pathogens, PCR products were sequenced; obtained sequences were matched to available reference databases (BLAST against GenBank and MalAvi) for molecular identification of pathogens.

Results

Altogether 29,734 female mosquitoes were collected. Although four species were firstly collected in Austria (*Culiseta longiareolata*, *Orthopodomyia pulcripalpis*, *Anopheles hyrcanus* and *Ochlerotatus japonicus japonicus*, the Asian Bush mosquito), no invasive behaviour was observed during the three year sampling period (Zittra et a. 2017a, Zittra et al. 2017b, Lebl et al. 2013). Statistical analyses revealed significant differences in mosquito abundance between sampling years and provinces. Incidence and abundance patterns were found to be linked to 14-day mean sunshine duration, humidity, water–level maxima and the amount of precipitation. However, land cover classes were found to be the most important factor, effectively assigning both indigenous and non-native mosquito species to various communities. Taxa of the *Culex pipiens* complex, competent vectors of the West Nile virus, were strongly associated with urban areas, especially continuous and discontinuous urban fabric land cover types, instead of natural wetland areas as the National Park Donau-Auen (Zittra et al. 2016, Zittra et al. 2017a). Pathogen screening recorded no pathogens of human medical importance in any of the pools tested.

Discussion

The assessment of mosquito diversity and abundance patterns in Eastern Austria indicates a low relevance of protected areas as sources for mosquitoes of medical interest. However, our results suggest an increased potential of West Nile Virus (WNV) transmission in urbanized areas due to the distribution patterns of the Northern house mosquitoes, which are the main vectors of WNV. Potentially invasive species like the Asian Bush mosquito and the Asian tiger mosquito primarily use artificial breeding habitats in Central Europe. Moreover, these species are mostly dispersed through global trade and transcontinental movement (Becker et al. 2010). The other three species firstly recorded in Austria must be considered as remnants of immigrations during the Holocene Climatic Optimum or later (recent) immigrations during warmer periods. Also, *Cs. longiareolata* and *Or. pulcripalpis* seem to have limited distribution areas and low population densities in Austria (Zittra et al. 2014, Zittra et al. 2017a, Zittra et al. 2017b) and are of no medical interest due to non-mammal hosts. In contrast, *An. hyrcanus* can occur locally in high abundances despite their present limited distribution areas and more investigations are needed to fully access the status of this species in Austria.

Despite the presence of a quite diverse mosquito fauna, no mosquito-borne pathogens potentially affecting humans were detected. However, our results suggest an increased risk of West Nile Virus transmission in urbanized areas compared to natural areas due to the distribution patterns of the *Cx. pipiens* complex, the most important WNV vector.

Conclusion

Our results demonstrate that protected areas, while providing a wide range of potential breeding habitats or containing a wide range of different mosquito species do not consequently represent hotspots for mosquito-borne pathogens. Also, nature reserves benefit from information created by carefully designed mosquito monitoring programs: the identification of seasonal and spatial distribution patterns of mosquito species and screening for mosquito-borne pathogens can support decision-making concerning public-health related mosquito management.

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