Biodiversity decline can increase the spread of infectious diseases like Hantavirus

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Short title: Biodiversity decline can increase the spread of infectious diseases

Key Message: The loss of biodiversity increases the risk for the transmission of diseases like the hantavirus.

Reviewer: Hans Keune

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What is the problem?

Intuitively one might expect that higher overall biodiversity leads to greater diversity and abundance of pathogens and thus more incidences of the transmission of diseases. Therefore, species-rich environments might be seen to exhibit a higher infection risk than anthropogenic disturbed environments with a low biodiversity. However, research results show the opposite. Several studies suggest that with the loss of biodiversity the transmission of diseases increases (Keesing *et al.* 2010). Thus biodiversity loss causes the loss of an important ecosystem service: buffering the spreading of infectious diseases to humans, animals and plants (Pongsiri *et al.* 2009). The decline of biodiversity might lead to a faster rate of emergence and re-emergence of infectious diseases, such as the Hantavirus, and therefore the infection of a greater proportion of the human population (Keesing *et al.* 2010, Pongsiri *et al.* 2009, Suzan *et al.* 2008, Peixoto and Abramson 2006). Regionally different genotypes of Hantaviruses cause hemorrhagic fever with renal syndrome (HFRS) in Asia and Europe and the Hantavirus pulmonary syndrom (HPS) in the Americas (Pongsiri *et al.* 2009).

Which ecosystem services were examined? And how?

The examination of circumstances of recent Hantavirus outbreaks, transmitted from host animals to humans, so called zoonoses, showed that all outbreaks occurred in anthropogenic highly disturbed habitats with reduced biodiversity (Pongsiri *et al.* 2009, Suzan *et al.* 2008).

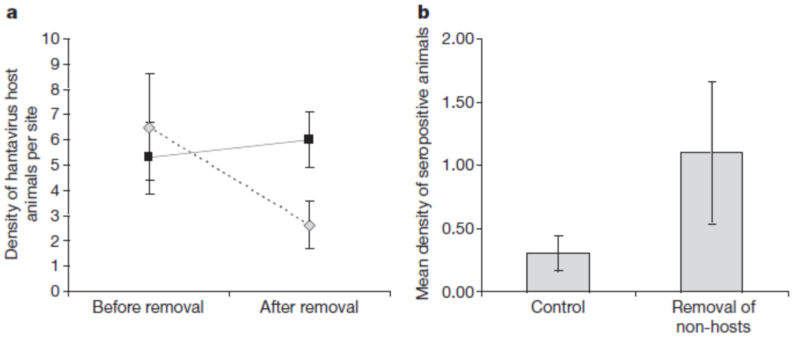
Host species of Hantaviruses are rodents and the viruses are transmitted to humans by aerosolized rodent excreta or by direct contact with the animals. Among rodents, the virus spreads through physical contacts (aggressive encounters). In general, each Hantavirus genotype is associated with a certain rodent (host) species. Therefore, the probability that a certain Hantavirus genotype infects other rodent species successfully is very low.

A study in Utah, USA, found a negative correlation between small-mammal diversity and Sin Nombre Hantavirus (SNV) infection prevalence in deer mice (Clay et al. 2009). High mammalian species diversity reduced the infection prevalence mainly by reducing the intraspecific encounters rather than by reducing host density. A result also supported by experiments. Deer mouse population density was not statistically associated with SNV infection prevalence. This suggests that high diversity reduced intraspecific encounters rather than host abundance (Clay et al. 2009).

There seems to be evidence that in recent outbreaks the rodent species transmitting the virus was a generalist species (Suzan et al. 2008). Generalist species have a high adaptability to a wide range of habitats and can subsist on a variety of food sources. Keesing *et al.* (2010) speculate that species usually amplifying pathogens tend to invest less energy into immune defence and are more vulnerable to pathogens. In contrast, specialist species are highly adapted to a narrowly defined habitat and require one or a few specific food resources and may invest more into immune defence and hence buffering pathogens (Keesing *et al.* 2010). Anthropogenic disturbance to natural ecosystems frequently results in extensive simplification of the environment. Often, many specialist species become locally extinct whereas the population density of certain opportunistic species rises dramatically due to their better adaptability to a changing environment and the decrease of competitive pressure.

Reduced diversity of rodent species subsequently means that the virus spreads most efficiently as there are fewer encounters with other species. Thus, it can be expected that Hantaviruses are transmitted and spread most efficiently within host communities of low diversity. Furthermore, the population of a generalist species tends to increase when species biodiversity decreases in highly disturbed regions, resulting in a higher risk of disease transmission to humans (Suzan *et al.* 2008).

Hence, if biodiversity decreases, transmission events rise due to an increase in encounter rates among infected and between infected and susceptible hosts. Assuming that a rodent has a certain amount of aggressive encounters during its life, it transmits the virus in more cases if the small-mammal diversity is low, since aggressive encounters happen more often within the same species. A recent experimental field study conducted on wild rodent populations of different species in southwestern Panama backs this view. It showed that the relative abundance of Hantavirus hosts increases with a decrease in small-mammal species diversity (See figure below from Keesing et al. 2010). This in turn increases human infection risk (Pongsiri *et al*. 2009, Suzan *et al*. 2008).



Box 2 figure | Effects of experimental removal of species. a, Mean (± standard error) population abundance of hantavirus hosts in Panamá in field plots before and after non-host species had been removed (solid line), and in unmanipulated controls (dashed line). Hosts on control plots underwent a strong seasonal decline in abundance, whereas those on plots where non-hosts were experimentally removed did not. **b,** Mean (± standard error) density of seropositive (currently or previously infected) animals on plots from which non-hosts had been removed and on control plots. Analysed from data provided in ref. 23.

Source: Keesing et al. 2010

Lessons learned

As a consequence of these findings Montira *et al.* (2009) suggest supporting policies that maintain or enhance biodiversity rather than trying to support or eliminate a certain species. Focusing on one species can have unexpected implications such as enhancing further biodiversity loss when eliminating a rodent species that might serve as food for others or as a buffer for diseases. Keesing *et al.* (2010) discuss that for certain diseases it can be considered to add a species (i.e. natural enemy or competitor) in order to control the host of the disease. It is also essential to reduce antibiotic overuse in order to avoid adaptation and resistance of pathogens. Further, it is important to identify potential emergence hotspots. The conservation of natural habitats can provide protection against emerging pathogens as it does not only foster biodiversity but also helps to reduce human-wildlife contact. It is also suggested to reduce contact between domestic animals and wildlife. However, the elimination of disease hotspots has the risk to “backfire” by resulting in pathogen transmission (Keesing et al. 2010).

More research on different disease systems is needed as well as a more profound understanding of how global trends – such as for example climate change or nutrient pollution are correlated to biodiversity loss and disease systems (Keesing *et al.* 2010). Furthermore, some economical decision making tools are needed. Cost-effectiveness analysis (CEA) and benefit-cost analysis (BCA) can be applied to human health protection measures, but additional research is needed here (Pongsiri *et al*. 2009).

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