Effects of host and vector diversity on disease dynamics

Abstract

Disease dynamics are affected by a number of factors including climate change, density of the population, and the interactions of different species with each other. It was also found however that host and vector diversity can also have a major impact on disease dynamics. Research on these two variables has not been as extensive as it should be considering the effect they have. The research done on host and vector diversity is presented here as to gather the information and show the gaps of knowledge present. Most importantly this review shows the problems surrounding this subject with conflicting evidence from different studies and it highlights the fact that what applies to one species of host, vector, or pathogen may not necessarily be generally applicable as a rule.

Introduction

An infectious disease occurrence consists of at least two species interacting which are the pathogen and the host; however in cases of vector transmitted diseases a third species, the vector, also takes part in the infection (Keesing *et al.* , 2006) . Vectors are mostly arthropods but can also include rodents or even surfaces that may be contaminated by the pathogen (Lemon & Institute of Medicine . Forum on Microbial Threats, 2008). Species diversity in all of these different stages of the infection can affect disease dynamics and in this review the analysis of this impact is presented.

Host Diversity

Different pathogens were found to be affected differently as species richness increases (Miller & Huppert, 2013). A number of studies have showed that when species diversity is increased in an ecosystem the pathogen abundance decreases (Schmidt & Ostfeld, 2001; Ezenwa *et al.* , 2006) . This is because of the dilution effect hypothesis, which states that by increasing the number of species there is a lower probability that the vector will infect a susceptible host and also a lower probability that the vector will uptake the pathogen resulting in a lower disease risk for the ecosystem. This was adapted from the concept of zooprophylaxis where it was argued that livestock could be placed around human settlements in order to divert the vectors from humans (Keesing *et al.* , 2006) . The hypothesis also states that even in the case of multi-host pathogens an increase in diversity will still result in decreased disease risk. This is based on host competence where different hosts have different uptake success of the pathogen meaning that the pathogen will not be able to infect as many individuals due to its lower succesfull (Ostfeld *et al.* , 2008) .

However on the other hand there is research showing that in some cases pathogen abundance increased with host diversity. For example in the case of Lyme disease (Ostfeld & Keesing, 2000) showed that as bird species richness increases the abundance of the pathogen increases as well. This was further investigated by (Loss *et al.* , 2009) where they disproved the hypothesis that species richness has a negative correlation with the abundance of the west Nile virus (WNV). While studying the effects of zooprophylaxis (Saul, 2003) showed that the increase of individuals provides the mosquitoes with a lower search time when foraging thus increasing their survival rate, essentially negating the positive effects of the dilution effect.

When a new species is introduced to an ecosystem spillover of a disease may occur. This is because the new species brings in a new pathogen and thus increases the exposure of native species to that particular pathogen. The new species can also act as a site for production of new strains of the pathogen that may result in the successful transition of the pathogen from one host to another (Parrish *et al.* , 2008) . However even if a new species does not introduce a pathogen it may act as a reservoir for the pathogen already present in the ecosystem thus again increasing the overall disease risk (Poulin *et al.* , 2011) .

Inter-species host diversity is not the only factor in relation to diversity concepts. Intra-species diversity which is the genetic diversity of the population also affects disease dynamics. (Lively, 2010) produced a model that showed that the more diverse the genetic composition of a population is the less effect a pathogen will have. The model was run under the assumption that each host genotype is susceptible to only one pathogen strain while immune to the rest. A similar model was done with livestock populations by (Springbett *et al.* , 2003) that had similar results thus reinforcing the hypothesis.

This hypothesis originated from research done in plants where empirical evidence was gathered that as genetic diversity increases in a population then the susceptibility of the population to a specific pathogen decreases (Mundt *et al.* , 2011) . Research was also done in bacteria again showing that as the genetic diversity of the host bacteria *Pseudomonas phaseolicola* increases then the abundance of the bacteriophage Φ6 increases. The experiment showed that by having only 50% of the population susceptible to this phage then the abundance of the phage decreases almost tenfold (Dennehy *et al.* , 2007) .

These experiments are being applied to animals however it is proving more difficult since you can't manipulate genetic diversity so easily in animals in relation to plants and bacteria. An experiment with water fleas, *Dapnia magna* showed that populations that had a higher genetic diversity had lower infection levels of the parasite *Octosporea bayeri (Altermatt & Ebert, 2008)* .

This hypothesis is also based on the concepts mentioned earlier which are the dilution effect caused by increased diversity of hosts and also on the competence of hosts with specific genotypes. This means that again for some diseases the hypothesis may be acceptable however other species of pathogens may not have the same mechanisms thus the hypothesis can be rejected (Ostfeld & Keesing 2012).

Vector Diversity

Even though it is known that vector diversity plays an important role in disease dynamics it has not been researched as much and it is poorly understood. Almost all research done on vector diversity is done for plant pathogen carrying vectors. This is because plants allow for large controlled experiments where different hosts, vector or pathogen strains can be studied (Lemon 2008). Most of the research done on vectors carrying animal diseases are in genetic sequencing so that the genes that enable the pathogen to complete its life cycle in the vector are found and eliminated

(Sinkins 2007). However by taking into account the factors that affect disease dynamics in plants we can try to apply them to animal pathogens.

One of the ways in which vector diversity affects the disease dynamics is the way that transmission actually occurs. For insects, pathogens can be transmitted by the pathogen going through the foregut or other organs of the vectors body, thus allowing for a greater pathogen persistence in the vector or they can be mechanically transmitted where the pathogen is not actually taken up by the vector but is on its mouthparts thus allowing for transmission for a limited amount of time. So a pathogen has its persistence in the vector population dependent on the species of the vector (Gray & Banerjee 1999). The life history of the species also plays an important role in disease dynamics. Univoltine vectors only have one generation per year while multivoltine species have more than two generations per year. This means that the disease dynamics are strongly correlated to vector life history since multivoltine species can generate a greater population that can more easily spread a disease in an ecosystem. The WNV for example can be transmitted by univoltine but also by multivoltine species allowing for different disease dynamics depending on the composition of vector populations (Crans 2004).

Disease dynamics can also be affected by intra-species diversity in the way that vectors with different genotypes or developmental stages can uptake the virus differently. This means that some individuals may be more susceptible to the virus, which is the same concept as host competence. For example young individuals may not be as efficient in transmitting the pathogen as adults are. So in a population of vector species the disease transmission may change over time as the genotype of the population as a whole changes or as the population changes demographics i. e. the population had more young individuals that are now adults hence changing the disease transmission rates(Ostfeld, keesing book 2008).

Diversity can also occur in terms of behaviour. Different species have different host preferences meaning that the range of hosts is only limited by the feeding range of the vector. So introduction of new vector species that can transmit a pathogen can result in an increase in the disease prevalence since the new vector may feed on different hosts thus allowing the pathogen to infect other species not previously infected. It was found that feeding preferences play a very important role in the case of WNV where the authors found that it was the most influential factor regarding disease transmission (Simpson et al 2012).

As mentioned before we can use these examples from plants to study vector diversity impact on animal diseases. However it is important to understand that even though there are a lot of similarities between vector-borne animal and plant disease the population there are factors that affect the diseases differently including host population movement and the differences between animal and plant immune systems (Ostfeld keesing book 2008).

Conclusion

It is obvious that host and vector diversity play an important role in disease dynamics and as shown in this review higher diversity can mean either an increase or a decrease of disease transmission. Also diversity is present in different aspects of an ecosystem including inter-species, intra-species and behavioural diversity. It is mandatory to research the effects of diversity in disease dynamics especially in vector diversity for animal pathogens since they are very inadequately studied. As more information is found on wildlife disease dynamics and the factors that affect them, we can prepare strategies for controlling the spread of a disease and use them in cases of an epidemic. This will allow us to correctly handle disease outbreaks both in the wild but also we can use these strategies for captive animals where disease is introduced thus allowing for the population to recover.