



Shift or stick? Untangling the signatures of biased host switching, and host-parasite co-speciation

Lucy Anne Weinert

Department of Veterinary Medicine, University of Cambridge -- Cambridge, UK
Correspondence to Lucy Anne Weinert (lucy.weinert@googlemail.com)

doi: [10.24072/pci.evolbiol.100049](https://doi.org/10.24072/pci.evolbiol.100049)

Published: 5th June 2018

Cite as: Weinert LA. 2018. Shift or stick? Untangling the signatures of biased host switching, and host-parasite co-speciation. Peer Community In Evolutionary Biology, 100049 doi: [10.24072/pci.evolbiol.100049](https://doi.org/10.24072/pci.evolbiol.100049)

A recommendation – based on reviews by Damien de Vienne and Nathan Medd – of

Engelstädter J and Fortuna NZ. 2018. The dynamics of preferential host switching: host phylogeny as a key predictor of parasite prevalence and distribution. bioRxiv 209254, ver. 5 peer-reviewed by Peer Community In Evolutionary Biology doi: [10.1101/209254](https://doi.org/10.1101/209254)

Open Access

Copyright: This work is licensed under the Creative Commons Attribution-NoDerivatives 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-nd/4.0/>

Many emerging diseases arise by parasites switching to new host species, while other parasites seem to remain with same host lineage for very long periods of time, even over timescales where an ancestral host species splits into two or more new species. The ability to understand these dynamics would form an important part of our understanding of infectious disease.

Experiments are clearly important for understanding these processes, but so are comparative studies, investigating the variation that we find in nature. Such comparative data do show strong signs of non-randomness, and this suggests that the epidemiological and ecological processes might be predictable, at least in part. For example, when we map patterns of parasite presence/absence onto host phylogenies, we often find that certain host clades harbour many more parasites than expected, or that closely-related hosts harbour closely-related parasites. Nevertheless, it remains difficult to interpret these patterns to make inferences about ecological and epidemiological processes. This is partly because non-random associations can arise in multiple ways. For example, parasites might be inherited from the common ancestor of related hosts, or might switch to new

hosts, but preferentially establish on novel hosts that are closely related to their existing host. Infection might also influence the shape of host phylogeny, either by increasing the rate of host extinction or, conversely, increasing the rate of speciation (as with manipulative symbionts that might induce reproductive isolation).

These various processes have, by and large, been studied in isolation, but the model introduced by Engelstädter and Fortuna [1], makes an important first step towards studying them together. Without such combined analyses, we will not be able to tell if the processes have their own unique signatures, or whether the same sort of non-randomness can arise in multiple ways.

A major finding of the work is that the size of a host clade can be an important determinant of its overall infection level. This had been shown in previous work, assuming that the host phylogeny was fixed, but the current paper shows that it extends also to situations where host extinction and speciation takes place at a comparable rate to host shifting. This finding, then, calls into question the natural assumption that a clade of host species that is highly parasite ridden, must have some genetic or ecological characteristic that makes them particularly prone to infection, arguing that the clade size, rather than any characteristic of the clade members, might be the important factor. It will be interesting to see whether this prediction about clade size is borne out with comparative studies.

Another feature of the study is that the framework is naturally extendable, to include further processes, such as the influence of parasite presence on extinction or speciation rates. No doubt extensions of this kind will form the basis of important future work.

References

[1] Engelstädter J and Fortuna NZ. 2018. The dynamics of preferential host switching: host phylogeny as a key predictor of parasite prevalence and distribution. bioRxiv 209254, ver. 5 peer-reviewed by Peer Community In Evolutionary Biology. doi: <https://doi.org/10.1101/209254>

Appendix

Reviews by Damien de Vienne and Nathan Medd: <https://doi.org/10.24072/pci.evolbiol.100049>