

Variation in susceptibility to a virus is the key to understanding infection biology

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A new study shows that differences in the vulnerability of animals to a virus are crucial to understanding patterns of infection, and that variation in susceptibility to two marginally different viruses increases the number of infections when the two virus variants are present in the same animal. This study, by researchers from the Netherlands and Spain, will be published on June 30th in the open-access journal *PLoS Computational Biology*.

Models of [virus infection](#) often fail to predict how many animals will become infected and which virus variants will be present in the infected animals, even under controlled laboratory conditions. To discover whether these models are fundamentally wrong or simply not detailed enough, the researchers created four mathematical models of virus infection. They subsequently tested the predictive ability of the models against data from [laboratory experiments](#) in which they exposed [caterpillars](#), Lepidopteran larvae, to insect viruses.

"We were surprised to find that a relatively simple model could describe the data", says Mark Zwart, one of the study's authors and currently a postdoctoral fellow at the Instituto de Biología Molecular y Celular de Plantas, Spain. "The only ingredient we needed to add to an infection model was differences in caterpillar vulnerability to the virus. Our work confirms that virus particles independently infect animals, even in situations where we thought they might be working together."

The study improves our understanding of how virus particles interact

with each other and the host animal during infection, and concludes that "Most deviations from [model] predictions may be caused by variation in host susceptibility". The extent to which this conclusion applies to other viruses and pathogens is not yet clear and a follow-up study on a wide range of different pathogens is currently being carried out.

More information: van der Werf W, Hemerik L, Vlak JM, Zwart MP (2011) Heterogeneous Host Susceptibility Enhances Prevalence of Mixed-Genotype Micro-Parasite Infections. *PLoS Comput Biol* 7(6): e1002097. [doi:10.1371/journal.pcbi.1002097](https://doi.org/10.1371/journal.pcbi.1002097)

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