



Evidence of epistasis provides further support to the Red Queen theory of host-parasite coevolution

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According to the Red Queen theory of antagonistic host-parasite coevolution, adaptation of parasites to the most common host genotype results in negative frequency-dependent selection whereby rare host genotypes are favoured. Assuming that host resistance relies on a genetic host-parasite (mis)match involving several linked loci, then recombination appears as much more efficient than parthenogenesis in generating new resistant host genotypes. This has long been proposed to explain one of the biggest so-called paradoxes in evolutionary biology, i.e. the maintenance of recombination despite its twofold cost.

Evidence from various study systems indicates that successful infection (and hence host resistance) depends on a genetic match between the parasite's and the host's genotype via molecular interactions involving elicitor/receptor mechanisms. However the key assumption of epistasis, i.e. that this genetic host-parasite match involves several linked resistance loci, remained unsupported so far. Metzger and coauthors [1] now provide empirical support for it.

Daphnia magna can reproduce both sexually and clonally and their well-studied interaction with *Pasteuria ramosa* makes them an excellent model system to investigate the genetics of host resistance. *D. magna* hosts were found to be either resistant (complete lack of attachment of parasite spores to the host's foregut) or

susceptible (full attachment). In this study the authors carried out an elegant Mendelian genetic investigation by performing multiple crosses between four host genotypes differing in their resistance to two different parasite isolates [1].

Their results show that resistance of *D. magna* to each of the two *P. ramosa* isolates relies on Mendelian inheritance at two loci that are linked (A and B), each of them having two alleles with dominant resistance; furthermore resistance to one parasite isolate confers susceptibility to the other. They also show that a third locus appears to confer double resistance (C), but that even double resistant hosts remain susceptible to other parasite isolates, and hence that universal host resistance is lacking – all of this supporting the Red Queen theory.

This paper demonstrates with a high level of clarity that host resistance is governed by multiple linked loci. The assumption of epistasis between resistance loci is supported, which makes it possible for sexual recombination to be maintained by antagonistic host-parasite coevolution.

References

- [1] Metzger CMJA, Luijckx P, Bento G, Mariadassou M, Ebert D. 2016. The Red Queen lives: epistasis between linked resistance loci. *Evolution* 70: 480-487. doi: [10.1111/evo.12854](https://doi.org/10.1111/evo.12854)