

Functional immunogenetic variation, rather than local adaptation, predicts ectoparasite infection intensity in a model fish species

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Abstract

Natural host populations differ in their susceptibility to infection by parasites, and these intra-population differences are still an incompletely understood component of host-parasite dynamics. In this study, we used controlled infection experiments with wild-caught guppies (*Poecilia reticulata*) and their ectoparasite *Gyrodactylus turnbulli* to investigate the roles of local adaptation and host genetic composition (immunogenetic and neutral) in explaining differences in susceptibility to infection. We found differences between our four study host populations that were consistent between two parasite source populations, with no indication of local adaptation by either host or parasite at two tested spatial scales. Greater host population genetic variability metrics broadly aligned with lower population mean infection intensity, with the best alignments associated with Major Histocompatibility Complex (MHC) ‘supertypes’. Controlling for intra-population differences and potential inbreeding variance, we found a significant negative relationship between individual-level functional MHC variability and infection: fish carrying more MHC supertypes experienced infections of lower severity, with limited evidence for supertype-specific effects. We conclude that population-level differences in host infection susceptibility likely reflect variation in parasite selective pressure and/or host evolutionary potential, underpinned by functional immunogenetic variation.

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