

Genotype-environment associations reveal genes potentially linked to avian malaria infection in populations of an endemic island bird

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Abstract

Patterns of pathogen prevalence are, at least partially, the result of coevolutionary host-pathogen interactions. Thus, exploring the distribution of host genetic variation in relation to infection by a pathogen within and across populations can provide important insights into mechanisms of host defence and adaptation. Here we use a landscape genomics approach (Bayenv) in conjunction with genome-wide data (ddRADseq) to test for associations between avian malaria (*Plasmodium*) prevalence and host genetic variation across 13 populations of the island endemic Berthelot's pipit (*Anthus berthelotii*). Considerable and consistent spatial heterogeneity in malaria prevalence was observed among populations over a period of 15 years. The prevalence of malaria infection was also strongly positively correlated with pox (Avipoxvirus) prevalence. Multiple host loci showed significant associations with malaria prevalence after controlling for genome-wide neutral genetic structure. These sites were located near to or within genes linked to metabolism, stress response, transcriptional regulation, complement activity and the inflammatory response, many previously implicated in vertebrate responses to malarial infection. Our findings identify diverse genes - not just limited to the immune system - that may be involved in host protection against malaria and suggests that spatially variable pathogen pressure may be an important evolutionary driver of genetic divergence among wild animal populations, such as Berthelot's pipit. Further, our data indicate that spatio-temporal variation in multiple different pathogens (e.g., malaria and pox in this case) may have to be studied together to develop a more holistic understanding of host pathogen-mediated evolution.

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