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**Optimizing pathogen fitness: the role of the antigenic archive for African Trypanosomes**

Antigenic variation processes play a central role in vector-borne infectious diseases and are likely to respond to host immune mechanisms and epidemiological characteristics. A key priority in disease control and understanding pathogen evolution is the investigation of mechanisms by which pathogens regulate antigenic diversity and how these affect larger-scale population processes. While the within-host population ecology of antigen switching pathogens is not a new topic, increasing access to genetic data provides us with a rapidly widening opportunity to understand the evolutionary ecology of antigenic variation. In this work, we study the interactions between the structure and function of the antigenic archive of the African Trypanosome, the parasite responsible for sleeping sickness. We show that the genetic architecture of the archive has important consequences for pathogen fitness within and between hosts. The optimality criteria we find for the antigenic archive arise as a result of typical trade-offs between transmission and virulence. Our analysis suggests that different traits of the host population can select for different aspects of the antigenic archive, reinforcing once more the importance of host heterogeneity in the evolutionary dynamics of parasites.