



Ascaris: The Neglected Parasite: Chapter 8. Genetic Epidemiology of Ascaris: Cross- transmission between Humans and Pigs, Focal Transmission, and Effective Population Size

Charles D. Criscione

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The fields of conservation genetics and genetic epidemiology share many parallel questions. Hence, methodologies can be adapted from the former to the latter. Three applications of population genetics are presented to further our understanding of *Ascaris* epidemiology. (1) I address if *Ascaris* infections in humans and pigs constitute a single population or subdivided host-affiliated populations with potential for cross-transmission and hybridization. (2) I discuss the use of landscape genetics as a means to identify transmission foci and epidemiologically relevant variables correlated to parasite population substructure. (3) I propose the novel integration of the effective population size (N_e) parameter into population monitoring and epidemiological studies of parasites in general. Using microsatellite data from a metapopulation of *A. lumbricoides* in Nepal, I demonstrate the utility of estimating N_e with single-sample contemporary estimators, offer epidemiologically related questions that can be addressed with N_e , and highlight assumptions of N_e estimation related to *Ascaris* biology.

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