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## Epidemic Models for Leishmaniasis: Elucidation of Key Processes and Parameters

Leishmaniasis is a vector-borne Neglected Tropical Disease. It is caused by Leishmania protozoa transmitted between humans by infected female sandflies. Previously associated with the impoverished in Africa, Leishmaniasis is now considered to be an emerging disease as it spreads across a range of locations from South America to the Mediterranean Basin. We present a mathematical model for the epidemiology of Leishmaniasis. We use a range of techniques including elasticity analysis to make a comprehensive assessment of the importance of various processes and parameters in both the ignition and maintenance of disease spread. We show that the vector population is the critical link when determining whether an infection can become established in a naive population, but that the host population is key in the perpetuation of endemic infection. We conclude by discussing the implications of our analysis for the control of Leishmaniasis in different parts of the world.