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MODELING INFECTIOUS DISEASE TRANSMISSION IN WILD PRIMATE POPULATIONS: A CASE STUDY WITH MOUNTAIN GORILLAS.

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Infectious diseases have become a major conservation concern for populations of wild primates. The endangered mountain gorillas (*Gorilla beringei beringei*) of the Virunga massif in east-central Africa suffer periodic disease outbreaks and are believed to be exposed to and to have suffered infection from exogenous pathogens. However, even in this well studied population the spread and ultimate impact of an introduced infection is very difficult to quantify. Here we present and evaluate an individual-based, stochastic, discrete time disease transmission model to predict epidemic outcomes and better understand health risks to the mountain gorilla population. Modeling the gorilla population as a realistic network of interconnected groups is shown to be an essential element of outbreak outcome. The model predicts that in the absence of humans, gorilla group dispersal and limited group interactions are strong factors in preventing widespread population level outbreaks of infectious disease. Model outbreak severity from a point source infection is dependent on the number of gorillas in the initially infected group and in their neighboring groups. The relative influence of either depends upon the magnitude of model parameters for gorilla interaction, migration, and pathogen transmission. The model also suggests that even a small group of regular human visitors can potentially have a dramatic effect on spreading infection throughout the gorilla population.

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