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Host mating system and the spread of a disease-resistant allele in a population. (English)

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Summary: The model presented here modifies a susceptible-infected (SI) host-pathogen model to determine the influence of mating systems on the outcome of a host-pathogen interaction. Both deterministic and stochastic (individual-based) versions of the model were used. This model considers the potential consequences of varying mating systems on the rate of spread of both the pathogen and resistance alleles within the population. We assumed that a single allele for disease resistance was sufficient to confer complete resistance in an individual, and that both homozygote and heterozygote resistant individuals had the same mean birth and death rates. When disease invaded a population with only an initial small fraction of resistant genes, inbreeding (selfing) tended to increase the probability that the disease would soon be eliminated from a small population rather than become endemic, while outcrossing greatly increased the probability that the population would become extinct due to the disease.

MSC:

92D30 Epidemiology

92D10 Genetics and epigenetics

92C80 Plant biology

37N25 Dynamical systems in biology

Keywords:

plant pathogens; pathogen spread; disease resistance; resistant alleles; allele spread; susceptible-infected-resistant model; inbreeding; ordinary differential equations

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