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Resistance threshold in spatially explicit epidemic model: Finite size scaling applied to dynamic percolation in epidemic processes with mixed cultivar planting

We examine the fraction of resistant cultivars necessary to prevent a global pathogen outbreak (the resistance threshold) using a spatially explicit epidemiological model (SIR model) in a finite, two-dimensional, lattice-structured host population[1]. Threshold behaviour of this spatially explicit SIR model cannot be reduced to that of bond percolation, as was previously noted in the literature, unless extremely unrealistic assumptions are imposed on infection process. The resistance threshold is significantly lower than that of conventional mean-field epidemic models, and is even lower if the spatial configuration of resistant and susceptible crops are negatively correlated. Finite size scaling applied to the resistance threshold reveals that its difference from static percolation threshold (0.41) is inversely proportional to the basic reproductive ratio of pathogen. Estimated value, 4.7, of critical basic reproductive ratio in a universally susceptible population is much larger than the corresponding critical value (1) in the mean-field model and nearly three times larger than that of SIS model.

References

[1] Suzuki, S.U. and Sasaki, A. *How does the resistance threshold in spatially explicit epidemic dynamics depend on the basic reproductive ratio and spatial correlation of crop genotypes?* Journal of Theoretical Biology **276** 117–125 (2011).