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How do spatial heterogeneity, habitat connectivity, and different movement rates among subpopulations combine to influence the observed spatial patterns of an infectious disease? To find out, we formulated and analyzed a discrete-time SIS patch model. Patch differences in local disease transmission and recovery rates characterize whether patches are low-risk or high-risk, and these differences collectively determine whether the spatial domain, or habitat, is low-risk or high-risk. In low-risk habitats, the infection disappears whenever the mobility of infected individuals lies above some threshold value, but for high-risk habitats, the infection can never be completely eliminated. When the disease-free equilibrium (DFE) is unstable, there exists an endemic equilibrium (EE) which is unique and positive everywhere. The EE tends to a spatially inhomogeneous DFE as the mobility of susceptible individuals tends to zero. Sufficient conditions for whether high-risk patches in the limiting DFE have susceptible individuals or not are given in terms of disease transmission and recovery rates as well as habitat connectivity, and these conditions are illustrated using numerical examples. (Received September 17, 2007)