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Human monocytic ehrlichiosis (HME) is a tick-transmitted disease with growing impact in the USA. Risk of a tick-borne disease to humans can be estimated using the prevalence of that disease in the tick population. A deterministic model for HME is explored to investigate the underlying dynamics of prevalence in tick populations. The dynamics in a single spatial patch are considered first to determine which model components are most important to predicting disease dynamics in a local ecology. The model is then expanded to spatially-explicit patches on which patch connectivity, the surrounding environment, and boundary effects are studied. The results of this investigation show that predicting risk of this disease to humans is determined by many complicated interactions. Areas that would be endemic in isolation may or may not sustain the disease depending on the surrounding habitat. Similarly, control efforts are shown to be far more effective when applied in wooded habitats than in neighboring grassy habitats. Boundary assumptions which describe the reality of increasing habitat fragmentation additionally play a large role in predicting the endemicity of an HME outbreak. Overall, HME and all tick-borne diseases are complex, nonlinear systems that have just begun to be explored. (Received August 27, 2008)