Dynamics of Vector-Host Interaction and Emergence Eastern Equine Encephalitis in Northeastern USA

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Abstract. Eastern equine encephalitis virus (EEEV) is a highly pathogenic mosquito-borne zoonosis responsible for outbreaks of severe disease in humans and equines. During the last decade, we have witnessed annual reoccurrence of virus activity with human and equine cases, and expansion into new regions in the northeastern (NE) U.S. Entomological factors, and changes in the pathogen's abiotic and biotic environment might be responsible for the recent emergent foci. In the NE U.S., EEEV is maintained in an enzootic cycle involving *Culiseta melanura,* and passerine birds in freshwater swamp habitats. However, the role this mosquito plays in transmission of EEEV to humans and equines is not well defined. A PCR-based method and direct sequencing of the mitochondrial *cytochrome b* gene were used for profiling of blood meals in *Cs. melanura* to quantify its contact with vertebrate hosts, and to infer epidemiologic implications of its feeding behavior in four historic EEEV foci in Connecticut. Avian point count surveys were conducted to determine spatio-temporal host community composition experienced by *Cs. melanura* and EEEV. Of 1127 blood meals identified to species level, only seven were from mammalian hosts. However, >99% of blood meals were from 65 avian species. An empirically informed transmission model was developed for EEEV in the four sites using *Cs. melanura* abundance and preferred and non-preferred avian hosts. We measured strong feeding preferences for American Robin, Tufted Titmouse, Common Grackle, Wood Thrush and a few other virus competent species, quantified as the proportion of mosquito blood meals from these bird species in relation to their frequencies. Our study clarifies the host associations of *Cs. melanura* in four EEEV foci in Connecticut. We identified vector host preferences as the most important transmission parameter and quantified the contribution of preference-induced contact heterogeneity to enzootic transmission. Our study elucidates spatio-temporal host species utilization by *Cs. melanura* in relation to avian host abundance, and indicates that heterogeneity induced by host preference is a key mediator of vector-borne pathogen epizootics in host communities.