

Abstracts of the Wildlife and Fisheries Poster Session

Genetic Structure of Striped Skunk Populations: Implications for Disease Transmission in an Urban Landscape

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Abstract: The striped skunk (*Mephitis mephitis*) is widely distributed in North America and a common inhabitant of urban areas. Striped skunks represent a reservoir and vector for the transmission of diseases that pose a significant human health risk, including rabies and the parasite *Toxoplasma gondii*. Therefore, understanding population structure and movements among striped skunk populations will assist in the management of disease issues within urban landscapes. Here we present a spatial analysis of striped skunk population structure within greater Houston, Texas, based on 7 microsatellite DNA markers amplified in 102 adult striped skunks. Although this highly developed urban landscape is bisected by major highways with high traffic volume (including Interstate 10 and US Hwy 59), we found no evidence for unique genetic clusters that might indicate barriers to dispersal. We detected weak genetic structure over the entire data set ($F_{ST} = 0.031$, $P < 0.001$). An analysis of spatial autocorrelation based on Moran's I revealed a large neighborhood size, where genetic structure was a function of geographic distance between individuals. Samples collected within 8–10 km were not genetically independent. Disparity of assignment index and F_{ST} values between males and females supports a male bias in dispersal. Estimates of Nm calculated from pairwise F_{ST} among three sampling sites ranged from 6.2–10.6 migrants per generation. Our results indicate that local populations of urban skunks in this region encompass a relatively large geographic area. Thus, management of disease risk will require spatially extensive efforts.

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