

Genetic Analysis of Population Dynamics of the Southeastern Coyote

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Abstract: Coyotes (*Canis latrans*) have been extremely successful in dispersing and expanding their range that now includes all 50 states of the United States in addition to Canada and parts of Central America. The southeastern United States is hypothesized as the last area of colonization for this species. Origins of coyotes in Alabama are being investigated using a phylogenetic approach integrated in our genetic analysis. Coyotes have generally been considered a pest species due to their adaptive ability, high reproductivity, and impact as a top predator on commercial agricultural business. Population dynamics of coyotes is still poorly understood, yet such knowledge will be beneficial to management practices of these individuals. The goal of this study was to determine population structure in Alabama by using microsatellite DNA markers. Bayesian clustering analysis was used to incorporate spatial data with the genotypes to identify potential populations. In addition we examined patterns of gene flow across an urban to rural gradient. ArcGIS was employed to define urban and rural populations within a 97-km radius of the Auburn/Opelika Metropolitan Area. High genetic diversity was detected across the sampled individuals within Alabama. In addition, some genetic differentiation was measured between urban and rural populations. Tracing patterns of gene flow within and among groups of coyotes in proximity to municipal localities is extremely applicable in urban coyote management. Information gained about population structure among coyotes in east-central Alabama could be informative about populations across the southeastern region. It is our expectation that such biological data will be consolidated with the vast knowledge of the ecology of the southeastern coyote gathered to date to inform and aid management plans and decisions across the region.

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