

High Spatial Homogeneity in a Sex-Biased Mating System: The Genetic Population Structure of Greater Prairie Chickens (*Tympanuchus cupido pinnatus*) in Kansas, Missouri, and Nebraska

by

Mayee Wong

B.S.-B.A., University of California, San Diego, 1994

ABSTRACT

This study characterizes the genetic pattern of great prairie chicken (*Tympanuchus cupido*) populations and investigates factors likely influencing these patterns in an effort to provide information critical to the management efforts of this imperiled species. I describe the genetic differentiation of lek groups in three states: Kansas, Missouri, and Oklahoma; and examine the relative influences of geographic distance and mating system on the apparent population structure. One hundred eighty-four individuals from fifteen leks were surveyed at four variable loci by amplification with primers initially found to amplify microsatellite loci in poultry (*Gallus gallus*). Genotypic distributions across the entire region differed significantly from Hardy-Weinberg expectations for panmixia. Statistically significant geographic heterogeneity was detected among leks ($F_{ST} = 0.056$; $p = 0.000$). However, analyses of molecular variation (AMOVA) showed geographic partitioning of total genetic variability to be slight: more than 90% was attributable to among individual variation within leks; of the remaining variance, approximately 2% occurred among leks within a state and approximately 5% among states. The average proportion of total gene diversity allocated by AMOVA between leks at a proximity of 2 to 5 km was comparable to that found among leks in regions more than 161 km apart.

The genetic structure of greater prairie chicken populations was greatly influenced by gender-biased dispersal. AMOVA tests conducted separately for each sex indicate males exhibited twice as much among-lek variation as do females. Additionally, estimates of average relatedness among males at a lek site were markedly higher than that among females by lek ($R_{MALES} = 0.146$, $SE = 0.046$; $R_{FEMALES} = 0.004$, $SE = 0.024$). These findings suggest males were largely responsible for the degree of population differentiation seen among greater prairie chicken leks whereas females promoted gene flow.