

A Landscape Genetics Approach to Assessing the Risk of CWD-infected White-tailed Deer Dispersing from Wisconsin to Iowa

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Collaborators:
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Goals and Objectives:

- o Characterize population genetic structure (i.e., relative rates of dispersal) among deer harvested from counties in Iowa and Wisconsin that border the Mississippi River
 - o Characterize the influence of features of the Mississippi River on genetic connectivity between Iowa and Wisconsin deer populations (i.e., the permeability/ resistance to deer movement)
 - o Use results from objectives 1+2 to identify regions of Iowa where deer are at highest risk of CWD infection based on rates of genetic exchange with Wisconsin deer.
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Progress:

Krista Eucken, an MS student, began work on the project in January 2008. Samples of hunter-harvested deer from Iowa and Wisconsin counties bordering the Mississippi River were obtained from the respective Departments of Natural Resources and cataloged. Twelve microsatellite genetic markers were selected based on their use in other studies of white-tailed deer and optimized for use in our lab. A pilot study was conducted using 92 female deer distributed across the study area (46 from each state) genotyped at 12 microsatellite markers with the objectives of: 1. obtaining a preliminary picture of genetic variation and population genetic structure in the study region and 2. guiding the sampling scheme for the overall project. Results of the pilot study indicate high levels of genetic diversity in deer in both Iowa and Wisconsin, as measured by allelic diversity and heterozygosity. Preliminary analyses of population structure, based on the pilot dataset, suggest there is a low degree of genetic differentiation between the states.

Future Plans:

Future plans include:

1. Characterizing population genetic structure over the entire study area by genotyping additional deer (~400) at the 12 microsatellite loci indicated above.
2. The high levels of variation within states and the low degree of differentiation between states indicates the desirability of adding a mitochondrial DNA marker, which is expected to show more structure than microsatellites to the project.
3. Collect landscape data on features hypothesized to influence deer movement in the Mississippi River and study area counties.
4. Following genotyping, we will conduct genetic data analysis and characterize deer population genetic structure in the study area.
5. Using our genetic data and landscape data, we will identify landscape features that influence deer gene flow, and potentially CWD infection risk, between Iowa and Wisconsin.