

**Environment and Natural Resources Trust Fund  
2012-2013 Request for Proposals (RFP)**

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**Project Title:**

**ENRTF ID: 009-A**

A Proactive Approach to Managing CWD in Minnesota

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**Topic Area:** A. Fisheries & Wildlife Research

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**Total Project Budget:** \$ 459,463

**Proposed Project Time Period for the Funding Requested:** 3 yrs, July 2013 - June 2016

**Other Non-State Funds:** \$ 0

**Summary:**

We provide a scientifically generated map of the genetic and habitat relationships of Minnesota deer to guide rapid management response in the event of a disease outbreak, such as CWD.

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**Sponsoring Organization:** U of MN

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**Location**

**Region:** Statewide

**County Name:** Statewide

**City / Township:**

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_____ Funding Priorities	_____ Multiple Benefits	_____ Outcomes	_____ Knowledge Base
_____ Extent of Impact	_____ Innovation	_____ Scientific/Tech Basis	_____ Urgency
_____ Capacity Readiness	_____ Leverage	_____ Employment	_____ TOTAL _____%



# Environment and Natural Resources Trust Fund (ENRTF)

## 2012-2013 Main Proposal

**PROJECT TITLE: A proactive approach to managing CWD in Minnesota**

### I. PROJECT STATEMENT

Chronic wasting disease (CWD) could threaten the experience of the 500,000 Minnesotans who annually stalk the estimated 1,000,000 white-tailed deer in our state, spending \$450 million in the process. CWD is a *fatal disease with no known vaccines or cure*. CWD has a strong foothold in Wisconsin, and alarmingly, it has recently (April 2012) spread to NW WI. Furthermore, unlike western states, the frequency of infected animals in some WI areas has risen to 25%, and some models predict a catastrophic decline in deer numbers. Despite the MN-DNR’s skillful management of Minnesota’s deer population, our herd is vulnerable to CWD. The primary question is what information would allow a biologically appropriate response to an outbreak? We suggest that knowledge of the genetic structure and broad-scale movement patterns of the deer herd would provide Minnesota’s resource managers with the tools to limit and contain spread. Biologists in WI and IA are currently documenting the genetic structure of their deer herds to inform managers, and we intend to do the same for Minnesota.

*Intriguingly, there is evidence that some deer have some genetic resistance to CWD.* CWD is unlike most diseases because the infectious agent is a normally occurring protein that becomes misshapen (termed a “prion”), makes contact with normal copies of the protein and causes them to misfold, builds up in the body and eventually causes death. Nonetheless, some deer have a genotype that confers some resistance to prion attack. We will determine the prevalence of this resistance, while also developing tools allowing a timely and efficient response to a potential CWD outbreak. Our goals are to:

**1) Develop the first statewide genetic map of Minnesota’s white-tailed deer herd.**

We will determine how genetically similar deer are within MN and their genetic relationships to deer in WI and IA. We will also identify the frequency and distribution of genetically resistant deer in the state.

**2) Develop a habitat-based connectivity map to explain the observed genetic patterns.**

We will develop habitat-specific landscape models that predict how deer move in the various habitats in Minnesota. We will use the genetic data (Goal 1) to refine this landscape model.

**3) Provide guidelines for rapid response to disease outbreaks in MN deer.**

Our information on genetically-tested corridors of deer movement will be used to develop models of CWD (or any other disease) spread. We will predict how fast and in what directions a CWD outbreak would spread given any starting point and different assumptions about transmission.

### II. DESCRIPTION OF PROJECT ACTIVITIES

**Activity 1:** Develop a statewide genetic map of Minnesota’s white-tailed deer herd. **Budget:** \$235,513 We will work with the MNDNR and hunting organizations to collect tissue samples throughout the state. We will use the same DNA markers used in Wisconsin and Iowa, allowing us to merge results. We will determine whether deer from different parts of MN are genetically differentiated and how similar MN deer are to deer from elsewhere. These results will be compared with the habitat connectivity models to refine our understanding of current and historical patterns of deer movements. To date, we have determined the DNA sequences of 14 deer from the Metro Zone and compared them to deer from NE Iowa and SW Wisconsin (part of the CWD zone). The comparison (Fig. 1) showed considerable intermingling, meaning there are no natural impediments to dispersal that would prevent deer or their diseases from moving into Minnesota. Using a second genetic test we will discover the distribution of the prion-resistant genotypes, creating a contour map of the relative frequency of resistance. We have found that approximately 15% of deer in the Metro Zone possess a degree of resistance.

Outcome	Completion Date
1. A detailed map of the genetic structure within the MN deer herd.	May 2014
2. Identification of any prion-resistant sub-populations within the MN deer herd.	November 2014

**Activity 2:** Develop a movement-based connectivity map to explain deer dispersal. **Budget:** \$111,975  
 We will combine maps of habitat and patterns of urban development into a Geographic Information System to produce a map of movement “resistance” throughout Minnesota. These models will include preferred habitats and potential dispersal barriers, and yield connectivity maps (Figure 2) that describe likely pathways of deer dispersal. We will fit our model to the genetic data (Activity 1) so that our model best explains observed patterns of connectivity within the MN herd.

Outcome	Completion Date
1. <i>An initial model, based on circuit theory, of deer population connectivity.</i>	November 2014
2. <i>A connectivity model fit to observed genetic patterns of the deer population.</i>	May 2015

**Activity 3:** Provide guidelines for rapid response to disease outbreaks in MN deer. **Budget:** \$111,975  
 It is unclear how CWD passes from one deer to another, but there are at least two pathways. First, scientific studies showed that if fawns are given enough concentrated CWD<sup>+</sup> saliva, they contract CWD. Second, prions are shed in feces and could be ingested by uninfected deer. Both types of transmission will be included in epidemiological models based on deer movements. These models will predict the likely routes of disease spread, allowing rapid and targeted response by managers.

Outcome	Completion Date
1. <i>A flexible modeling framework that describes the dynamics of CWD spread.</i>	November 2015
2. <i>Identification of areas in MN at high-risk for spreading disease within deer.</i>	June 2016

### III. PROJECT STRATEGY

#### A. Project Team/Partners

This project is a partnership between three University of Minnesota researchers. Dr. Robert Zink (Dept. of EEB, College of Biological Sciences) is an expert in landscape genetics and will direct the genetic analysis of the deer population. Dr. James Forester (Dept. of FWCB, College of Food, Agricultural and Natural Resource Sciences) is a quantitative ecologist and will develop the deer dispersal model. Dr. Meggan Craft (Dept. of VPM, College of Veterinary Medicine) is a disease ecologist who will develop the CWD epidemiological model. No other organization in the state possesses the expertise to undertake these studies.

#### B. Timeline Requirements

We will collect 500 tissue samples from deer in yr 1. After analyzing the samples during 2013-14, we will fit a deer dispersal model to the resulting genetic data. The following year we will collect 500 additional samples to rigorously test and refine the dispersal model. During the third year we will sample areas needed to construct a final epidemiological model to predict how CWD would spread through the state.

#### C. Long-Term Strategy and Future Funding Needs

*Forewarned is forearmed:* Neighboring states are collecting genetic and landscape data to predict deer movements and disease corridors. We believe the time for gathering this information is now -- before any outbreaks. Our studies will guide informed responses to a CWD outbreak, or any other infectious deer diseases (including bovine tuberculosis or foot and mouth disease). In addition, if we find areas with a high level of resistant genotypes, this will further modify potential monitoring efforts. **Once we identify routes of deer movements from the landscape and genetic data we can recommend the best-suited places for culling, intensive harvest or monitoring.** Waiting for an outbreak is a risky strategy when a resource so important to Minnesotans hangs in the balance. This project will produce important management tools, and will also provide critical data to help us procure federal grants (from NSF, NIH, and USDA) to expand and refine the research produced from this project.

## 2012-2013 Detailed Project Budget

### IV. TOTAL ENRTF REQUEST BUDGET 3 years

<u>BUDGET ITEM</u>	<u>AMOUNT</u>
Personnel (All UM): Postdoctoral associate (100% full time salary for 3 years, \$129818, fringe for 3 years, \$29,495) - will develop model for disease spread across state and perform habitat suitability models Lab technician (100% full time salary for 3 years, 122,091, fringe 50,423) - will obtain tissue samples, isolated DNA and perform sequencing of DNA and basic data analysis Faculty member (Forester) – 1 month summer salary (\$24,044) plus 7% fringe (\$1683; excluding retirement benefits), oversee habitat model Undergraduate Assistant – (\$30909) will assist postdoc and faculty	\$ 388,463
<b>Equipment/Tools/Supplies:</b> shipping tissue samples from across state (\$1,500), DNA laboratory supplies and services (\$54,000; \$36/sample for 1500 samples), dedicated computer workstation for simulations often taking weeks (\$6000), GIS software required for project (\$2000)	\$ 63,500
<b>Acquisition (Fee Title or Permanent Easements):</b> NA	\$ -
<b>Travel:</b> \$7500 (mileage to collect tissues samples around state)	\$ 7,500
<b>Additional Budget Items:</b> NA	\$ -
<b>TOTAL ENVIRONMENT AND NATURAL RESOURCES TRUST FUND \$ REQUEST =</b>	<b>\$ 459,463</b>

### V. OTHER FUNDS

<u>SOURCE OF FUNDS</u>	<u>AMOUNT</u>	<u>Status</u>
<b>Other Non-State \$ Being Applied to Project During Project Period:</b>	none	
<b>Other State \$ Being Applied to Project During Project Period:</b>	none	
<b>In-kind Services During Project Period:</b> Salaries for Zink (10% match), Forester (10% match), Craft (5% match) = \$67,962; fringe for Zink, Forester & Craft = \$24,065	\$ 92,027	secured
<b>Remaining \$ from Current ENRTF Appropriation (if applicable):</b>	none	
<b>Funding History:</b>	none	



2012-2013 Main Proposal

PROJECT TITLE: A proactive approach to managing CWD in Minnesota

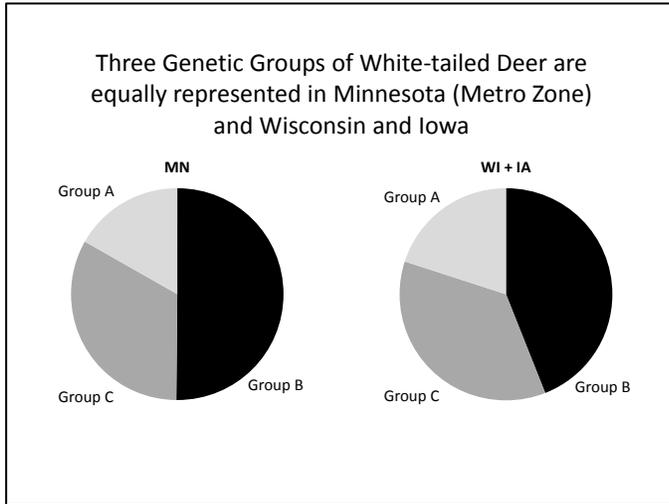


Figure 1. Pie charts showing relative percentages of three different genetic groupings of white-tailed deer in Minnesota (Metro Zone, 601) and southwestern Wisconsin and Northeastern Iowa. The charts show a high degree of genetic similarity between these areas, one of which (WI) has CWD and the others do not. The explanation for the lack of differences is either recent historical or ongoing dispersal, which could easily spread disease from one area to the other.

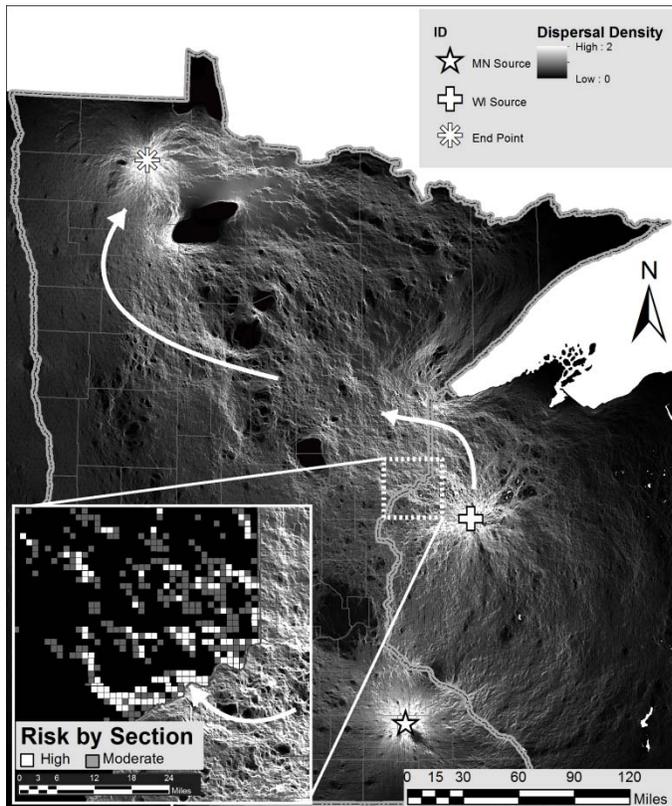


Figure 2. Predicted paths of connectivity between three locations. If a disease outbreak were found at the cross, a map based on genetic connectivity would show where section-level monitoring (see inset) would do the most good (i.e., where to put up a CWD roadblock). The three locations are for illustration but represent the first occurrence of CWD in Minnesota (star), the recent CWD case in NW WI (cross) and the location where bovine TB was discovered in cattle and deer (asterisk).

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Project manager qualifications

Dr. Robert M. Zink is a full professor in the Department of Ecology, Evolution and Behavior, and the Breckenridge Chair in Ornithology at the Bell Museum. He has conducted sponsored research for 30 years, and is a leading expert in the genetics of natural populations. He has over 150 peer reviewed publications and has received awards for excellence in both research and teaching.