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A standardized, high-throughput genetic resource to inform white-tailed deer population and disease management

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Understanding how deer move on the landscape is key to predicting the spread of Chronic Wasting Disease (CWD). Most often, deer movements are investigated by capturing, collaring, and following individual animals, but this approach is time-consuming and expensive.

Using genetic techniques, specifically the use of specific genetic markers termed SNPs (pronounced 'snips' – specific locations within an animal's genome that can vary between individuals), researchers can compare the genetics of individual deer to the genetic characteristics of groups of deer to identify where an animal originated. Researchers can then compare the genetics of CWD positive animals to the genetics of other groups of deer to infer where the infected animal originated.

A team led by Caitlin Ott-Conn, a Laboratory Scientist with the Michigan Department of Natural Resources, was awarded funding through PA207 of 2018 to use recent technological advances to design and to create panels of selected SNPs that many CWD researchers will have access to. The panels will give researchers the ability to efficiently and inexpensively determine the population of origin and to do landscape level investigations of CWD prion gene variation. These panels, once complete, will provide information for studies of disease spread at roughly half the cost of current techniques.

To date, the Ott-Conn collaboration has selected 60,000 SNPs (out of over 5 million locations of variability) for their first assessment tool. This tool has been used to analyze 400 samples across 16 states. The research team has secured additional support from the Association of Fish and Wildlife Agencies in the form of deer tissue samples to help create these panels. Samples will come from researchers or state agencies in Alabama, Florida, Georgia, Indiana, Iowa, Louisiana, Maryland, Michigan, Minnesota, Mississippi, Missouri, New York, Oklahoma, Pennsylvania, South Carolina, South Dakota, Texas, Vermont, Virginia, and Wisconsin. This effort has even gone international with collaborating partners in Mexico.

Several steps are planned for completion by 2023. One of these is to conduct an association study to determine links between SNPs on the panel and their relation to CWD across the Midwest. Another is to apply the genetics of Michigan's deer herd to understand population level patterns of movement and to identify 'populations-of-origin' from across the range.

Ott-Conn's work promises to move the needle at the landscape level by providing managers across jurisdictions with a new and powerful tool to inform their disease management efforts and to assure healthy populations of white-tailed deer.

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