ML 2015, ML 2016 Project Abstract
For the Period Ending June 30, 2023

PROJECT TITLE: Building a mechanistic and process-based species distribution model for tansy and leafy spurge
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FUNDING SOURCE: Environment and Natural Resources Trust Fund
LEGAL CITATION: MINNESOTA INVASIVE TERRESTRIAL PLANTS AND PESTS CENTER
ML 2015, Ch. 76, Art. 2, Sec. 6a
ML 2016, Ch 186, Sec 2, Subd 6a

ML 2015
APPROPRIATION AMOUNT: $70,812
AMOUNT SPENT: $70,812
AMOUNT REMAINING: $0

ML 2016
APPROPRIATION AMOUNT: $351,188
AMOUNT SPENT: $351,188
AMOUNT REMAINING: $0

Sound bite of Project Outcomes and Results

Cutting-edge deep learning computer models, large scale field experiment, and genomic analyses were used to improve predictions of invasive range expansion for leafy spurge and common tansy. In both species, we found substantial genetic and phenotypic evolution that may impact their invasive risk and change future strategic decision making.

Overall Project Outcome and Results

In our project, we used cutting-edge deep learning computer models, large scale field experiments, and genomic analyses to improve predictions of invasive range expansion for the two problematic weeds, leafy spurge and common tansy. In both species, we found substantial genetic and phenotypic evolution that may impact their invasive risk and change future strategic decision making. In the leafy spurge system, we built highly accurate detection models that leveraged publicly-available satellite imagery, which allowed us to predict occurrences across large landscapes. Predictions of this magnitude allow for rapid field detection and monitoring as well as the identification of environmental factors that promote leafy spurge invasion. Population genomics and trait analysis of leafy spurge further revealed that, despite relatively similar genetic variation across the expanding range, populations from different regions of the state may have evolved differences in germination niche. In the common tansy system, we focused on understanding potentially adaptive genetic and trait variation using growth chamber experiments and a large common garden experiment with climate manipulations. Data reveal important trait evolution occurred during range expansion which has the potential to impact further invasion and that may influence the response to climate change. Landscape genomic analysis of common tansy revealed that there are two distinct genetic clusters in Minnesota that are distinguished by changes in soil features and land usage.

Project Results Use and Dissemination

Lake, T.A., R.D. Briscoe Runquist & D.A. Moeller. 2023. Chronosequence of invasion reveals minimal losses of population genomic diversity, niche expansion, and trait divergence in the polyploid, leafy spurge. Evolutionary Applications, in revision; https://www.biorxiv.org/content/10.1101/2023.04.04.535556v2

Lake, T.A. Lake, R.D. Briscoe Runquist, & D.A. Moeller. 2022. Deep learning detects invasive plant species across complex landscapes using Worldview-2 and Planetscope satellite imagery. Remote Sensing in Ecology and Conservation 8:875–889.

Briscoe Runquist, R.D., T.A. Lake, & D.A. Moeller. 2021. Improving predictions of range expansion for invasive species using joint species distribution models and surrogate co-occurring species. Journal of Biogeography 48:1693-1705.

Lake, T.A., R.D. Briscoe Runquist, & D.A. Moeller. 2020. Predicting range expansion of invasive species: pitfalls and best practices for obtaining biologically realistic projections. Diversity and Distributions 26:1767–1779.