

Integrating DNA fingerprinting of invasive watermilfoil strains into aquatic vegetation monitoring and assessment

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ABSTRACT

Eurasian watermilfoil (*Myriophyllum spicatum* L.) and its hybrids with native northern watermilfoil (*Myriophyllum spicatum* L. × *Myriophyllum sibiricum* Komarov) are among the most heavily managed invasive aquatic plants in the United States. Previous genetic studies have identified numerous distinct Eurasian and hybrid strains that can spread within and among waterbodies via clonal propagation. Strains can differ in their invasiveness (e.g., growth and potential for spread) and response to herbicides. Characterizing particularly problematic or invasive strains of watermilfoil could help inform management decisions. However, identifying strains for laboratory study (e.g., herbicide response) is a significant logistical challenge. One promising tool to address this problem is strain-level monitoring. In this study, we integrated genetic fingerprinting that can distinguish different watermilfoil strains into aquatic vegetation monitoring in eight Minnesota lakes over the course of 3 yr. Specifically, we looked for changes in strain composition of watermilfoil populations over time to identify strains of specific interest for further characterization of growth and herbicide response. Using a simulation-based chi-square analysis, we documented significant changes in strain composition in six of the eight waterbodies monitored, and we identified three strains of invasive watermilfoil and two strains of native northern watermilfoil to prioritize for further investigation. Although more work is needed to determine the best sampling strategies and statistical analysis of spatiotemporal strain data, our study suggests that integrating genetic fingerprinting into aquatic vegetation management could help to more efficiently identify and manage the most troublesome watermilfoil strains.

Key words: genetic monitoring, herbicide resistance evolution, *Myriophyllum spicatum* L., northern watermilfoil, strain identification.

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