

Results Summary Sheet
GenPass, LLC

Samples Sent From: WIDNR
Samples Received on: 8/30/17
Received By: Syndell Parks

Send Results to:
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Chris Acy (chris@fwwa.org)

Book: Milfoil Book 11

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Sample Summary:

Lake Name	Location	Lat/Lon	WBIC	Putative ID	Sample ID Code	Well Position
Winnebago	Boat Landing	44.026212/ -88.520730	NA	EWM/HWM	WI469-001	2B
Winnebago	Boat Landing	44.026212/ -88.520730	NA	EWM/HWM	WI469-002	2C
Winnebago	Boat Landing	44.203900/ -88.424990	NA	EWM/HWM	WI469-003	2D
Winnebago	South Asylum Bay	44.4045572/ -88.514576	NA	EWM/HWM	WI469-004	2E
Winnebago	South Asylum Bay	44.045572/ -88.514576	NA	EWM/HWM	WI469-005	2F

Plate Diagram:

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
A	X	Extraction (-) Control	PCR (-) Control									
B	X	WI149-001	EWM (+) Control									
C	X	WI149-002	HWM (+) Control									
D	X	WI149-003	NWM (+) Control									
E	X	WI149-004	Restriction (-) Control									
F	X	WI149-005										
G	X	X										
H	X	Extraction (-) Control										

*(-) Control: Well run with water to ensure no contamination of samples during processing, (+) Control: Samples with know/verified ID to ensure process is working as desired.

Results Summary:

Lake Name	Sample ID Code	Analysis Type	Identification Result	Comments
Winnebago	WI469-001	ITS RA	Eurasian Watermilfoil (<i>Myriophyllum spicatum</i>)	
Winnebago	WI469-002	ITS RA	Eurasian Watermilfoil (<i>Myriophyllum spicatum</i>)	
Winnebago	WI469-003	ITS RA	Eurasian Watermilfoil (<i>Myriophyllum spicatum</i>)	
Winnebago	WI469-004	ITS RA	Eurasian Watermilfoil (<i>Myriophyllum spicatum</i>)	
Winnebago	WI469-005	ITS RA	Hybrid Watermilfoil (<i>Myriophyllum spicatum</i> x <i>M. sibiricum</i>)	

*ITS RA: ITS gene Rapid Assay; **SS-ITS: Straight Sequencing of the ITS gene; **SS-trnLF- Straight sequencing of the trnLF gene.

Additional Notes: NA

*DNA extractions were performed using the Qiagen DNeasy Plant mini kit and associated protocol (CAT# 69106). Samples processed were identified using an Internal Transcribed Spacer (ITS) rapid assay.

For more information on the downstream analysis, see:

Thum R.A., Lennon, J.T., Connor, J., Smagula, A.P. 2006. A DNA fingerprinting approach for distinguishing native and non-native milfoils. *Lake and Reservoir Management*. 22(1):1-6.

Sturtevant, A.P., Hatley, N., Pullman, G.D., Sheick, R., Shorez, D., Bordine, A., Mausolf, R., Lewis, A., Sutter, R., Mortimer, A. 2009. Molecular characterization of Eurasian watermilfoil, northern watermilfoil, and the invasive interspecific hybrid in Michigan lakes. *Journal of Aquatic Plant Management*. 47:128-135.

Grafe, S.F., Boutin, C., Pick, F.R., Bull, R.D. 2015. A PCR-RFLP method to detect hybridization between the invasive Eurasian watermilfoil (*Myriophyllum spicatum*) and the native northern watermilfoil (*Myriophyllum sibiricum*), and its application in Ontario lakes. *Botany*. 93:117-121.

** DNA extractions were performed using the Qiagen DNeasy Plant mini kit and associated protocol (CAT# 69106). Samples processed were identified by analysis of either the Internal Transcribed Spacer (ITS) gene or the trnLF gene.

For more information on the downstream analysis, see:

Moody, M. L., Les, D. H. (2002). Evidence of hybridity in invasive watermilfoil (*Myriophyllum*) populations. *Proceedings of the National Academy of Sciences of the United States of America*, 99(23), 14867–71. <http://doi.org/10.1073/pnas.172391499>

Moody, M. L., & Les, D. H. (2007). Geographic distribution and genotypic composition of invasive hybrid watermilfoil (*Myriophyllum spicatum* x *M. sibiricum*) populations in North America. *Biological Invasions*, 9(5), 559–570. <http://doi.org/10.1007/s10530-006-9058-9>