

Results Summary Sheet  
GenPass, LLC

**Samples Sent From:** Onterra  
**Samples Received on:** 7/25/2017  
**Received By:** Syndell Parks

**Send Results to:**  
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**Book:** Milfoil Book 11

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**Sample Summary:**

Lake Name	Location	Lat/Lon	WBIC	Putative ID	Sample ID Code	Well Position
Bullhead	South end of lake	44.101195/-88.035721	68300	EWM	WI198-003	2A
McCarry	Northeast Corner	46.519655/-91.370259	293400	EWM	WI448-01	2B

**Plate Diagram:**

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
<b>A</b>	x	WI198-003	Extraction (-) Control	x	Restriction (-) Control							
<b>B</b>	x	WI448-001	x	Extraction (-) Control								
<b>C</b>	x	x	x	PCR (-) Control								
<b>D</b>	x	x	x	x								
<b>E</b>	x	x	x	EWM (+) Control								
<b>F</b>	x	x	x	M.q. (+) Control								
<b>G</b>	x	x	x	HWM (+) Control								
<b>H</b>	Extraction (-) Control	x	x	NWM (+) 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
Bullhead	WI198-003	ITS RA	Eurasian Watermilfoil ( <i>Myriophyllum spicatum</i> )	NA
McCarry	WI448-01	ITS RA	Eurasian Watermilfoil ( <i>Myriophyllum spicatum</i> )	NA

\*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>