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Lake Erie Center

Dr. Carol Stepien sizing up the walleye run at the Maumee River.

# Great Lakes Genetics/Genomics Laboratory at the Lake Erie Center, Department of Environmental Sciences

*The Great Lakes Genetics/Genomics Laboratory (GLGL) at the LEC, directed by Dr. Carol Stepien, focuses on:*

1. Evaluating the evolutionary relationships, population genetics, genomic adaptations, and biogeographic structure of fishes.
2. Understanding the vector pathways, population dynamics, evolutionary relationships, and genetic time course of nonindigenous species invasions.
3. Interpreting gene flow patterns and genomic differentiation of fishes as influenced by dams, habitat changes, and other anthropogenic factors.
4. Developing rapid genetic tests for discerning fish disease, and identifying biological communities from eDNA water samples, in conjunction with the lab of Dr. James Willey of the Health Science Campus.

*For all of these problems, we work closely with federal and state agency fishery and conservation managers, who partner with us and often serve on graduate student committees. Our laboratory emphasizes tiered mentorship and our graduate students first-author many publications, obtain grants and scholarships, win best-paper awards, and are recognized as top environmental professional students nationally and internationally. We are funded by the NSF, USEPA, USDA, NOAA Sea Grant, and others.*

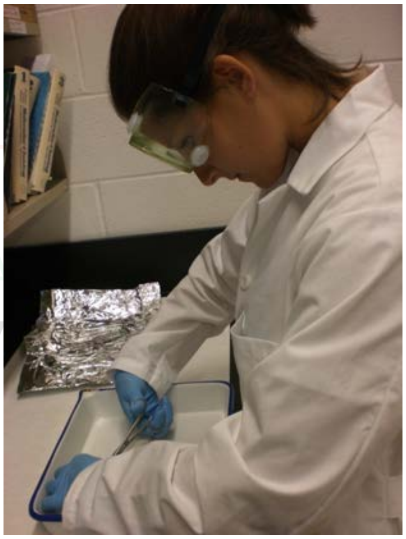
## Our most important recent findings are:

**1. The primary source of the Eurasian round goby invasion in the Great Lakes genetically traces to the port of Kherson in the Black Sea Ukraine, at the mouth of the Dnieper River. Some other Black Sea riverine sources, including the Danube and Dniester Rivers, also contributed. This invasion has tremendous genetic diversity, which likely has fueled its success.**

**2. The zebra and quagga mussel invasions in the Great Lakes also are characterized by very high genetic diversity. The eastern Lakes (but not those closer to the west) contributed founders to new expansion populations in western states, including the Colorado River system and California resevoirs, transported via boats on trailors.**

**3. Using high-resolution DNA microsatellite markers, we found that Great Lakes populations of native walleye, yellow perch, and smallmouthbass show greater genetic variability and patterning than previously known. State and federal agencies are using our results to conserve their genetic structure and manage the fisheries.**

**4. We developed a new rapid, accurate PCR test with internal controls to detect and quantify the VHS fish virus that outbroke in the Great Lakes, which also distinguishes whether the virus is active and replicating (collaboration with Dr. James Willey).**



GLGL Ph.D. sutdent Lindsey Pierce collects tissue samples from fish infected with Viral Hemorrhagic Septicemia.

GLGL Ph.D. student Jhonatan Sepulveda Villet, and REU undergraduate students electrofish in Lake Erie.

## Selected Recent Publications with our GLGL graduate students(*):

Sepulveda-Villet, O.J.* and C.A Stepien. 2012. Waterscape genetics of the yellow perch (*Perca flavescens*): patterns across large connected ecosystems and isolated relict populations. *Molecular Ecology,* doi: 10.1111/mec.12044.

Stepien C.A., J.A. Banda*, D.M. Murphy* & A.E. Haponski*. 2012. Temporal and spatial genetic consistency of walleye spawning groups. *Transactions of the American Fisheries Society,* 141: 660-674.

Pierce, L.R.*, C.A. Stepien. 2012. Evolution and biogeography of an emerging quasispecies: Diversity patterns of the fish Viral Hemorrhagic Septicemia virus (VHSv). *Molecular Phylogenetics and Evolution,* 63: 327-341.

Karsiotis, S.I.*, L.R. Pierce*, J.E. Brown*, C.A. Stepien. 2012. Salinity tolerance of the invasive round goby: Experimental implications for seawater ballast exchange and spread to North American estuaries. *Journal of Great Lakes Research,* 38: 121-128.

Neilson, M.E.* and C.A. Stepien. 2011. Historic speciation and recent colonization of Eurasian monkey gobies (*Neogobius fluviatilis* and *N. pallasi*) revealed by DNA sequences, microsatellites, and morphology. *Diversity and Distributions*, 17: 699-702.

Brown, J.E.* and C.A. Stepien. 2010. Population genetic history of the dreissenid mussel invasion: Expansion patterns across North America. *Biological Invasions*, 12(11): 3687-3710.

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