**John W. Martinson, Research Biologist, in EPA's National Exposure Research Laboratory**

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**Area of Expertise:** Currently I am pursuing a Ph.D. in bioinformatics at the University of Cincinnati. Most of my work involves working with nucleic acid sequences generated by high throughput DNA sequencing (HTS). My primary focus currently is being part of team working to improve draft genome assemblies of the Fathead minnow. The improved assemblies will in turn will be used to help develop robust methods for using RNAseq-based gene expression assays as indicators and/or diagnosers of exposure(s); genome annotation and development of a reference transcriptome will also be part of this effort. I am also part of a team that is developing ways to use HTS data to monitor for aquatic invasive species and to do community profiling (metagenetics/metagenomics) that can be applied to bioassessments. The goal is to develop tools that use DNA sequences from bulk extractions of environmental samples to determine the community composition (biodiversity) present in samples, and to correlate such results with other measures of condition in order to better understand the full impact of various stressors on the environment. Prior to my current activities, I gained considerable experience with "DNA barcoding" using the COI gene, particularly in fish.

**Select Publications:**

Nacci, D., Proestou, D., Champlin, D., Martinson, J., Waits, E. 2016. Genetic basis for evolved tolerance to dioxin-like pollutants in wild Atlantic killifish: more than the aryl hydrocarbon receptor. Molecular Ecology – under review

Waits, E., Nacci, D., Martinson, J., Champlin, D., Morris, S., Rinner, B., Proestou, D., 2016. An integrated genetic linkage map and comparative genome analysis for the estuarine Atlantic killifish, Fundulus heteroclitus. Open Journal of Genetics – in press

Kostich, M., Flick, R., Martinson, J., 2013. Comparing predicted estrogen concentrations with measurements in US waters. Environ. Pollut. 178C, 271-277

Maddaloni, M., Santella, D., Itkin, C., Kahn, H., Stephansen, S., Chang, M., Borst, M., Bourbon, J., Elsen, F., Martinson, J., O'Neil, M., Henning, C. 2013. Fish Tissue Analysis for Mercury and PCBs from a New York City Commercial Fish/Seafood Market, EPA/600/R-11/066F; U.S. Environmental Protection Agency.

Lamendella, R., Domingo, J. W., Ghosh, S., Martinson, J., Oerther, D.B. 2011. Comparative fecal metagenomics unveils unique functional capacity of the swine gut. BMC Microbiol. (11):103

Maki, N., Martinson, J., Nishimura O., et al. 2010. Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. Molecular Vision, (16):72–78

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**Education:**

- Ph.D. candidate, Bioinformatics, 2009-present, University of Cincinnati
- M.S. in Chemistry, 1995, University of Cincinnati
- B.A. in Zoology, 1981, Miami University

**Professional Experience:**

- Research Biologist/Bioinformaticist, USEPA, ORD/NERL, Cincinnati, OH, 2004 to Present
- Acting Branch Chief, MERB, USEPA, ORD/NERL, Cincinnati, OH, November, 2009 to May, 2010
- Quality Assurance Manager, USEPA, ORD/NERL Cincinnati, OH, 1994 to 2003
- Project Coordinator, TAI/DynCorp, Cincinnati, OH, 1992 to 1994
- Analytical Support Chemist/Group Leader/Acting Program Manager, TAI/DynCorp, Cincinnati, OH, 1990 to 1992
- Pilot Plant Operator/Research Associate/Analytical Support Chemist, University of Cincinnati, Cincinnati, OH, 1982 to 1989