

SEA GRANT PROJECT SUMMARY FORM 90-2 DEVELOPMENT PROPOSAL

- (1) **INSTITUTION:** Purdue University (1a) **ICODE:**
- (2) **TITLE:** Utilization of genomic signatures from *Hyalella azteca* as a way to quickly evaluate toxicity and need of sediment remediation in the Great Lakes basin.
- (3) **PROJECT NUMBER:** (4) **REVISION DATE:**
- (5) **PROJECT STATUS:** (6) **INITIATION DATE:** 03/01/10
(7) **COMPLETION DATE:** 09/30/10
- (8) **SUB PROGRAM:**
- (9) **PRINCIPAL INVESTIGATOR:** Sepúlveda, Maria S. (9a) **EFFORT:** 2.0
(9b) **AFFILIATION:** Forestry and Natural Resources and School of Civil Engineering, Purdue University
(9c) **AFFILIATION CODE:**
- (10) **CO-PRINCIPAL INVESTIGATOR:** Colbourne, John K. (10a) **EFFORT:** 1.0
(10b) **AFFILIATION:** The Center for Genomics and Bioinformatics, Indiana University
(10c) **AFFILIATION CODE:**
- (11) **ASSOCIATE INVESTIGATOR 1:** (11a) **EFFORT:**
(11b) **AFFILIATION:**
(11c) **AFFILIATION CODE:**
- (12) **ASSOCIATE INVESTIGATOR 2:** (12a) **EFFORT:**
(12b) **AFFILIATION:**
(12c) **AFFILIATION CODE:**
- (13) **S.G. FUNDS:** \$10,000 (14) **STATE MATCHING FUNDS:** N/A
(15) **LAST YEAR'S SG FUNDS:** \$0 (16) **LAST YEAR'S MATCHING FUNDS:** N/A
(17) **PASS-THROUGH FUNDS:** \$0 (18) **LAST YEAR'S PASS-THROUGH FUNDS:** N/A
(19) **RELATED PROJECTS:** Collaboration in Life Sciences & Informatics Research Grant (Indiana/Purdue Universities) "Construction of cDNA libraries for developing genomic signatures of sediment toxicity" <https://projects.cgb.indiana.edu/display/grp/Hyalella+azteca>
(20) **PARENT PROJECTS:**
(21) **SEA GRANT STRATEGIC PLAN CLASSIFICATION:**
(22) **OBJECTIVES:**

The main objective of the proposed studies is to apply state-of-the-art technologies for a quick and accurate evaluation of the hazards posed by contaminated sediments across the Great Lakes basin. More specifically, *we propose to utilize microarrays for the evaluation of gene expression signatures after exposure to different sediment pollutants and to correlate these changes with phenotypic responses of ecological significance in order to determine ecological risk from direct exposure to contaminated sediments.* We will achieve this goal by utilizing a recently developed microarray for the evaluation of gene expression signatures after exposure of the amphipod

Hyalella azteca to different pollutants commonly found in sediments across the Great Lakes basin and by correlating these changes with phenotypic responses of ecological significance in order to determine ecological risk from direct exposure to contaminated sediments. Our specific objectives are to:

- 1) Test our newly developed *H. azteca* microarray after exposure to three major classes of contaminants: heavy metals (mercury), polychlorinated biphenyls (PCBs), and polycyclic aromatic hydrocarbons (PAHs).
- 2) Compare gene responses from above experiments to standard ecological endpoints (growth and reproduction).
- 3) Test our microarray with Great Lakes contaminated sediments and compare our results with previous toxicity studies that have evaluated them with standard toxicity tests using *H. azteca*.

(23) PROBLEM:

Decades of point and non-point pollution sources to the Great lakes and its tributaries have resulted in major sediment contamination. Indeed, sediments from this basin are known to contain many different types of contaminants, such as heavy metals (mercury, lead, cadmium), herbicides (atrazine), PCBs, and PAHs. More recently, emerging contaminants, such as polybrominated flame retardants, have also been detected in Great Lakes sediments. Sediments contaminated with organic and inorganic contaminants have the potential to negatively affect ecosystem health through impacts on aquatic organisms, wildlife, and humans. The problem is so widespread, that over 2,000 miles (20%) of the Great Lakes shoreline is considered impaired because of sediment contamination and fish consumption advisories. Altogether, these areas fall into the category of Areas of Concern (AOC) and are defined as “places where beneficial uses of water resources such as drinking, swimming, fishing, and navigation are impaired by anthropogenic pollution or perturbation” (Adriaens et al., 2002, “Great Lakes Sediments: Contamination, Toxicity and Beneficial Re-Use”, White paper commissioned by Michigan Sea Grant and the School for Natural Resources and the Environment, 37 pp.). Since it is impossible to remediate this vast geographical area, it is imperative that contaminated areas get ranked in terms of sediment toxicity and ecological impacts.

(24) RATIONALE (IMPACT OF PROBLEM):

The expense involved with removing or treating contaminated sediments requires an accurate characterization of risks. Currently, one of the standard approaches is to evaluate sediments through the sediment triad approach, which includes sub-chronic and chronic toxicity testing using the benthic invertebrate *H. azteca*. The high cost of these tests results in either very high evaluation costs, or remedial decisions based on very limited data. A gene microarray chip specific to *H. azteca* can eventually be used as a surrogate for chronic tests, resulting in significant money and time savings.

Gene arrays (also called microarrays), are a relatively new research tool where thousands of genes specific to an organism are spotted onto a solid support matrix and queried with RNA samples from animals exposed to stressors, which are compared to controls. Our own work and that of others has shown that classes of chemicals, and perhaps even individual chemicals, are likely to display their own “chemical signatures” in terms of the specific genes that are differentially activated upon exposure. A major advantage of this approach is that these “chemical signatures” can be elicited rapidly (within hours of exposure), even though the physiological responses to which they are correlated may require much prolonged exposures.

Moreover, such biomarkers can provide early warnings of ecological duress, even when there is limited knowledge about the mode of action of individual toxicants or of chemical mixtures. The application of such arrays for screening is already proven in the diagnosis of several human diseases. However, their application in ecotoxicological studies have yet to be rigorously tested, largely because the production of microarrays for such purpose requires substantial resources, including characterized and relevant cDNA databases to source the DNA probes on the arrays.

Our research has the potential to revolutionize toxicogenomics using model species whose genomes are not yet fully sequenced. If we succeed in producing a proof of principle in extracting genomic signatures that are diagnostic of the toxicological effects using this model aquatic crustacean for toxicological evaluations, then other species will follow for cross-species extrapolations of environmental toxic effects from contaminants. This project is similar in design to the recent endeavors by the *Daphnia* Genomics Consortium – based within Indiana University’s Center for Genomics and Bioinformatics (CGB) – to develop a comprehensive database of genomic signatures of environmental compounds for this distantly related limnetic crustacean. Moreover, given the paucity of functional genomic data for Arthropods other than *Drosophila* and its insect allies, the comparative value of microarray experiments in crustaceans that root the insect phylogenetic tree will provide important insights into the evolution of toxicological responses and their gene regulatory networks.

Since all organisms respond to environmental stressors by regulating the expression of genes, we propose to utilize recently developed microarrays for measuring these fundamental changes. Over the last year, we have produced over one million cDNA sequences for *H. azteca* using a recently published procedure from one of our labs that characterizes the full transcriptome from single runs of next-generation sequencers. This constitutes the largest catalog of transcribed genes for an amphipod species. In collaboration with Roche NimbleGen (Madison, WI) we have also produced a multiplex microarray containing three probes for every predicted gene for genome wide expression analysis. Our main goal now is to evaluate gene expression signatures after exposure to different sediment pollutants and to correlate these changes with whole animal toxicity. The use of microarrays will allow replacing long, expensive toxicity tests with short exposures using microarrays for the identification of DNA signatures that predict chronic toxicity.

(25) METHODOLOGY:

First, we will conduct laboratory experiments exposing *H. azteca* to sediments spiked with contaminants singly and in mixtures and evaluate changes on gene expression using microarrays. Changes at the gene level will be correlated to phenotypic changes. Second, we will replicate these experiments with sediments from a couple of AOC (likely Indiana Harbor and Saginaw River). Results from our microarray studies will be compared with published data on *Hyalella* toxicity tests using these same sediments (USEPA, 1993, "Biological and Chemical Assessment of Contaminated Great Lakes Sediment", USEPA 905-R93-006).

Controlled contaminant exposures: *H. azteca* will be exposed to contaminants commonly associated with Great Lakes sediments. These will include a heavy metal (mercury), a mixture of PCBs, and a mixture of PAHs. Contaminants will resemble environmental conditions both in concentration and mixture composition. Endpoints to be measured during the 42-day tests include somatic growth (which will also be measured at 10 days), fecundity, and survival. Three toxicant concentrations and a control will be tested using three replicates each. Tests will start by introducing fifty 7-day-old organisms into 600-mL glass beakers. Animals will be maintained

at standard experimental conditions (22 ± 2 °C with a photoperiod of 16 h light: 8 h dark) and fed fish flakes and *Selenastrum* algae. A minimum of six organisms from each flask will be collected at days 2 and 10 during the exposure period, photographed and flash-frozen for RNA extraction. At day 10, the remaining animals will be counted and promptly returned to their respective treatment chambers. The experiment will be terminated after 42 days when the total numbers of animals, gravid females, and precopula pairs will be counted. Note: These experiments will begin regardless of whether this seed grant gets funded and should be completed by spring 2010.

Exposure to naturally contaminated sediments: These experiments will mirror those already described, but will be conducted with sediments collected from at least two AOC. We are proposing to conduct these experiments with sediments from Indiana Harbor and Saginaw River for several reasons. First, their contaminant profiles have been well characterized. Second, their toxicity has been tested using standard toxicity assays with *H. azteca*. And third, we can easily access these sites for the collection of sediments.

Microarrays: For the modest investment of a single run of the Roche 454 genome sequencer, we assembled over one million Expressed Sequence Tags (ESTs) into 59,650 contigs (overlapping sequence fragments) of which 14,869 have average lengths of 1,000 bases. Our bioinformatics pipeline then generated 135,799 long oligonucleotide (60 bp) sequences that match uniquely to the gene transcripts, which were then synthesized onto 12 sub-arrays of a single glass slide. Therefore, by processing up to four glass slides in a single day, we can generate transcription profiles from 96 independent RNA samples (4 chips x 12 sub arrays x 2 co-hybridizing samples using different fluors).

(26) EXPECTED RESULTS AND IMPACT:

This type of study will help determine if remediation or regulation will be necessary for maintaining ecosystem health, especially in urban coastal environments where these compounds are found in higher concentrations. It also directly addresses the goal of improving Great Lakes ecosystem health and water quality by providing information on sediment toxicity and informing the risk assessment process.

There are three main areas where this project is of major significance. First, the proposed work will greatly facilitate the development of a streamlined sediment evaluation approach. The expense involved with removing or treating contaminated sediments requires an accurate characterization of risks. Currently, the standard approach is to evaluate sediment toxicity by measuring effects on *H. azteca* reproduction, which can be cost-prohibitive (> \$5,000/sample) and very time consuming (each test lasts 42 days). A gene microarray chip based on *H. azteca* can eventually be used as a surrogate for chronic 42-d toxicity tests. Second, the development of gene arrays for a distinctive invertebrate species will enhance efforts to better extrapolate results from toxicity studies on test species to other organisms. The extrapolation of results observed in one test species is often problematic when there is no information as to the mechanism by which a chemical induces a certain response. Gene expression profiles may be able to define global biochemical pathways that are affected and thus clarify the mechanisms by which compounds act. Finally, this proposal will immediately provide the first sequence survey of genes responding to environmental stressors in this sentinel species. To date, there are no sequence data for nuclear genes for this amphipod within public databases.

SEA GRANT BUDGET FORM 90-4

GRANTEE: Purdue University			GRANT/PROJECT NO.:		
PRINCIPAL INVESTIGATOR Maria S. Sepulveda Co-PI: John K. Colbourne			DURATION: 12 months Yr. 1 4/1/10-3/31/11		
A. SALARIES AND WAGES:		man-months			
	No. of People	Amount of Effort	Sea Grant Funds	Matching Funds	
1. Senior Personnel					
a. (Co) Principal Investigator:	0	0	0	0	
b. Associate (Faculty or Staff):	0	0	0	0	
Subtotal:	0	0	0	0	
2. Other Personnel					
a. Professionals:	0	0	0	0	
b. Research Associates:	0	0	0	0	
c. Res. Asst./Grad Students:	0	0	0	0	
d. Prof. School Students:	0	0	0	0	
e. Pre-Bachelor Student(s):	1	0	1499	0	
f. Secretarial-Clerical:	0	0	0	0	
g. Technicians:	0	0	0	0	
h. Other:	0	0	0	0	
Total Salaries and Wages:	1	0	1499	0	
B. FRINGE BENEFITS:			127	0	
Total Personnel (A and B)			1626	0	
C. PERMANENT EQUIPMENT:			0	0	
D. EXPENDABLE SUPPLIES AND EQUIPMENT:			3731	0	
E. TRAVEL:					
1. Domestic			1200	0	
2. International			0	0	
Total Travel:			1200	0	
F. PUBLICATION AND DOCUMENTATION COSTS:			0	0	
G. OTHER COSTS:					
1. Communications			0	0	
2. Copying			0	0	
3. Postage/Mailing			0	0	
4. Contractual Services			0	0	
5. Membership/Sponsorship Fees			0	0	
6. Training/Continuing Education			0	0	
7. Project/Person Recognition			0	0	
8. Housing/Board/Research			0	0	
9. Tuition Remission			0	0	
10. Other			0	0	
11. Other:			0	0	
Total Other Costs:			0	0	
TOTAL DIRECT COST (A through G):			6557	0	
INDIRECT COST					
	On campus	52.50%	3443	0	
	Off campus	0.00%	0	0	
Total Indirect Cost:			3443	0	
TOTAL COSTS:			10000	0	

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Web: <http://www.agriculture.purdue.edu/fnr/faculty/sepulveda/index.htm>

(i) Professional Preparation

B.S. Universidad de Chile, Veterinary Sciences (1988)
D.V.M. Universidad de Chile, Veterinary Medicine (1991)
M.S. University of Florida, Wildlife ecology (1997)
Ph.D. University of Florida, Veterinary Medicine, Concentration: Toxicology (2000)

(ii) Appointments

Associate Professor of Ecotoxicology and Aquatic Animal Health
Department of Forestry and Natural Resources, Purdue University, West Lafayette, Indiana (May 2009 – Present).
Assistant Professor of Ecotoxicology and Aquatic Animal Health
Department of Forestry and Natural Resources, Purdue University, West Lafayette, Indiana (October 2004 – April 2009).
Assistant Scientist
Department of Physiological Sciences, College of Veterinary Medicine, University of Florida, Gainesville, Florida (April 2002-September 2004).
Assistant Instructor
Department of Physiological Sciences, College of Veterinary Medicine, University of Florida, Gainesville, Florida (June 2000-February 2002).

(iii) Publications (selected out of 48)

- Sepúlveda MS**, Williams GE Jr., Frederick PC, and Spalding MG. 1999. Effects of mercury on health and first-year survival of free-ranging great egrets (*Ardea albus*) from southern Florida. *Arch. Environ. Toxicol. Chem.* 37:369-376.
- Sepúlveda MS**, Ruessler DS, Denslow ND, Holm SE, Schoeb TR, and Gross TS. 2001. Assessment of reproductive effects in largemouth bass (*Micropterus salmoides*) exposed to bleached/unbleached kraft mill effluents. *Arch. Environ. Contam. Toxicol.* 41:475-482.
- Sepúlveda MS**, Quinn BP, Denslow ND, Holm SE, and Gross TS. 2003. Effects of paper mill effluents on reproductive success of largemouth bass. *Environ. Toxicol. Chem.* 22:205-213.
- Sepúlveda MS**, Wiebe JJ, Honeyfield DC, Hinterkopf JP, Johnson WE, and Gross TS. 2004. Organochlorine pesticides and thiamine in eggs of largemouth bass and the American alligator, and their relationship with early life-stage mortality. *J. Wild. Dis.* 40:781-785.
- Garcia-Reyero N, Barber DS, Gross TS, Johnson KG, **Sepúlveda MS**, Szabo NJ, Denslow. 2006. Dietary exposure of largemouth bass to OCPs changes expression of genes important for reproduction. *Aquat. Toxicol.* 78:358-369.
- Sepúlveda MS**, Del Piero F, Wiebe JJ, Rauschenberger HR, Gross TS. 2006. Necropsy findings in American alligator late stage embryos and hatchlings from North-Central Florida lakes contaminated with organochlorine pesticides. *J. Wild. Dis.* 42:56-73.
- Lee LS, Carmosini N, Sassman SA, Dion HM, and **Sepúlveda MS**. 2007. Agricultural contributions of antimicrobials and hormones on soil and water quality. *Adv. Agr.* 93:2-69.
- Sanchez BC, Ochoa-Acuña H, Porterfield M, **Sepúlveda MS**. (2008). Oxygen flux as an indicator of physiological stress in fathead minnow embryos: a real-time biomonitoring system of water quality. *In Press. Environ. Sci. Technol.* 42:7070-7017.
- Ralston-Hooper K, Jannasch A, Oh C, Zhang X, Adamec J, **Sepúlveda MS**. (2008). Development of GCxGC/TOF-MS metabolomics for use in future invertebrate ecotoxicological studies. *Aquat. Toxicol.* 88:48-52.

- Ralston-Hooper K, Hardy J, Hahn L, Ochoa-Acuña HG, Lee LS, Mollenhauer R, **Sepúlveda MS**. (2009). Acute and chronic toxicity of atrazine and its metabolites deethylatrazine and deisopropylatrazine on aquatic organisms. *Ecotoxicology*. In Press.
- Garcia-Reyero N, Kroll KJ, Liu L, Orlando EF, Watanabe KH, **Sepúlveda MS**, Villeneuve DL, Perkins EJ, Ankley GT, Denslow ND. (2009). Chemical probing in fathead minnow testis reveals estrogenic mode of action. *BMC Genomics*. In Press.
- Watanabe KH, Li Z, Kroll KJ, Villeneuve DL, Garcia-Reyero N, Orlando EF, **Sepúlveda MS**, Collette TW, Ekman DR, Ankley GT, Denslow ND. (2009). Computational model of the hypothalamic-pituitary-gonadal axis in male fathead minnows exposed to 17 α -ethinylestradiol and 17 β -estradiol. *Toxico. Sci.* 109:180-192.

(iv) Synergistic Activities

Dr. Sepúlveda's main areas of research are ecotoxicology and animal health. Over the last 15 years, she has conducted extensive research evaluating the sublethal effects of a wide-range of environmental contaminants and other environmental stressors on the physiology of numerous terrestrial and aquatic species. For instance, she has worked with heavy metals (mercury); complex industrial mixtures (paper mill effluents); herbicides and pesticides (e.g. atrazine, dieldrin, DDT and derivatives, and toxaphene); industrial pollutants (polychlorinated biphenyls and polyaromatic hydrocarbons); and emerging contaminants (nanoparticles and pharmaceuticals). In terms of species, although most of her work has been focused using vertebrates (including marine mammals, birds, and fishes) as animal models, Dr. Sepúlveda has recently begun research with aquatic invertebrates (*Hyalella* and *Diporeia*). Within the field of ecotoxicology, Dr. Sepúlveda's main area of interest involves studying the potential health effects of environmental contaminants in populations of free-ranging fish and wildlife. Specifically, Dr. Sepúlveda's research has focused on understanding the effects of pollutants on reproduction and early life-stage development. Besides examining whole animal and tissue-level responses to environmental contaminants, in recent years Dr. Sepúlveda has begun investigating the effects of chemicals at the sub-cellular and molecular levels and over the past few years she has incorporated the use of genomics, proteomics, and metabolomics in her research.

(v) Collaborators and Other Affiliations

a) Collaborators and Co-Authors

- 1) Nancy Denslow, University of Florida.
- 2) Jiri Adamec, Purdue University.
- 3) Krista Nichols, Purdue University.
- 4) Inez Hua, Purdue University.
- 5) Reuben Goforth, Purdue University.
- 6) Tomas Höök, Purdue University.
- 7) Tom Nalepa, National Oceanographic Atmospheric Administration.
- 8) Hugo Ochoa-Acuña, Purdue University.
- 9) Michael Kane, Purdue University.
- 10) Trent Sutton, University of Alaska Fairbanks.
- 11) John Bickham, Purdue University.
- 12) Linda Lee, Purdue University.
- 13) Marshall Porterfield, Purdue University.
- 14) Gary Ankley, United States Environmental Protection Agency.
- 15) James Lazorchak, United States Environmental Protection Agency.
- 16) Loring Nies, Purdue University.
- 17) Ron Turco, Purdue University.
- 18) Eric Stach, Purdue University.
- 19) John Coulborne, Indiana University.
- 18) Feng Zhou, Indiana University.
- 19) Karen Watanabe, Oregon Health State University.
- 20) Ed Orlando, University of Maryland.

b) Graduate and Post-doctoral Advisors

Total Number of Graduated Students Advised: Ph.D., 2; M.S., 2

Number of Currently Supervised Students and Post-Doctoral: 4 Ph.D., 0 M.S., 1 Post-Doc

c) Thesis Advisees and Postgraduate Scholars Sponsored:

Stephanie Baker (M.S. 5/07)

Kimberly Ralston-Hooper (Ph.D. 5/09)

Sonia Johns (M.S., 5/09)

Brian Sanchez (Ph.D. 8/09)

BIOGRAPHICAL SKETCH

NAME		POSITION TITLE	
John Kenneth Colbourne		Genomics Director, Associate Scientist	
EDUCATION/TRAINING			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
University of Toronto	B.Sc.	1993	Zoology
University of Guelph	Ph.D.	1999	Evolution
University of Oregon	Post-doc	1999-2001	Evol. genetics
University of Indiana	Post-doc	2001-2002	Functional genomics

Positions and Employment

1999-2001	NSERC Post-doctoral fellow, Department of Biology, Univ. of Oregon
2001-2002	Post-doctoral fellow, Center for Genomics and Bioinformatics, Indiana Univ. Bloomington
2002-2005	Senior Staff Scientist and Project Leader, Center for Genomics and Bioinformatics
2005-present	Genomics Director, Center for Genomics and Bioinformatics, Indiana Univ. Bloomington
2005-2006	Assistant Scientist, Biology, Indiana Univ. Bloomington
2006-present	Associate Scientist, Biology, Indiana Univ. Bloomington

Professional Activities

1) I lead the *Daphnia* Genomics Consortium (DGC), an international group of biologists from 17 countries, with the goal to develop *Daphnia* species into model systems for ecological and evolutionary genomics. I hosted the first DGC meeting at Indiana University on October 3-4, 2002 and the third (January 17-19, 2006) and fourth (July 7-9, 2007) meetings.

2) I develop *Daphnia* genomic tools and protocols, including genetic maps, encyclopedic cDNA resources and microarrays for functional genomic studies. I launched wFleaBase with D. Gilbert (Indiana University), a genome information system for *Daphnia*. All resources, including the draft *D. pulex* genomes sequence and annotation, are made available to researchers via the DGC web pages and mailing list, which are maintained by the Center for Genomics and Bioinformatics.

3) I lead the *Daphnia* Genome Steering Committee, which is charged by the DGC and the Joint Genome Institute (Department of Energy) to direct the first crustacean whole-genome sequencing project. The genome sequence assembly and annotation was pre-released to the public on July 7, 2007, at the DGC meeting.

Daphnia Genomics Consortium (DGC) – <http://daphnia.cgb.indiana.edu>

NIH Model Organism for Biomedical Research – <http://www.nih.gov/science/models/daphnia/>

wFleaBase *Daphnia* Water Flea Genome Database – <http://wfleabase.org>

D. pulex cDNA sequenced libraries – <https://dgc.cgb.indiana.edu/display/DGC/cDNA+Libraries>

D. pulex microarrays – <https://dgc.cgb.indiana.edu/display/DGC/Microarrays>

DGC Collaboration Wiki – <https://dgc.cgb.indiana.edu/>

D. magna genome sequencing project – <https://projects.cgb.indiana.edu/display/grp/D.+magna+Genome>

Honors

- Invited speaker at Gordon Research Conference on Ecological and Evolutionary Functional Genomics. Tilton, USA, 2009
- Invitee for the US Environmental Protection Agency and US Army Engineer Research and Development Division panel of the “TSERAWG Joint Winter Meeting on Environmental Risk Assessment”. Vicksburg, USA; 2009.
- Associate Editor for the Journal of Experimental Zoology, Part A: *Ecological Genetics and Physiology*; 2008-present.
- Executive Advisor for The Center for Research in Environmental Science, Indiana University; 2008-present.
- Invitee for the US Environmental Protection Agency review panel of the “Ecological Exposure Research

Division”. Cincinnati, USA; 2008.

- Panel Member for Environment Canada / Genome Canada panel “Toxicogenomic applications at the Water Science & Technology Directorate”. Burlington, Canada; 2007
- Panel Member for the US Department of Energy panel “Assessing environmental health and ecosystem function using molecular tools”. Oak Ridge National Laboratory, USA; 2005.
- Nominee and finalist for Directorship of Max-Planck-Institut für Limnologie; 2005
- Panel Member for Society of Environmental Toxicology and Chemistry – Society of Toxicology (SETAC-SOT) “Pellston workshop”. Portland, USA; 2004.
- High Performance Computing Award, Sponsored by IEEE Computer Society; 2003.
- Panel Member for Society of Environmental Toxicology and Chemistry (SETAC) Ecotoxicogenomic panel “An ecological perspective of genomics, assessing ecological risk through partnerships.” Pensacola, USA; 2002.
- Post Doctoral Fellowship, University of Oregon, Sponsored by Natural Sciences and Engineering Research Council of Canada (NSERC); 1999-2001.
- Research Fellowship, Sponsored by Max Planck Gesellschaft; 1997.

Referee Activities and Memberships

• I regularly serve as referee for fourteen international journals and six granting agencies: Evolution, Hydrobiologia, Aquatic Ecology, Canadian Journal of Fisheries and Aquatic Sciences, Archiv für Hydrobiologie, BioTechniques, Molecular Ecology, Ecography, Trends in Ecology and Evolution, Evolution and Development, Invertebrate Reproduction and Development, Molecular Phylogenetics and Evolution, Environmental Pollution, Genesis, BMC Research Notes, PLOS One, The Wellcome Trust, The College of Science at Utah State University, The Kansas State university Targeted Excellence Program, The U.S. Environmental Protection Agency, The U.S. National Science Foundation, the Netherlands Organization for Scientific Research NOW, Ghent University.

• I participate in the following professional consortia and societies:

The *Daphnia* Genomics Consortium, The *Nasonia* Genome Sequencing Committee, The *Fundulus* Genomics Consortium, The Arthropod Base Consortium, Society of Environmental Toxicity and Chemistry, The Black Fly Genome Sequencing Initiative, The International Aphid Genomics Consortium, the Consortium for Environmental Genomics and Toxicology.

Publications and Presentations

- Peer reviewed publications (manuscripts, book chapters): 37
- Invited presentation (keynotes, plenary speaker, workshop speaker, symposia speaker): 39
- Presentations at international meetings: 43

SEA GRANT PROJECT SUMMARY FORM

(Continued)

PAPERWORK REDUCTION ACT, PRIVACY ACT, AND PUBLIC BURDEN

NOAA's National Sea Grant College Program exists to increase the understanding, assessment, development, utilization, and conservation of the Nation's ocean, coastal, and Great Lakes resources. It does this by providing grant monies to promote a strong educational base, responsive research, and training. The information requested on this form is required in order to be considered for an award under the authority of the National Sea Grant College Act, as amended. The Project Summary provides information on the project status (for continuing projects applying for additional funding), the investigators and their level of effort, the objectives and methodology of the project, and similar summary information. The information requested may be disclosed to qualified reviewers and staff assistants as part of the application review process; to applicant institutions/grantees to provide or obtain data regarding the application review process, award decisions, or the administration of awards; to government contractors, experts, volunteers and researchers as necessary to complete assigned work; to other government agencies needing information as part of the review process or in order to coordinate programs; and to another Federal agency, court or party in a court or Federal administrative proceeding if the Government is a party. Notwithstanding any other provision of the law, no person is required to respond to, nor shall any person be subject to a penalty for failure to comply with, a collection of information subject to the requirements of the Paperwork Reduction Act, unless that collection of information displays a currently valid OMB Control Number.

Public reporting burden for this collection of information is estimated to average 20 minutes per response, including the time necessary for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions to reduce this burden, to National Sea Grant College Program, R/SG, NOAA, 1315 East-West Highway, Silver Spring, MD 20910 (Attn: Paperwork Reduction Act - Dr. Fritz Schuler).