

UTAH DIVISION OF WATER QUALITY

195 North 1950 West
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Willard Bay Project Proposal Form

Applicant Name: Dr. David C. Richards

Co-Applicant Name(s) (if applicable): Dr. Scott Blankenship; Dr. Gregg Schumer; Brett Marshall; and Dr. Theron Miller

Project Title: Development of Macroinvertebrate DNA Barcodes: A Superior Method for Monitoring Water Quality in Willard Bay and Surrounding Wetlands

Agency or Business Name (if applicable): Oreohelix Consulting; Genidaqs; River Continuum Concepts; and Jordan River/Farmington Bay Water Quality Council

Mailing Address: P. O. Box 996 City: Moab State: UT Zip: 84532

Phone: (406) 580- 7816 E-mail: oreohelix@icloud.com

Individual Non-Profit Govt. Agency Academic **X** Commercial Other

1. Estimated Project Costs:

Labor	\$70,000
Materials	\$40,000
Equipment	\$30,000
Administration	\$10,000
Miscellaneous	\$7,000
TOTAL	\$157,000

Other sources of project funding:

Source: Jordan River/Farmington Bay Water Quality Council Amount: \$40,000

Total project cost including other sources of funding: \$197,000
(please include bids for labor, equipment, rentals, etc.)

2. Describe the purpose and need of the project:

Willard Spur and Surrounding Wetlands

Great Salt Lake (GLS) has approximately 250,000 ha of freshwater wetlands on its eastern shorelines, including Willard Bay (Spur). Over 50,000 ha are managed by private owners and federal and local governments. Managing freshwater inflows and water quality of these wetlands is crucial for maintaining fish and wildlife habitat, ecosystem function, and resistance and resilience to future perturbations, including global climate change. Anthropogenic influences on the Great Salt Lake wetlands are extensive, including a recent diesel oil spill in March 2013 along the shore of Willard Bay in Willard Bay State Park. Salt Lake County alone is home to 10 Superfund sites. Salt Lake County borders the shoreline of Farmington Bay. Most contamination is related to high trace metal content in soil, sediments, and groundwater attributable to historic mining and smelting operations in the Salt Lake Valley. These contaminants have primarily been transported down the

Jordan River and continue to threaten Farmington Bay wetlands. Urbanization and agricultural runoff, including nutrients, sedimentation and pesticides also present a risk to all GSL wetlands. Additional anthropogenic impacts, including adequate water supply may also have undesirable effects on wetland resources and water quality as human communities expand in the northeastern region of GSL shores and the Bear River watershed. Given its current relatively high-quality condition, the Willard Spur Science Panel concluded that Willard Spur and the surrounding wetlands are unique and critically important ecosystems in an otherwise desert environment and that closely monitoring their water quality was crucial.

Water Quality Assessment and Monitoring

One of the most important water quality assessment tools is the use of macroinvertebrates as indicators. Most state, tribal, and federal agencies have well-established biomonitoring programs that focus on macroinvertebrate assemblages. However, the costs of sample processing, taxonomic expertise needed, and subsequent subsampling methods, prohibit the full utilization of the wealth of information that macroinvertebrate assemblages can provide to assess and monitor water quality. This constraint is primarily due to the limited number of samples that can affordably be processed and the associated effects of subsampling on statistical power.

The power ($1-\beta$) to detect changes in metrics due to water quality impairment is primarily dependent on: the number of samples (N), the variability of the metric (σ), and the level of statistical significance (δ) that managers find acceptable (Type I error, α). For example, a U.S. EPA (2008) report conducted a power analysis case study to determine how many years it would take to detect decreases in taxa richness due to expected increased temperatures due to global climate change. Taxa richness is the cornerstone metric in multimetric based indices and in O/E methods. The EPA study estimated it would take 15 years to detect taxa richness losses under a high loss rate and high temperature change scenario. Under a low loss rate and low temperature change scenario, they estimated it would take 100 years to detect losses in taxa richness. It was not apparent whether the U. S. EPA (2008) analysis included the effects of using data that were based on 100 organism count subsamples, which if not included would have increased their estimates substantially more and decreased their ability to detect taxa losses.

As is often the case in bioassessment programs, the problem and the solution for detecting changes are one- in- the same: N , sample size. Increased sample size substantially increases our ability to detect losses of taxa: taxa richness estimates are directly related to the size and number of samples (species area/sample rule, MacArthur and Wilson 1967). Increased sampling can be done either by increasing the number of sites sampled each year within a watershed or by increasing the number of replicate samples taken within a wetland pond, depending on management goals based on properly designed strategies.

Economic and Ecological Costs of Sampling and Subsampling

Collecting more samples does not substantially increase the cost of field sampling. This is because the time and energy required to collect and field process samples are relatively minor compared to taxonomic laboratory costs. Taxonomic laboratory processing is quite cost prohibitive and is the limiting factor in the number of samples that can be collected and analyzed in every bioassessment. Taxonomic costs often exceed \$500/sample. All bioassessment programs have to deal with these costs and an entire bioassessment culture based on these obvious limitations has evolved. Because of vastly reduced budgets, every bioassessment program now limits the number of samples collected and further reduces the statistical and discriminatory power of replicate sampling by either collecting far too few samples or by composite sampling. Subsampling then further reduces the ability to detect impairment. The consequence of processing too few samples often results in an assessment that can only detect extreme differences between reference conditions and highly impaired conditions. Therefore, it is possible that an ecologically relevant impairment that wasn't extreme often remains as 'reference' condition or 'in need of further analysis'. Obviously, better methods that allow for dramatically more samples to be economically processed are urgently needed.

DNA Barcoding

There is an increased emphasis on using genetic bar coding (species-specific DNA fingerprints), including using environmental sampling (i.e. eDNA) in taxonomic surveys and to estimate taxa richness. Indeed, genetic bar coding is one of the most promising developments in species sampling methods this century and is rapidly becoming the method of choice, including water quality biomonitoring (Stein et al. 2014). Genetic bar coding analyses can result in a presence/absence detection signal or relative DNA composition of a given sample. Current leading laboratory instrumentation allows for concentrations of a dynamic number of bar codes (from 24 up to 96 species) to be simultaneously tested for within-samples. This information can be directly used in richness based metrics and to establish the presence or absence of species known to be sensitive to specific stressors that otherwise might be too rare or uncommon to be included during subsampling. Additionally, if standard dose curves have been developed for target species, the proportion of total DNA represented by each species at time of collection can be quantified, which can provide important ecological/food web information as well as can be incorporated into modified abundance based metrics. In addition, this database can be supplemented with taxa lists from other crucial wetlands, particularly those in Farmington Bay, where other key research is being conducted to identify sensitive taxa and elucidate more subtle, but important responses to various water, sediment and habitat quality stressors.

One of the most important contributions of genetic bar coding to bioassessment programs is the cost of processing samples. Once a genetic bar code database has been established for relevant species type specimens, sample processing costs can be reduced by as much as twenty times using molecular methods. This improvement in data generation efficiency will allow managers to collect greater than twenty times more samples (e.g., temporal or geographic expansion) for the same budget, vastly increasing the power of their studies. Alternatively data analyses and projects could be completed using standard metrics at a fraction of typical times and budgets.

3. Estimated time frame of the project with significant milestones (Note: Project must be completed with final reports filed by January 1, 2018):

July through October 2014: Macroinvertebrate field sampling and processing, DNA Library, Taxonomic identification and library museum collection

November 2014: Progress Report

November through February 2014/2015: DNA Barcoding

March 2014: Progress Report

June through October 2015: Additional Macroinvertebrate Collection and Processing, and DNA Barcoding, if necessary

November 2015: Final Report, Formal Consultation

4. Describe the location of the project with attached location map, including details on the total area that will be directly enhanced by the project:

Macroinvertebrate sampling will occur throughout Willard Spur and surrounding wetlands, including Farmington Bay area wetlands

5. Describe how the project will specifically enhance and protect waterways affected by the Willard Bay diesel release and improve the conditions of one or more of the following: wildlife, habitat, natural vegetation, water quality or emergency response:

The project will provide a superior water quality monitoring tool to guide enhancements and protection of WS and surrounding wetlands affected by human caused impacts, including diesel fuel release.

6. Describe project's connectivity to other natural areas or projects that further enhance wildlife, habitat, natural vegetation, water quality or emergency response:

This tool can be used for all wetlands in eastern GSL

7. Describe any additional social benefits of implementing this project:

This tool will be highly useful for assessing and monitoring water quality in GSL wetlands. Water quality and ecosystem services provided by these wetlands is of critical social benefit to of all the people of the GSL watershed.

8. Project plans and details, including rights to work on specified piece of land:

We will generate a taxonomic list of the macroinvertebrate species currently found in Willard Spur and surrounding wetlands. We already have a large database of these taxa, as does the State of UT and BLM Buglab in Logan and we are continuing to collect macroinvertebrate samples in these wetlands.

A complete search of the Barcode of Life database (BOLD) and the National Center for Biological Information (NCBI) nucleotide database for the mitochondrial genes COI (the “universal barcode gene”) and Cytochrome B (CytB) will be conducted to retrieve published and publically available DNA sequences for all species on the list. The database search will reveal:

- 1) which species have been barcoded and
- 2) which target species need to be DNA barcoded.

1) For the species that have publically available DNA sequences for the mitochondrial genes COI (the “universal barcode gene”) and Cytochrome B (CytB) the sequences will be downloaded and saved for future comparison to all target species.

2) DNA barcodes will be determined for target species for which there are no publically available DNA sequence data. For each of these species a minimum of 5- 10 vouchered individuals from across the broadest portion of their range and within the area of proposed monitoring will be collected and used for barcoding. This will likely from populations in Farmington Bay and Willard Spur. Sequence data for the mitochondrial genes COI and CYTB will be generated for each of the 5-10 individuals for all species. The DNA sequences generated will be used for future comparison to all target species. COI and CytB sequence data will be compiled and cross-referenced to identify short (~100- 400bp) nucleotides unique to each species. Additionally the species specific nucleotides will be compared to all published nucleotide sequences using NCBI GENBANK nucleotide Basic Local Alignment Software Tool (BLAST) or what is more commonly referred to as a nucleotide BLAST. The BLAST will ensure that all nucleotides for both COI and CytB are specific not only when compared to those species that are closely related and co-existing on the taxonomic list but unique when compared to all published nucleotide sequences for all species.

Assay Design and Validation

The COI and CytB nucleotide sequences identified as unique to each species will be used to generate species specific Quantitative Polymerase Chain Reaction (qPCR) assays using commercially available software and algorithms. QPCR is a commonly used technique in molecular biology that enables both detection and quantification for one or more specific DNA sequences in a sample. The qPCR assay is both extremely specific and sensitive. All assays will be validated for specificity and sensitivity to ensure that each assay does not cross- react with other closely related co-existing species. Only after each assay has been validated will it be used to identify the DNA from control and field samples.

While individual qPCR assays are ideal for species-specific detection our goal is to produce a high throughput qPCR method for the simultaneous identification of all our target species. To accomplish this we will use the Fluidigm® BioMark™ microfluidic chip platform. Using qPCR assays on the BioMark chip will allow us to simultaneously detect the presence of DNA from as few as 24 up to 96 unique species within as many as 124 samples within hours. The BioMark microfluidic chip platform is dynamic and can be adapted to meet sampling requirements as needed (e.g depending on which species are being targeted species specific assays can be alternated on the BioMark). The dynamic nature of the BioMark will give us the capability to create chips that are regionally and even project specific.

Field and Taxonomic Laboratory Work

We will field sort the specimens to the best taxonomic resolution feasible using a field binocular dissecting scope. Specimens will be placed in properly labeled vials and delivered to the taxonomic laboratory for further taxonomic identification and verification. In the laboratory, again we will sort the specimens to the best taxonomic resolution possible. In some cases this will require slide-mounting specimens. Note that slide mounting the specimen destroys the specimen and it is no longer available for

DNA-related laboratory work. Specimens will be stored in a 70% ethanol solution made with distilled water in glass vials. They will be kept at room temperature in a taxonomic library collection with only external labels to prevent contamination from the laboratory environment. It will take several field visits to accumulate sufficient specimens for genetic analyses. When a sufficient amount of material from a sufficient number of species has been accumulated, specimens will be available for DNA barcoding by the genetic laboratory.

Literature Cited

MacArthur R. H. and E. O. Wilson. 1967. The theory of island biogeography. Princeton University Press. N. J.

Stein, E. D., Bryan P. White, Raphael D. Mazor, John K. Jackson, Juliann M. Battle, Peter E. Miller, Erik M. Pilgrim, and Bernard W. Sweeney. 2014. Does DNA barcoding improve performance of traditional stream bioassessment metrics? *FreshwaterScience*, Vol. 33, No. 1. pp. 302-311

U.S. Environmental Protection Agency (U.S. EPA). 2008. Climate change effects on stream and river biological indicators: A preliminary analysis. Global Change Research Program, National Center for Environmental Assessment, Washington, DC; EPA/600/R-07/085.

9. Describe your experience in implementing projects of similar scope and magnitude:

This consortium of scientists is highly experienced in these specific types of projects. Please review our resumes, C.V.s, and Statements of Qualifications that are attached.

10. Describe how ongoing maintenance of the project will be funded and carried out: NA

11. List consultants or agency partners that have participated in project development (below):

All of the applicants and co-applicants have participated in the project development. No additional consultants or agency partners were involved.

Applicant

Signature: *David C. Richards*

Date: April 24, 2014

Signature *Scott Blankenship*

Date: April 24, 2014

Co-Applicant (if applicable)

Signature *Gregg Schumer*

Date: April 24, 2014

Co-Applicant (if applicable)

Signature *Brett Marshall*

Date April 28, 2014

Co-Applicant (if applicable)

Signature *Theron Miller*

Date: April 28, 2014

Co-Applicant (if applicable)

Website address for:

Dr. Scott Blankenship and Dr. Gregg Schumer, Genidaqs, West Sacramento, CA
<http://www.genidaqs.com>

Brett Marshall, River Continuum Concepts, Manhattan, MT
<http://www.rivercontinuum.org>

SCOTT M. BLANKENSHIP PH.D.

Senior Scientist – Cramer Fish Sciences
Science Director – GENIDAQS
scott.blankenship@fishsciences.net
www.fishsciences.net

Associate – University of California, Davis,
College of Agriculture and Environmental Sciences
sblankenship@ucdavis.edu

Scott Blankenship received his Ph.D. in genetics from the University of California, Davis (2001) studying the relationship between genetic diversity and population boundaries. He then went on to a postdoc at UC Santa Cruz / NOAA studying population genetics of California Chinook salmon and related data system infrastructure. He became a geneticist with the Washington Department of Fish and Wildlife's Molecular Genetics Laboratory, becoming Director of the WDFW genetics program prior to joining the Cramer Fish Sciences team. He is also currently an Associate at UC Davis College of Agriculture and Environmental Sciences. Dr. Blankenship interests focus on combining the newest tools of molecular biology and genetics theory with field observations of aquatic organism populations and their habitat to create solutions for some of the most challenging issues in fishery management, hatchery operations, and population recovery. In addition to technical expertise, Dr. Blankenship is also known for his can-do attitude, enthusiasm, and leadership within multi-interest group collaborations.

Education and Training

Ph.D. Genetics. University of California, Davis. 2001.

B.S. Biology. Cal Poly San Luis Obispo, CA. 1993.

Employment History

Applied Geneticist/Senior Scientist, Cramer Fish Sciences. 2011–present.

Science Director, GENIDAQS. 2011–present.

Genetics Laboratory Director, Washington Department of Fish and Wildlife's Molecular Genetics Laboratory, Olympia, Washington. 2010–2011.

Geneticist/Biologist III, Washington Department of Fish and Wildlife's Molecular Genetics Laboratory. 2006–2010.

Post doc, University of California, Santa Cruz. 2003–2006.

Research Assistant, University of California, Davis. 1994–2001.

Student Intern, Diablo Canyon Nuclear Power Plant, Tenera Environmental Inc., 1992–1993.

Teaching Assistant, Invertebrate Zoology, Cal Poly, San Luis Obispo, 1991-1993

Selected Publications

Author	Publication
<p>Blankenship, Scott M.</p>	<p>D. J. Rawding, C. S. Sharpe, and S. M. Blankenship. (In Press) Genetic-based Estimates of Adult Chinook Salmon (<i>Oncorhynchus tshawytscha</i>) Spawner Abundance from Carcass Surveys and Juvenile Outmigrant Traps. Submitted to Transactions of American Fisheries Society.</p> <p>S. Blankenship G. Schumer, and B. Cavallo. 2013. Genetic Identification of Salvaged Winter Run Chinook Salmon and pilot study for Parental Based Tagging salvage identification methodology. Report to California Department of Water Resources</p> <p>P. Moran, D. J. Teel, M. A. Banks, T. D. Beacham, M. R. Bellinger, S. M. Blankenship, J. R. Candy, J. C. Garza, J. E. Hess, S. R. Narum, L. W. Seeb, W. D. Templin, C. G. Wallace, and C. T. Smith. 2013. Divergent life-history races do not represent Chinook salmon coast-wide: the importance of scale in Quaternary biogeography. Canadian Journal of Fisheries and Aquatic Sciences 70:415-435 DOI: 10.1139/cjfas-2012-013</p> <p>J. E. Merz, P. Skvorc, S. M. Sogard, C. Watry, S. M. Blankenship, and E. E. Van Nieuwenhuysse. 2012. Onset of Melanophore Patterns in the Head Region of Chinook Salmon – A Natural Marker for the Re-identification of Individual Fish. North American Journal of Fisheries Management 32: 806-816. DOI: 10.1080/02755947.2012.681014</p> <p>S. Blankenship, M. Teply, and G. Schumer. 2012. Sampling and analysis to assess brook trout (<i>Salvelinus fontinalis</i>) population trends in High Lake (Oregon) using environmental DNA monitoring. Report to Burns Paiute Tribe</p> <p>M. T. Limborg, S.M. Blankenship, S.F. Young, F.M. Utter, L.W. Seeb, M.H.H. Hansen, and J.E. Seeb. 2011. Signatures of natural selection among lineages and habitats in <i>Oncorhynchus mykiss</i>. Ecology and Evolution. DOI: 10.1002/ece3.59/abstract</p> <p>S. M. Blankenship, M. R. Campbell, J. E. Hess, M. A. Hess, T. W. Kassler, C. C. Kozfkay, A. P. Matala, S. R. Narum, M. M. Paquin, M. P. Small, J. J. Stephenson, K. I. Warheit, and P. Moran 2011. Major lineages and metapopulations in Columbia River <i>Oncorhynchus mykiss</i> are structured by dynamic landscape features and environments. Transactions of American Fisheries Society 140:665–684</p> <p>S. M. Blankenship, M. P. Small, and J. D. Bumgarner. 2009. Temporal stability of genetic variation within natural populations of summer steelhead (<i>Oncorhynchus mykiss</i>) receiving mitigation hatchery fish. Transactions of the American Fisheries Society 138: 1052</p> <p>L.W. Seeb, A. Antonovich, M.A. Banks, T.D. Beacham, M.R. Bellinger, S. M. Blankenship, M. Campbell, N.A. Decovich, J.C. Garza, C.M. Guthrie III, T. A. Lundrigan, P. Moran, S.R. Narum, J.J. Stephenson, K.J. Supernault, D.J. Teel, W.D. Templin, J.K.Wenburg, S.F. Young, C.T. Smith (2007) Development of a Standardized DNA Database for Chinook Salmon. Fisheries 32 (11): 540 - 552</p> <p>D. Hedgecock, M. D. Banks, V. K. Rashbrook, C. A. Dean, and S. M. Blankenship. 2001. Applications of population genetics to conservation of Chinook salmon diversity in the Central Valley. In: Brown RL, editor. Fish. Bul. 179: Contributions to the biology of Central Valley salmonids. Sacramento (CA): California Department Fish and Game.</p>

SCOTT M. BLANKENSHIP PH.D.

Applied Geneticist – Senior Scientist
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Education

Ph.D., Genetics, University of California, Davis. November 2001.

Dissertation: Assessing the validity of DNA tandem repeat genetic markers for population analysis, patterns of neutral variation and the coalescent approach to modeling molecular evolution. Advisor: Dr. Dennis Hedgecock.

Bachelor of Science: Biological Sciences, California Polytechnic State University, San Luis Obispo. June 1993.

Research Experience

Current Positions:

Applied Geneticist – Senior Scientist, Cramer Fish Sciences, Gresham Oregon

- Science Director for the GENIDAQS Division of Cramer Fish Sciences, services specializing in quantitative molecular detection of species and genetic tagging enhancements to population monitoring.
- Coordinating, directing, implementing, and managing projects combining the newest tools of molecular biology and genetics theory with field observations of fish populations and their habitat.
- Informing and educating clients and staff about genetics research capabilities.
- Applying technical expertise in genetics to critique and advise on all issues requiring or related to genetics information.
- Fiscal management

Associate – College of Agriculture and Environmental Sciences, University of California, Davis

- Collaborating with UCD faculty, staff, and students on fishery genetics projects in the Central Valley of California

Previous Positions:

Genetics Laboratory Director, Washington Department of Fish and Wildlife's Molecular Genetics Laboratory, Olympia, Washington – Coordinate, direct, and supervise State of Washington fish and wildlife genetics research program; Fiscal management – grants, budgeting, contracting, billing; Professional consultation – Apply technical expertise to inform processes related to species interactions, hatchery reform, population recovery, and harvest management.

Biologist/Geneticist, Washington Department Fish and Wildlife – Designs, leads, and participates in genetic studies; directs and/or coordinates samplers, lab technicians, students, and other researchers; Analyzes and manages genetic data; Communicates results in a variety of technical and non-technical formats; Critically reviews genetics-related reports, proposals, and publications; Implements novel analytical techniques; Develops specialized genetic databases; Creates research grant proposals; Oversees contractual obligations; Advises on issues related to population monitoring and fishery science.

Postdoctoral Fellow, UC Santa Cruz / NMFS - Lead scientist on research projects regarding the population genetics and molecular ecology of California Chinook.

Technical Experience

Certified Wildlife Forensics Analyst 2010 – present

Consulting geneticist on wildlife research project development and analysis. Passed with 100% score the Wildlife Genetics Proficiency Testing Program –Test # 022311

Data Standardization

Participating scientist in international consortium tasked with standardizing genetic data acquisition for Chinook and steelhead salmon (species wide) to enhance research capabilities and facilitate innovations in population analysis. I was lead scientist on publishing data product regarding application of reference baseline within Columbia Basin steelhead.

Yakima Klickitat Fishery Project's Monitoring Implementation and Planning Team, 2008 – 2011

Participating member of the MIPT, which guides population monitoring in the Yakima Basin and advises State, Federal, and Tribal policy makers on science issues.

South Fork Nooksack Technical Advisory Workgroup, 2008 – 2011

Consulting geneticist on issues related to recovering the South Fork Nooksack spring Chinook population and captive breeding program operations.

Hatchery Action Implementation Plans (HAIPs), 2010 – 2011

Consulting geneticist during development of HAIPs. The purpose of HAIPs were to consolidate comanager priorities, legal requirements of the Puget Sound Salmon Management Plan and Endangered Species Act, and recommendations of the Hatchery Scientific Review Group.

West Coast Salmon Collaborative, 2008 – present

Participating member and co-chair of the data standards and sampling methodology committee. The goal of the West Coast Salmon Genetic Stock Identification Collaboration is to utilize evolving technologies and pilot project research to strengthen west coast salmon fisheries by rebuilding weak stocks, providing sustainable harvest, enhancing ecosystem-based science, modernizing fishery management, and to improve economic opportunities and fishing practices.

Specialized Genetic databases 2009 - present

In association with Paul Moran (NOAA), I have collaborated on the design of a regional fisheries genetic data management system. An aspect of this process was the development of a fisheries genetic database analogous to the regional coded-wire tag database (RMIS). Within the WDFW Molecular Genetics Laboratory, I designed a prototype database using the PROGENY laboratory management software. This database is currently being tested.

Integration of genetic and geospatial information 2009 – present

Through collaboration with researchers and commercial anglers, I designed and implemented a mechanism to integrate genetic information with environmental and geospatial datastreams. This protocol may enhance WDFW's ability to transition into ecosystem management objectives.

Funded Grants (Lead PI only for 2011 - 2013)

California Department of Water Resources. Real-time Genetic Identification of Salvaged Winter Run Chinook Salmon - \$60,000

California Department of Water Resources. Investigation of predation in Clifton Court Forebay using genetic analysis of predatory fish gut contents - \$900,000

California Department of Water Resources. Real-time Genetic Identification of Salvaged Winter Run Chinook Salmon, and pilot study for Parental Based Tagging salvage identification methodology - \$330,000

Pacific Salmon Commission, U.S. Chinook Technical Committee. Escapement Estimates using Genetic Mark-Recapture and Sibship Distributions: an Application to the Coweeman River Tule Fall Chinook Salmon - \$220,000.

Pacific Salmon Commission, Sentinel Stock Committee. Abundance Estimates for Green River Chinook Salmon - \$440,000

Funded Grants (Lead PI only)

Pacific Salmon Commission, U.S. Chinook Technical Committee. Escapement Estimates using Genetic Mark-Recapture and Sibship Distributions: an Application to the Coweeman River Tule Fall Chinook Salmon - \$142,000.

Saltonstall-Kennedy Grant Program. Validating Current Method For Forecasting Impacts Of Chinook Fisheries: Integrating Genetic, Geospatial And Environmental Information To Verify Timing And Occurrence Of ESA-Listed Chinook In Washington Ocean Fisheries - \$249,000.

National Oceanic and Atmospheric Administration. Yakima Basin Steelhead Genetics Project 2008 - Developing technical resources and methods for using genetic information to estimate tributary specific abundance - \$50,000

Pacific Salmon Commission. Workshop to help resolve issues concerning the CTC-GAPS baseline and fishery databases. Subsidy to offset cost of hosting the biennial Coastwide Salmonid Genetic Conference - \$10,482

National Oceanic and Atmospheric Administration. Yakima Basin Steelhead Genetics Project (2007) – Developing technical resources and methods for using genetic information to estimate tributary specific abundance - \$50,000

Academic Service/Affiliations

Society for Wildlife Forensic Sciences

American Fisheries Society (Genetic Section) Member

Bodega Marine Science Association Member (President 1998 – 2001)

Beta Beta Beta Biological Honor Society Member (Cal Poly President 1991 – 1992)

S.M.A.R.T. (Minority Outreach Program) Advisor

Publications

- D. J. Rawding, C. S. Sharpe, and S. M. Blankenship. (In Press) Genetic-based Estimates of Adult Chinook Salmon (*Oncorhynchus tshawytscha*) Spawner Abundance from Carcass Surveys and Juvenile Outmigrant Traps. Submitted to Transactions of American Fisheries Society.
- S. Blankenship G. Schumer, and B. Cavallo. 2013. Genetic Identification of Salvaged Winter Run Chinook Salmon and pilot study for Parental Based Tagging salvage identification methodology. Report to California Department of Water Resources
- P. Moran, D. J. Teel, M. A. Banks, T. D. Beacham, M. R. Bellinger, S. M. Blankenship, J. R. Candy, J. C. Garza, J. E. Hess, S. R. Narum, L. W. Seeb, W. D. Templin, C. G. Wallace, and C. T. Smith. 2013. Divergent life-history races do not represent Chinook salmon coast-wide: the importance of scale in Quaternary biogeography. *Canadian Journal of Fisheries and Aquatic Sciences* 70:415-435 DOI: 10.1139/cjfas-2012-013
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- S. Blankenship, M. Teply, and G. Schumer. 2012. Sampling and analysis to assess brook trout (*Salvelinus fontinalis*) population trends in High Lake (Oregon) using environmental DNA monitoring. Report to Burns Paiute Tribe
- M. T. Limborg, S.M. Blankenship, S.F. Young, F.M. Utter, L.W. Seeb, M.H.H. Hansen, and J.E. Seeb. 2011. Signatures of natural selection among lineages and habitats in *Oncorhynchus mykiss*. *Ecology and Evolution*. DOI: 10.1002/ece3.59/abstract

- S. M. Blankenship, M. R. Campbell, J. E. Hess, M. A. Hess, T. W. Kassler, C. C. Kozfkay, A. P. Matala, S. R. Narum, M. M. Paquin, M. P. Small, J. J. Stephenson, K. I. Warheit, and P. Moran 2011. Major lineages and metapopulations in Columbia River *Oncorhynchus mykiss* are structured by dynamic landscape features and environments. *Transactions of American Fisheries Society* 140:665–684
- S. M. Blankenship, T. W. Kassler, and K. I. Warheit. 2011. The Origin of Marked-Untagged Chinook Found on the Skagit River Spawning Grounds. Report to Pacific Salmon Commission – Southern Boundary Restoration and Enhancement Fund. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- S. M. Blankenship, C. A. Dean, and K. I. Warheit. 2011. Genetic Analysis of greater sage-grouse (*Centrocercus urophasianus*) at the Yakima Training Center post-Augmentation. Report to Department of Defense under Cooperative Management Agreement W911S8-08-G-4000. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- T. W. Kassler, S. M. Blankenship, and A. R. Murdoch. 2011. Genetic Structure of upper Columbia River Summer Chinook and Evaluation of the Effects of Supplementation Programs. Report to Habitat Conservation Plan’s Hatchery Committee. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- T. W. Kassler, S. M. Blankenship, K. I. Warheit, and C. A. Busack. 2010. Yakima River spring Chinook Pedigree. Report to Yakama Nation under Bonneville Power Authority contract. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- S. M. Blankenship, and J. A. Henning. 2010. The Differentiation of Fall and Spring Chinook Stocks at Mayfield Collection Facility, 2006 - 2009. Report for Tacoma Public Utilities, Tacoma Power. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- S. M. Blankenship, M. P. Small, and J. D. Bumgarner. 2009. Temporal stability of genetic variation within natural populations of summer steelhead (*Oncorhynchus mykiss*) receiving mitigation hatchery fish. *Transactions of the American Fisheries Society* 138: 1052
- J. A. Henning and S. M. Blankenship. 2009. The Differentiation of Fall and Spring Chinook Stocks at Mayfield Collection Facility, 2008. Report for Tacoma Public Utilities, Tacoma Power. (Available at Washington Department Fish and Wildlife, Olympia, WA).
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- S. M. Blankenship, C. A. Dean, M. P. Small. 2007. Comparison of Adult Steelhead and Resident Trout Collected at Roza Dam in 2006 to Available DNA-based Microsatellite Genetic Data. Yakima Klickitat Fishery Project report. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- S. M. Blankenship, T. W. Kassler, C.A. Dean, K. I. Warheit. 2007. Genetic baseline additions of Washington Chinook salmon populations to enhance mixed stock fishery analyses in the Southern Boundary area. Report to Pacific Salmon Commission – Southern Boundary Restoration and Enhancement Fund. (Available at Washington Department Fish and Wildlife, Olympia, WA).
- J. C. Garza , S. M. Blankenship , C. Lemaire, and G. Charrier. 2007. Genetic population structure of Chinook salmon (*Oncorhynchus tshawytscha*) in California's Central Valley. Report to CalFed.
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Research Interests: Ecological studies of freshwater ecosystems in desert regions; biological and ecological assessment and monitoring; post-secondary teaching

Professional Experiences:

2014 to present Director, Oreohelix Consulting, Moab, UT
2013- 2014 Aquatic Ecologist, Cramer Fish Sciences, West Sacramento, CA
1999-2012 Senior Research Ecologist, EcoAnalysts, Inc.
2009 Instructor. Introduction to Ecological Statistics. Northwest Environmental Training Center, Seattle WA.
2007-2009 Adjunct Assistant Professor, Department of Ecology, Montana State University, Bozeman, MT
2006-2008 Affiliate Assistant Professor, Land Resources and Environmental Sciences, Montana State University, Bozeman, MT
1997-1999 Biologist, USFWS/Puerto Rico Dept. Natural Resources, San Juan, Puerto Rico
1986-1997 Backcountry Ranger and Trail Crew Leader, Absaroka-Beartooth and Bob Marshal Wilderness, and Yellowstone and Glacier National Parks, fisheries technician Yellowstone National Park

Education

Ph.D. 2004 Montana State University; Biology (Dept. Ecology) with minor in Statistics
M. S. 1996 Montana State University; Entomology and Mountain Research Center
B. S. 1987 Montana State University; Biology, Fish and Wildlife Management Option

Awards, Achievements, and Certificates

2011 PADI Open Water Scuba Certification
1983-2004 Red Cross Advanced First Aid and CPR
1993 Montana Board of Regents Academic Scholarship
1993 Outstanding Biology Student of the Year, Flathead Valley Community College

Professional and Public Service Activities

2006-present Topic-Editor
Encyclopedia of Earth, <http://www.eoearth.org/>
2001-present Peer-review referee:
American Malacological Society Bulletin
Journal of North American Benthological Society
Western North American Naturalist

Southwest Naturalist
Biological Invasions
Northwest Science

North American Journal of Aquaculture

2001-2005 Initiated and organized 1st, 2nd, 3rd, 4th, and 5th Annual Conference on New Zealand Mudsail in Western USA, July 9-10, 2001, August 26-28, 2002, August 26-27, 2003, 2005, Bozeman, MT and June 2007, Davis, CA

Field and classroom lecturer: Aquatic Ecology, Stream Ecology, Science Teachers Institute of the Rockies, Montana State University; and local grade schools

Professional Societies, Conservation Organizations, and Committees

American Malacological Society

Freshwater Mollusk Conservation Society

American Fisheries Society

Ecological Society of America

Montana Academy of Science

Society for Freshwater Science

PADI Diving Society

Snake River Snail Conservation Plan Technical Committee

Society for Conservation Biology

Working Group for Ecological Economics and Sustainability Science

Western Regional Panel Aquatic Nuisance Species

Publications

Carling, G.T, Richards, D.C., Hoven, H., Miller, T., Fernandez, D.P., Rudd, A, Pazmino, E., and W. P. Johnson. 2013. Relationships of surface water, pore water, and sediment chemistry in wetlands adjacent to Great Salt Lake, Utah and potential impacts on plant community health. *Science of the Total Environment*.

Richards, D. C., T. Arrington, S. Sing, and B. L. Kerans. In revision. Competition and coexistence between an invasive aquatic snail and its threatened native congener. *American Malacological Society Bulletin*.

Richards, D. C. and T, Arrington. In review. Spatial and environmental relationships of three snail taxa in a freshwater spring: with estimates of their abundance. *Journal North American Benthological Society*.

Richards, D. C., C. M. Falter, G. T. Lester, and R. Myers. In revision. Mollusk survey of Hells Canyon reservoirs and free flowing Snake River, Idaho and Oregon, USA: with focus on rare and listed taxa, including a newly described *Taylorconcha* sp. *American Malacological Society Bulletin*.

Richards, D. C., P. O'Connell, and D. C. Shinn. In preparation. Growth Rates of the threatened Bliss Rapids Snail, *Taylorconcha serpenticola* and the invasive New Zealand mudsnail *Potamopyrgus antipodarum* at six temperatures.

Richards, D. C. 2010. Mollusk diversity and estimated predation rates by gastropod shell borehole drillers on *Turritella* spp. at Playa Grande, Las Baulas National Park, Costa Rica. *American Malacological Society Newsletter*. Vol. 41. No. 2. Pg 5-7.

- Richards, D. C. and T. Arrington. 2008. Evaluation of Threatened Bliss Rapids Snail, *Taylorconcha serpenticola* susceptibility to exposure: potential impact of 'load following' from hydroelectric facilities. *American Malacological Society Bulletin*.
- Richards, D. C. In review. Some life history studies of the threatened Bliss Rapids snail and invasive New Zealand mudsnail. *Western North American Naturalist*.
- Richards, D. C. 2004. Competition between the threatened Bliss Rapids Snail, *Taylorconcha serpenticola* and the invader New Zealand Mud Snail, *Potamopyrgus antipodarum*. Ph D. Dissertation. Montana State University, Bozeman, Montana. 175 pp.
- Richards, D. C. and D. C. Shinn. 2004. Intraspecific competition and development of size structure in the invasive snail, *Potamopyrgus antipodarum*. *American Malacological Society Bulletin*. 19. 1.2.
- Richards, D. C., P. O'Connell, and D. C. Shinn. 2004. Simple control method for the New Zealand mudsnail, *Potamopyrgus antipodarum*. *Journal North American Fisheries Management*. 24:114-117.
- Richards, D. C., L. D. Cazier, and G. T. Lester. 2001. Spatial distribution of three snail species, including the invader *Potamopyrgus antipodarum*, in a freshwater spring. *Western North American Naturalist*. 61: 375-380.
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- Richards, D. C. 1996. The use of aquatic macroinvertebrates as water quality indicators in mountain streams of Montana. Masters thesis. Montana State University. Bozeman, MT. 199 pp.
- Sriharan, S., A. Wright, P. Singh, F. V. Dunkel, D. C. Richards, W. Bertsch, and C. Wells. 1994. Insecticidal activity of floral and root extracts of *Tagetes minuta* and *Tagetes patula* (marigold against the Mexican bean weevil, (*Zabrotes subfasciatus*), a non-target fish (*Gambusia affinis*), and the predatory warehouse pirate bug (*Xylocoris flavipes*). in D. L. Weigmann, ed. *New directions in pesticide research, development, management, and policy*. Proc. Fourth National Conference on Pesticides. Blacksburg, Virginia, November 1-3, 1993. pp. 542-556.
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Technical Reports

- Richards, D. C. 2013. Arizona Intermittent Streams Macroinvertebrate Index of Biological Integrity. Developed for the *Arizona/New Mexico Mountain Ecoregion*. Final Report. Biocriteria Program Monitoring Unit, Water Quality Division, Arizona Department of Environmental Quality, Phoenix AZ. 59 pp.
- Richards, D. C. 2013. Development of Idaho Macroinvertebrate Temperature Occurrence Models. Report to Dept. Water Quality, ID Department of Environmental Quality, Boise, ID. 32 pp.

- Richards, D. C. 2012. Development of an Arizona Intermittent Streams Macroinvertebrate IBI. Final Draft Report to Arizona Department of Water Quality. 95pp.
- Richards, D. C., J. Rensel, and Z. Siegrist. 2011. Rufus Woods Lake – Columbia River reservoir morphometrics, initial food web, and rainbow trout fishery studies. Report to Colville Confederated Tribes. Nespelem, WA. 138pp.
- Miller, T. G., D. C. Richards, Hoven, H. M., Johnson, W. P., Hogset, M., and G. T. Carling. 2011. Macroinvertebrate communities in Great Salt Lake impounded wetlands and their relationship to water and sediment quality and plant communities. Preliminary report to: Jordan River / Farmington Bay Water Quality Council, Salt Lake City, UT. 67pp.
- Hoven, H. M., D. Richards, W. P. Johnson, and G.T. Carling. 2011. Plant metric refinement for condition assessment of Great Salt Lake impounded wetlands. Preliminary report to: Jordan River / Farmington Bay Water Quality Council, Salt Lake City, UT. 44pp.
- Johnson, W. P., G. T. Carling, and D. Richards. 2011. Chemistry of surface water, pore water, and sediment in seven impounded wetlands bordering Great Salt Lake. Preliminary report to: Jordan River / Farmington Bay Water Quality Council, Salt Lake City, UT. 31pp.
- Richards, D. C., 2011. Colville streams fertilization study: Final report to: Colville Confederated Tribes, Fish and Wildlife Department, Nespelem, WA. 44pp.
- Richards, D. C. 2010. Possible effects of selective withdrawal-temperature control at Hungry Horse Dam, nuisance growth of *Didymosphenia geminata*, and other factors, on benthic macroinvertebrate assemblages in the Flathead River. Final report to: Montana Fish, Wildlife & Parks, Kalispell, MT. 142pp.
- Richards, D. C. 2010. Characterization of temperature, dissolved oxygen, and macroinvertebrate communities of targeted intermittent streams. Report to Idaho Department of Environmental Quality, Boise, Idaho. 189 pp.
- Richards, D. C., W. VanWinkle, and T. Arrington. 2009. Metapopulation viability analysis of the threatened Bliss Rapids Snail, *Taylorconcha serpenticola* in the Snake River, Idaho: effects of load following. EcoAnalysts Center for Aquatic Studies. Bozeman, MT. 162 pp.
- Stephenson, M., D. Bates, D. C. Richards, and T. Arrington. 2009. Risk Assessment of Hydroelectric Operations on the Bliss Rapids Snail in the Middle Snake River, Idaho with a Focus on Load Following. 63pp.
- Richards, D. C. and T. Arrington. 2009. Bliss Rapids Snail abundance estimates in springs and tributaries of the Middle Snake River, Idaho. EcoAnalysts Center for Aquatic Studies. Bozeman, MT. 195pp.
- Richards, D. C., W. Van Winkle, and T. Arrington. 2009. Estimates of Bliss Rapids Snail, *Taylorconcha serpenticola*, abundances in the Lower Salmon Falls Reach and Bliss Reach of the Snake River, Idaho. EcoAnalysts Center for Aquatic Studies. Bozeman, MT. 24pp.
- Richards, D. C., W. Van Winkle, and T. Arrington. 2009. Spatial and temporal patterns of Bliss Rapids Snail, *Taylorconcha serpenticola*, in the Middle Snake River, Idaho in Relation to Population Viability Analysis. EcoAnalysts Center for Aquatic Studies. Bozeman, MT. 47 pp.
- Richards, D. C., C. M. Falter, and K. Steinhorst. 2006. Status review of the Bliss Rapids snail, *Taylorconcha serpenticola* in the Mid-Snake River, Idaho. 170pp.

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- Richards, D. C., C. M. Falter, G. T. Lester, and R. Myers. 2005. Listed Mollusks. Responses to FERC Additional Information Request AR-2. Hells Canyon Project. FERC No. P-1971-079. 180 pp.
- Richards, D. C. 2004. Population dynamics of *Taylorconcha serpenticola* and *Potamopyrgus antipodarum* at Banbury Springs outlet: 1999 to 2004 using time series analysis. EcoAnalysts Inc. Moscow, Idaho. 16pp.
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- Richards, D. C., Gustafson, D.L., Kerans, B.L., and C. Cada. 2002. New Zealand mudsnail in the Western USA. Web site. www2.montana.edu/nzms
- Richards, D. C. and G. T. Lester. 2002. Survey for the endangered *Pyrgulopsis idahoensis* at the Cove Recreation Site, CJ Strike Reservoir. Prepared for North Wind, Inc. Idaho Falls, Idaho. EcoAnalysts Inc., Moscow, Idaho. 12pp.
- Richards, D. C. 2002. The New Zealand Mudsnail invades the Western United States. *Aquatic Nuisance Species Digest*. Vol. 4. (4): 42-44.
- Richards, D. C. and L. D. Cazier Shinn. 2001. Intraspecific and interspecific competition between *Taylorconcha serpenticola* and *Potamopyrgus antipodarum* under laboratory conditions. EcoAnalysts Inc. Report. 14pp.
- Richards, D. C., P. O'Connell, and L. D. Cazier Shinn. 2001. Growth rates of the Bliss Rapids Snail, *Taylorconcha serpenticola* and the New Zealand mudsnail, *Potamopyrgus antipodarum* at six temperatures. EcoAnalysts Inc. Report. 10pp.
- Richards, D. C. and L.D.Cazier Shinn. 2001. Distribution and abundance of the Bliss Rapids Snail, *Taylorconcha serpenticola* in Banbury Springs in relation to two hydrobiid snail species and eight environmental gradients. EcoAnalysts Inc. Report. 23pp.
- Richards, D. C. and L.D. Cazier Shinn. 2001. *Taylorconcha serpenticola* densities at Banbury Springs 1999-2001. EcoAnalysts Inc. Report. 16pp.
- Richards, D. C. and L.D.Cazier Shinn. 2001. Densities of *Taylorconcha serpenticola* and *Potamopyrgus antipodarum* in cobble habitat at the outlet of Banbury Springs 1999-2001. EcoAnalysts Inc. Report. 11pp.
- Richards, D. C., L. D. Cazier, and G. T. Lester. 2001. Spatial distribution of three snail species, including the invader *Potamopyrgus antipodarum*, in Banbury Springs, Snake River Drainage, Southern Idaho, USA. EcoAnalysts Inc. Report. 19 pp.
- Richards, D. C. and D. L. Gustafson. 2001. Compilation workbook for Mollusk Identification Workshop: New Zealand mudsnail in Western USA . First Annual Conference. July 9 and 10, 2001. Montana State University, Bozeman, MT.
- Richards, D. C. and G. T. Lester. 2000. Intraspecific competition of *Potamopyrgus antipodarum* (Gray) at different densities for a limiting resource under laboratory conditions. EcoAnalysts Inc. Report. 22 pp.
- Richards, D. C. and G. T. Lester. 2000. Growth rates of the New Zealand Mud Snail, *Potamopyrgus antipodarum* (Gray) at five temperatures. EcoAnalysts Inc. Report. 19 pp.
- Richards, D. C. and G. T. Lester. 2000. Competition between two freshwater snail species: the invasive New Zealand Mud Snail, *Potamopyrgus antipodarum* and the native, threatened

- Bliss Rapids Snail, *Taylorconcha serpenticola* in an enclosure study, 1999 and 2000. EcoAnalysts Inc. Report. 25 pp.
- Richards, D. C. and G. T. Lester. 2000. Comparison of the number of *Potamopyrgus antipodarum* neonates produced seasonally, between habitats, and in two freshwater springs, Idaho and Montana: a preliminary investigation. EcoAnalysts Inc. Report. 18 pp.
- Richards, D. C. and G. T. Lester. 1999. Seasonal changes in densities of three snail species at Banbury Springs, 1999. EcoAnalysts Inc. Moscow, Idaho. 9 pp.
- Richards, D. C. and G. T. Lester. 1999. Exploratory population analysis of the Banbury Limpet (*Lanx* sp. undescribed) colony in Banbury Springs, Snake River drainage, southern Idaho. EcoAnalysts Inc. Moscow, Idaho. 7 pp.
- Richards, D. C. and G. T. Lester. 1999. Evidence for competition between two freshwater snail species, the exotic, biological invader *Potamopyrgus antipodarum* and the native, threatened *Taylorconcha serpenticola* in an enclosure study. EcoAnalysts Inc. Moscow, Idaho. 30 pp.
- Richards, D. C. and G. T. Lester. 1999. Abiotic and biotic factors influencing the distribution and abundance of three species of freshwater snails in Banbury Springs. EcoAnalysts Inc. 17 pp.
- Richards, D. C. 1998. Assessment of the 1997 release of captive-reared *Hispaniola amazons* (*Amazona ventralis*) in the Dominican Republic as related to their training at the parent facility training cage (PFTC), Rio Abajo Aviary, Puerto Rico. Report to Puerto Rico Department of Natural Resources and Environment. San Juan. 14 pp.
- Richards, D. C. 1996. Relationship of the number of taxa and the number of organisms in macroinvertebrate samples from mountain streams of Montana. Report to State of Montana, Water Quality Division Department of Environmental Quality. Helena, MT. 5pp.
- Richards, D. C. 1996. Effects of an unbiased 300 organism subsample on macroinvertebrate samples from mountain streams of Montana. Report to State of Montana, Water Quality Division Department of Environmental Quality. Helena, MT 12pp.
- Shannon, J. P., E. P. Benenati, H. Kloeppel, and D. C. Richards. 2003. Monitoring the aquatic food base in the Colorado River, Arizona during June and October 2002. Annual Report. Grand Canyon Monitoring and Research Center. USGS. Cooperative Agreement-02WRAG0028.
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- Marcus, W. A., J. A. Stoughton, S. C. Ladd, and D. C. Richards. 1995. Trace metal concentrations in sediments and their ecological impacts in Soda Butte Creek, Montana and Wyoming. In: Meyer G (ed), 1995 Field conference guidebook, friends of the Pleistocene-Rocky Mountain cell: Late Pleistocene-Holocene evolution of the northeastern Yellowstone landscape, Middlebury College, Vermont, 9 pp.

Invited Presentations

- Richards, D. C. and P. Spindler. 2013. Development of Arizona Intermittent Streams Macroinvertebrate Index of Biological Integrity. California Aquatic Bioassessment Workgroup Annual Meeting. Davis, CA.
- Author and co-author of three talks on Salt Lake wetlands. 2013. Society for Wetland Scientists Annual Conference, Duluth, MN. May 2013. Need citations.
- Richards, D. C., J. Rensel, and Z. Siegrist. 2012. Food web and fisheries studies: Rufus Woods Lake, Columbia River, WA. Large river ecology section moderator; Society for Freshwater Science Annual Meeting. Louisville, KY.
- Richards, D. C. and T. Arrington. 2012. Predicting and monitoring the effects of a habitat restoration project on metapopulation viability of two federally listed species in a tributary of the Columbia River. Columbia River Estuary Conference. Astoria, OR. May 15-17.
- Farley, J. and D. C. Richards. 2008. A critique of economic valuation of ecosystem services and its applicability to sustainable economic policy. Symposium on Economic Growth and Biodiversity: The Elemental Arguments. Society for Conservation Biology Annual Meeting. Chatanooga, TN. July 13-17.
- Richards, D. C. and T. Arrington. 2007. Morgan Lake restoration project: Does *Lanx* sp. have a problem with that? Mid-Snake River Technical Work Group: Quarterly Meeting. September 19. Boise, ID.
- Richards, D. C. and T. Arrington. 2007. Evolutionary consequences of a rapidly evolving invasive species to the viability of a native threatened species. Presented Poster. International Summit: Evolutionary Consequences of a Changing Environment. University of California. Los Angeles, CA. February, 2007.
- T. Arrington and D. C. Richards. 2007. Predicting the effects of a habitat restoration project on the population viability of one threatened and one endangered lotic gastropod. Mid-Snake River Technical Work Group: Quarterly Meeting. September 19. Boise, ID.
- T. Arrington and D. C. Richards. 2007. Predicting the effects of a habitat restoration project on the population viability of one threatened and one endangered lotic gastropod. World Malacological Congress Annual Meeting. Antwerp, Netherlands. July.
- Richards, D. C. and T. Arrington. 2006. Empirical estimates of extinction and colonization rates of the threatened Bliss Rapids Snail for use in metapopulation viability analyses. Presented Paper. Snake River Snail Technical Committee Quarterly Meeting. December 12.
- Richards, D. C., C. Smith, and B. Marshall. 2006. Effects of New Zealand mudsnail on water quality bioassessment metrics. Presented paper. California Water Quality Bioassessment Annual Meeting. Davis California. November 28-29th.
- Richards, D. C., C. M. Falter, G. T. Lester, and R. Myers. 2005. Mollusk survey and basic ecological studies in Hells Canyon, Snake River, USA. Presented paper. 38th Annual Western Society of Malacologists Conference. Asilomar, Pacific Grove, CA. June 26th-30th.
- Richards, D. C., B. L. Kerans, G. T. Lester, and D. C. Shinn. 2004. Competition between a threatened and invasive snail in a freshwater spring. Presented paper. North American Benthological Society Annual Meeting. Vancouver, BC.
- Richards, D. C. 2004. The invasive New Zealand mudsnail: case study. Invited speaker. Western Division American Fisheries Society Annual Meeting. Salt Lake City, Utah. March 1-4.

- Richards, D. C. 2004. Conducted New Zealand mudsnail identification workshop. Western Division American Fisheries Society Annual Meeting. Salt Lake City, Utah. March 1-4.
- Richards, D. C. and D. C. Shinn. 2003. Spatial distribution of Bliss Rapids Snail and New Zealand mudsnail in a freshwater spring, Idaho, USA. Presented paper. North American Benthological Society Annual Meeting. Athens GA.
- Richards, D. C. and D. C. Shinn. 2003. Intra and interspecific competition between Bliss Rapids Snail and New Zealand mudsnail. Presented paper. Society for Conservation Biology Annual Meeting. Duluth, MN.
- Richards, D. C. 2002. The New Zealand Mudsnail in the Western USA. 2002. Presented paper. American Malacological Society Annual Conference. Charleston, SC. August 2002.
- Richards, D. C. 2002. The New Zealand Mudsnail in the Western USA. Presented paper. Orvis Fishing Guides National Rendezvous, Cody, Wyoming. April 12.
- Richards, D. C. 2002. New Zealand mudsnail in the western USA.. Invited paper. Western Regional Panel on Aquatic Nuisance Species Annual Meeting. Las Vegas, Nevada. January 9-10.
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