FINAL

SUMMARY REPORT

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

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Prepared for:

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RECLAMATION
Managing Water in the West

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Executive Summary

The Middle Rio Grande Endangered Species Collaborative Program (Program) is comprised of multiple stakeholders (federal, state and local entities) representing diverse interests on the Middle Rio Grande. The Program works to support the recovery of listed species in the Middle Rio Grande and to protect existing and future water uses while complying with applicable state and federal laws, existing water rights, and the Rio Grande Compact. The Program Area is defined as the headwaters of the Rio Chama watershed and the Rio Grande from the New Mexico-Colorado state line downstream to elevation 4,450 feet mean sea level, the elevation of the spillway crest of the Elephant Butte Dam. One of the species managed by the Program is the Rio Grande silvery minnow (RGSM; *Hybognathus amarus*). RGSM has been confined to a small fraction of its historic range and may have experienced severe genetic bottlenecks over time. An ongoing Genetics Project provides a genetic sampling and assessment program, which refers to the estimation of population genetic parameters, such as gene diversity, heterozygosity, allelic richness, and genetic effective size of RGSM.

The purpose of this peer review was to review the RGSM Genetics Project and related management activities, including the annual reports from the Genetics Project, the genetics management and propagation plan, and the work products and management approaches that are informed by or inform the Genetics Project, such as the augmentation reports and population monitoring reports. The peer reviewers also interviewed the Science Workgroup, Captive Propagation and Genetics Workgroup, and the Principal Investigators of the Genetic Project on 4 February 2016 and toured one of the hatchery facilities on 5 February 2016.

The peer reviewers responded to sixteen Focus Area Questions, summarized their conclusions, and generated sixteen recommendations. The recommendations included specific guidance relating to hatchery and broodstock protocols, various genetic studies and monitoring, and some additional research that would provide additional information on the genetics of RGSM, contribute to the maintenance of genetic diversity of RGSM, and assist with maintenance and potential recovery of the species. Recommendations for changes to hatchery and broodstock protocols included monitoring genetic status of year classes, using one female-one male breeding pairs (or assessing genetic contributions in offspring of 10 x 10 pairings), keeping more detailed and shared hatchery records, and using younger fish for spawning. The recommendations related to genetic studies and monitoring included developing a single nucleotide polymorphic (SNP) panel, determining broodstock relatedness, assessing offspring lots before release, monitoring changes in genetic status within year classes held in hatcheries, using next-generation sequencing to assess the changes in the whole genome of RGSM. Other recommendations included evaluating quantitative traits over year classes in the hatcheries to assess for changes and measuring the contributions and survival of different lots and hatcheries in fish released back into the Middle Rio Grande.

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

1.0 Background

The Middle Rio Grande Endangered Species Collaborative Program (Program) is comprised of multiple stakeholders (federal, state and local entities) representing diverse interests on the Middle Rio Grande. The primary federal agencies are the Bureau of Reclamation (Reclamation), US Army Corps of Engineers (USACE), and the US Fish and Wildlife Service (USFWS). An Executive Committee governs the Program in accordance with the Program By-Laws. The Program works to support the recovery of listed species in the Middle Rio Grande and to protect existing and future water uses while complying with applicable state and federal laws, existing water rights, and the Rio Grande Compact. The Program Area is defined as the headwaters of the Rio Chama watershed and the Rio Grande, including tributaries, from the New Mexico-Colorado state line downstream to elevation 4,450 feet mean sea level, the elevation of the spillway crest of the Elephant Butte Dam. Additional information about the Program may be accessed at http://mrgescp.dbstephens.com/#Home.

One of the species managed by the Program is the Rio Grande silvery minnow (RGSM; *Hybognathus amarus*). RGSM has been confined to a small fraction of its historic range and has likely experienced severe population bottlenecks over time. An ongoing Genetics Project provides a genetic sampling and assessment program, which refers to the estimation of population genetic parameters, such as gene diversity, heterozygosity, allelic richness, and genetic effective size of RGSM (e.g., Osborne et al. 2012). Understanding of trends in genetic diversity parameters such as genetic variation and effective population size and minimizing risks (e.g., loss of genetic variation, population fragmentation and reduced population size) to the existing RGSM population are a key component of the RGSM Recovery Plan (USFWS 2010).

Genetic samples were collected beginning in 1999, prior to augmentation. Genetic monitoring has focused on nine microsatellite loci and the mitochondrial ND4 region, and includes both wild-caught individuals and hatchery-reared individuals. Augmentation of the species began in 2002, with the goal of capturing eggs from the Middle Rio Grande and rearing them in hatcheries to a larger size and then releasing back into the river to ensure a baseline population every year regardless of water levels that year (e.g., Archdeacon 2015). To supplement these fish, other individuals are held in the hatcheries to propagate additional offspring, which also returned to the river. The Program has funded the Genetics Project since 2004 (except for 2013); prior to 2004 funding was provided through a variety of sources. Population monitoring along the Middle Rio Grande is also occurring to monitor the existing population of RGSM in nature (e.g., Dudley et al. 2015).

The Science Workgroup of the Program was formed to oversee scientific studies and related investigative projects, including the RGSM Genetics Project. While the RGSM Genetics Project is not a specific requirement of the *Biological Opinion on the Bureau of Reclamation's*

(Reclamation) Water and River Maintenance Operations, Army Corps of Engineers' Flood Control Operations, and Non-Federal Actions (USFWS 2003), it is an essential component in tracking the genetic status of RGSM and assessing the effectiveness of the Program's population augmentation program in the Middle Rio Grande, and the USFWS's RGSM Genetics Management and Propagation Plan (City of Albuquerque et al. 2013) and RGSM Recovery Plan (USFWS 2010). Annual reports, along with additional publications, authored by the Principal Investigators (PIs) of the Genetics Project summarize the goals, methods, results, and conclusions over the duration of the project. In addition to the Science Workgroup of the Program, the USFWS has established a Captive Propagation and Genetics Workgroup for RGSM, which includes some of the same members of the Science Workgroup, but is independent from the Program. Both workgroups provide some oversight and review of the RGSM Genetics Project.

There are also other components of recovery that are designed to aid in maintenance and ensure against the loss of valuable alleles in wild and captive RGSM (see Glossary for definition of ‘wild’ and ‘captive’). Some of the most discussed components include understanding the RGSM life history, effects of population fragmentation, augmentation with captive reared or captive bred individuals, and fluctuating environmental conditions.

The purpose of this peer review is to review the RGSM Genetics Project and related management activities, including the annual reports from the Genetics Project (Turner et al. 2003; Turner & Osborne 2004, 2005, 2006, 2007; Osborne & Turner 2008, 2009, 2010, 2011, 2012; Carson et al. 2014; Osborne et al. 2015), the genetics management and propagation plan (City of Albuquerque et al. 2013), and the work products and management approaches that are informed by or inform the Genetics Project, such as the augmentation reports and population monitoring reports. The peer reviewers also interviewed the Science Workgroup, Captive Propagation and Genetics Workgroup, and the PIs of the Genetic Project on 4 February 2016. The peer reviewers then produced this report synthesizing findings (conclusions, recommendations, and responses to the Focus Area Questions) and providing recommendations. The full list of materials provided is presented in Appendix A.

The peer reviewers reviewed the materials provided as listed in Appendix A. The reviewers also interviewed the Science Workgroup, Captive Propagation Workgroup and the PIs of the Genetics Project during a meeting held 4-5 February 2016 in Albuquerque, New Mexico. The draft report was discussed with the Workgroups and the PIs during a meeting held 12 May 2016 in Albuquerque, New Mexico. The meeting agendas and attendee lists for both meetings is provided in Appendix B.

2.0 Peer Reviewers

The selection of peer reviewers followed the guidance provided in the Office of Management and Budget's *Final Information Quality Bulletin on Peer Review* (OMB Bulletin; December 16, 2004) to ensure scientific integrity of the peer review. Appropriate expertise and an appropriate balance of that expertise was identified for this peer review panel during the process of identifying potential reviewers. Panelists with expertise in fish genetics and fish conservation were essential for this peer review. All peer reviewers were provided the language from the OMB Bulletin (2004) with regard to independence and conflicts of interest and any potential issues were identified and evaluated during the selection of the panelists, both with respect to both Reclamation and the program under peer review. The five peer reviewers all have experience with freshwater fish genetics and conservation and with peer reviews of scientific publications. The reviewers are all independent of Reclamation and have no conflicts of interest. The resumes for the peer reviewers are presented in Appendix C. The peer reviewers are:

- Dylan Fraser, PhD, Concordia University (Canada);
- Andrew Martin, PhD, University of Colorado at Boulder;
- Bernard May, PhD, University of California at Davis;
- Craig Stockwell, PhD, North Dakota State University; and
- Amy Welsh, PhD, West Virginia University.

3.0 Responses to Focus Area Questions

The peer reviewers considered and responded to the Focus Area Questions provided by the Science Workgroup and Reclamation, based on the documents provided (listed in Appendix A) and the interviews during the meeting (agenda provided in Appendix B).

Question 1

Do the techniques, methods, and data used and the results provided support the conclusions and interpretations that are provided in the annual reports issued and peer reviewed articles authored by the PIs for the Genetics Project?

The panel commends the PIs of the Genetics Project on the breadth and scope of their RGSM monitoring research. Now in the 17th year, the annual time series of genetic data on RGSM surely represents one of the most comprehensive genetic monitoring programs conducted to date on an imperiled freshwater fish. In general, the data are well-analyzed and well-interpreted in relation to the results. A central conclusion of the collective annual genetic reports is that there has been no change in genetic diversity between pre- and post-augmentation time periods (based on allelic richness [N_a or N_{ac}] or observed heterozygosity [H_o]). Interpretation of effective population size (N_e) estimates and possible changes to N_e over time is less clear owing to a number of factors discussed in detail below. Occasionally, conclusions are somewhat overstated (specifically, emphasizing annual changes in genetic diversity when allelic richness changes are not significant

and point estimates of N_e have large, overlapping confidence intervals).

The panel offers the following suggestions for improvements to future genetic reports:

HIGH PRIORITY

1) Sometimes it is not clear how N_e estimators relate to purpose. The reports could improve the explanations for why certain approaches were adopted.

2) Develop a biological relevant and realistic benchmark for critically low levels of genetic diversity. One possible way to set a benchmark would be to estimate the 95% confidence interval (CI) for genetic diversity (expected heterozygosity [H_e] and number of alleles [N_a]) using all samples across time and space. If the diversity falls below the CI, then more aggressive management actions may be warranted.

MEDIUM PRIORITY

3) There needs to be a clear statement of the hypothesis and predictions being tested. For example, a simple hypothesis is whether there is a difference in estimates of genetic diversity between the pre- and post-augmentation periods. If this is the case, one approach would be to use a linear model to compare the estimates pre- and post- augmentation. Although time should be included as a co-variate, there is no effect of augmentation on observed heterozygosity corrected for sample size (H_{oc}) ($t = 1.95$, $p = 0.071$).

4) The authors need to redefine pre-augmentation (1987, 1999) and augmentation periods (post 1999) given the augmentation that took place in 2000 and 2001. They may not be able to conclude strongly whether genetic diversity of the natural spawning population has changed. However, the authors can say that augmentation has maintained genetic diversity throughout the augmentation period, with the provision that this conclusion is based on the nine microsatellite loci evaluated, which might not reflect genome-wide variation.

5) Microsatellite loci may no longer be the most effective markers for the purpose as the cost of newer, genotyping-by-sequencing (GBS) approaches has become more affordable for largescale throughput of many individuals. The limitations of microsatellites relative to other genetic markers such as single nucleotide polymorphisms (SNPs), and trade-offs associated with different genetic markers in relation to RGSM genetic monitoring goals, are discussed in detail under Questions 2, 8, 9, 10, and 13 (particularly 13).

LOW PRIORITY

6) The Genetic Project PIs may also wish to examine genetic diversity / N_e variation over time using a piecewise regression as these can be used to find any breakpoints in the data; also referred to as segmented regression. If a breakpoint is identified say for pre- versus post-augmentation, then separate regressions can be run for each section. This approach can also identify points in time where there are temporal changes in genetic diversity.

Question 2

Do the techniques, methods, and data used and the results provided support the conclusions and interpretations that are provided in the Genetics Management and Propagation Plan and updates to that Plan, authored by the RGSM Captive Propagation and Genetics Workgroup?

The loss of genetic diversity as defined in the Genetics Management and Propagation Plan is the loss of alleles that are present at a higher than 10% frequency in the population. The panel feels this criterion is arbitrary. See Question 11 for an alternative approach.

The plan also suggests spawning multiple year classes to offset temporal variation. We agree that this approach is likely better at conserving genetic diversity than the current strategy of primarily spawning 4-year old fish at the Dexter facility (and 3-year old fish at the BioPark facility). Unintentional selection may be occurring when 4-year old fish are used as the primary spawners. There may have been selection for fish that are better adapted to surviving in captivity. With high mortality throughout life in captivity, the broodstock is comprised of the remaining survivors, so there could be inadvertent selection for fish that live longer in captivity. Fish collected in a single year represent the reproductive effort of fish that had the highest reproductive success in that particular year, which could result in artificial selection for traits that were best suited to the environmental conditions in that particular year. Crossing fish from multiple years would likely reduce the effects of some of these risks. In addition, relatedness among parents would likely be reduced by using fish from different cohorts. Also, the variance in fecundity is likely to be lower among the smaller/younger fish than among older fish, so using smaller/younger fish as broodstock should reduce the negative impacts on N_e. A simple solution would be to pull broodstock from the younger cohorts and increase the number of individuals used to compensate for the lower age-related fecundity, or using a one female to one male mating strategy.

The plan also states that monitoring should continue using the nine microsatellite loci and mitochondrial DNA (mtDNA) ND4. However, as new technologies become more accessible for non-model organisms, the plan should allow for the flexibility to use different genetic markers instead of only microsatellites and mtDNA. The microsatellites are selectively neutral and likely do not capture genome-wide genetic diversity; new technologies provide the opportunity to explore adaptive loci that may be under selection, providing a better assessment of genetic diversity and the evolutionary potential of the species (discussed at length under Question 13). These methods have only recently become accessible to fisheries geneticists. Previously, techniques were not available for cost-effective, high-throughput genetic screening and the PIs were using accepted techniques for genetic monitoring.

Question 3

Are the RGSM genetic parameters appropriate in relation to the life history of RGSM (as is supported by relevant, peer-reviewed reports or other references in the Genetics Project work products)?

1) The key genetic parameter relevant to life history is N_e. This is an appropriate statistic because it attempts to quantify the number of breeders that contribute to the population each generation. This number, more than any other, determines the amount of variation that is transmitted from one generation to the next.

2) The genetic parameters of number of alleles, corrected for sample size (N_{ac}) and H_e are also relevant and are used to estimate N_e. In terms of thresholds, there appears to be less spatial/temporal variance in N_{ac} and H_e compared to N_e, so critical thresholds should be set using these parameters (see Question 11).

3) Fragmentation of the river by the dams is a concern, and given the short lifespan of RGSM, this could have an effect on population structure. F_{ST} values (a measure of genetic differentiation between populations) between river reaches are low, but sometimes significant. Additionally, many of the loci are out of Hardy-Weinberg equilibrium (HWE), which may indicate the inadvertent sampling of multiple genetically distinct populations. If this is the case, additional genetic analyses on the existing data may help to shed light on the biology of RGSM in different river sections (e.g., Are certain families distributed non-randomly in different river sections? Are particular river sections more likely to harbor substructure and hence be particularly prone to river dam fragmentation), but also to refute/confirm that augmentation has homogenized the species and that, in fact it should be treated as a single population. Analyses such as spatial genetic Principal Components Analysis (PCA) (http://adegenet.r-forge.r-project.org/files/tutorial-spca.pdf) could be used to explore population structure; traditional clustering programs such as STRUCTURE can be sensitive to family structure, which may be present in the sample collections. Family reconstruction using analyses like COLONY could also be conducted to determine the number of families represented in sample collections. Simulations or analysis using known families from the hatchery should first be conducted to determine whether the existing microsatellite loci have sufficient power to accurately delineate families. Other analyses for detecting population structure that are less sensitive to family structure could also be used, such as the software FLOCK (Duchesne & Turgeon 2012). If there is evidence of structure, it will be useful to evaluate if the structure is correlated with the variance in “wild productivity” among segments. This will be most apparent when looking to see if the genetic structure varies temporally, so that structure increases following years where there was high among-segment variance in wild-productivity.

4) There are a large number of loci out of HWE and this has been explained by the presumed presence of null alleles. We wonder if some non-random element may be playing a role. Null alleles could be important in some circumstances, as a higher frequency of null alleles will depress H_o. Thus, a decrease in heterozygosity in the future could actually represent an

increase in the frequency of null alleles. The design of species-specific genetic markers (either additional microsatellite loci or single nucleotide polymorphisms [SNPs]) may eliminate the problem of null alleles.

5) Do different reaches have more natural spawning, rearing, retention, and recruitment than other reaches? If so, this could affect the relative abundance of naturally spawned vs. augmented fish, and thus reduce N_e for reaches where naturally spawned fish are relatively low in abundance relative to hatchery spawned fish (Ryman-Laikre effect). This may in turn influence genetic divergence among river segments as measured by F_{ST}.

6) Did the 'wild' fish % vary among reaches within years? See number 5.

7) N_e from broodstock was comparable to the genetic N_e if looking at just allele frequencies. This suggests it is an appropriate genetic parameter.

8) There was insufficient description of when and from what they collected data for the genetics studies. Did they measure from mixed collection of lots or from individual lots? Did it vary by hatchery? Such information is important to have to determine if the genetic monitoring is best positioned and is sufficiently standardized across hatcheries to detect changes in genetic diversity or N_e over time.

Question 4

Was the experimental design and sampling methodology appropriate and did the methods have sufficient power to detect the trends and findings that were reported?

1) The appropriateness of the experimental design depends on the particular parameter being estimated. If the goal is to monitor the effective population size, it would be worthwhile for the PIs/Genetics Workgroup (and others) to carefully assess how their sampling strategy influences effective population size. While they have relatively large sample sizes, there is a strong effect of sample size on the estimate of effective population size ($t = 3.360$, $p < 0.01$) and this is not expected. A similar result was obtained for the estimate of N_eD—after omitting infinity values—($t = 2.63$, $p = 0.03$). It is not clear why there is an association between sample size and estimated effective population size, but this should cause some concern and perhaps the Genetics group should sort this out.

2) The PIs need to make it clear why they are calculating multiple estimates of N_e, why the estimates are expected to differ, and the biological meaning of differences in the estimates of N_e using different methods.

3) Because one of the goals of the genetic monitoring is establish whether there is "drift" in the gene pool due to sampling effects and population bottlenecks, the PIs should test whether the composition of the gene pool shifts from generation to generation. Ideally, if it is a large panmictic population—as suggested by the data—it should be statistically impossible to distinguish year classes based on analyses of allele frequencies. However, the consistent

lack of HWE at many loci suggests that allele/genotype frequencies may not be consistent across generations. Waples (2015) provides a good review about possible causes of HWE deviations and their evaluation.

4) One important issue is that when the genetic composition of two subsequent year classes are expected to differ because of augmentation effects, temporal estimates of the variance in effective population size will be biased low; thus, it is important for the geneticists to clearly explain what bias, if any, exists when estimating relevant parameters.

Question 5

Does the study design, and methods of genetic monitoring and assessment achieve the goals and objectives of the Genetics Project?

We have evaluated the study design and methods of genetic monitoring and assessment in relation to the goals and objectives of the Recovery Plan, the Propagation Plan, and the Scope of Work for the Genetics Project. Text in italics is from the document listed by the arrow bullet above it.

- **RGSM Recovery Plan**

Three goals have been established for the recovery of the Rio Grande silvery minnow:
1. Prevent the extinction of the Rio Grande silvery minnow in the middle Rio Grande of New Mexico.
2. Recover the Rio Grande silvery minnow to an extent sufficient to change its status on the List of Endangered and Threatened Wildlife from endangered to threatened (downlisting).
3. Recover the Rio Grande silvery minnow to an extent sufficient to remove it from the List of Endangered and Threatened Wildlife (delisting).

The augmentation program as a whole has clearly played an important role in achieving the first goal of the RGSM Recovery Plan. It is likely that, without the augmentation program, the species would have gone extinct in the Middle Rio Grande. However, achievement of the other two goals will be more difficult. The criteria for both downlisting and delisting are the existence of at least two self-sustaining populations. Currently, the Middle Rio Grande population is dependent on the augmentation program and it is unlikely the population will become self-sustaining without hydrological changes. Habitat fragmentation along the river also likely plays a role in preventing the establishment of a self-sustaining population along the river. These challenges are especially difficult as a water deficit is expected to persist and become more acute due to climate change. Thus, changes in hydrological resources for RGSM habitat would most likely have to come from significant changes in re-allocation.

In the immediate future, RGSM persistence in the wild appears to highly depend on augmentation. It is difficult for the panel to recommend appropriate levels or % of augmentation relative to the wild population: few theoretical and empirical generalizations have been made in the literature,

and existing modeling on this topic has not factored in all conditions that might influence demographic and genetic outcomes of augmentation jointly (see Fraser 2008, pages 543-546 and references therein). With improved, annual data on the relative number of RGSM produced in the wild vs. the hatchery, future recovery efforts could reduce augmentation inputs in years where a demographically stable number of RGSM were sustained in the wild. This would be part of a balancing act between not constraining the RGSM population in the wild with likely maladapted augmentation fish, whilst giving a demographic boost to the population size when necessary to avoid extirpation.

- **Propagation Plan**

Genetic Monitoring and Management (Recovery Goal 1; Recovery Objectives 1-A and 1-B)
Recovery Action 1.3: Continue genetic studies on Rio Grande silvery minnow populations.
Recovery Action 3.1.3: Continue genetic monitoring and study of propagated Rio Grande silvery minnow.

One issue with the genetic monitoring is that genetic data are collected immediately prior to the release of the offspring and data are then analyzed after release. This approach can lead to situations where the released offspring reflect a small number of families which would further reduce the effective population size of the population. Thus, genetic sample collection and analysis should be conducted well in advance of release so that changes can be made in which family lots are released to avoid a reduction in the effective population size of the overall population. Such sampling could be done in real time if a standardized genetic analysis protocol was established at the Southwestern Native Aquatic Resources & Recovery Center (in Dexter, New Mexico). If this approach is taken, it will be prudent to re-run a randomly selected set of samples for quality assurance.

Stabilize and enhance populations of RGSM in the middle Rio Grande Valley (Recovery Goal 1; Recovery Objective 1-A and 1-B).

A) Propagation activities to maintain genetic diversity
Recovery Action 3.0: Ensure the survival of the Rio Grande silvery minnow in its current habitat and reestablish the species into suitable habitats in its historical range.
Recovery Action 3.1: Continue Rio Grande silvery minnow captive propagation activities.
1) Maintain a captive stock of at least 15,000 and up to 25,000 adults to represent the Middle Rio Grande.
2) Maintain and maximize the effective population size and genetic diversity of the captive population.
3) Ensure production fish contain acceptable genetic variation such that the overall diversity of the augmented population is not reduced.
4) Complete the comparison of communal spawning vs. paired mating spawning. (Complete)
5) Optimize recommendation for paired mating or designate number for communal spawning to maximize number of parental contributors.

It appears there may be activities in the hatchery that can result in a reduced effective population

size of released offspring. As mentioned in other responses, more data are needed on the variance in family size and actual number of contributing breeders. Further data on the effectiveness of communal spawning should also be generated to determine the number of breeders that are actually represented in communal spawning. Sperm competition commonly occurs in broadcast spawners (Furness et al. 2015), so communal spawning in this species should be studied further. Hatcheries and grow-out facilities should share the spawning and release records, with these data being combined in a central location in a clear and understandable way.

B) Production goals for augmentation: *Provide up to 321,000 age-0 (30-40 mm) RGSM for release into the Middle Rio Grande annually.*

Recovery Action 3.2: Continue Rio Grande silvery minnow augmentation activities.
1) Annual collection of a minimum of 500,000 eggs (when possible) for captive rearing and subsequent stocking of RGSM in the middle Rio Grande.
3) Continue to assess the use of existing and additional facilities to refine the capabilities and roles to facilitate the RGSM propagation program.

There are differences between the facilities in terms of spawning practices and rearing conditions. This could have an effect on survival of released offspring. The panel encourages research on differential survival between offspring reared in different facilities, and subsequent post-release survival. While it is tempting to use every captively produced fish, such an approach can undermine the goals of the entire project. It is better to equalize family sizes and NOT use any surplus fish. Surplus fish are those fish that are produced either by accident or do not meet genetic criteria/composition.

Reestablish the RGSM in at least two other areas within the historic range (Recovery Goal 2; Recovery Criterion 2-A-3)

Recovery Action 3.3: Reestablish Rio Grande silvery minnow at appropriate locations in its historical range.
1) Replicate the Middle Rio Grande population in the Big Bend reach of the Rio Grande.

These other established populations may ultimately serve as “back-up” populations if the population on the Middle Rio Grande is extirpated. Therefore, the same principles and practices recommended here should be applied to these programs as well.

- **Scope of Work for Genetics Project**

Objective 1) Determine levels of genetic variability in the wild population of RGSM and compare to past results.

There is limited information on the genetic variability of the wild-caught RGSM as there are only two years of data available from the pre-augmentation period. Additionally, it is unlikely that RGSM of a wild origin exists in the Middle Rio Grande because most captured fish and eggs likely had hatchery/captive rearing in its lineage (see glossary under ‘wild and captive RGSM’).

Therefore, the first objective will be difficult to achieve with existing data and the absence of a truly wild origin population.

Objective 2) Compute genetic effective population size and explain how it relates to long-term population viability.

It is difficult to assess the relationship between effective population size and a population's long-term viability. Instead, practices can be implemented to maximize the effective population size with the genetic variability that currently exists in the population. Implementation of the practices suggested in this review will help to maximize N_e, such as those included in Overall Recommendations.

Objective 3) Assess genetic impacts of captive propagation and augmentation on wild stocks.

Our response to Question 7 addressing a potential Ryman-Laikre effect applies to this objective.

Objective 4) Evaluate RGSM propagation practices and how they relate to genetic diversity.

Additional evaluations need to be conducted to determine if artificial selection may be occurring and to determine how hatchery practices may be affecting effective population size, particularly variance in family size. Also, it is critical that all hatcheries use the same breeding protocols, and that hatchery personnel be extensively trained in the important costs of deviating from the protocols. For instance, there may be circumstances where hatchery personnel see an opportunity to breed some extra fish, but if the standard protocol is not followed, then the entire program is put at risk.

Objective 5) Provide recommendations regarding genetic management of RGSM.

As currently practiced, the timing of genetic sampling of released offspring does not permit the development of recommendations for stocking in that year. Although there may be some lots with a small effective population size, those lots are released and information about their effective population size is not obtained until after their release. Real-time genotyping could provide more direct recommendations that could influence release decisions that same year.

Question 6

What statistical analyses were used and were the assumptions of those analyses met?

1) None of the assumptions were met for any of the analyses, which is common in population genetic studies. The question is whether the violations of the assumptions cause the estimates of relevant parameters to have significant systematic error. We did not see much discussion of whether assumptions were violated, but it does not appear that there are problems with the estimates. Nonetheless, this issue should be addressed more explicitly by the genetics group. For instance, there is evidence of disequilibrium among loci and it is not clear whether this is due to physical linkage or sampling effects.

If it is physical linkage, then the estimates of effective population size may be biased (most likely a downwards bias), although the magnitude of the bias is not clear. For more on the effect of violations of the assumptions of N_eD, see Waples & England (2011).

2) None of the assumptions were met for F_{ST} comparisons – additional analyses that could be done include relatedness approaches discussed above. This would also help to discern if temporal differences/fluctuations are in fact due to drift and not sampling noise.

Question 7

What other scientifically-robust interpretations could be made using the same data and results of the Genetics Project?

Given the dependence of effective population size estimates on sample size, one could argue that all of the results reflect differences in sample size and how fish were sampled each year.

The effective population size estimates are often much smaller than the census population size and the interpretation is often that the low effective population size is due to factors that are occurring in nature, such as environmental conditions. However, another scientifically-robust interpretation is that the small effective population size is due to hatchery production. The reports sometimes mention the Ryman-Laikre effect, which is a reduction in N_e (and corresponding genetic diversity) that occurs when a captive population is supplemented with numerous captive individuals generated from proportionally fewer breeders, but more attention should be given to this interpretation. Analyses such as generalized linear mixed effects modeling (GLMM) could be conducted to determine how different environmental factors, sample sizes, and the extent of annual hatchery releases affect N_e, and to determine the most important factors. Additional genetic screening of egg lots in the hatchery would also permit an evaluation of the degree to which variance in family size of released offspring is occurring, and hence the degree to which hatchery practices and augmentation may be reducing N_e and possibly generating a Ryman-Laikre effect.

Question 8

When there are gaps or uncertainties in the information or data collected for the Genetics Project, are they clearly identified in the reports and publications issued? Does the Panel unanimously recommend remedies to address any gaps or uncertainties?

The genetic reports do a good job of addressing some of the gaps and uncertainties related to the effective population size estimates and often do a thorough job describing the assumptions and differences between the various estimates. However, the different estimates of N_e and the high variability associated with those estimates make those estimates less suitable for management decisions. Instead, determination of the number of breeders through parentage analysis and/or sibship reconstruction may be more useful for management decisions. The power

of the existing genetic markers or newly developed markers should be assessed to determine if there is sufficient power to identify the number of parents and sibship relationships (determined by using COLONY software or something similar).

There is also uncertainty surrounding estimates of pre-augmentation genetic diversity. Considering there was a substantial number of individuals released in 2000 (203,600 larval fish), pre-augmentation samples would conservatively consist of samples from 1987 and 1999. This provides some data about pre-augmentation genetic diversity, but interpretations about pre-augmentation are limited by the few number of years available. Unless there are additional samples from years prior to any augmentation, interpretations of pre-augmentation genetic diversity are limited and the focus should instead be on maintaining remaining genetic diversity.

There is a gap in knowledge about the effect of hatchery practices on effective population size. Sampling of the released offspring occurs, but these data are not linked with sampling of the broodstock. As a result, there is uncertainty about the contribution of the different parents and whether there is high variance in family size, both of which could contribute to a reduced effective population size. We recommend that the broodstock also be genotyped so that parental contribution can be assessed. This would also help confirm whether communal spawning is capturing maximum genetic diversity.

Microsatellite loci are the genetic markers providing most of the data for the genetic monitoring program. However, there is uncertainty whether genetic diversity at nine neutral microsatellite loci reflects genome-wide variation or genetic diversity at adaptive loci. The geneticists had examined the *Clock* gene in the Rio Grande silvery minnow and found that this species had lower genetic diversity at this gene relative to other closely-related non-imperiled species. This loss of diversity could be due to genetic drift or selection and indicates the possibility that the species could be losing adaptive variation. For the next few years, there is a still a benefit to continue some degree of genetic monitoring using the same nine microsatellite loci because of the ease with which a temporal perspective on genetic diversity in RGSM can be generated, and because next generation sequencing (NGS) approaches will not necessarily generate results for conservation action right away as these are implemented. Nevertheless, the panel recommends that the time has come to concurrently initiate the transition from population genetics to population genomics in the RGSM recovery program through implementing NGS approaches (such as genotyping-by-sequencing [GBS]) to assess genome-wide variation in the species, which would include both additional neutral and adaptive loci. Once an initial NGS assessment is completed and contrasted with microsatellite data, the RGSM recovery team will be in a better position to determine whether maintaining further microsatellite research is worthwhile. Ultimately, once adaptive loci are identified, these could then be targeted in future studies using a candidate gene approach in order to better monitor adaptive variation in the species – i.e. a candidate gene approach would track genetic variation over time at gene loci of functional significance in RGSM.

Question 9

Are there additional genetic techniques that could be utilized that would improve the Genetics Project that can better provide the Program with additional information to guide RGSM management actions?

Many population genetics monitoring programs (e.g., salmonids) have moved to SNP panels in which a large number of individual polymorphisms are assessed using high-throughput technology. While the start-up costs of developing the SNP panels can be significant, the panels allow for cheap and quick large-scale (1000s of individuals) genotyping once the panels have been created. If the plan is to continue monitoring into the foreseeable future, these approaches should be seriously considered. For an example, see Palti et al. (2015).

The molecular surveys can be complemented by evaluation of quantitative trait variation within and among the various groups (reaches, captive cohorts, lots). Selection operates on important life history traits, morphology and behavior, and evolution has been shown for many quantitative traits in captive populations (domestication selection, or relaxed selection). Thus, evaluating phenotypic variation within and among the captive cohorts would be a very efficient and inexpensive means to assess potential domestication selection.

Sequencing of the mtDNA ND4 does not seem to add any information beyond the microsatellite data. The mtDNA ND4 is a coding gene that is highly conserved and is better suited for studying relationships between different species. In comparison, microsatellite loci will detect genetic changes more quickly. This locus could be dropped and new genetic markers be explored instead. With GBS, one can often generate sequences for the complete mitochondrial genome.

Question 10

What genetic parameters should be measured and reported that will most efficiently track the maintenance of genetic diversity or genetic integrity of RGSM?

Given the data being collected, relevant parameters have been calculated, including theta (a measure of genetic diversity using coalescent analysis), effective population size, disequilibrium and departures from HWE, expected and observed heterozygosity, and effective number of alleles. Additional analyses can also be conducted that may better track the maintenance of genetic diversity in the population. Annual genotyping of broodstock adults and using that data to assess their respective contributions to the resulting offspring will provide a more accurate estimate of the effective number of breeders. Sibship reconstruction may be done on existing data to determine the number of contributing parents; however, this is contingent on having sufficient power with the microsatellite loci to distinguish full- and half-siblings. Relatedness could also be calculated among the broodstock to ensure that unrelated individuals are breeding. If communal spawning is continued, then relatedness estimates can be used to ensure that the 10 females and 10 males have low relatedness. If pairwise mating is used, then relatedness values can be used to select unrelated mates.

Question 11

Are there thresholds of genetic diversity (e.g., percent loss of allelic diversity, effective population size) where management actions should be taken? If so, what management actions would be recommended?

Rather than focus on loss of relatively common alleles (>10%), another approach would be to look at changes in overall diversity that fall below a critical threshold. The data collected to date can be used to create 95% CI of diversity across space and time. Thus, any time a new sample falls below this threshold would signal reduced genetic diversity, and require evaluating the likely factors that may have caused the decrease. For instance, during our tour, we learned that a specific tank held RGSM brood-stock that had been produced "fortuitously". Our concern was that this tank of fish may had been produced from one pair and could completely undermine attempts to equalize family sizes. Approaches for maintaining or enhancing current effective population size in RGSM are detailed above under Questions 2-4, 8, and 10.

Question 12

Based on the life history of RGSM, at what frequency should genetics monitoring be implemented on wild and hatchery populations to improve/maintain genetic diversity, or other identified goal. To support this answer, what are examples of effective fish genetic monitoring programs? And how are the results used by decision makers?

If monitoring includes the four year classes maintained in the hatcheries, monitoring should be done each year on the actual broodstock used in the hatcheries, in part to assess whether mortality, for whatever reason, causes a non-random shift in genotypic frequencies. Annual monitoring of genetic diversity in the generated progeny before pooling of lots and release into nature will also help to ensure that genetic diversity is maximized. Annual or bi-annual monitoring of genetic variation underlying putatively adaptive loci (e.g., SNPs linked to functional traits) will also help to track whether hatchery practices are minimizing domestication selection. The refugial populations should also be monitored regularly (preferably every two years at a minimum) to ensure that the gene pool remains robust (see Conclusion 8).

Question 13

What changes would the Panelists recommend to improve the Genetics Project? Please support recommendations with relevant citations, reasoning, and estimates of the relative power to detect changes in genetic diversity and integrity in RGSM compared with the current techniques and methods of the Genetics Project as is currently being implemented?

In addition to the aforementioned discussion on enhancing effective population size through hatchery breeding protocols, the panel recommends three different avenues of improvements relating to (1) assessing standing levels of neutral genetic variation and genetic variation underlying adaptive traits, (2) ensuring that domestication selection is minimized in all propagation activities, and (3) implementing experimentation with controls to assess performance (survival, reproductive success) to assist real-time, adaptive management decision-making on a short-term basis. Genetic monitoring can complement each of these monitoring avenues.

1) Monitoring both neutral and adaptive genetic variation over time

RGSM genetic diversity has been monitored annually using a panel of nine microsatellite loci. For a number of reasons (including ascertainment bias, use of loci developed for different species other than RGSM), this modest number of loci likely does not adequately portray genome-wide, standing levels of neutral genetic diversity within RGSM. 'Neutral' here refers to gene loci that are not (presently) under selection. In being selectively neutral, the microsatellite panel employed in current RGSM genetic monitoring also cannot assess how genetic changes might have occurred over time at gene loci linked to traits of adaptive significance in RGSM.

a) *MEDIUM PRIORITY*: The panel therefore recommends that both neutral and adaptive genetic variation be monitored over time in RGSM in the future using a larger, more diverse set of genetic markers. Genotyping-by-sequencing (GBS) or related equivalent would provide more confident estimates of genome-wide neutral genetic variation (N_{ac}, H_o) in RGSM because it would more likely represent the entire genome (for more information on GBS and related NGS approaches and their practical benefits for conservation genetics monitoring, see the review of Allendorf et al. 2010). GBS would also likely help to provide more accurate and precise N_e estimates in the future, and even permit simulating complex demographic histories of RGSM, if this is desired. Furthermore, a large panel of SNPs (e.g., several thousand at a minimum) would permit the researchers to monitor changes in putatively adaptive genetic variation over time by separating out SNPs under putative selection from those that behave as selectively neutral, and then contrasting the dynamics of the two loci groups across time. Historical samples are available in sufficient numbers from some sampled years. Hence, the researchers could also go back into time and assess whether or not changes in adaptive or neutral genetic variation correspond to periods of supplementation, including whether selective sweeps have occurred for certain traits (even if the extent of neutral genetic variation remains the same across time). Monitoring of adaptive genetic variation could be supplemented using major histocompatibility complex (MHC) genes that have been screened in a few previous years of the monitoring project (Osborne & Turner 2009), if sufficient resources are available

and if a more direct link to functional traits is needed. Finally, selection often operates on quantitative traits that are coded by numerous loci, thus we recommend examining phenotypic variation for important life history traits (size/age maturity, growth rate), behavioral traits (anti-predator behavior, risking taking behavioral syndromes) and morphology (body shape as it relates to flow regime).

For instance, Collyer et al. (2011) found rapid evolution of body shape for a refuge population of White Sands pupfish. The ancestral population was comprised of streamlined-bodied fish that occupied a lotic habitat (saline creek) whereas the refuge population was comprised of deep-bodied fish that occupied a lentic habitat (brackish spring). This evolution occurred within a few decades. In another example, Heath et al. (2003) reported a case where conditions at a chinook salmon hatchery relaxed selection on egg size, leading to evolution of smaller eggs. Populations supplemented with from this hatchery showed trends toward small egg size, despite widespread evidence that large egg size was selectively advantageous in the wild. Thus, managers should evaluate how the hatchery environments differ from the wild and consider the types of traits that may evolve. For instance, a population of fish introduced from the river in year zero, may show "evolution" with the deep bodied fishes outperforming the streamlined fishes over the course of a 4 year period – prior to their use as broodstock. A general approach would be to conduct work to evaluate life history variation and body shape variation by sub-sampling cohorts during each year they are held to evaluate if there are noticeable changes occurring. Life history evaluations can focus on evaluating important fitness correlates such as size at maturity, growth rate, egg size, reproductive allocation, fat storage and clutch size (for methodology see Reznick & Braun 1987 and Reznick & Bryga 1987). Body shape variation within cohorts across the four years in captivity can follow methodology outlined by Collyer et al. (2011).

b) *HIGH PRIORITY*: Sampling of floodplains should be considered and included where feasible to ensure that the genetic characteristics of RGSM are adequately represented in egg collection samples.

2) <u>Minimizing domestication selection in propagation activities</u>

While there has been some consideration in the existing genetic project of how neutral genetic diversity might be affected by propagation practices, the panel recommends that a more thorough consideration of domestication selection be implemented in all propagation activities and that procedures be set up to minimize such selection. There is a large body of literature which indicates that domestication selection (either through a relaxation of natural selection or unintentional selection in the captive/hatchery environment) operates regularly in fish propagation through non-random changes to phenotypes and genotypes (e.g., Waples 1999; Araki et al. 2007; Fraser 2008; Christie et al. 2012; Evans et al. 2014). Such domestication selection can also happen very quickly (within 1-2 generations) and have severe impacts on the fitness of released fish (Christie et al. 2012; Milot et al. 2013). Furthermore, plastic changes in fish induced by the propagation process can have what are termed 'carry over effects' into the next generation (Evans et al. 2014; Clarke et al. 2016). For example, maternal effects in fishes can influence the subsequent survival and fitness of their offspring. What this all means for the RGSM recovery plan is that changes to

phenotypes within the propagated environment, whether plastic or genetic, whether generated between or within generations of propagation, can impinge substantially on survival and fitness post-release, and hence influence the probability of recovery.

The panel is concerned that the potential for domestication selection is high in the RGSM propagation program. Specifically, although mortality is normally high in wild RGSM within the natural, riverine environment, the drivers/causes of high mortality of captive RGSM individuals (approximately 75-90%, starting from the initial egg stages all the way through to age 4 adult broodstock) may differ from those in nature. Domestication selection in captive RGSM may also occur in a number of life stages/ways.

HIGH PRIORITY

The following procedures are recommended for future propagation to minimize domestication selection; this is not an exhaustive list but is based on what was described in the materials provided and discussions during the interviews:

a) Conduct random sampling of annual egg collections from nature, to include not only the main channel but also the floodplains, for subsequent hatchery rearing (e.g., current collections only come from the main channel of the Rio Grande River, not on floodplains)

b) Rear RGSM in environmental conditions that resemble natural environmental conditions as much as possible. This will reduce relaxation of selection or non-random survival at egg/early life stages in relation to habitat selection/settlement, behavioral/physiological characteristics, anti-predator responses etc. Specific recommendations for RGSM hatcheries include: (i) early juvenile environmental enrichment that resembles critical floodplain habitat (temperature, substrate, flow, turbidity, pH, conductivity, food sources, natural daylight); and (ii) some exposure to natural predators, or at the very least, mimicking of predators to stimulate anti-predator conditioning.

c) RGSM live longer in captivity and the breeding program uses 4-year old fish as brood stock. By contrast, in the wild the breeding population is comprised largely of 1-year old fish. Thus, it will be prudent to evaluate the phenotypic effects of older brood-stock. Also, because larger fish have about 4x as many eggs as younger adults (10,000 vs. 2,500), and there is also likely higher variance in egg production among 4-year old fish compared to the variation in egg production among 1-year old fish. This could undermine efforts to equalize family sizes. Thus, using younger fish as brood stock will reduce the likelihood of un-intentional domestication selection, and also result in higher effective population sizes (due to reduced variance in egg production among females).

d) Equalize contributions of different adults in the captive broodstock to new broods/lots as much as possible.

e) Rear RGSM so as to maintain the growth trajectories typical of wild-raised fish (i.e., Age 1 fish in captivity should exhibit the same range of sizes of Age 1 fish in the wild). At present,

either faster growing individuals may be unintentionally selected for, or other fish phenotypes (e.g., size, condition, body shape) may not match natural sizes upon release.

f) Rear RGSM on natural diet if possible; diet appears natural at early life stages, but diet appears supplemented in later life stages (pellet feed).

g) Minimize the duration in captivity as much as possible before release; domestication selection is reduced with less captive exposure (see Frankham 2008 and Fraser 2008)

3) Implement experimentation with controls to assess performance (survival, reproductive success) and assist real-time, adaptive management decision-making on a short-term basis.

Genetic monitoring of changes at neutral loci and loci putatively under selection would shed light on whether genetic variation is or is not being maintained over time in RGSM recovery efforts. Nevertheless, how much the genetic changes translate into relative differences in survival and fitness can only be assessed by conducting experimentation on the performance of propagated progeny and naturally spawned ('wild') progeny in nature. The panel recognizes the challenges to conducting such field experiments, but suggests the working groups consider geographical locations where this might be feasible to carry out.

a) *MEDIUM PRIORITY*: Maximize the information gained from re-stocking efforts of hatchery-raised fish back into the river in order to test particular scientific hypotheses and inform adaptive management. One possible experiment would release several groups of RGSM (i.e., different treatment groups) in relatively large numbers into several sampling sites where treatment fish could be feasibly recaptured at later time points. Different treatment groups could be different hatchery sources, different cohorts, different diets, different size at release, etc. The duration of time will be influenced by logistical constraints, environmental variation, etc. The survival of these fish, but preferably reproductive success in the next generation of egg collections, would then be compared among the treatment groups, based on genotyping of the released fish and assignment back to parents. Treatment groups could be (i) fish from different hatcheries and hence different degrees of exposure to (more or less) naturalized rearing environments; and (ii) fish with a different extent of captive exposure (egg to hatch only; to early juvenile; late juvenile, adult etc.). Such an experiment would be highly useful to adaptive management by revealing which stocking and rearing strategies reduce maladaptation from propagation, and by what extent, to ensure that the adaptive potential of RGSM is maintained as much as possible. Within two or three years, we might learn if more naturalized hatcheries produce better survival. Again if subsets of breeders could be DNA printed, we could track performance of these three hatchery types to the following generation at the spawning stage.

b) *MEDIUM PRIORITY*: In addition (or alternatively if resources are limited), the genetics survey could focus on characterizing whether the year classes maintained in the hatcheries change over time in their genetic constitution as a consequence of differential mortality. So for instance, the year class 1 fish could be genotyped and the same population sampled in year two, three and four to assess whether mortality causes a significant non-random shift in the

gene pool (which would be consistent with selection in the hatchery, and not random genetic drift).

c) *LOW PRIORITY*: Monitoring of domestication selection could include DNA fingerprinting (GBS) of wild-caught egg collections. An investigation into whether non-random changes to genome-wide variation were occurring at successive early life stages relative to the same stages in the wild would provide evidence that the hatchery environment is resulting in domestication selection.

Question 14

Do the results of the Genetics Project facilitate the Program and management agencies' efforts to manage RGSM risk of extinction and support recovery efforts?

Yes, but the genetic characterizations can be improved. The key to maintaining the genetic diversity within RGSM depends on (i) using large numbers of breeders that contribute equally to the augmentation population, and (ii) minimizing domestication selection during propagation. The breeders in the hatchery should ALWAYS be derived from river-collected eggs or larvae, unless a major calamity occurs at the hatchery or there are years of drought preventing natural reproduction. The genetic analysis should focus on exhaustive characterization of the potential and actual broodstock from the four year classes present in the hatchery.

Question 15

Does the Genetics Project provide the Program with reliable information based on repeatable methodologies so as to accurately detect trends in the genetic parameters measured in a timely manner, allowing the Program to quickly adjust its Genetics Project and captive propagation approaches and other agency management actions in order to quickly reduce the risk of deleterious changes in both the wild and captive RGSM populations?

The short answer is yes, but there are methods that permit more rapid genotyping. Given the scale of fish production, it seems reasonable for the program to develop a panel of polymorphic SNPs and use high throughput methods for genotyping (for example, see Larson et al. 2014 and Ali et al. 2015).

Question 16

Does the genetic monitoring component of the Genetics Project inform the Program of any loss of genetic diversity adequately so as to maintain genetic variance in wild and captive RGSM in a timely manner?

Yes but the focus should shift to the analysis of all fish used for spawning in the hatchery system. If this is done, it should be possible to know the genetic composition of the augmentation fish PRIOR to the release rather than the current strategy in which fin clips are obtained at the time of release. In this way, the program will know the genetic composition of the augmentation fish early enough to make changes if necessary. This would be necessary if the current spawning strategy of a breeding matrix of 10 females x 10 males is continued which leads to differential individual and family contributions to the resultant progeny. Unequal combinations of these 10 x 10 lots can further differentially represent individual and family contributions to the augmentation fish.

4.0 Conclusions and Recommendations

The panel recognizes the professional and dedicated efforts of the PIs. The majority of our answers to the questions posed above, and the recommendations listed below, are meant to relay what we consider to be constructive critiques of the work from independent evaluations of the program. While we have many suggestions, we recognize their considerable efforts towards the goal of staving off extinction and enacting positive actions towards conservation of the RGSM. Their efforts have played an important role in preventing this species from going extinct. This is a definite success.

CONCLUSIONS

1) The timing and duration of the pre-augmentation period depends on whether hatchery spawned, hatchery adults or naturally spawned, hatchery reared adults are counted as augmentation.

2) There is no difference in genetic diversity between pre- and post-augmentation based on the microsatellite suite of loci used when pre-augmentation is categorized as 1999-2000 (if larvae count as a release).

3) The eggs or juveniles recovered in the river come from and represent selection for fish that can survive and spawn naturally in the river. The fish that spawn naturally are primarily one year old fish.

4) The current use of exclusively three and four year old broodstock is selecting for broodstock that can survive from eggs (or juveniles) captured in the river and live in a hatchery setting until ages three and four.

5) Remaining genetic diversity in the population has been maintained. There is no trend in estimates of genetic diversity over time since augmentation has occurred. Estimates of diversity remain more or less constant over the period surveyed, with no significant

differences in genetic diversity observed between years

6) There is no trend in the estimate of effective population size over time spanning the period from 1987 to 2014. Estimated effective population size for individuals captured from the Middle Rio Grande varies over time and ranges from 596 in 2004 to infinity—a biological impossibility. An infinite population size was estimated in six different years. From this we conclude that little information is gained from these estimates of effective population size and recommend (see Recommendation #7 below) using broodstock genotypes and resultant progeny to gain a more realistic estimate of effective population size for the driving force for genetic diversity which are the augmentation fish.

7) The vast majority of fish in the river today descend from fish that were either produced for augmentation in the hatcheries, or that experienced some degree of hatchery rearing for a part of their life cycle, as a result of severe droughts in 2002-2003, 2006 and 2011-2014.

8) Fish spawn in the river and there are usually sufficient eggs or larvae for hatchery-aided augmentation efforts.

9) Monitoring the status of the gene pool of a species or the gene pool of a population of a species requires an understanding of the genetic life history of that gene pool. What constitutes the gene pool of the RGSM at any one time? Below are our conclusions from discussions with members of the RGSM augmentation team. Taking these into consideration can help inform process, inform appropriate sampling, and guide genetic analysis.

    - Assuming random sampling, when naturally spawned eggs are taken from the river and incubated in the hatchery, the resultant larvae represent that generation's gene pool. This egg collection was derived from former generations of naturally produced fish, but also from former generations of hatchery produced juveniles released into nature. These parental fish are primarily one year old fish.

    - When there is a significant drought and there are essentially no eggs (from collections for augmentation) or adults (from population status surveys) recovered from the river, then the collective genomes of the augmentation fish released that year are likely to constitute the gene pool. This has happened several times and likely will in the future without an emergency plan to maintain river flow in drought years. Hence, we conclude that the hatchery broodstock are driving the gene pool of this species.

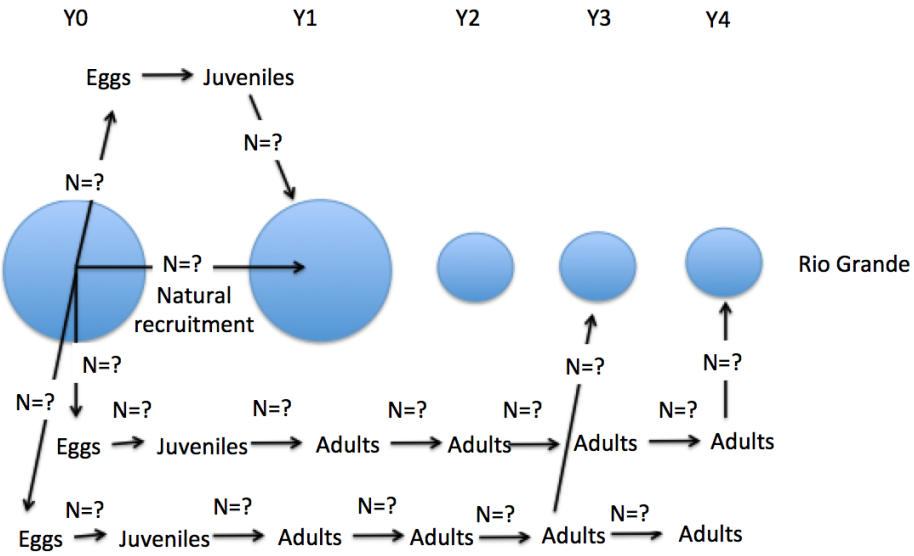
    - Based on these observations, yearly genetic monitoring of the broodstock fish and precisely the quantity of genomes that each broodstock member contributes each year along with the number of broodstock used should be emphasized. Determining these contribution ratios among broodstock, along with the number of broodstock, and the ratio of sexes will provide a measure of the effective population size.

RECOMMENDATIONS

HIGH PRIORITY

1) A flow chart should be constructed for each year that gives detailed numbers for: eggs and dates taken, disposition of eggs/larvae to specific rearing sites, broodstock maintained, actual breeding strategy, disposition of eggs/larvae to specific rearing sites, pooling of larvae prior to stocking, stocking sites, source of juveniles, and dates. These data should be standardized and collected for each hatchery engaged in fish production and the data should be made available electronically to all interested parties. Deviations from planned methodologies (such as the inclusion of approximately 10,000 eggs from unplanned spawning in a broodstock tank) should be noted in the flow chart.

   We provide one mock up of a model of what we imagine is going on with arrows indicative of movement of fish either in space or through time. This model, we realize, is not as complex as the actual program, but it provides a template for organizing the information, describing the program, and developing a quantitative model of the recovery effort that can be used to investigate the importance of particular parameters.



2) When deviations from planned methodologies result in the production of offspring, those offspring should not be released into the wild. Release of these offspring into the river could have a negative effect on the overall genetic diversity of the population. Providing flexibility in the next recovery permit should allow such surplus fish to be properly handled, whether used for research or held until natural death in the hatchery.

3) All broodstock and sufficient subset of the pre-release juveniles should be genotyped and the contribution of each broodstock individual determined. These results can be used to gain a more accurate, precise and biologically relevant estimate of N_e for each year class. This approach avoids the inherent assumptions and excessive variance associated with the N_e

estimators currently employed. This should be done every year. Developing a high throughput method would facilitate more rapid genotyping.

4) The Genetics Management and Propagation Plan and/or the Augmentation Plan should have a detailed methodology as to what will be done should a drought lasting more than three/four years occurs or all four year classes of broodstock are lost to a major hatchery accident.

5) The Science Workgroup (led by the Program) and the Genetics Workgroup (led by the USFWS) should integrate the genetics data and the decision-making more carefully. Specifically, there should be more translation of the genetics research into the adaptive management process, hatchery broodstock practices, and the integration of the past 15 years of research (genetics and ecology combined).

6) A more stable, consistent funding stream for the genetics research (e.g. an extended funding cycle) would ensure that all critical, temporally important genetic studies are accomplished each year (e.g., broodstock genotyping, pre-release juvenile genotyping). Cost will vary depending on the analysis and goal. At the time of writing this report, the RGSM program can expect to require approximately $50-150/individual for GBS or RAD-seq if outsourced to a genomics facility (including individual sample preparation, but not including salary for a research associate for sample preparation, data filtering and data analysis); a minimum of 30-40 individuals per year is recommended. Other genetic assessments do not require the amount of genetic data generated from GBS; any parentage assignments of offspring generating from mixed matings in the hatchery, for example, would be expected to cost approximately $5-10/individual (not including personnel salaries), and so could be (and should be) conducted on larger numbers of individuals (1000s).

7) The use of only four year fish as broodstock may compromise the maintenance of genetic diversity because of the possibility of non-random, differential survival of individuals in the hatchery. Crosses should include younger fish. As a consequence of using younger fish as broodstock with lower fecundity, more fish will be needed to produce the quota of eggs and this will increase the effective number of breeders.

8) It will be useful to conduct an evaluation of whether domestication selection is occurring in the hatcheries. This could be done using an appropriate genetic analysis and/or measuring quantitative traits to assess phenotypic variation of each captive cohort during each year in captivity.

MEDIUM PRIORITY

9) We recommend the use of the term “naturally spawned” in place of the term “wild” to refer to fish captured in the river that do not have an elastomeric tag; this assumes that all augmentation fish received a tag. It is likely that all fish captured in the wild have experienced some hatchery influence in their ancestry.

10) If possible, the augmentation team should consider artificially spawning broodstock in a one female by one male mating scheme, all the while maintaining the same total number of broodstock adults spawned (or increasing this number). This would allow equalizing family size as families are combined.

11) Relatedness should be calculated for broodstock prior to use to choose specific crosses that avoid inbreeding. If group spawning continues, relatedness estimates could be used to ensure that potential spawners in a group have low kinship.

12) To facilitate adaptive management, experimental studies comparing the survival and reproductive success of subsets of RGSM from different stocking strategies and hatchery facilities in nature would also shed light on the extent to which domestication selection is a concern in the recovery program.

13) A study using next-generation sequencing technology (e.g., GBS, RAD-seq) should be done with pre-augmentation samples and post-augmentation year classes to determine how the genome as a whole has changed over time. At the time of writing this report, the RGSM program can expect to require approximately $50-150/individual for such an assessment (more for RAD-seq) if outsourced to a genomics facility (including individual sample preparation, but not including salary for a research associate for sample preparation, data filtering and data analysis); a minimum of 30-40 individuals per year is recommended.

5.0 References

In addition to the references included in Appendix A, the following references were cited in this report.

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6.0 Acronyms and Glossary

ACRONYMS

CI	confidence interval
H_o	observed heterozygosity at a locus
H_{oc}	observed heterozygosity at a locus estimated from a randomization procedure
H_e	expected heterozygosity at a locus
HWE	Hardy-Weinberg equilibrium
F_{ST}	measure of genetic differentiation among populations
GBS	genotyping-by-sequencing
GLMM	generalized linear mixed effects modeling
MHC	major histocompatibility
mtDNA	mitochondrial DNA
N_a	allelic richness, typically the average number of alleles per locus in a study
N_{ac}	allelic richness (number of alleles per locus) corrected for sample size
N_e	effective population size
N_eD	effective population size, based on Waples & Do (2010)
NGS	next generation sequencing
PCA	Principal Components Analysis
PIs	Principal Investigators
QTL	quantitative trait loci
Reclamation	US Bureau of Reclamation
RGSM	Rio Grande silvery minnow
SNP	single nucleotide polymorphisms
USACE	US Army Corps of Engineers
USFWS	US Fish and Wildlife Service

GLOSSARY

Allelic richness – The total number of alleles in a population.

Broodstock – Individuals used (or likely to be used) for generating new offspring.

Candidate genes - Genes believed to be related to a particular phenotype or condition. Candidate genes can be identified on the basis of position or function. A positional candidate gene is located in a chromosomal region suspected of being linked to the phenotype. A functional candidate gene is a gene encoding a product connected with the phenotype.

Genetic bottleneck - A brief, often substantial, reduction in size of a population which usually leads to a rapid loss of genetic variation and subsequent random genetic drift.

Gene diversity – Expected heterozygosity, assuming Hardy-Weinberg equilibrium.

Genetic effective size – The effective size of a breeding population under idealized conditions meeting the assumptions of Hardy-Weinberg (i.e., equal sex ratio, random mating).

Genotyping-by-sequencing – A method to discover single nucleotide polymorphisms (SNP) in order to determine the genotype of an individual.

Hardy-Weinberg equilibrium - The stable frequency distribution of genotypes (AA, Aa, and aa) in the proportions (p^2, 2pq, and q^2) respectively (where p and q are the frequencies of the alleles, A and a). It is a consequence of random mating in the absence of mutation, migration, natural selection, or random drift.

Heterozygosity - The presence of different alleles at one or more loci on homologous chromosomes. The more outbred a population is the higher the heterozygosity will be and, conversely, the more inbred a population the lower the heterozygosity.

Null allele – An allele whose effect is either an absence of normal gene product at the molecular level or an absence of normal function at the phenotypic level; a genotyping error in which an individual appears to be homozygotic because one allele for a diploid individual failed to be detected.

Refugial population – Protected group of individuals maintained to safeguard the persistence of a species.

Ryman-Laikre effect – The reduction in N_e due to augmenting, resulting in wild populations with hatchery brood-stock derived from a limited number of breeders.

'Wild' vs. 'captive' – For the purposes of this report, the authors define a 'wild RGSM individual', 'wild-caught individual' or a 'naturally spawned individual' as one that was captured as a fish or egg in the natural environment, without showing any elastomer tag that is normally placed on fish released from the hatchery. By this definition, wild individuals may or may not have a purely wild origin (i.e., one in which both parents themselves completed their entire lives in the natural environment). Some 'wild' individuals may have had one or two parents that were reared for some part of their lifecycle in the captive environment, or one or more grandparents with such rearing, etc. In other words, individuals with a 'wild origin' are also 'wild' individuals, but 'wild' individuals may not have a 'wild origin'. This definition also assumes that elastomer tags are not lost on fish originating from hatchery/captive rearing environments. Conversely, a 'captive RGSM individual' or 'hatchery-reared individual' is a fish (or egg) that is reared for some part of its lifecycle (or solely) within the captive environment, and that has an elastomer tag if captured in nature.

APPENDIX A

Documents Provided

Genetics Reports

Augmentation Reports

Spawning and Egg Monitoring Reports

Life History Reports and Publications

Other Relevant Documents

Other Published Literature

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation

Documents Distributed to Panel

Annual Genetics Reports

Carson, E. W., M. J. Osborne, and T. F. Turner. 2014. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2014. University of New Mexico, Albuquerque, NM.

Osborne, M. J., T. J. Pilger, and T. F. Turner. 2015. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2015. University of New Mexico, Albuquerque, NM.

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Osborne, M. J., and T. F. Turner. 2009. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2009. University of New Mexico, Albuquerque, NM.

Osborne, M. J., and T. F. Turner. 2010. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2010. University of New Mexico, Albuquerque, NM.

Osborne, M. J., and T. F. Turner. 2011. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2011. University of New Mexico, Albuquerque, NM.

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Turner, T. F., and M. J. Osborne. 2006. Genetic monitoring of the Rio Grande silvery minnow: Genetic status in 2006. University of New Mexico, Albuquerque, NM.

Turner, T. F., and M. J. Osborne. 2007. Genetic monitoring of the Rio Grande silvery minnow: Genetic status of wild and captive stocks in 2007. University of New Mexico, Albuquerque, NM.

Turner, T. F., M. J. Osborne, and D. Alò. 2003. Conservation genetics of Rio Grande silvery minnow, *Hybognathus amarus*: genetic evaluation of wild and captive stocks, 1999-2003. University of New Mexico, Albuquerque, NM.

Augmentation Reports

Archdeacon, T. P. 2013, November 19. Subject: Final Rio Grande silvery minnow release calculation for November, 2013.

Archdeacon, T. P. 2014. Rio Grande Silvery Minnow Augmentation in the Middle Rio Grande, New Mexico: Annual Report 2013. US Fish & Wildlife Service, Albuquerque, NM.

Archdeacon, T. P. 2015. Rio Grande Silvery Minnow Augmentation in the Middle Rio Grande, New Mexico: Annual Report 2014. US Fish & Wildlife Service, Albuquerque, NM.

Archdeacon, T. P., and W. J. Remshardt. 2013. Rio Grande Silvery Minnow Augmentation in the Middle Rio Grande, New Mexico: Annual Report 2012. US Fish & Wildlife Service, Albuquerque, NM.

Remshardt, W. J. 2005. Experimental Augmentation and Monitoring of Rio Grande Silvery Minnow in the Middle Rio Grande, New Mexico: Annual Report June 2003 - May 2004. US Fish & Wildlife Service, Albuquerque, NM.

Remshardt, W. J. 2008a. Rio Grande Silvery Minnow Augmentation in the Middle Rio Grande, New Mexico: Annual Report 2006. US Fish & Wildlife Service, Albuquerque, NM.

Remshardt, W. J. 2008b. Rio Grande Silvery Minnow Augmentation in the Middle Rio Grande, New Mexico: Annual Report 2007. US Fish & Wildlife Service, Albuquerque, NM.

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Dudley, R. K., and S. P. Platania. 2011. Spatial spawning periodicity of Rio Grande silvery minnow during 2011. American Southwest Ichthyological Researchers, LLC, Albuquerque, NM.

Dudley, R. K., and S. P. Platania. 2013. Spatial spawning periodicity of Rio Grande silvery minnow during 2013. American Southwest Ichthyological Researchers, LLC, Albuquerque, NM.

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Dudley, R. K., and S. P. Platania. 2015. Monitoring of the Rio Grande silvery minnow reproductive effort during 2015 in the Rio Grande and selected irrigation canals. American Southwest Ichthyological Researchers, LLC, Albuquerque, NM.

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Horwitz, R. J., D. H. Keller, P. F. Overbeck, S. P. Platania, and R. K. Dudley. 2011. Age and Growth of Rio Grande Silvery Minnow. Patrick Center for Environmental Research and American Southwest Ichthyological Researchers, LLC, Albuquerque, NM.

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Pease, A. A., J. J. Davis, M. S. Edwards, and T. F. Turner. 2006. Habitat and resource use by larval and juvenile fishes in an arid-land river (Rio Grande, New Mexico). Freshwater Biology **51**:475–486.

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Platania, S. P., M. A. Farrington, W. H. Brandenburg, S. J. Gottlieb, and R. K. Dudley. 2003. Movement Patterns of Rio Grande Silvery Minnow *Hybognathus amarus*, in the San Acacia Reach of the Rio Grande During 2002. American Southwest Ichthyological Research Foundation, Albuquerque, NM.

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Remshardt, J., T. Turner, T. Perez, M. Ulibarri, P. Hines, C. Altenbach, C. Keeler-Foster, M. Osborne, C. Caldwell, and J. Parody. 2009. Rio Grande Silvery Minnow Genetics Management and Propagation Plan. City of Albuquerque BioPark, Albuquerque, NM.

USFWS. 2003. Biological and Conference Opinions on the Effects of Actions Associated with the Programmatic Biological Assessment of Bureau of Reclamation's Water and River Maintenance Operations, Army Corps of Engineers' Flood Control Operation, and Related Non-Federal Actions on the Middle Rio Grande, New Mexico. Available from http://www.fws.gov/southwest/es/newmexico/ES_bio_op.cfm.

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Osborne, M. J., M. A. Benavides, and T. F. Turner. 2005. Genetic heterogeneity among pelagic egg samples and variance in reproductive success in an endangered freshwater fish, *Hybognathus amarus* (Cyprinidae). Environmental Biology of Fishes **73**:463–472.

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Osborne, M. J., T. L. Perez, C. S. Altenbach, and T. F. Turner. 2013. Genetic Analysis of Captive Spawning Strategies for the Endangered Rio Grande Silvery Minnow. Journal of Heredity **104**:437–446.

Osborne, M. J., and T. F. Turner. 2011. Isolation and characterization of major histocompatibility class IIβ genes in an endangered North American cyprinid fish, the Rio Grande silvery minnow (*Hybognathus amarus*). Fish & Shellfish Immunology **30**:1275–1282.

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Watson, J. M., C. Sykes, and T. H. Bonner. 2009. Foods of Age-0 Rio Grande Silvery Minnows (*Hybognathus amarus*) Reared in Hatchery Ponds. The Southwestern Naturalist 54:475–479.

APPENDIX B

Meeting Agendas and Attendees

Final Meeting Agenda – February 2016

Meeting Attendees – February 2016

Final Meeting Agenda – May 2016

Meeting Attendees – May 2016

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation
Albuquerque, New Mexico

Panel Interviews and Meeting
February 4-5, 2016

Location:
U.S. Bureau of Reclamation
Albuquerque Area Office
555 Broadway Blvd NE Suite 100
Albuquerque, NM 87102

Agenda

Day 1 (February 4, 2016)

8:00	Welcome and Introductions
8:15	Presentation: Background of Program and Genetics Project
8:30	Overview of the Peer Review objectives, agenda, and process
8:45	Review the Focus Areas questions
9:00	Meeting with Science Workgroup and other Program members (Key discussion points: goals and objectives, definition of genetic integrity, appropriate to life history of RGSM)
10:15	Break
10:30	Meeting with RGSM Captive Propagation and Genetics Workgroup
12:00	Lunch with Panel Only
1:30	Meeting with the PIs of the Genetics Project
4:30	Panel Discussion
5:00	End of Day 1

Day 2 (February 5, 2016)

8:30	Panel Discussion (including identification of missing information)
12:00	Lunch
1:30	Visit to BioPark Facility (2601 Central Ave NW, Albuquerque, NM 87104)
3:30	Panel Discussion
5:00	End of Workshop

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation
Albuquerque, New Mexico

Meeting Attendees – February 2016

Peer Review Panelists

Dylan Fraser, PhD	Concordia University
Bernard (Bernie) May, PhD	University of California at Davis
Andrew Martin, PhD	University of Colorado at Boulder
Craig Stockwell, PhD	North Dakota State University
Amy Welsh, PhD	West Virginia University

Facilitator: Dawn Johnson, PhD — Amec Foster Wheeler

Attendees

Ann Demint[1]	MRG Project Manager	Bureau of Reclamation
Jen Bachus[1, 2]	Biologist	Bureau of Reclamation
Alighieni Saenz	MRG Program Analyst	Bureau of Reclamation
Brian Hobbs[1]	Fish Biologist	Bureau of Reclamation
Michael Porter[1]	Fishery Biologist	U.S. Army Corps of Engineers
Dana Price[1]	Botanist	U.S. Army Corps of Engineers
Wade Wilson[2]	Fish and Wildlife Biologist	U.S. Fish and Wildlife Service
Thomas Archdeacon[2]	Fish Biologist	U.S. Fish and Wildlife Service
Joel Lusk[1]	Fish and Wildlife Biologist	U.S. Fish and Wildlife Service
Manuel Ulibarri[2]	Project Leader, Southwestern ARRC	U.S. Fish and Wildlife Service
Kim Ward[2]	Head Aquarist	City of Albuquerque, BioPark
Kathy Lang[1, 2]	Curator	City of Albuquerque, BioPark
Grace Haggerty[1]	Hydrologist	New Mexico Interstate Stream Commission
Rich Valdez	Fish Biologist	SWCA (for NMISC)
Alison Hutson[2]	Manager, Los Lunas Silvery Minnow Refuge	New Mexico Interstate Stream Commission
Rick Billings[3]	Biologist	Albuquerque Bernalillo County Water Utility Authority
Mike Marcus[1]	Biologist	Assessment Payers Association
Megan Osborne[2]	Research Faculty	University of New Mexico
Tom Turner	Faculty	University of New Mexico

[1] Member of Science Workgroup
[2] Member of Genetics Workgroup
[3] Co-Chair of Executive Committee

Draft Report Review
May 12, 2016

Location:
U.S. Bureau of Reclamation
Albuquerque Area Office
555 Broadway Blvd NE Suite 100
Albuquerque, NM 87102

Agenda

9:00	Review of Comments Received
9:45	Break
10:00	Review of Draft Priorities for Recommendations
10:45	End

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation
Albuquerque, New Mexico

Meeting Attendees – May 2016

Peer Review Panelists

Dylan Fraser, PhD	Concordia University
Bernard (Bernie) May, PhD	University of California at Davis
Craig Stockwell, PhD	North Dakota State University
Amy Welsh, PhD	West Virginia University

Facilitator: Dawn Johnson, PhD — Amec Foster Wheeler

Attendees

Jen Bachus[1, 2]	Biologist	Bureau of Reclamation
Brian Hobbs[1]	Fish Biologist	Bureau of Reclamation
Eric Gonzalez[1]	Biologist	Bureau of Reclamation
Michael Porter[1]	Fishery Biologist	U.S. Army Corps of Engineers
Dana Price[1]	Botanist	U.S. Army Corps of Engineers
Stephen Ryan	Biologist	U.S. Army Corps of Engineers
Danielle Galloway	Biologist	U.S. Army Corps of Engineers
Susan Bittick	Collaborative Program Manager	U.S. Army Corps of Engineers
Wade Wilson[2]	Fish and Wildlife Biologist	U.S. Fish and Wildlife Service
Thomas Archdeacon[2]	Fish Biologist	U.S. Fish and Wildlife Service
Joel Lusk[1]	Fish and Wildlife Biologist	U.S. Fish and Wildlife Service
Manuel Ulibarri[2]	Project Leader, Southwestern ARRC	U.S. Fish and Wildlife Service
Kathy Lang[1, 2]	Curator	City of Albuquerque, BioPark
Grace Haggerty[1]	Hydrologist	New Mexico Interstate Stream Commission
Rich Valdez	Fish Biologist	SWCA (for NMISC)
Alison Hutson[2]	Manager, Los Lunas Silvery Minnow Refuge	New Mexico Interstate Stream Commission
Ken Richard	ESA Project Manager	New Mexico Interstate Stream Commission
Rick Billings[3]	Biologist	Albuquerque Bernalillo County Water Utility Authority
Mike Marcus[1]	Biologist	Assessment Payers Association
Janet Jarret		Assessment Payers Association
Brooke Wyman[1]	Biologist	Middle Rio Grande Conservancy District
Megan Osborne[2]	Research Faculty	University of New Mexico
Tom Turner	Faculty	University of New Mexico
Tyler Pilger	Post-doctoral researcher	University of New Mexico

[1] Member of Science Workgroup
[2] Member of Genetics Workgroup
[3] Co-Chair of Executive Committee

APPENDIX C

Reviewer's Curricula Vitae (Alphabetical)

Dylan Fraser, PhD

Andrew Martin, PhD

Bernard May, PhD

Craig Stockwell, PhD

Amy Welsh, PhD

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation

DYLAN JOHN FRASER

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LAB WEBSITE: www.dylanfraser.com

EMPLOYMENT HISTORY

- 2014-present Associate Professor, Department of Biology, Concordia University, Montréal, QC
- 2009-present Adjunct Professor, Department of Biology, Dalhousie University, Halifax, NS
- 2009-2014 Assistant Professor, Department of Biology, Concordia University, Montréal, QC
- 2006 Temporary Assistant Professor, Ecology, Dalhousie University, Halifax, NS
- 2000-04 Molecular Ecology Laboratory Techniques and Data Analysis, Université Laval, QC
- 2000-02 Field Coordinator, Université Laval, Cree Nation of Mistissini, QC
- 1999 Field Assistant, US Fish & Wildlife Service, AK
- 1998 Field Assistant, Department of Fisheries and Oceans, ON
- 1997 Field Assistant, Ontario Ministry of Natural Resources, ON

ACADEMIC BACKGROUND

- 2005-09 NSERC Postdoctoral Fellow, Conservation biology and quantitative genetics
  Department of Biology, Dalhousie University, Halifax, NS
- 2000-05 PhD, Evolutionary biology and population genetics
  Département de Biologie, Université Laval, Québec City, QC
- 1996-00 BSc, Fisheries biology (Specialized Honours, with distinction)
  Department of Zoology, University of Guelph, Guelph, ON

DISTINGUISHED AWARDS

- 2012 J.C. Stevenson Memorial Lecturer, Canadian Conference for Fisheries Research (Distinguishes an outstanding, young aquatic ecologist)
- 2006 TWM Cameron Award, Canadian Society of Zoologists (Outstanding PhD thesis in zoology in Canada for 2005; $1500)
- 2005 Tableau d'honneur de la Faculté des études supérieures, Université Laval (PhD placed on the Faculty of Graduate Studies excellence List)
- 2004 Best Student Paper Award, American Fisheries Society Annual Meeting (1 of 2 winners out of 200 student oral presentations; $500)

DISTINGUISHED EXTERNAL SCIENTIFIC COMMITTEES

- 2008-present Committee on the Status of Endangered Wildlife in Canada (COSEWIC)
  Freshwater Fish Species Specialist Committee

EDITORSHIPS

- 2014-present Associate Editor, *Evolutionary Applications*
- 2012-2013 Advisory Editorial Board member for *Evolutionary Applications*
- 2009-2013 Associate Editor, *Canadian Journal of Fisheries and Aquatic Sciences*

RESEARCH ACTIVITIES

SUBMITTED ARTICLES FOR PUBLICATION

***Supervised or co-supervised undergraduate or graduate students (academic level in parentheses)*

47. *Yates MC (BSc), PV Debes (PhD)*, DJ Fraser, JA Hutchings (2015) The influence of hybridization with domesticated conspecifics on alternative reproduction phenotypes in male Atlantic salmon in multiple temperature regimes. ***submitted***
46. *Clarke CN (MSc), DJ Fraser, CF Purchase (2015) Life-long and carry-over effects of early captive exposure in Atlantic salmon. ***In revision***
45. *Wood JLA (PhD), D Tezel (BSc)*, D Joyal (BSc)*, DJ Fraser (2015) Population size is not associated with quantitative genetic variation and differentiation in a stream fish. ***In revision***

PUBLICATIONS IN REFEREED JOURNALS

***Supervised or co-supervised undergraduate or graduate students (academic level in parentheses); Number of citations per article in parentheses at the end of the title (based on Google Scholar, last accessed January 2014); total citations: 2013; citations since 2010: 1374*

44. *Wood JLA (PhD), DJ Fraser (2015) Similar plastic responses to elevated temperature among different sized brook trout populations. ***Ecology***
43. *Harbicht AB (MSc), CC Wilson, DJ Fraser (2014) Does human-induced hybridization have long-term genetic effects? Empirical testing with domesticated, wild and hybridized fish populations. ***Evolutionary Applications*** *(1)*
42. Fraser DJ, PV Debes (Postdoc)*, L Bernatchez, JA Hutchings (2014) Population size, habitat fragmentation, and the nature of adaptive variation in a stream fish. ***Proceedings of the Royal Society of London Biological Sciences*** *(1)*
41. *Yates MC (PhD), DJ Fraser (2014) Does source population size affect performance in new environments? ***Evolutionary Applications***
40. *Debes PV (PhD), DJ Fraser, MC Yates, JA Hutchings (2014) The between-population genetic architecture of growth, maturation and plasticity in Atlantic salmon. ***Genetics*** 196:1277-1291.
39. *Wood JLA (PhD), S Belmar-Lucero (MSc)*, JA Hutchings, DJ Fraser (2014) Relationship of habitat variability to population size in a stream fish. ***Ecological Applications*** 24: 1085-1100. *(3)*
38. *Harbicht AB (MSc), M Al Shamlih, CC Wilson, DJ Fraser (2014) Anthropogenic and habitat correlates of hybridization between hatchery and wild brook trout. ***Canadian Journal of Fisheries and Aquatic Sciences*** 71: 688-697. *(1)*
37. *Gray QZ (MSc), JWA Grant, DJ Fraser (2014) Extirpation for conservation: applying predictors of extinction risk to eradicate introduced trout populations for lake restoration. ***Ecological Restoration*** 32: 59-67.
36. Fraser DJ (2014) Evolutionary hypotheses for a constraint to life history resilience in depleted Atlantic salmon populations. ***Journal of Fish Biology*** 85: 199-131 *(2)*
35. Sloat MR, Fraser DJ, Dunham J, Falke J, Jordan B, MacMillan B, Olms H (2014) Ecological and evolutionary patterns of freshwater maturation in Pacific and Atlantic Salmonines. ***Reviews in Fish Biology and Fisheries*** *(2)*
34. Fraser DJ, AM Calvert, L Bernatchez, A Coon (2013) Multidisciplinary population monitoring when demographic data are sparse: a case study of remote trout populations. ***Ecology and Evolution 3:*** 4954-4969. *(2)*
33. Fraser DJ (2013) The emerging synthesis of evolution with ecology in fisheries science. ***Canadian Journal of Fisheries and Aquatic Sciences*** 70:1417-1428. *(3)*
32. *Debes PV (PhD), DJ Fraser, MV McBride, JA Hutchings (2013) Multigenerational hybridisation and its consequences for maternal effects in Atlantic salmon. ***Heredity*** 111: 238-247 *(6)*
31. Moore J-S, DJ Fraser (2013) Puny males punch above their weight class to conserve genetic diversity in a declining salmon population. ***Molecular Ecology*** 22: 2364-2365 *(2)*
30. *Meli A (BSc), DJ Fraser (2013) Kinship analysis of brook trout during their breeding migration. ***Journal of Fish Biology*** 82:1514-1522.
29. Palstra FP, DJ Fraser (2012) Effective/census population size ratio estimation: a compendium and appraisal. ***Ecology and Evolution*** 2: 2357-2365. *(35)*
28. *Debes PV (PhD), E Normandeau, DJ Fraser, L Bernatchez, JA Hutchings (2012) Differences in transcription levels among wild, domesticated and hybrid Atlantic salmon (*Salmo salar*) from two environments. ***Molecular Ecology*** 21: 2574-2587. *(20)*
27. *Belmar-Lucero S (MSc), JLA Wood (PhD)*, S Scott (BSc)*, AB Harbicht (MSc)*, JA Hutchings, DJ Fraser (2012) Concurrent habitat and life history influences on effective/census population size ratios in stream-dwelling trout. ***Ecology and Evolution*** 2: 562-573. *(10)*
26. *Houde ALS (MSc), DJ Fraser, PT O'Reilly, JA Hutchings (2011) Relative risks of inbreeding and outbreeding depression in the wild in endangered salmon. ***Evolutionary Applications*** 4: 634-647. *(17)*
25. *Morris MRJ (BSc), DJ Fraser, JD Eddington, JA Hutchings (2011) Hybridization effects on phenotypic plasticity: experimental compensatory growth responses in farmed-wild Atlantic salmon. ***Evolutionary Applications*** 4: 444-458. *(9)*
24. *Houde ALS (MSc), DJ Fraser, PT O'Reilly, JA Hutchings (2011) Maternal and paternal effects on fitness correlates in outbred and inbred Atlantic salmon (*Salmo salar*). ***Canadian Journal of Fisheries and Aquatic Sciences*** 68: 534-549. *(18)*

23. Fraser DJ, LK Weir, L Bernatchez, MM Hansen, EB Taylor (2011) Extent and scale of local adaptation in salmonid fishes: review and meta-analysis. ***Heredity*** 106:404-420. (Invited) *(132)*
22. Fraser DJ, C Minto, AM Calvert, JD Eddington, JA Hutchings (2010) Potential for domesticated-wild interbreeding to induce maladaptive phenology across multiple populations of wild Atlantic salmon. ***Canadian Journal of Fisheries and Aquatic Sciences*** 67:1768-1775. *(8)*
21. Fraser DJ, ALS Houde (MSc)*, PV Debes (PhD)*, PT O'Reilly, JD Eddington, JA Hutchings (2010) Consequences of farmed-wild hybridization across divergent wild populations and multiple traits in salmon. ***Ecological Applications*** 20: 935-953. *(37)*
20. *Houde ALS (BSc), DJ Fraser, JA Hutchings (2010) Fitness-related consequences of competitive ability between farmed and wild Atlantic salmon at different proportional representations of wild-farmed hybrids. ***ICES Journal of Marine Science*** 67: 657-667. *(14)*
19. *Houde ALS (BSc), DJ Fraser, JA Hutchings (2010) Reduced anti-predator responses in multi-generational hybrids between farmed and wild Atlantic salmon. ***Conservation Genetics*** 11: 785-794. *(23)*
18. Normandeau E, JA Hutchings, DJ Fraser, L Bernatchez (2009) Population-specific gene expression responses to hybridization between farm and wild Atlantic salmon. ***Evolutionary Applications*** 2: 489-503. *(33)*
17. Hansen MM, DJ Fraser, K Meier, KLD Mensberg (2009) Sixty years of anthropogenic pressure: a spatio-temporal genetic analysis of brown trout populations subject to stocking and population declines. ***Molecular Ecology*** 18: 2549-2562. *(68)*
16. *Morris MRJ (BSc), DJ Fraser, AJ Heggelin (BSc)*, JW Carr, SF O'Neil, FG Whoriskey, JA Hutchings (2008) Prevalence and recurrence of escaped farmed Atlantic salmon in eastern North American rivers. ***Canadian Journal of Fisheries and Aquatic Sciences*** 65: 2807-2826. *(35)*
15. Fraser DJ (2008) How well can captive breeding programs conserve biodiversity? A review of salmonids. ***Evolutionary Applications*** 1: 535-586. *(186)*
14. Fraser DJ, AM Cook, JD Eddington, P Bentzen, JA Hutchings (2008) Mixed evidence for reduced local adaptation in wild salmon resulting from interbreeding with escaped farmed salmon: complexities in hybrid fitness. ***Evolutionary Applications*** 1: 501-512. *(54)*
13. Hansen MM, DJ Fraser, TD Als, KLD Mensberg (2008) Reproductive isolation, evolutionary distinctiveness, and setting conservation priorities: the case of European lake whitefish and endangered North Sea houting (*Coregonus* spp.). ***BMC Evolutionary Biology*** 8: 137. *(14)*
12. Hutchings JA, DJ Fraser (2008) The nature of fisheries- and farming-induced evolution. ***Molecular Ecology*** 17: 294-313. (Invited) *(213)*
11. Fraser DJ, L Bernatchez (2008) Ecology, evolution and conservation of lake-migratory brook trout: a perspective from pristine populations. ***Transactions of the American Fisheries Society*** 137:1192-1202. *(12)*
10. Fraser DJ, MM Hansen, N Tessier, S Ostergaard, M Legault, L Bernatchez (2007) Comparative estimation of effective population sizes and temporal gene flow in two contrasting population systems. ***Molecular Ecology*** 16: 3866-3889. *(104)*
9. Fraser DJ, LK Weir, TL Darwish, JD Eddington, JA Hutchings (2007) Divergent compensatory growth responses within species: linked to contrasting migrations in salmon? ***Oecologia*** 153: 543-553. *(29)*
8. Fraser DJ, MW Jones, TL McParland, JA Hutchings (2007) Loss of historical immigration and the unsuccessful rehabilitation of extirpated salmon populations. ***Conservation Genetics*** 8:527-546. *(50)*
7. Fraser DJ, T Coon, MR Prince, R Dion, L Bernatchez (2006) Integrating traditional and evolutionary knowledge in biodiversity conservation: a population level case study. ***Ecology and Society*** 11: 4. *(63)*
6. Fraser DJ, P Duchesne, L Bernatchez (2005) Migratory charr schools exhibit population and kin associations beyond juvenile stages. ***Molecular Ecology*** 14: 3133-3146. *(47)*
5. Fraser DJ, L Bernatchez (2005) Allopatric origins of sympatric brook charr populations: colonization history and admixture. ***Molecular Ecology*** 14: 1497-1509. *(41)*
4. Fraser DJ, L Bernatchez (2005) Adaptive migratory divergence among sympatric brook charr populations. ***Evolution*** 59: 611-624. *(46)*

3. Fraser DJ, C Lippé (BSc)*, L Bernatchez (2004) Consequences of unequal population size, asymmetric gene flow and sex-biased dispersal for population structure in brook charr (*Salvelinus fontinalis*). ***Molecular Ecology*** 13: 67-80. *(104)*
2. Gatt MH, DJ Fraser, AP Liskauskas, MM Ferguson (2002) Mitochondrial DNA variation and stock structure of walleyes from eastern Lake Huron: an analysis of contemporary and historical samples. ***Transactions of the American Fisheries Society*** 131: 99-108. *(18)*
1. Fraser DJ, L Bernatchez (2001) Adaptive evolutionary conservation: towards a unified concept for defining conservation units. ***Molecular Ecology*** 10: 2741-2752. *(551)*

OTHER PUBLICATIONS

Hutchings JA, DJ Fraser (2009) Adaptive phenotypic plasticity in Atlantic salmon and Atlantic cod and its relevance to risk assessments of aquaculture. International Council for the Exploration of the Sea (ICES) CM 2009/Q:04. 32 pages.

Heggelin AJ, DJ Fraser, DC Hardie, JA Hutchings (2008) Environmental and human influences affecting the population biology of Nova Scotia brook trout (*Salvelinus fontinalis*). Dalhousie University, NS. 34 pages.

Bernatchez L, Fraser DJ (2005) Mémoire relatif à la creation du Parc Albanel-Témiscamie-Otish, un premier parc habité en forêt boréale – l'omble de fontaine (*Salvelinus fontinalis*) du Lac Mistassini. Technical Report, Développement durable, Environnement et Parcs, Gouvernement du Québec. 12 pages.

Fraser DJ, V Castric, F Bonney, L Bernatchez (2004) Genetic diversity of brook trout (*Salvelinus fontinalis*) in Rapid River, Maine. Technical Report, Maine Department of Inland Fisheries and Wildlife, Strong ME, U.S.A. 10 pages.

INVITED PRESENTATIONS AT INTERNATIONAL/NATIONAL MEETINGS; DISTINCTIVE GUEST LECTURES

13. Fraser DJ (2012) Evolutionary principles in fisheries management: promises and challenges. *J. C. Stevenson Memorial Lecture, Canadian Conference for Fisheries Research, Moncton, NB.*
12. Fraser DJ (2011) Shifting conservation paradigms of local adaptation along the continuum from population declines to population reintroductions. *American Fisheries Society Annual Meeting, Seattle, WA, USA.*
11. Fraser DJ (2011) Lack of resilience? Evolutionary hypotheses for the continual expression of an apparently maladaptive life history in an endangered lineage of Atlantic salmon. *American Fisheries Society Annual Meeting, Seattle, WA, USA.*
10. Fraser DJ (2010) Conceptual issues in restoring species: perspectives for salmonids. *Rubenstein School of Natural Resources & Dept. of Biology, University of Vermont, Burlington, VT, U.S.A.*
9. Fraser DJ (2009) A critique of pathways of effects of aquaculture escapes in Canada. *Pathways of effects of aquaculture workshop, Department of Fisheries and Oceans, Ottawa, ON*
8. Hutchings JA, DJ Fraser (2009) Adaptive phenotypic plasticity in Atlantic salmon and Atlantic cod and its relevance to risk assessments of aquaculture. *International Council for the Exploration of the Sea (ICES), Berlin, Germany.*
7. Fraser DJ (2009) To supplement or not to supplement: genetic considerations associated with stocking of declining fish populations. *Atlantic salmon stocking as a tool in the restoration toolbox – a workshop for community groups. Antigonish, NS.*
6. Fraser DJ (2008) Interbreeding between farmed and wild, endangered Atlantic salmon: conservation conundrum? *Young Investigators Series, University of Washington, Seattle, WA, U.S.A.*
5. Hutchings JA, DJ Fraser (2007) Fishing, farming, and their evolutionary consequences to fishes. *Evolutionary change in human-altered environments, Los Angeles, CA, U.S.A.*
4. Fraser DJ (2006) Recognizing and maintaining diversity within species for viable fisheries. *Genetic consequences of fisheries and fisheries management, Bornholm, Denmark.*
3. Fraser DJ (2006) The interplay between adaptive divergence and evolutionary history in brook charr (*Salvelinus fontinalis*) population divergence: relevance to biodiversity conservation. *TWM Cameron Lecture, Canadian Society of Zoologists, Edmonton, AB.*
2. Fraser DJ, L Bernatchez (2004) Evolution and coaster brook trout conservation: implications from underexploited populations in northern Québec. *American Fisheries Society Symposium, Madison, WI, U.S.A.*
1. Fraser DJ, L Bernatchez (2002) Conserving lineages below the species level: lessons from a review of the Evolutionarily Significant Unit (ESU) concept. *Annual conference of the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), Ottawa, ON.*

OTHER ORAL PRESENTATIONS AT INTERNATIONAL/NATIONAL MEETINGS

**Supervised or co-supervised undergraduate or graduate students as presenters*

- 2015 Canadian Conference for Fisheries Research, Ottawa, ON
- 2015 *Canadian Conference for Fisheries Research, Ottawa, ON (4 presentations)
- 2014 *American Fisheries Society Symposium, Quebec City, QC (4 presentations, 1 poster)
- 2014 *Forum National sur les lacs, Mont Tremblant, QC
- 2014 *Canadian Society for Ecology and Evolution, Montreal, QC (2 presentations, 2 posters)
- 2014 *Groupe Inter-universitaire de Recherche en Limnologie (GRIL) (3 posters)
- 2013 *US Fish & Wildlife Service and Vermont Fish & Wildlife, Burlington, VT, U.S.A
- 2013 Groupe Inter-universitaire de Recherche en Limnologie (GRIL), St. Hippolyte, QC
- 2013 *Groupe Inter-universitaire de Recherche en Limnologie (GRIL) (2 presentations)
- 2012 American Fisheries Society Symposium, Minneapolis, MN, U.S.A.
- 2012 *Evolution first international joint annual meeting, Ottawa, ON (3 presentations)
- 2012 *Groupe Inter-universitaire de Recherche en Limnologie (GRIL), Trois Rivieres, QC
- 2012 *Canadian Conference for Fisheries Research, Moncton, NB (2 presentations)
- 2010 *Canadian Society for Ecology and Evolution, Quebec City, QC (2 presentations)
- 2010 *Canadian Conference for Fisheries Research, Winnipeg, MB
- 2009 European Society of Evolutionary Biology, Torino, Italy
- 2009 Canadian Society for Ecology and Evolution, Halifax, NS (Poster)
- 2008 American Fisheries Society Symposium, Ottawa, ON
- 2008 *Canadian Society for Ecology and Evolution, Vancouver, BC
- 2008 Canadian Conference for Fisheries Research, Halifax, NS
- 2008 *Canadian Conference for Fisheries Research, Halifax, NS (2 presentations)
- 2007 Ecosystem Sciences Division, Department of Fisheries and Oceans, Ottawa, ON
- 2007 Six decades of fishery genetics, Seattle, WA, U.S.A. (Poster)
- 2007 Challenges for diadromous fishes in a dynamic global environment, Halifax, NS (Poster)
- 2007 Evolutionary change in human-altered environments, Los Angeles, CA, U.S.A. (Poster)
- 2006 International Congress on the Biology of Fish, St. John's, NF
- 2004 American Fisheries Society Symposium, Madison, WI, U.S.A. (Poster)
- 2003 American Fisheries Society Symposium, Québec City, QC
- 2003 Canadian Conference for Fisheries Research, Ottawa, ON
- 2002 Ecological and Evolutionary Ethology of Fishes Symposium, Québec City, QC
- 2002 Lowell Wakefield Fisheries Symposium - Genetics of Subpolar fishes, Juneau, AK, U.S.A.

INVITED UNIVERSITY DEPARTMENTAL SEMINARS

- 2015 McGill University, Montreal, QC
- 2015 University of Windsor, Windsor, ON
- 2013 Université de Québec, Montreal, QC
- 2012 Université de Québec, Trois Rivieres, QC
- 2011 Universidad de Chile, Santiago, Chile
- 2011 Memorial University, St. John's, NF
- 2011 Université de Sherbrooke, Sherbrooke, QC
- 2010 Université de Québec, Montreal, QC
- 2010 University of Vermont, Burlington, VE, U.S.A.
- 2010 Université de Montreal, Montreal, QC
- 2010 Concordia University, Montreal, QC
- 2009 McGill University, Montreal, QC
- 2009 University of Alberta, Edmonton, AB
- 2009 Dalhousie University, Halifax, NS
- 2008 University of Washington, Seattle, WA, U.S.A.
- 2007 Concordia University, Montreal, QC
- 2006 Dalhousie University, Halifax, NS

ORAL PRESENTATIONS AT PROVINCIAL MEETINGS/INSTITUTIONS

**Supervised or co-supervised students, or collaborators as first authors and presenters*

- 2014 *Quebec Centre for Biodiversity Science annual meeting (2 posters)
- 2014 *Mistaken Point Ecological Reserve, NL, public outreach talk (presentation with 3 students)

- 2014 *Cree Nation of Mistissini, Mistissini, QC
- 2013 Cree Nation of Mistissini, Mistissini, QC
- 2013 *Concordia University Faculty of Arts & Science Undergraduate Research Day
- 2012 *Quebec Centre for Biodiversity Science annual meeting (three presentations)
- 2012 Marianopolis College, Montreal, QC (Evolutionary principles in conservation biology)
- 2012 Cree Nation of Mistissini, Mistissini, QC
- 2009 Nova Scotia Atlantic Salmon Association Annual Meeting, Guest Speaker, Truro, NS
- 2008 *Trout Nova Scotia Annual General Meeting, Sportsman Show, Halifax, NS
- 2007 *****Atlantic Provinces Council on the Sciences Aquaculture Conference, Saint John, NB
- 2007 *****Atlantic Provinces Council on the Sciences Biology Conference, Saint John, NB
- 2007 Trout Nova Scotia Annual General Meeting, Sportsman Show, Halifax, NS
- 2006 Environnement et Parcs, Gouvernement du Québec, Chibougamau, QC
- 2005 Cree Nation of Mistissini, Société de la faune et des Parcs du Québec (FAPAQ), Société des établissements de plein air du Québec (SEPAQ), Mistissini, QC
- 2004 Conférence annuelle du Québec Océan, Rimouski, QC (Poster)
- 2004 Cree Nation of Mistissini, Cree Trapper's Association, Mistissini, QC
- 2004 Hydro Québec, Eeyou Namess Corporation, Montréal, QC
- 2003 Grand Council of the Crees, Ouje-Bougamau, QC
- 2003 Cree Nation of Mistissini, Société de la faune et des Parcs du Québec (FAPAQ), Société des établissements de plein air du Québec (SEPAQ), Mistissini, QC
- 2002 Société de la faune et des Parcs du Québec (FAPAQ) et la Société des établissements de plein air du Québec (SEPAQ), Chibougamau, QC
- 2001 Cree Nation of Mistissini, Société de la faune et des Parcs du Québec (FAPAQ), Société des établissements de plein air du Québec (SEPAQ), Mistissini, QC
- 2000 Cree Nation of Mistissini, Société de la faune et des Parcs du Québec (FAPAQ), Société des établissements de plein air du Québec (SEPAQ), Mistissini, QC

RESEARCH IN THE MEDIA, OR COMMENTARY ON OTHER RESEARCH IN THE MEDIA

- 2014 Radio: Fish studies in Algonquin Park (CBC, Sudbury, Ontario)
- 2014 Web: Call of the wild: fish stocks adapt more quickly than previously thought (Science Media Centre of Canada)
- 2014 Web: Small populations have more diversity than previously thought (Science Media Centre of Canada)
- 2014 Web & newspapers: 'Why nature adores a hybrid' or 'Farmed fish evolve to be like wild fish' (5 media outlets, including Le Journal du Montreal, and Science Daily)
- 2013 CBC news (PEI): 'Lack of GMO salmon egg export limit puzzles scientists'
- 2012 Newspaper interview: 'Zoos: do they work for captive breeding?' Gulf News, Dubai, UAE
- 2011 Radio: Quirks & Quarks (show); topic: Fish evolution in Canada (CBC, national)
- 2011 Web & newspapers: 'Transplanted fish tend to do better closer to home, study finds' (>30 different media outlets, including the Montreal Gazette, Ottawa Citizen, Vancouver Sun, Calgary Herald**,** and Science Daily)
- 2010 Panel discussion: 'Transformation and biodiversity in art and biology', Concordia U.
- 2010 Web: Mature females key to Beluga Sturgeon survival (www.sciencenews.org)
- 2010 Magazine: Climate change and Fraser River salmon (Canadian Geographic)
- 2009 Web: Molecular Ecology article (18: 2549-2562) highlighted for significant contributions to fisheries science in the 'News & Views' section of the journal
- 2009 Radio: Concerns regarding escaped farmed salmon in the wild (CBC, NS)
- 2009 Radio: Concerns regarding escaped farmed salmon in the wild (CBC, NB)
- 2008 Radio: Will captive breeding bring back endangered wild salmon? (CBC, BC)
- 2008 Web: Fisheries catch-22 - captive breeding aims to conserve biodiversity but plunders genetic diversity (press release to several scientific research, science education, fisheries, and fishing magazine websites)
- 2007 Web: Genetic issues related to re-establishing endangered Atlantic salmon in the Bay of Fundy, eastern Canada (Atlantic Salmon Federation)
- 2007 Newspaper: Why causeway removal on the Petitcodiac River, NB is good for wild salmon and other fishes (Moncton Times, NB)
- 2005 Magazine: Diversité chez l'omble de fontaine du Lac Mistassini (Chasse et Pêche, QC)

- 2004 Magazine: Mistassini Lake fish study (The Nation, a First-Nations publication, QC)
- 2002 Television: Genetics and conservation of brook trout (Canadian Sportfishing TV show)

FUNDING (EXTERNAL AND INTERNAL)

MAJOR SCHOLARSHIPS, GRANTS OR CONTRACTS

$1,380,178.00 in external funding or external in-kind contributions since commencing Assistant Professorship at Concordia U. in 2009 (>$250K/annum)

- 2014-17 NSERC Discovery Accelerator Award ($120,000 over three years; PI)
- 2014-19 NSERC Discovery Grant ($210,000 over 5 years; PI) Adapting to environmental change: driving factors and the persistence of small populations
- 2013-14 Fisheries Health Grant, Niskamoon Corporation ($113,650, one year; PI) Lakescape genetic population structure of lake trout in Mistassini Lake.
- 2013-15 US Fish & Wildlife Service ($170,254 US over three years, PI). Restoration of Atlantic salmon in Lake Champlain.
- 2014 FQRNT Regroupement Strategique Grant (student and field assistant supplement)
- 2013 FQRNT Regroupement Strategique Grant (student and field assistant supplement)
- 2012 NSERC RTI Grant ($33,500, 1 of 7 co-applicants). Field truck for ecology research.
- 2012-13 CFI Leaders Opportunity Fund: DNA Analyzer for high throughput research in molecular ecology and conservation biology ($158,247, PI)
- 2011-12 Fisheries Health Grant, Niskamoon Corporation ($110,000, one year; PI) Genetic monitoring of brook trout in northern Quebec
- 2011-12 In-kind research contribution: Parks Canada Waterton Lakes National Park ($80,000 over 2 years) Restoration of fishless, mountain lakes
- 2011-12 In-kind research contribution: Parks Canada Fundy National Park ($80,000 over 2 years) Reintroduction biology of Atlantic salmon
- 2010-11 In-kind research contribution: Ontario Ministry of Natural Resources ($50,000 over 2 years) Adaptation and plasticity of hybrid and parental trout populations
- 2010-11 FQRNT Nouveaux Chercheurs Grant ($84,797 over 2 years; PI) Long-term consequences of human-induced hybridization between populations
- 2010 NSERC RTI Grant ($31,736; PI, 5 co-applicants) Field truck for ecological research
- 2009-14 NSERC Discovery Grant ($130,000 over 5 years; PI) The nature of genetic diversity, population size and adaptation: applications to conservation biology
- 2009-11 Concordia University new professor equipment start-up fund ($85,000; PI)
- 2007-08 Department of Fisheries and Oceans Contract ($20,000) The role of hatcheries in the conservation of fish biodiversity in Canada
- 2006-09 NSERC Strategic Project research grant ($510,000 over 3 years) Principal writer: Multi-generational interactions between escaped farm and wild Atlantic salmon: a risk assessment perspective (JA Hutchings & L Bernatchez)
- 2005-07 NSERC Postdoctoral Fellowship ($80,000 over 2 years)
- 2002-04 NSERC Postgraduate Scholarship (doctoral) ($42,000 over 2 years)
- 2002-04 NSERC Northern Research Scholarship ($10,000 over 2 years)
- 2002-03 Eeyou Namess Corporation. Conservation genetics of brook charr (research grant) with L Bernatchez ($30,000)

OTHER SCHOLARSHIPS, GRANTS OR CONTRACTS

- 2013 Aid to Research-related events Grant, Concordia University ($5,000)
- 2013 Faculty Optimization Grant, Concordia University ($8,404; PI)
- 2013 Atlantic Salmon Federation Olin Fellowship ($1,000, 1 year)
- 2011 Faculty Optimization Grant, Concordia University ($6,539; PI)
- 2010 Faculty Optimization Grant, Concordia University ($5,200; PI)
- 2009 Center for Independent Experts (CIE) – Pacific salmon biological opinion ($8,000)
- 2007 Trout Nova Scotia, Trout Unlimited Canada and the Ecology Action Centre of Halifax conservation research grant, with DC Hardie and JA Hutchings ($7,500)
- 2007 Evolutionary change in human-altered environments (travel grant) ($500)
- 2006 Atlantic Salmon Federation Olin Fellowship ($1,000, 1 year)
- 2004 Fonds Richard-Bernard et Société Provancher (scholarship) ($2,500)
- 2002 Clemens Rigler Award (travel grant) ($300)

- 2001 Le Fonds Écologique de Anne Vallée (scholarship) ($1,500)

TEACHING ACTIVITIES

COURSE LECTURING

Concordia University
- 2012 Lecturer: Meta-analysis in ecology (Winter – 1 student)
- 2012-now Lecturer: Conservation Biology (Winter – 40 students)(offered every two years)
- 2011 Lecturer: Effects of invasive species on aquatic ecosystems (Winter – 2 students)
- 2010-now Lecturer: Scientific Communication (Fall – 20 students)(offered every year)
- 2010-now Lecturer: Vertebrate Biology (Winter – 72 students)(offered every year)

Dalhousie University
- 2006 Lecturer: Introductory Ecology (Fall -150 students)
- 2006-08 Assistant Lecturer: Conservation Biology (Winter - 40 students) (11 lectures)
- 2006 Assistant Lecturer: Introductory Ecology (Winter - 150 students) (2 lectures)
- 2005-08 Assistant Lecturer: Fish Ecology and Evolution (Fall, Winter-30 students) (8 lectures)
- 2005 Assistant Lecturer: Molecular Ecology (Fall - 10 students) (3 lectures)

Université Laval
- 2004 Assistant Lecturer: Molecular Ecology (Winter - 30 students) (3 lectures)

Guest Lecturing
- 2011 Evolution and genetics in conservation biology (Universidad de Chile, Santiago, Chile)
- 2006 Defining intraspecific conservation units. Graduate Course (Dalhousie U.)
- 2005 How humans cause evolutionary change. Evolution (Dalhousie U.)

STUDENT MENTORING

Postdoctoral Fellows
- 2014-present Paul Debes (Concordia U.)

Research Associates
- 2014 Jacquelyn Wood (Concordia U.)
- 2012-14 Robert Carson (Concordia U.)

PhD Thesis Supervisor or Co-supervisor
- 2013-present Andrew Harbicht “Eco-evolutionary applications to restoring salmon” (Concordia Graduate Scholarship, Concordia U.)
- 2011-present Matthew Yates “Empirical test of the small population paradigm of conservation genetics” (NSERC Postgraduate Scholarship, Concordia U.)
- 2009-14 Jacquelyn Wood “Population size and evolutionary potential in brook trout” (NSERC Postgraduate Scholarship, Concordia U.)
- 2008-13 Paul Debes “Genetic, genomic, and physiological effects of inter-population hybridization in Atlantic salmon” (Dalhousie U. – co-supervised with Dr. Jeff Hutchings)

MSc Thesis Supervisor or Co-supervisor
- 2014-present Elizabeth Lawrence “Population diversity: extent and loss in Canada” (Concordia NSER Scholarship)
- 2014-present Carol Zastavniouk “Effects of habitat fragmentation on sexually-selected and life history traits among different-sized trout populations” (FQRNT Postgraduate Scholarship)
- 2014-present Zachery Wells “Inbreeding and outbreeding depression among different sized trout populations” (Concordia entrance scholarship)
- 2013-present Eric Brunsdon “Meta-analysis of habitat requirements for Atlantic salmon: implications for species restoration (Concordia U., co-supervised by Dr. Jim Grant)
- 2013-present Thais Bernos “Bidirectional pathways between demography and genetics in affecting population persistence”
- 2013-present Kia Marin “Lakescape population structure of lake trout in Mistassini Lake”
- 2010-14 Corey Clarke “Transgenerational effects of early captive exposure in Atlantic salmon” (NSERC Canada Scholar Postgraduate Scholarship, Memorial U., co-supervised by Dr. Craig Purchase)
- 2011-13 Queenie Gray “Prioritizing mountain lakes for restoration after fish introductions”

(Concordia U., co-supervised by Dr. Jim Grant)
- 2010-12 Andrew Harbicht "Ecological correlates of long-term hybridization" (Concordia U.)
- 2010-12 Sebastian Belmar-Lucero "Trout population genetics" (did not finish, Concordia U.)
- 2007-10 Aimee Houde "Inbreeding and outbreeding depression in endangered salmon rehabilitation programs" (NSERC Canada Scholar Postgraduate Scholarship, Dalhousie U.- co-supervised with Dr. Jeff Hutchings)

BSc Thesis Supervisor or Co-supervisor
- 2014-present Lisa Walker (Concordia U.) "Effects of captivity of female reproductive allotment among varying-sized trout populations"
- 2014-present Jessica Mantha (Concordia U.) "Chronosequential assessment of morphological and physiological changes during smoltification in Atlantic salmon"
- 2014-15 Alana Di Vito (Concordia U.) "Effects of outbreeding on fitness among varying sized populations of brook trout"
- 2014-15 Megan Heath (Concordia U.) "Ecological correlates of juvenile dispersal distance among six varying –sized brook trout populations"
- 2012-13 Tom Burdon "Estimating fine-scale divergence times between trout populations" (Concordia U.)
- 2012-13 Thais Bernos "Patterns and correlates of reproductive success across small trout populations" (Concordia U.)
- 2012-13 Defne Tezel "Population size and heritabilities underlying behavioural traits among trout populations" (Concordia U.)
- 2011-12 Alexandre Meli "Density dependence and juvenile dispersal across ten trout populations" (Concordia U.)
- 2011-12 Mikayla Wujec "Genetic and traditional ecological monitoring of northern brook trout populations" (Concordia U.)
- 2010-11 Sherylyne Scott "Environmental correlates of effective size-census size ratios in two brook charr populations" (Concordia U.)
- 2010-11 Matthew Yates "The effects of temperature on the incidence of precocial male maturity in Atlantic salmon (NSERC Undergraduate Scholarship, Dalhousie U., co supervised with Dr. Jeff Hutchings)
- 2008-09 Matthew Morris "Hybridization effects on phenotypic plasticity: a comparison of compensatory growth between farmed, wild and hybrid salmon" (NSERC Undergraduate Scholarship, Dalhousie U.-co-supervised with Dr. Jeff Hutchings)
- 2007-08 Anthony Heggelin "Environmental and human factors affecting the population biology of Nova Scotia brook trout (*Salvelinus fontinalis*)" (Dalhousie U. – co supervised with Dr. Jeff Hutchings and Dr. David Hardie)
- 2006-07 Aimee Houde "Ecological and behavioural interactions at individual and population levels between wild salmon and farmed-wild hybrids" (NSERC Undergraduate Scholarship, Dalhousie U.-co-supervised with Dr. Jeff Hutchings)
- 2003-04 Karen Allard "Origine de l'omble de fontaine du Lac Mistassini/ Phylogeographic origin of brook charr in Mistassini Lake" (U. Laval)
- 2002-03 Catherine Lippé "Structure génétique et la stabilité temporelle des populations d'omble de fontaine du Lac Mistassini/ Population genetic structure and temporal stability of brook charr in Mistassini Lake" (U. Laval, co-supervised by Dr. Louis Bernatchez)

Other training of highly-qualified personnel (HQP)
- 2014 Megan Heath, Summer Research Assistant (Concordia U.)
- 2013 Ryan Beach, Summer Research Assistant (Concordia U.)
- 2013 Sarah Smart-Yates, Summer Research Assistant (Concordia U.)
- 2013 Thais Bernos, Concordia Undergraduate Summer Research Award (Concordia U.)
- 2012 Christine Gaudreau, Fall Research Assistant (Concordia U.)
- 2012 Alexandre Meli, Molecular Genetics Lab Research Assistant (Concordia U.)
- 2012 Pablo Munoz, Visiting MSc Student, Universidad de Chile (Apr-Jun 2012)
- 2012 Philippe Thompson-Leduc, Molecular Genetics Lab Research Assistant (Concordia U.)
- 2012 Destin Joyal, Quantitative Genetics Assistant (Concordia U.)
- 2011-12 Alexandre Meli, NSERC USRA Summer Research Assistant (Concordia U.)
- 2011 Mikayla Wujec, Summer Research Assistant (Concordia U.)

- 2011-12 Morgane Bonamy, Summer/Fall Research Assistant (Concordia U.)
- 2011 Cyndy Desjardins, Fall Research Assistant (Concordia U.)
- 2011 Emily Fobert, Fall Research Assistant (Concordia U.)

STUDENT COMMITTEES AND OTHER SERVICE

- 2012 PhD defense, external examiner: Diana Sharpe, McGill University, Montreal, QC
- 2012 PhD defense, external examiner: Jessica Cote, INRS, Rennes, France
- 2010-14 Chair for thesis defenses (4 students-biology or biochemistry)(Concordia U.)
- 2010 Undergraduate Co-op Student Supervisor (1 student, Dalhousie U.; two semesters)
- 2010-13 Graduate student (PhD) advisory committee (1 student-geography) (Concordia U.)
- 2009-13 Graduate student (PhD) advisory committee (3 students-biology) (Concordia U.)
- 2009-now Graduate student (MSc) advisory committee (8 students-biology) (Concordia U.)
- 2009-now Undergraduate student (BSc) advisory committee (8 students-biology) (Concordia U.)
- 2014-now External examiner, PhD student preliminary exam (1 student-biology)(UQTR)
- 2013-now External examiner, PhD student preliminary exam (2 students-biology)(UQAM)
- 2009-now External examiner, PhD student preliminary exam (4 students-biology)(Concordia U.)
- 2009-now External examiner, PhD defenses (2 students-biology)(Concordia U.)
- 2014-now External examiner, MSc defense (1 student-geography)(Concordia U.)
- 2009-now External examiner, MSc defense (1 student-biology)(Concordia U.)
- 2009 External examiner, PhD student preliminary exam (1 student-biology)(McGill U.)
- 2007-09 Graduate student (MSc) advisory committees (2 students) (Dalhousie U.)
- 2007 Undergraduate Co-op Student Supervisor (2 students, Dalhousie U.; two semesters)
- 2005-06 Teaching Assistant: Evolution (2 semesters, Dalhousie U.)
- 2005 Teaching Assistant: Undergraduate Integrated Science Program (Dalhousie U.)
- 2003 Teaching Assistant: Ichthyology (U. Laval)

ACADEMIC SERVICE

ACADEMIC COMMITTEES AT CONCORDIA UNIVERSITY

- 2014-now Animal Rights and Ethics Committee
- 2014-now Department of Biology Tenure Committee
- 2014-now Faculty Research Committee
- 2014 Search Committee, full-time teaching/equipment technician, Department of Biology
- 2012-13 Search Committee, tenure-track position for community ecology, D. of Biology
- 2011-12 Department of Biology Appraisal Committee
- 2011 Advisory Search Committee for Unit head, Department of Geography
- 2010 Advisory Search Committee for Unit head, Department of Biology
- 2010-11 Steering Committee of Faculty Council
- 2010-14 Arts & Science Elections Evaluation Committee
- 2009-14 Co-organizer, Department of Biology Seminar Committee

PEER REVIEWING EXPERIENCE

Scientific journals and funding organizations

I am presently an associate editor of *Evolutionary Applications*, where I review 20-30 paper submissions per year.

I was also an associate editor of *Canadian Journal of Fisheries and Aquatic Sciences* between 2009 and 2013 where I reviewed on average one paper per month.

I also review on average one paper or grant application every six-eight weeks and have served as a reviewer for the following 36 journals and funding organizations: *National Science Foundation (NSF), Natural Sciences and Engineering Research Council of Canada (NSERC, Discovery and Strategic Grants Research Programs), National Geographic Society, Washington Sea Grant, Ecology Letters, Ecology, Evolution, Molecular Ecology, Proceedings of the Royal Society of London Biological Sciences, Philosophical Transactions of the Royal Society Biological Sciences, Conservation Biology, Evolutionary Applications, Ecological Applications, Journal of Evolutionary Biology, Oecologia, Evolutionary Ecology, Journal of Animal Ecology, Heredity, PLOS (Public Library of Science) One, Conservation Genetics, Biological Conservation, Biological Journal of the Linnean Society, Canadian*

Journal of Fisheries and Aquatic Sciences, BMC Ecology, BMC Evolutionary Biology, Transactions of the American Fisheries Society, Ecology of Freshwater Fish, Journal of Fish Biology, Great Lakes Fishery Trust (GLFT), Invertebrate Biology, Animal Genetics, Environmental Biology of Fishes, Hydrobiologia, Aquatic Living Resources, Journal of Great Lakes Research, Chinese Journal of Oceanology and Limnology

Non-governmental organizations

As a member of COSEWIC's Freshwater Fish Species Specialist Committee, I am responsible for routinely reviewing status reports of endangered/threatened fish species in Canada, and for recommending status designations according to criteria stipulated in the *Species At Risk Act* (*SARA*).

Governmental agencies

- 2013 Department of Fisheries and Oceans Canada, Biotechnology division, Risk assessment of genetically-modified Atlantic salmon production
- 2009 U.S. National Marine Fisheries Service, Pacific salmon biological opinion
- 2009 Department of Fisheries and Oceans Canada, Pathway of effects of escaped aquaculture organisms or their reproductive material on natural ecosystems in Canada
- 2009 Department of Fisheries and Oceans Canada, Atlantic salmon captive breeding program
- 2008 U.S. Fish and Wildlife Service, Endangered Species Act (Coaster brook trout petition)
- 2008 Department of Fisheries and Oceans Canada, Atlantic salmon captive breeding program
- 2007 Pacific Scientific Advice Review Committee, Department of Fisheries and Oceans Canada, Conservation units for Pacific salmon under the Wild Salmon Policy

VOLUNTEER WORK, CURRENT OR PAST PROFESSIONAL SOCIETY MEMBERSHIPS

- 2011 Judge, Undergraduate Research Day, Concordia University
- 2010 Co-founder: Charity for an educational book trust for a Tanzanian village through CODE (*Canadian Organization for Development through Education*) (raised and donated $2305 thus far)
- 2010 Judge, Quebec Provincial High School Science Fair, Montreal, QC
- 2009 Symposium Co-chair, Canadian Society for Ecology and Evolution annual meeting
- 2008 Session Chair, Evolutionary Ecology, Canadian Conference for Fisheries Research
- 2007-2008 Department of Biology Seminar Committee, Dalhousie University
- Society for Conservation Biology
- Society for the Study of Evolution
- European Society of Evolutionary Biology
- Canadian Society for Ecology and Evolution
- Canadian Society of Zoologists

Andrew P. Martin, Ph.D.

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University of Colorado, Boulder, CO 80309-0334
Phone: 303-325-1790 FAX: 303-492-8699
Email: am@colorado.edu

Present Position

Professor

Employment & Professional Experience

2010-present	Professor, Dept of EBIO, University of Colorado
2002-2010	Associate Professor, Dept of EBIO, University of Colorado
2004-present	Affiliate Professor, Dept of Molecular and Microbiology, Colorado State University
2004-2005	Associate Chair, Dept of EBIO, University of Colorado
1998-2002	Assistant professor, Dept of EPOB, University of Colorado
1994-1998	Adjunct professor, Friday Harbor Marine Labs, Univ. of Washington.
1994-1998	Assistant professor, University of Nevada-Las Vegas
1992-1994	Postdoctoral scientist, Smithsonian Tropical Research Institute
1990	Contractor, National Marine Fisheries Service, NOAA.

Degrees

PhD	1992	Zoology, University of Hawaii
MS	1990	Zoology, University of Hawaii
BS	1986	Renewable Natural Resources, University of Arizona

Awards and Fellowships

2013	CU College Scholar Award
2012	National Academies Education Fellow in Life Sciences
2005	CU Faculty Fellowship
1997	Smithsonian Institute Senior Scientist Fellowship
1992	Smithsonian Institution Tupper 3-year Fellowship

Record of Grant Support

1) National Park Service, 2013-2016, "Genetics analysis of trout populations", $45,000.
2) UC Seed Grant Program, 2013-2014, "Genomics of Genetic Rescue", $48,000.
3) Science Education Initiative, 2011-2014, "Reforming EBIO's educational mission." $480,000.
4) National Park Service, 2010-2014, "Genetic analysis of trout populations", $51,000.
5) CDOW, 2009-2011, "Range Wide Survey of Gunnison Prairie Dogs", $50,000.
6) National Park Service, USFS, BLM, etc., 2009-2012, "Using DNA from museum specimens to explore the heritage and native range of Colorado's state fish", $105,000.
7) NIH, 2009-2012, "New tools for understanding the composition and dynamics of microbial communities in human body habitats", Co-PI (R. Knight, PI), $1,130,600.
8) NSF, 2008-2009, Population and Systematic Biology, "Islands on islands on islands: phylogenetic analysis of microbial communities in fleas on prairie dogs in Boulder County." $11,470.
9) USFWS, 2008-2010, "Genetics of the endangered Mojave niterwort", $27,000.
10) USFWS, 2007-2009, "Genetics of pupfish populations", $71,000.
11) National Park Service, 2007-2008, "Genetic analysis of trout populations", $39,000.
12) NSF, Integrative and Organismal Biology, Collaborative Research, 2007-2009, "Evolution of hammerhead shark cephalofoil", $400,000.
13) USFWS, 2005-2006, "Analysis of MHC Diversity in Historic and Restoration Populations of Greenback Cutthroat Trout", $2700.
14) NSF, Microbial Observatory Program, 2005-2010, "Microbial Biogeochemistry and functional diversity across the Forest-Tundra ecotone in the Rocky Mountains", Co-PI (w/ S. Schmidt, J. Neff, and R. Guralnick), $2,000,000.
15) NDOW/USFWS, 2005-2006. "Conservation Genetics of Devils Hole Pupfish", $7,000.
16) NSF, Biotic Surveys and Inventory, 2004-2007, "Discovery, Description and Biogeography of Novel Alpine Fungi", Co-PI (w/ S. Schmidt), $280,000.
17) National Park Service, 2003-2004, "Determine and Establish appropriate source populations for restoration of native trout subspecies in Rocky Mountain National Park", $61,870.
18) NSF, GK-12 Training grant. 2002-2005, "Partners in Science Education: GK-12 Fellows at CU Boulder, Co-PI, $1,359,348.
19) NSF, Doctoral Dissertation Improvement, 2002-2003, "Phylogeography of alpine butterflies and their host plants. $10,000.
20) NSF/NIH, 2002-2007, "Landscape Effects on Disease Dynamics in Prairie Dogs", Co-PI (w/ S. Collinge), $1,750,000.

21) NSF, Molecular and Cellular Biology, 2000-2004, "Microbial Biogeochemistry and functional diversity across the Forest-Tundra ecotone in the Rocky Mountains", Co-PI (w/ S. Schmidt), $1,000,000.
22) Nevada Division of Wildlife, 2000-2002, "Conservation genetics of endangered poolfishes", $7,500.
23) CU-CRCW, 2000-2001, "Conservation genetics of endangered poolfishes", $5,539.
24) NSF, 2000-2001, REU Supplement, $5,000.
25) Smithsonian Institution, 1999, Senior Scientist Fellowship, "Biogeography of freshwater fishes", $8,000.
26) NSF, Systematic Biology, 1999-2002, "Using complex multigene family trees in systematics: the hsp 70 gene family $150,000.
27) NSF, Doctoral Dissertation Improvement, 1999-2000, "Evolutionary genetics of small populations", $10,000 (with J. Wilcox).
28) NSF, REU Supplement, 1997, $5,000.
29) NSF EPSCoR Program, 1997, Seed Grant, $5,000.
30) UNLV, Faculty Development Award, 1997, $3,000.
31) University of Nevada, Las Vegas, 1997-1999, "Development of a conservation genetics program for endangered fishes", $7,500.
32) Nevada Division of Wildlife, 1997-1999, "Development of a conservation genetics program for endangered fishes", $7,500.
33) USFWS, Endangered Species Grant, 1997-2000, "Conservation genetics of pupfish", $9,500.
34) NSF, Systematic Biology, 1996-1999, "Molecular systematics of lamniform sharks using creatine kinase genes", $90,000.
35) National Geographic Society, 1993, "Historical biogeography of the Amazon basin", $21,000.
36) Smithsonian 3-year fellowship, Tupper Fellowship, 1992-1994, "Historical biogeography of neotropical freshwater fishes", $105,000.
37) RCUH, Predoctoral Fellowship, 1990-1992, University of Hawaii, 2 years, $28,000.

Peer-reviewed publications

1)Gubili, C., C. S. Jones, G. Cliff, S. P. Wintner, E. de Sabata, R. M. Aspden, A. P. Martin, D. W. Sims, and L. R. Noble. 2014. Insights into white shark colonization and genetic diversity from historical artifacts. Endangered Species Journal (in press).
2)Mara, K, A. P. Martin, R.Hueter, and P. Motta. 2014, Constructional morphology within the head of hammerhead sharks (Sphyrnidae). Journal of Morphology (in press).
3)Keepers, K. G., A. P. Martin. 2014. Fitness landscapes of sympatric pupfish: a useful tool for visualizing speciation. Molecular Ecology 23: 2144-2145. http://onlinelibrary.wiley.com/doi/10.1111/mec.12727/full
4)Sackett, L. C., A. Seglund, R.P. Guralnick, M.M Mazzella, D.M. Wagner, J.D. Busch, A.P. Martin. 2014. Evidence for two subspecies of Gunnison's prairie dogs (*Cynomys gunnisoni*), and the general importance of the subspecies concept. *Biological*

Conservation, in press. http://dx.doi.org/10.1016/j.biocon.2014.03.010
5)Paulson, E. L., A. P. Martin. 2013. Discerning invasion history in an ephemerally connected system: landscape genetics of *Procambaraus clarki* in Ash Meadows, Nevada. Biological Invasions DOI 10.1007/s10530-013-0621-x
6)Martin, A. P., E. L. Paulson, and R. Graham. 2013. Geographically disjunct and widepread genets in an endangered halophilic plant, the Amargosa Niterwort (*Nitrophila mohavensis*). Conservation Genetics DOI 10.1007/s10592-013-0486-7.
7)Sackett, L. C., S. K. Collinge, and A. P. Martin. 2013. Do pathogens reduce the genetic diversity of their hosts? Variable effects of sylvatic plague in black-tailed prairie dogs. Molecular Ecology 22: 2441-2455.
8)Knight, R., M. E. Lladser, A. P. Martin, S. E. Brenner. 2012. New tools for understanding the composition and dynamics of microbial communities. Encyclopedia of Metagenomics (in press).
9)McCafferty, S. S., A. P. Martin and E. Bermingham 2012. Pliocene diversification and phylogeography of the lower Mesoamerican cichlid *Aquidens coeruleopunctuatus* (Cihlidae). International Journal of Evolutionary Biology (in press).
10) Metcalf, J. L., S. Love-Stowell, C. M. Kennedy, K. B. Rogers, D. McDonald, J. Epp, K. Keepers, A. Cooper, J. J. Austin, A. P. Martin. 2012. Historical stocking data and 19th century DNA reveal human-induced changes to native diversity and distribution of cutthroat trout. Molecular Ecology 21: 5194-5207.
11) Gubili, C, C. A. J. Duffy, G, Cliff, S. P. Wintner, M. Shivji, D. Chapman, B. D. Bruce, A. P. Martin, D. W. Sims, C. S. Jones and L. R. Noble. 2012. Application of molecular genetics for conservation of the White Shark, *Carcharodon carcharias*. Ch. 24 in M. L. Domeier (ed.) Global Perspectives on the Biology and Life History of the White Shark, CRC Press.
12) Jones, R. T., S. A. Bernhardt, A. P. Martin, K. L. Gage. 2012. Interactions among symbionts of *Oropsylla* spp. (Siphonoptera: Ceratophyllidae). Journal of Medical Entomology 49: 492-496..
13) Martin, A. P., A. A. Echelle, G. Zegers, S. Baker, and C. L. Keeler-Foster. 2012. Dramatic shifts in the gene pool of a managed population of an endangered species may be exacerbated by high genetic load. Conservation Genetics: 13: 349-358
14) Sackett, L. C., T. B. Cross, R. T. Jones, W. Johnson, K. Ballare, C. Ray, S. K. Collinge and A. P. Martin. 2012. Connectivity of prairie dog colonies in an altered landscape: inferences from analysis of microsatellite DNA variation. Conservation Genetics 13: 407-418.
15) Brinkerhoff, R. J., A. P. Martin, R. T. Jones, and S. K. Collinge. 2011. Population genetic structure of the prairie dog flea and plague vector *Oropsylla hirsuta*. Parasitology 138: 71-79.
16) Robeson, M., A. P. Martin, S. K. Schmidt,, A. King, et al. 2011. Bdelloid rotifer communities: extremely diverse at global scales and spatially autocorrelated at local scales. Proceedings National Academy of Sciences USA 108: 4406-4410..
17) Gubili, C., R. Bilgin, E. Kalkan, S. U. Karhan, D. W. Sims, H. Kabasakal, A. P. Martin, C. S. Jones, L. R. Noble. 2011. Antipodean white sharks on a Mediterranean walkabout?: historical dispersal of a top marine predator accounts for an endangered anomalous population. Proceedings Royal Academy of Sciences B 278: 1679-1686. *Media coverage included*

Time, Nature, BBC, Discovery, MSNBC.

18) Martin, A. P. 2010. Conservation genetics of Ash Meadows pupfish populations. I. The Warm Springs pupfish *Cyprinodon nevadensis pectoralis*. Conservation Genetics 11: 1847-1857.
19) Robeson, M, S., E. K. Costello, K. R. Freeman, J. Whiting, B. Adams, A. P. Martin, S. K. Schmidt. 2010. Environmental DNA sequencing primers for eutardigrades and bdelloid rotifers. BMC Ecology 9: 25.
20) Lim, D., K. Mara, P. Motta and A. P. Martin. 2010. Phylogeny of hammerhead sharks (Family Sphyrnidae) inferred from mitochondrial and nuclear genes. Molecular Phylogenetics and Evolution 55: 572-579. *Media coverage included ScienceDaily, Discovery*.
21) Sackett, L. C., L.K. Etchberger, M.N. Mazzella, D.D. Lim, A. P. Martin. 2009. Characterization of 18 microsatellite loci for three species of prairie dogs. Molecular Ecology Resources 10: 232-236.
22) Freeman, K. R., A. P. Martin, D. Karki, M. S. Mitter, A. F. Meyer, J. E. Longcore, D. R. Simmons, and S. K. Schmidt. 2009. Evidence that Chytrids dominate fungal communities and decomposition processes in high-elevation soils. Proceedings of the National Academy of Sciences USA 106: 18315-18320.
23) Jones, R. J, R. K. Knight, and A. P. Martin. 2009. Bacterial communities of prairie dog fleas sampled across time, space and flea species. ISME J. 4: 223-231.
24) Eaton, M. J., G. L. Myers, S.-O. Kolokotronis, M. Leslie, A. P. Martin, and G. Amato. 2009. Barcoding bushmeat: molecular identification of Central African and South American harvested vertebrates. Conservation Genetics 11: 1389-1404. *Media coverage included ScienceDaily*,
25) Pritchard, V. L., J. L. Metcalf, K. Jones, A. P. Martin and D. E. Crowley. 2008. Population structure and genetic management of Rio Grande cutthroat trout (*Oncorhynchus clarkii virginalis*). Conservation Genetics 10: 1209-1221.
26) Eaton, M. J., A. P. Martin, and G. Amato. 2008. Molecular and geographic evidence of speciation of African dwarf crocodiles (*Osteolaemus tetraspis* ssp.) across Central and West Africa. Molecular Phylogenetics and Evolution (In press).
27) Mayhew, L. E. D. Swanner, A. P. Martin and A. Templeton. 2008. Phylogenetic relationships and functional genes: distribution of a manganese-oxidizing gene (mnxG) in *Bacillus* species. Applied and Environmental Microbiology 74: 7265-7271.
28) Schmidt, S. K., S.C. Reed, D. R. Nemergut…and A.P. Martin. 2008. The early stages of ecosystem succession in high-elevation (5000 meters above sea level) recently deglaciated soils. Proceedings of the Royal Society B 275: 2793-2802.
29) Nemergut, D.R., M. S. Robeson, R. F. Kysela, A. P. Martin, S. K. Schmidt and R. Knight. 2008. Insights and inferences about integron evolution from genomic data. BMC Genomics 9: 261-271.
30) Bai, Y., M. Kosoy, A. Martin, C. Ray, K. Sheff, L. Chalcraft and S. K. Collinge. 2008. Characterization of *Bartonella* strains isolated from Black-tailed Prairie Dogs (*Cynoyms ludovicianus*). Vector Borne Zoonotic Diseases 8: 1-5.

31) Porter, T. M., C. W. Schadt, L. Rizvi, A. P. Martin, S. K. Schmidt, L. Scott-Denton, R. Vilgalys, J.-M. Moncalvo. 2008. Widespread occurrence and phylogenetic placement of a soil clone group adds a prominent new branch to the fungal tree of life. Molecular Phylogenetics and Evolution 46: 635-644.
32) Metcalf, J. L. M. Siegel and A. P. Martin. 2008. Hybridization dynamics between greenback cutthroat trout and rainbow trout. Heredity 99: 149-156.
33) Jones, R. J, K. McCormick and A. P. Martin. 2008. Bacterial symbionts of fleas that vector diseases in small mammals. Applied and Environmental Microbiology 74: 1667-1670.
34) Metcalf, J. L., V. L. Pritchard, S. M. Silvestri, J. B. Jenkins, J. S. Wood,, D. E. Cowley, P. R. Evans, D. K. Shiozawa and A. P. Martin. 2007. Across the Great Divide: genetic forensics reveals misindentification of endangered cutthroat trout populations. Molecular Ecology 16: 4445-4454. *Media coverage included NY Times, Science Daily, Nature, Daily Camera, Rocky Mountain News, Earthwatch Radio.*
35) Pritchard, V. L., K. Jones, J. L. Metcalf, A. P. Martin, Y. Perot, K. Patten, P. Wilkinson, and D. E. Crowley. 2007. Characterization of tetranucleotide microsatellitees for Rio Grande cutthroat trout (*Onchorhynchus clarkii virginalis*) and rainbow trout (*O. mykiss*), and their cross-amplification in other cutthroat trout subspecies. Molecular Ecology Notes 7: 594-596.
36) Schmidt, S. K., E. K. Costello, D. R. Nemergut, C. C. Cleveland, M. N., Weintraub, A. F. Meyer and A. P. Martin. 2007. Biogeochemical consequences of rapid microbial turnover and seasonal succession in soil. Ecology 88: 1379-1385.
37) Nemergut, D. R., S. P. Anderson, C. C. Cleveland, A. P. Martin, A. E. Miller, A. Seimon and S. K. Schmidt. 2007. Microbial community succession in an unvegetated deglaciated soil. Microbial Ecology 53: 110-122.
38) Vignieri, S. N., E. M. Halllerman, B. J. Bergstrom, D. J. Hafner, A. P. Martin, P. Devers, P. Grobler and N. Hitt. 2006. A wolf in sheep's clothing: Ramey et al.'s semantic debate of "taxonomic validity undermines conservation of an evolutionary distinctive lineage. Animal Conservation 9: 237-243.
39) Martin, A. P. 2006. Advocacy dressed up as science: a comment on Ramey et al. 2005. Animal Conservation 9: 248-249.
40) Jones, R. T. and A. P. Martin. 2006. Testing for differentiation of microbial communities using phylogenetic methods: accounting for uncertainty of phylogenetic inference and character state mapping. Microbial Ecology 52: 408-17.
41) Wilcox, J. L. and A. P. Martin. 2006. The Devil's in the Details: Genetic and phenotypic divergence between artificial and native populations of the endangered pupfish *Cyprinodon diabolis* Animal Conservation 9: 316-321.
42) DeChaine, E. G. and A. P. Martin. 2006. Quaternary climate cycles inhibited co-divergence in an alpine plant-insect association. Evolution 60: 1004-1013.
43) Duncan, K. M., A. P. Martin, B. W. Bowen and H. G. de Couet. 2006. Global phylogeography and population structure in the scalloped hammerhead shark (*Sphyrna lewini*). Molecular Ecology 15: 2239-2251.

44) DeChaine, E. G. and A. P. Martin. 2005. Historical biogeography of two alpine butterflies in the Rocky Mountains: broad scale concordance and local-scale discordance. Journal of Biogeography 32: 1943-1952.
45) Collinge, S.K., W.C. Johnson, C. Ray, R. Matchett, J. Grensten, J.F. Cully, Jr., K.L. Gage, M.Y. Kosoy, J.E. Loye, and A.P. Martin. 2005. Landscape structure and plague occurrence in black-tailed prairie dogs. Landscape Ecology 20: 941-955..
46) Collinge, S. K., W. C. Johnson, C. Ray, R. Matchett, J. Grensten, J. F. Cully, Jr., K. L. Gage, M. Y. Kosoy, J. E. Loye, and A. P. Martin. 2005. Testing the generality of a trophic cascade model for plague. Ecohealth 2: 1-11.
47) Jones, R, A. Mitchell, S. Collinge, C. Ray and A. P. Martin. 2005. Characterization of 14 polymorphic microsatellites markers for the black-tailed prairie dog (*Cynomys ludovicianus*). Molecular Ecology Notes 5: 71-74.
48) DeChaine, E. G. and A. P. Martin. 2005. Marked genetic divergence among sky island populations of *Sedum lanceolatum* (Crassulaceae) in the Rocky Mountains. American Journal of Botany 92: 477-486.
49) Martin, A. P. and J. L. Wilcox. 2004. Evolutionary history of Ash Meadows pupfish (genus *Cyprinodon*) populations inferred using microsatellite markers. Conservation Genetics 5: 769-782.
50) Davelos, A.L., K. Xiao, A. P. Martin, D. A. Sumac and L. L. Kinkel. 2004. Spatial variation in *Streptomyces* genetic composition and diversity in a prairie soil. Microbial Ecology 48: 601-612.
51) Martin, A. P., E. K. Costello, A. Meyer, D. R. Nemergut and S. K. Schmidt. 2004. The rate and pattern of cladogenesis in microbes. Evolution 58: 946-955.
52) Nemergut, D. R., A. P. Martin and S. K. Schmidt. 2004. Integron diversity in heavy metal contaminated mine tailings and inferences about integron evolution. Applied Environmental Microbiology 70: 1160-1168.
53) Winchell, C. W., A. P. Martin and J. A. Mallet. 2004. Molecular phylogeny of d7ifferentiation: Using LSU andd SSU ribosomal RNA genes to evaluate morphology-based hypotheses. Molecular Phylogenetics and Evolution 31: 214-224.
54) Meyer, A., D. Lipson, A. Martin, C. Schadt and S. Schmidt. 2004. Molecular and metabolic characterization of cold tolerant, alpine soil Pseudomonas Sensu Stricto. Applied and Environmental Microbiology 70: 483-489.
55) DeChaine, E. G. and A. P. Martin. 2004. Historic cycles of expansion and contraction in *Parnassius smintheus* (Papilionidae) inferred using mitochondrial DNA. Evolution 58: 113-127.
56) Schadt, C. W, A. P. Martin, D. A. Lipson and S. K. Schmidt. 2003. Seasonal dynamics of previously unknown fungal lineages in tundra soils. Science 301: 1359-1361.
57) Martin, A. P. 2002. Phylogenetic approaches for describing and comparing microbial communities. Applied and Environmental Microbiology 68: 3673-3682.
58) Martin, A. P. and T. M. Burg. 2002. Perils of paralogy: Using HSP70 genes for inferring organismal phylogenies. Systematic Biology 51: 570-587.

59) Martin, A. P., A. Pardini, C. Jones and L. Noble. 2002. Conservation of a microsatellite locus in sharks. Molecular Phylogenetics and Evolution 23: 205-213.
60) Burg, T. M., J. Wilcox, and A. P. Martin*. 2002. Polymorphic microsatellite loci from pupfish (genus *Cyprinodon*). Conservation Genetics 3: 197-204.
61) Martin, A. P. 2001. The phylogenetic placement of Chondrichthyes: Inferences from analysis of multiple genes and implications for comparative studies. Genetica 111: 349-357.
62) Pardini, A. T., C. S. Jones, L. R. Noble, B. Kreiser, H. Malcolm, B. D. Bruce, J. D. Stevens, G. Cliff, M. C. Scholl, M. Francis, C. A. J. Duffy and A. P. Martin*. 2001. Sex-biased dispersal in great white sharks. Nature 412: 139-140.
63) Martin, A. P. 2001. Is tetralogy real: testing the assumptions of the "one-to-four rule". Molecular Biology and Evolution 18: 89-93.
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77) Martin, A. P., R. Humphreys, and S. R. Palumbi. 1992. Population genetic structure of the armorhead, *Pseudopentaceros wheeleri*, in the North Pacific Ocean: Application of PCR to fisheries problems. Canadian Journal Fisheries & Aquatic Science 49: 2386-2391.
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82) Martin, A. P. and C. Simon. 1990. Variation in insect life cycles and its evolutionary significance: Lessons from periodical cicadas. Bioscience 40: 359-367.
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84) Simon, C. and A. P. Martin. Periodical cicadas. 1989. Nature 341: 288-289.
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86) Martin, A. P. & C. Simon. 1988. Anomalous distribution of nuclear and mitochondrial gene markers in periodical cicadas. Nature 336: 237-239.

Peer-reviewed book chapters

87) Jones, R. P., E. K. Costelllo, and A. P. Martin. 2007. Phylogenetic approaches for the study of soil microbial communities. Pp. 608-617 in Manual of Environmental Microbiology, 3rd Ed., AEM Press, Washington, DC.
88) Martin, A. P. 2007. Back from the brink of extinction: A tale of two fishes. Healing The West, Center for the American West, Island Press.
89) Martin, A. P. 1999. Molecular clocks. In Encyclopedia of Life Sciences, MacMillan Press.

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91) Martin, A. P. 1997. Systematics of the Lamnidae and the origination time of *Carcharodon carcharias* inferred from the comparative analysis of mitochondrial DNA sequences, pgs. 49-54 in P. Klimley and D. Ainsley (eds.) The Biology of the White Shark, Academic Press, NY.
92) Bermingham, E., S. MacCafferty, and A. P. Martin. 1997. The Isthmus of Panama, molecular clocks, and the historical biogeography of neotropical freshwater fishes. In T. D. Kocher and C. Stepien (eds.) Molecular Systematics of Fishes. Academic Press, New York.
93) Naylor, G. J. P., A. P. Martin, E. Mattison, and W. M. Brown. 1997. The inter-relationships of lamniform sharks: Testing phylogenetic hypotheses with sequence data. In T. D. Kocher and C. Stepien (eds.) Molecular Systematics of Fishes. Academic Press, New York.
94) Bermingham, E., H. Banford, A. P. Martin and V. Aswani. 1997. Smithsonian Tropical Research Institute Neotropical Fish Collections. Pp. 37-38 in L. Malabarba (ed.) Neotropical Fish Collections. Museo de Ciencias e Tecnologia, PUCRS, Puerto Alegre, Brazil.
95) Martin, A. P. 1991. Application of mitochondrial DNA sequence analysis to the problem of species identification of sharks. NOAA NMFS 115: 53-59.

Technical Reports and other Non-Peer Reviewed Publications

1) Martin, A. P. 2007. Genetics management plan for the Devils Hole pupfish. Technical report, USFWS, 122 p.
2) Martin, A. P. 2007. Genetics management plan for the Warm Springs pupfish, Technical report for the USFWS, 37 p.
3) Martin, A. P. 2005. Comparison of Sequence Variation in the Major Histocompatibility Complex Between Como Creek and Restoration Populations Originating from Como Creek Stock. Report submitted to the United States Fish and Wildlife Service.
4) Martin, A. P. 2005. Genetic Analysis of *Cyprinodon diabolis*: Hybridization With *C. nevadensis* in the Point of Rocks Refuge. Report submitted to the Nevada Division of Wildlife and the USFWS.
5) Martin, A. P., J. Mitton and J. Metcalf. 2005. Describe existing populations and determine the appropriate source populations for restoration of native trout subspecies in Rocky Mountain National Park utilizing mitochondrial and nuclear DNA markers. Submitted to National Park Service and US Fish and Wildlife Service.
6) Winchell, C. J., A. P. Martin and J. Mallatt. 2001. Phylogeny of living differentiation based on LSU and SSU rRNA-gene sequences. American Zoologist 1: 1627-1628.

7) Wilcox, J. & A. P. Martin*. 2001. Report on the studies of the Devil's Hole pupfish. National Parks Service Technical Report, 55 p.
8) Wilcox, J., C. Serway, J. Stein & A. P. Martin*. 2001. Systematics and conservation genetics of the tui chub (*Siphateles bicolor*) in Nevada. Nevada Division of Wildlife, Annual Report.
9) Martin, A. P. and J. Wilcox. 1999. Conservation genetics of Ash Meadows pupfish. Report to the United States Fish and Wildlife Service, 33 p.
10) Kessing, B. K., A. P. Martin, H. Croom, W. O. MacMillan, S. Romano, & S. R. Palumbi. 1991. The Simple Fool's Guide to PCR. University of Hawaii, Special Publication (over 3000 copies reproduced and distributed by the authors).

Popular Articles

1) Martin, A. P. 2004. Endangered Species, Daily Camera, August 1st.
2) Martin, A. P. 1993. If I had a hammerhead. BBC Nat. History. 12: 12-13.

Professional Peer Review

1) USFWS, Gunnison prairie dog, Durango, Colorado. 2013
2) USFWS, Greenback cutthroat trout, Lakewood Colorado, 2014
3) USWFS & NPS, Devils Hole Pupfish, Ft Collins, CO, 2008
4) USFWS, Lahontan cutthroat trout, Reno, NV, 2005

Manuscript reviews (regular service)

1) Molecular ecology
2) Microbial ecology
3) Evolution
4) Conservation genetics

Grant review panelist

1) National Science Foundation, Genealogy of Life panel, Washington DC, 2014
2) National Science Foundation, Systematics panel, Washington DC, 2013
3) National Science Foundation, Systematics panel, Washington DC, 2012
4) National Science Foundation, GK12 Education panel, Washington DC, 2008

Workshops Attended or Organized

1) SEI Summer Education Workshop, CU, 2014 (organizer/leader)
2) Summer Institute, National Academies Education Workshop, 2013 (participant)
3) CREATE Education Workshop, 2013 (participant)
4) SEI Summer Education Workshop, CU, 2013 (organizer/leader)
5) SEI Summer Education Workshop, CU, 2012 (organizer/leader)

Presentations at Symposia and Conferences and Invited Talks (since 2001)

1) 2014, “Network analysis in the classroom”, Evolution meetings, UNC, Chapell-Hill, NC.
2) 2014, “Genetic rescue of a small, isolated population”, Evolution meetings, UNC, Chapell-Hill, NC
3) 2014, “Measuring hard to measure learning goals using network analysis”, DBER, CU
4) 2014, “Genomics of cutthroat trout”, Desert Fish Council, Cabo San Lucas, Mexico (with Sierra Love-Stowell)
5) 2013, "Cultural traits as the focus for student demonstration of evolutionary analysis process skills", Evolution Meetings, Snowbird UT.
6) 2013, "Transforming Undergraduate Teaching: Three Recommendations", Keynote address, CSL Annual Meeting, University of Colorado (w/ N Barger and AM Hoskinson)
7) 2013, "Genetic Restoration of Small Spring Populations", Denver University
8) 2013, "Genetic Restoration of Small Spring Populations", University of Northern Colorado
9) 2012, "Flipping Out in the Classroom", Keynote speaker at a medical education meeting, University of Colorado Medical School
10) 2012, "Invasive crayfish in a desert spring system: Using landscape genetics to inform ecological restoration", E. Paulson, A. Martin, Ecological Society of America, Portland, OR.
11) 2010, “Sylvatic plague extirpation causes evolution in prairie dogs,” L. Sackett, A. Martin, and S.K. Collinge, Evolution, Portland, Oregon, June 2010 (Poster)
12) 2009, “Conservation Genetics of Spring Populations”, Desert Fish Council Meetings, Death Valley, CA.
13) 2009, Department of Ecology and Evolutionary Biology, University of Arizona. “Microbial Diversity: The Alpine Microbial Observatory and the Vector Microbiome Projects.”
14) 2008, International Meeting of the Desert Fish Council, “Genetics of Spring Populations”, Cuatro Cienagas, Mexico.
15) 2008, International Conference on Genetics, Berlin, “Population Genetics of Southern Rocky Mountain Cutthroat Trout” (D. Crowley, NMSU)
16) 2007, UCLA Conference on Evolution in a Changing World, “Genetic Forensics of Trout Populations”

17) 2006, Desert Fish Council, Invited Symposium Speaker, “Conservation Genetics of Species Suffering from Deleterious Mutations”
18) 2006, Ecological Society of America, Tennessee, Invited Symposium Speaker, “The Generation of Microbial Diversity”
19) 2006, Leigh Marine Laboratory, University of Auckland, “Revealing the Biology of Sharks Through Phylo- and Population Genetic Analyses”
20) 2006, University of Auckland, Department of Biology, Auckland, New Zealand, “The Alpine Microbial Observatory and Macroevolution of Microbes.”
21) 2006, LandCare Research, Lincoln, New Zealand, “The Alpine Microbial Observatory and Macroevolution of Microbes.”
22) 2006, University of Canterbury, Christchurch, New Zealand. “The Alpine Microbial Observatory and Macroevolution of Microbes.”
23) 2004, University of Colorado, Applied Math Department, “Phylogenetic Methods for Describing and Comparing Microbial Communities”.
24) 2003, Center for the American West, “Healing the West” series, “Restoration of native species: A tail of two fishes.”
25) 2003, American Society for Microbiology, w Nemergut and Schmidt.
26) 2003, Microbial Observatory Workshop, “Comparing the diversity of microbial communities”, National Science Foundation, Washington DC.
27) 2003, Evolution meetings, “Rate and pattern of cladogenesis in prokaryotes”, Chico, CA.
28) 2003, Evolution meetings, Chico, CA. “Evolutionary genetics of native Colorado cutthroat trout: a tail of two slopes”.
29) 2003, Evolution meetings, “Cycles of population fragmentation and expansion from multiple interglacial refugia inferred for the Rocky Mountain butterfly, Parrnassius smintheus”.
30) 2003, EPA Species at Risk Program, “Disease dynamics in a fragmented landscape”, EPA, Corvalis, OR.
31) 2003, Society of Integrative and Comparative Biology, “Gene duplication and phylogenetic inference: the perils of paralogy”, Toronto, CANADA.
32) 2002, University of Illinois-Chicago, “Gene duplication and phylogenetic inference: the perils of paralogy”, Chicago, IL.
33) 2002, National Science Foundation, Microbial Observatories Workshop, Washington, D. C.
34) 2002, American Fisheries Society, “Morphological and behavior 13ifferentiation between artificial and native populations of the Devil’s Hole pupfish”, Lake Tahoe, CA.
35) 2001, Regional Aquarist Association, Denver, “Species diversity of freshwater fishes in Central America”, Denver, CO.
36) 2001, University of Denver, “Gene duplication and the evolution of vertebrates”
37) 2001, Guild of Rocky Mountain Population Biologists, “The devil’s in the details: failure of artificial propagation to preserve the Devil’s Hole pupfish. Ghost Ranch, NM.

Bernard *(Bernie)* Paul May

PERSONAL

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EDUCATION

Ph.D., The Pennsylvania State University, in Genetics--1980
"The salmonid genome: evolutionary restructuring following a tetraploid event."
M.S., University of Washington, in Fisheries--1975
"Electrophoretic variation in the genus *Oncorhynchus*: the methodology, genetic basis, and practical applications to fisheries research and management."
B.S., University of Washington, in Molecular Biology--1973

PRESENT POSITION AND ADDRESS

1995 to present Adjunct Professor, Director, Genomic Variation Laboratory, Department of Animal Science, Meyer Hall, Univ. of California, Davis, CA 95616.

PREVIOUS POSITIONS

1992-1995	Senior Research Associate and Director, Genome Variation Analysis Facility, Dept. Natural Resources, Cornell University.
1988-1992	Senior Research Associate (SRA II in 1989) and Director, CLEEG, Dept. Natural Resources, Cornell University
1981-1988	Research Associate (SRA in 1985) and Director, The Cornell Laboratory for Ecological and Evolutionary Genetics (CLEEG), Section of Ecology and Systematics, Cornell University
1980-1981	Research Associate, Department of Plant Pathology,The Pennsylvania State University
1978	Instructor, The Pennsylvania State University at DuBois, Introductory Biology (lecture and lab) and Introductory Zoology (lecture and lab)
1977-1980	Research Assistant, Department of Biology, The Pennsylvania State University
1976-1977	Research Technician, Department of Botany and Plant Pathology, University of Maine
1974-1975	Consultant, Washington State Department of Fisheries
1972-1974	Research Technician, Department of Civil Engineering, University of Washington

TEACHING

"Introductory Biology" (lecture and lab) and "Introductory Zoology" (lecture and lab), Penn. State Univ., DuBois, PA (1978)
"Population Genetic Software" , lecture and computer lab course for graduate students (2004, 06)
"Detection of Genomic Variation", course for graduate students (1993, 96, 00, 02, 04)
Week long short courses in "Fisheries Genetics", Syracuse, NY (1992), Wellsboro, PA (1990), Smithville, TN (1987), Marcy, NY (1981), Leetown, WV (1980)
Guest Lectures in "Aquaculture", "Fishery Techniques", "Introductory Fish Biology", "Introductory Field Biology", "Conservation Biology", "Biochemistry Lab" and "Toxicology" (1981-2007)

RESEARCH INTERESTS

My research over the past three decades has centered around the use of discrete Mendelian data to answer biological questions. My interests are broad based, including studies of genomic structure, population analysis, mixed stock analysis, genomic manipulation, effects of non-indigenous species/populations, and isolate identification. I have worked on over 100 taxa (fish, fungi, birds, mammals, plants, and invertebrates). This research has involved riverine, marine tidal, lacustrine, and terrestrial systems. One of my primary roles has been to provide a genetics perspective to the collaborative projects with which I have been involved. During the past 18 years my laboratory has come to focus primarily on the use of direct measures of DNA variability, e.g., AFLPs, microsatellites, sequencing, and SNPs to study questions in social behavior, population structuring, subspecies identification, systematics, and maintenance of genetic variation in small isolated populations. One of my current interests is exploring the use of SNPs and microsatellites to address questions in conservation biology regarding the "genetic health" and "genetic integrity" of natural populations of threatened and endangered species, questions which have not been sufficiently addressable with prior data types. Examples of these questions include: How do we identify populations for preservation?, How do we measure loss of genetic variability?, What remnants of native populations remain after extensive stocking with non-indigenous populations?, How different must two populations be for them to be maintained and managed separately? My program also includes an emphasis on mapping QTLs in aquaculture species, such as growth, temperature toloerance, or disease resistance. I am currently developing expression technologies as an approach to examine the effects of environmental stressors, such as temperature, disease, or toxicants.

REVIEWER FOR

AAAS
Alaska EPSCoR
Alaska Sea Grant
An. Feed Sci. Tech.
Ann. of the Entomol. Soc. of Am.
Aqua. Liv. Res.
AK N. Pac. Res. Bd.
Army Corps of Engineers
AYK SSI
Biochem. Genetics
Biotechniques
BMC Genomics
CDFG Commission
Can. J. Bot.
Can. J. Fish. and Aqua. Sci.
Can. J. Zoology
Connecticut Sea Grant
Cons. Gen.
Coop. Grants Prog. for Former Soviet Union
Copeia
Delaware EPSCoR
Env. Tox. and Chem.
Evolution
Fish. Bull.
Genetics
Genome
Genome Canada
Genome Espana/Genome Canada
Great Lakes Fish Comm.
Hortscience
International Science Foundation
J. Agr. Sci. Tech.
J. An. Sci.
Jeffrees Memorial Trust
J. Fish Biol.
J. Food Sci.
J. Great Lakes Research
J. Hered. (assoc. ed. 1997 to 2001)
J. Mammal.
Maine COBRE
Mar. Biotech.
Mar. Ecol. Prog. Ser.
Michigan Life Sciences Corridor Fund
Michigan Sea Grant
Mol. Ecol.
Marine Ecology Progress Series
N. Amer. J. Fish. Science
National Marine Fisheries Service
NIH
NSF (panel member)
NSERC
Oregon Sea Grant
Phytopathology
PNAS
Rhode Island EPSCoR
Science
Sea Grant (National; Panel Chair)
SF Est. Watershed Sci.
Trans. of the Am. Fish. Soc.
UCDavis MEHP
UCMexus/Conacyt (panel member)
USDA Competitive Research Grants
USDA SBIR
Washington Sea Grant

PROFESSIONAL SOCIETIES

AAAS
American Fisheries Society

MANUSCRIPTS SUBMITTED

Caulder, M.E., E. Wictum, B. May. S.R. Fain, and H.B. Ernest. DNA discrimination of deer species: microsatellite marker panel for mule deer and white-tailed deer. To be submitted to For. Sci Intl: Gen.

Van Dam, A.R., L.P., Martinez, A.J. Chavez, and B.P. May. Revealing Pre-Columbian Trade Via Molecular Phylogenetics of The Cochineal Insect (Dactylopius coccus)". Submitted to J. Biogeogra.

MANUSCRIPTS IN PRESS

Brandl, S., G. Schumer, B. Schreier, J. L. Conrad, B. May and M. R. Baerwald. Ten real-time PCR assays for detection of fish predation at the community level in the San Francisco Estuary-Delta. Mol. Ecol. Res.

Finger, A.J. and B. May. Conservation genetics of a desert fish species: The Lahontan tui chub (*Siphateles bicolor ssp*.). Cons. Gen.

Gille, D., F.R. Famula, B.P. May, and A.D. Schreier. Evidence for a maternal origin of spontaneous autopolyploidy in cultured white sturgeon (*Acipenser transmontanus*). Aquaculture.

LaCava, M., K. Fisch, M., Nagel, J., Lindberg, B.P. May, A.J. Finger. Genetic analysis of the reproductive behavior of delta smelt (*Hypomesus transpacificus*). N. Amer. J. Aqua.

Lavretsky, P., R.S. Schwartz, M.R. Baerwald, and B. May. A Multi-Locus Approach Towards Assessing a Viable Breeding Program for Sacramento Perch (*Archoplites interruptus*) . J. Fish. Biol.

Mahardja, B., B. May, F.Feyrer, R. Coalter, N. Fangue, T. Foin, and M.R. Baerwald. Interannual variation in connectivity and comparison of contemporary effective population size between the two populations of splittail (*Pogonichthys macrolepidotus*) in the San Francisco Estuary. Cons. Gen.

Meek, M., M. Stephens, A. Wong. K. Tomalty, B. May, M. Baerwald. Genetic characterization of California's Central Valley Chinook salmon. Ecology.

Welsh, A.B., M.R. Baerwald, M. Friday, and B. May. Breeding number estimation based on fry genotypes for a remnant lake sturgeon population in a regulated river. Env. Biol. Fish.

MANUSCRIPTS PUBLISHED

2014 Fisch, K.M., B. Mahardja, R.S. Burton, and B. May. Hybridization between delta smelt and two other species within the family Osmeridae in the San Francisco Bay-Delta. Cons. Gen. 15:489–494.

Jones, K.L., D.H. Van Vuren, M.B. McEachern, K.R. Crooks, J.W. Dragoo, and B. May. Spatial and Genetic Organization of the Island Spotted Skunk, Spilogale gracilis amphiala. Soutwest. Nat., 58(4):481-486. 2013.

Meek, MH, MR Stephens, KM Tomalty, BP May, and MR Baerwald. Genetic considerations for sourcing steelhead reintroductions: investigating possibilities for the San Joaquin River. San Francisco Estuary and Watershed Science. 12(1).

Tomalty, K.M., M. Stephens, M. Baerwald, K. Bork, M. Meek, and B. May Genetic Considerations for fall-run Chinook salmon during the San Joaquin River Restoration. San Francisco Estuary and Watershed Science. 12(2).

2013 Chen, Y., S. Parmenter, and B. May. Genetic characterization of variation and management implications for the endangered Mohave tui chub. Cons. Gen. 14:11-20.

Deiner, K, J.M. Hull, and B. May. Eight novel microsatellite loci developed from vernal pool fairy shrimp. J. Fish & Wild. Man. 4:134-138.

Deiner, K.,R. Knapp, D. Boiano, and B. May Increased accuracy of species lists developed for alpine lakes using morphology and barcodes for identification. Mol. Ecol. Res. 13: 820–831.

Finger, A.J., S. Parmenter, and B. May. Conservation genetics of the Owens pupfish (*Cyprinodon radiosus):* Genetic effects of multiple population translocations and extirpations. Trans. Am. Fish. Soc. 142:1430-1443.

Fisch,K.M., J.A. Ivy, R. S. Burton, B. May. Evaluating the performance of captive breeding techniques for conservation hatcheries: A case study of the Delta smelt captive breeding program. J. Hered. 104:92-104.

Schreier, A.D., B. May, and D.A. Gille. Incidence of spontaneous autopolyploidy in cultured populations of white sturgeon, *Acipenser transmontanus*. Aquaculture 416–417: 141–145.

Schreier, A.D. B. Mahardja, and B. May. **Variable patterns of population structure revealed across the range of the ancient octoploid white sturgeon, Acipenser transmontanus**. Trans. Am. Fish. Soc. 142:1273-1286.

2012 Baerwald, M.R., B.M. Schreier, G. Schumer, and B. May. Detection of Threatened Delta Smelt in the Gut Contents of the Invasive Mississippi Silverside in the San Francisco Estuary Using TaqMan Assays. Trans. Am. Fish. Soc. 141:1600-1607.

Mahardja, B., B. May, and M.R. Baerwald. Characterization of 36 additional microsatellite loci in splittail (*Pogonichthys macrolepidotus*) and cross-amplification in five other native Sacramento-San Joaquin Delta cyprinid species. Cons. Gen. Res. 4(4):917-921.

Meek, M., A. Wintzer, N. Sheperd, and B. May. 2012. Genetic diversity and reproductive mode in two non-native hydromedusae, *Maeotias marginata* and *Moerisia sp.*, in the Upper San Francisco Estuary, California. Biological Invasions. DOI 10.1007/s10530-012-0279-9.

Meek, M.H., A.P. Wintzer, W.C. Wetzel, and B.P. May. Climate change likely to facilitate the invasion of the non-native hydroid, *Cordylophora caspia*, in the San Francisco Estuary. PLoS ONE. 7(10).

Petersen, J.L., M.R. Baerwald, J.M. Ibarra, and B. May. A first-generation linkage map of the Pacific lion-paw scallop: initial evidence of QTL for size traits and markers linked to orange shell color. Aquaculture. 350-353:200-209.

Schreier, A.D., B. Mahardja, and B. May. Hierarchical patterns of population structure in the endangered Fraser River white sturgeon, *Acipenser transmontanus*, and implications for conservation. Can. J. Fish. & Aquat. Sci. 69:1968-1980.

Schreier, A. D., J. Rodzen, S. Ireland, and B. May. Genetic techniques inform conservation aquaculture of the endangered Kootenai River white sturgeon, *Acipenser transmontanus.* Endang. Species Res. 16:65-75.

Sukmanomon, S., W. Kamonrat, S. Poompuang, T. Nguyen, D. M. Bartley, B. May, U. Na-Nakorn. Genetic changes, intra- and interspecific introgression in farmed Nile tilapia in Thailand. Aquaculture 324-325:44-54.

Van Dam, A.R. and B. May. A new species of Dactylopius Costa (*Dactylopius gracilipilus* sp. nov.) (Hemiptera: Coccoidea: Dactylopiidae) from the Chihuahuan Desert, Texas, U.S.A. . Zootaxa 3573:33-39.

2011 Baerwald, M., J. Petersen, R. Hedrick, G. Schisler, and B. May. A major effect quantitative trait locus for whirling disease resistance identified in rainbow trout (*Oncorhynchus mykiss*). Heredity. 106:920-926.

Baerwald, M., G. Schumer, B. Schreier, and B. May. TaqMan assays for the genetic identification of delta smelt (*Hypomesus transpacificus*) and wakasagi smelt (*Hypomesus nipponensis*). Mol. Ecol. Res. 11:784-785.

Finger, A. J., E. C. Anderson, M. R. Stephens, and B. P. May. Application of a method for estimating effective population size and admixture using diagnostic SNPs: Implications for conservation of threatened Paiute cutthroat trout (*Oncorhynchus clarkii seleniris*) in Silver King Creek, California. Can. J. Fish. Aquat. Sci. 68:1369-1386.

Fisch, K.M., J.M. Henderson, R.S. Burton, and B. May. Population genetics and conservation implications for the endangered delta smelt in the San Francisco Bay-Delta. Conservation Genetics. 12:1421-1434.

Floyd, C. H., D.H. Van Vuren, K.R. Crooks, K.L. Jones, D.K. Garcelon, N.M. Belfiore, J.W. Dragoo, and B. May. Genetic differentiation of island spotted skunks, *Spilogale gracilis amphiala*. J. Mam. 92(1):148-158.

McEachern, M.B., D.H. Van Vuren, C.H. Floyd, B. May, and J.M. Eadie. Bottlenecks and rescue effects in a fluctuating population of golden-mantled ground squirrels (Spermophilus lateralis). Con. Gen.12:285-296.

Mejia , O., L. G. Herrera, B. May, R. A. Medellin,and J. J. Flores-Martinez. Effective population size dynamics of *Myotis vivesi* during the Pleistocene and Holocene climatic changes. Acta Chiropterologica. 13:33-40.

Schreier, A.D., D. Gille, B. Mahardja, and B. May. Neutral markers confirm the octoploid origin and reveal spontaneous polyploidy in white sturgeon, *Acipenser transmontanus*. J. Appl. Ichthiol. 27:24-33.

Wintzer, A.P., M.H. Meek, P.B. Moyle, and B. May. Ecological insights into the polyp stage of non-native hydrozoans in the San Francisco Estuary. Aquat. Ecol. 45:151–161.

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Royse, D.J. and B. May. Identification and use of three new biochemcial markers in Agaricus bisporus. Agric. Biol. Chem. 53:2861-2866.

1988 Gavin, T. A. and B. May. Taxonomic status and genetic purity of Columbian white-tailed deer. J. Wildl. Man. 52:1-10

Krueger, C.C., and B. May. Stock identification of naturalized brown trout (*Salmo trutta*) in Lake Superior tributaries: differentiation based on allozyme data. Trans. Am. Fish. Soc. 116:785-794.

Krueger, C.C., and B. May. Genetic comparison of naturalized rainbow trout populations among Lake Superior tributaries: differentiation based on allozyme data. Trans. Am. Fish. Soc. 116:795-806.

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May, B., K.J. Henley, C.C. Krueger, and S.P. Gloss. Androgenesis as a mechanism for chromosome set manipulation in brook trout (*Salvelinus fontinalis*). Aquaculture 75: 57-70.

May, B. , K. J. Henley, C. G. Fisher and D. J. Royse. Linkage relationships of 19 allozyme encoding loci within the commercial mushroom genus *Pleurotus*. Genome 30:888-895.

May, B. and D. J. Royse. Interspecific allozyme variation within the fungal genus *Pleurotus*. Trans. Brit Mycol. Soc. 90:29-36.

1987 Johnson, K.R., J.E. Wright, and B. May. Linkage relationships reflecting ancestral tetraploidy in salmonid fish. Genetics. 116:579-591.

Kukuk, P.F., G.C. Eickwort, and B. May. Multiple maternity and multiple paternity in first generation brood from single foundress colonies of the sweat bee *Dialictus zephyrus* (Hymenoptera: Halictidae). Insectes Sociaux. 34:131-135

Marsden, J.E., C.C. Krueger, H.C. Kincaid, and B. May. Inheritance of duplicated fumarase and phosphoglucomutase loci in lake trout (*Salvelinus namaycush*). Heredity. 58:365-372.

Marsden, J. E., S. Schwager, and B. May. Single-locus inheritance in the tetraploid treefrog *Hyla versicolor* with an analysis of expected progeny ratios in tetraploid organisms. Genetics. 116:299-311.

Royse, D.J., and B. May. Identification of shiitake genotypes by multilocus enzyme electrophoresis: catalog of lines. Biochemical Genetics. 25:705-716.

Royse, D.J., M. Jodon, G.G. Antoun, and B. May. Confirmation of intraspecific crossing and single and joint segregation of biochemical loci of *Vovariella volvacea*. Exp. Mycol. 11:11-18.

Wright, J.E., K.R. Johnson, and B. May. Synthetic linkage map of salmonid fishes (*Salvelinus, Salmo, Oncorhynchus*). Pages 405-413. In: Genetic Maps 1987. O'Brien, S.J. (ed.). Cold Spring Harbor.

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1986 Krueger, C.C., J.E. Marsden, and B. May. Genetic comparison of New York hatchery strains of brown trout based on allozyme variation. NY Fish and Game J. 33: 16-27

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1985 Kukuk, P. K. and B. May. A reexamination of genetic variability *in Dialictus zephyrus* (Hymenoptera:Halcitidae). Evolution 39:226-228.

Ross, K. G., D. J. C. Fletcher, and B. May. Enzyme polymorphisms in the fire ant, *Solenopsis invicta* (Hymenoptera:Formicaidae). Biochem. Syst. Ecol. 13:29-33.

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1984 Bonde, M. R., G. L. Peterson, W. M. Dowler, and B. May. Isozyme analysis to differentiate species of *Peronosclerospora* causing downy mildews of maize. Phytopathology 74:1278-1283

Marsden, J. E. and B. May. Feather Pulp: a non-destructive sampling technique for electrophoretic studies in birds. The Auk 101:173-175.

Staub, J. E., L. J. Kuhns, P. Grun, and B. May. Genetic bases of isozyme variation for alkaline phosphatase and glucosephosphate isomerase in *Solanum*. Theor. Appl. Genet. 67:505-513.

1983 Royse, D. J., M. C. Spear, and B. May. Cell line authentication and genetic relatedness of lines of the shiitake mushroom, *Lentinus edodes*. J. Gen. Appl. Microbiol. 29:205-216.

Royse, D. J., M. C. Spear, and B. May. Single and joint segregation of marker loci in the shiitake mushroom, *Lentinus edodes*. J. Gen. Appl. Microbiol. 29:217-222.

Soper, R. S., B. May, and B. Martinell. *Entomophaga grylii* enzyme polymorphism as a technique for pathotype identification. Environ. Entomol. 12:720-723.

Spear, M. C., D. J. Royse, and B. May. Atypical meiosis and joint segregation of biochemical loci in *Agaricus brunnescens*. J. Hered.74:417-420.

Wright, J. E., K. Johnson, A. Hollister, and B. May. Meiotic models to explain classical linkage, pseudolinkage and chromosome pairing in tetraploid derivative salmonid genomes. Pages 239-260 in Isozymes: Current Topics in Biological and Medical Research 10.

1982 May, B. and D. J. Royse. Genetic variation and joint segregation of biochemical loci in the common meadow mushroom, *Agaricus campestris*. Biochem. Genet. 20:1165-1173.

May, B. and D. J. Royse. Confirmation of crosses between lines of *Agaricus brunnescens* by isozyme analysis. Exp. Mycol. 6:283-292.

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May, B., J. E. Wright, and K. R. Johnson. Joint segregation of biochemical loci in Salmonidae: III. Linkage associations in Salmonidae including data from rainbow trout (*Salmo gairdneri*). Biochem. Genet. 20:29-40.

Royse, D. J. and B. May. Use of isozyme variation to identify genotypic classes of *Agaricus brunnescens*. Mycologia 74:93-102.

Royse, D. J. and B. May. Genetic relatedness and selective breeding of *Agaricus brunnescens*. Mycologia 74:569-575.

Staub, J. E., L. J. Kuhns, P. Grun, and B. May. Stability of potato tuber isozymes under different storage regimes. J. Am. Soc. Hort. Sci. 107(3):405-408.

1981 May B. and D. J. Royse. Applications of the electrophoretic methodology to the elucidation of genetic life histories of edible mushrooms. Mush. Sci. XI:799-817.

Stoneking, M., B. May, and J. E. Wright. Loss of duplicate gene expression in salmonids: evidence for a null allele polymorphism at the duplicate asparatate aminotransferase loci in brook trout (*Salvelinus fontinalis*). Biochem. Genet. 19:1063-1077.

1980 Gagnon, P. S., R. L. Vadas, D. B. Burdick, and B. May. Genetic identity of annual and perennial forms of *Zostera marina* L. Aquatic Bot. 8:157-162.

May, B., M. Stoneking, and J. E. Wright. Joint segregation of biochemical loci in Salmonidae: II. Linkage associations from a hybridized *Salvelinus* genome (*S. namaycush x S. fontinalis*). Genetics 95:707-726.

Wright, J. E., B. May, M. Stoneking, and G. Lee. Pseudolinkage of two muscle asparatate aminotransferase loci in brook trout (*Salvelinus fontinalis*). J. Heredity 71:223-228.

1979 May, B., D. W. Roberts, and R. S. Soper. Intraspecific genetic variability in laboratory strains of *Entomophthora* as determined by enzyme electrophoresis. Exp. Mycol. 3:289-297.

May, B., M. Stoneking, and J. E. Wright. Joint segregation of malate dehydrogenase and diaphorase loci in brown trout (*Salmo trutta*). Trans. Am. Fish.Soc. 108:373-377.

May, B., J. E. Wright, and M. Stoneking. Joint segregation of biochemical loci in Salmonidae: results from experiments with *Salvelinus* and review of the literature on other species. J. Fish. Res. Bd. Can. 36:1114-1128.

Stoneking, M., B. May, and J. E. Wright. Genetic variation, inheritance, and quarternary structure of malic enzyme in brook trout (*Salvelinus fontinalis*). Biochem. Genet. 17:599-619.

Utter, R. M., F. W. Allendorf, and B. May. The genetic basis of creatine kinase variation in skeketal muscle of salmonid fishes. Biochem. Genet. 17:1079-1091.

1978 May, B. and F. R. Holbrook. Absence of genetic variability in the green peach aphid, *Myzus persicae* (Hemiptera: Aphidae). Ann. Entomol. Soc. Am. 71:809-812.

1977 May, B., L. S. Bauer, R. L. Vadas, and J. Granett. Biochemical genetic variation in the family Simuliidae: electrophoretic identification of the human biter in the isomorphic *Simulium jenningsi* group. Ann. Entomol. Soc. Am. 70:637-640.

May, B., D. E. Leonard, and R. L. Vadas. Electrophoretic variation and sex linkage in spruce budworm. J. Heredity 68:355-359.

1976 Utter, F. M., F. W. Allendorf, and B. May. Genetic delineation of salmonid populations based on electrophoretic data. Pages 8-11 in Salmonid Genetics: Status and Role in Aquaculture. University of Washington Sea Grant Program.

Utter, F. M., F. W. Allendorf, and B. May. The use of protein variation in the management of salmonid populations. North American Wildlife and Natural Resources Conference Transactions 41:373-384.

1975 Allendorf, F.W., F.M. Utter, and B. May. Gene duplication within the family Salmonidae: II. Detection and determination of the genetic control of duplicate loci through inheritance studies and the examination of populations. Pages 415-432 in Genetics and Evolution, C.L.Markert, (ed.). Academic Press, New York.

May, B., F. M. Utter, and F. W. Allendorf. Biochemical genetic variation in pink and chum salmon: inheritance of intraspecies variation and apparent absence of interspecies introgression following massive hybridization of hatchery stocks. J. Heredity 66:227-232.

TECHNICAL OR EXTENSION PUBLICATIONS

Welsh, A.B., R.F. Elliott, K.T. Scribner, H.R. Quinlan, E.A. Baker, B.T. Eggold, J.M. Holtgren, C.C. Krueger, and B.May. 2010. Genetic guidelines for the stocking of lake sturgeon (*Acipenser fulvescens*) in the Great Lakes basin. Great Lakes Fish. Comm. Misc. Publ. 2010-01.

Roach, J.L., R. Colayco, C. To, D. Batey, and B. May. 2003. Microsatellite Genotyping Using the BaseStation DNA Fragment Analyzer. MJ Research Application Note Vol.2, No.7. 4pp.

May, B. 1996. Identification of smelt species and their interspecific hybrids in the Sacramento-San Joaquin estuary by allozyme analysis. Interagency Ecological Program Newsletter 9:9-10.

Danforth, B.N., C.R. Freeman, S. Bogdanowicz, and B. May. 1994. Chemiluminescent DNA fingerprinting using PCR-labeled M13 and Jeffreys probes. Biochemica 11:17-19.

Gavin, T.A. and B. May. 1990. Conservation Biology - maintaining biotic and genetic diversity. New York Food and Life Sciences Quarterly. 19:9-13.

May, B. 1989. New varieties of trout being developed for New York. Agriculture News Service. Cornell Cooperative Extension. 2 pp.

Royse, D.J. and B. May. 1982. Selective breeding of the common cultivated mushroom. Parts I, II, and III. Mushroom News. Vol. 30 Nos. 8-10. 10 pp.

CURRICULUM VITAE

CRAIG ALAN STOCKWELL **PHONE: (701) 231-8449**
James A. Meier Professor
Department of Biological Sciences, Stevens Hall
North Dakota State University
Fargo, ND 58108
E-MAIL: Craig.Stockwell@ndsu.edu

EDUCATION

1995 **Doctor of Philosophy, Program in Ecology, Evolution & Conservation Biology** University of Nevada, Reno, Nevada; Advisor – Dr. Gary Vinyard (deceased)

1989 **Masters of Science, Biology**, Northern Arizona University, Flagstaff, Arizona; Advisor – Dr. Gary Bateman

1981 **Bachelor of Arts, Anthropology**, University of Colorado, Boulder, Colorado

RESEARCH & TEACHING EXPERIENCE

2013 - **Professor -** Department of Biological Sciences, North Dakota State University, Fargo, ND

2008-2013 **Director, Environmental & Conservation Sciences Graduate Program.,** North Dakota State University, Fargo, ND

2008 **James A. Meier Associate Professor -** Department of Biological Sciences, North Dakota State University, Fargo, ND

2004-2013 **Associate Professor** – Department of Biological Sciences, North Dakota State University, Fargo, ND

1998-2004 **Assistant Professor** -- Department of Biological Sciences, North Dakota State University, Fargo, ND

2007-2008 **Visiting Faculty –** Department of Fish, Wildlife & Conservation Biology, Colorado State University, Fort Collins, CO

1999-2000 **Visiting Professor** -- University of Nebraska's Cedar Point Biological Station, Lincoln, NE

1995-1997 **Postdoctoral Research Ecologist** -- University of Georgia's Savannah River Ecology Laboratory, Aiken, SC (Mentor: Dr. Margaret Mulvey)

1993-1995 **Research Fellow** -- Bioresources Research Center, Department of Biology, University of Nevada, Reno, NV

1992-1993 **Research Assistant** -- Department of Biology, University of Nevada, Reno, NV

1990-1992 **Teaching Assistant** (Ichthyology, Limnology, Animal Behavior, Introductory Biology) -- Department of Biology, University of Nevada, Reno, NV

RESEARCH & TEACHING EXPERIENCE (continued)

1988-1989 **Research Fellow** -- Department of Range, Wildlife & Forestry, University of Nevada, Reno, NV

1987 **Professional Biologist** -- United States Department of Agriculture, Denver Federal Center, Denver, CO

1983-1985 **Teaching Assistant** (General Zoology, General Biology) -- Northern Arizona University, Flagstaff, AZ

1984-1986 **Research Biologist** (Funded by Grant from Grand Canyon Natural History Association), Grand Canyon, AZ

NDSU SERVICE – ENVIRONMENTAL & CONSERVATION SCIENCES

Developed and submitted proposal for interdisciplinary Graduate Program in Environmental & Conservation Sciences (w/ B. Saini-Eidukat, Geosciences and W. Lin, Engineering) 2002-2004

Environmental & Conservation Sciences Graduate Program Director – 2008-2013

- Successfully pursued appropriated and non-appropriated funding ~$150K / year
  - Funded approximately 6-8 ECS graduate fellows each year
  - Organized competitive small research grant program for ECS students
  - Organized competitive seed grant program for ECS faculty
  - Supervised part-time administrative assistant
  - Provided small grants to support student travel to professional meetings
  - Organized and funded annual poster competition
  - Obtained funds and organized weekly "Greenbag Lunch" Seminar Series
- Organized and obtained funds to support periodic public lectures
- Worked with NDSU Administrators
  - Inter-disciplinary Graduate Program Directors monthly meetings 2008-2013
  - Graduate Leaders monthly meetings 2010-2013
  - University Chair's Council monthly meetings with Provost 2012-2013
  - Prepared and submitted annual reports to Graduate Dean
  - Prepared and submitted program review to NDSU Program Review Committee
- ECS Steering Committee – 2004-present – Chair 2008-2013
  - Recruited NDSU faculty members to participate in ECS program
  - Nominated ECS faculty for election to ECS Steering Committee
  - Worked with committee to evaluate and revise ECS Curriculum
  - Recruited faculty to teach ECS Environmental Law course
  - Developed Roadmap White Paper for Provost's office
- ECS Admissions Committee 2008-present, Chair 2008-2013
  - Managed Admissions Process in collaboration with Graduate School
  - Pursued funding from Graduate School to support competitive applicants
- ECS Recruiting Committee 2011- present, Chair 2011-2013
  - Pursued and obtained competitive funding to support annual recruiting efforts
  - Annual recruiting visits to regional universities
  - Hosted Annual Recruiting Fair
  - Developed recruiting materials
  - Developed and managed NDSU ECS Website using TYPO-III
  - Established ECS Graduate Student Ambassador Program

NDSU SERVICE – ENVIRONMENTAL & CONSERVATION SCIENCES (continued)

Organized Annual Workshops for ECS students and faculty
- 2013 – Multivariate Analyses – Aug 12-14, 2013
- 2012 – Scientific Communication with Press – Jan 5-6, 2012
- 2011 – Program R – Aug 15-17, 2011
- 2010 – Program R – May 9-11, 2010
- 2009 – STELLA – Aug 17-19, 2009

NDSU SERVICE – DEPARTMENTAL, COLLEGE, UNIVERSITY

Coordinated NDSU Response to US Fish & Wildlife Service Landscape Conservation Cooperative (Future Research opportunities). 2012

Lead NDSU Effort to Establish USGS Cooperative Research Unit for North Dakota
Meetings with ND Game and Fish, USGS Northern Prairie Wildlife Research Center

University Biosciences-Ag Research Task Force 2014-present

University Senate – College of Science and Mathematics Representative, 2010-2013

Promotion, Tenure and Evaluation Committee, College of Science & Mathematics, 2005-2007; Chair: 2006-2007

NDSU FORWARD Allies – 2011-present

Promotion, Tenure and Evaluation Committee, Biological Sciences, 2009-present; Chair 2012

Department of Biological Sciences, Faculty Affairs Committee, 2012-2013

Department of Biological Sciences, Graduate Affairs Committee, 2014-present

Faculty and Staff Search Committees:
- Ecology Faculty, Biological Sciences Department, Chair, 2011-2012
- Plant Conservation Biology Faculty, Biological Sciences Department, Chair, 2006-2007
- Environmental & Conservation Sciences Director, Chair, 2003-2004
- Insect Ecologist, Entomology Department, 2002
- Physiological Ecologist Faculty, Biological Sciences Department, 2001
- Wheat Geneticist Faculty, Plant Sciences Department, 2001
- Postdoctoral Researcher, Chair, 2009
- Postdoctoral Researcher, Chair, 2004
- Research Technician, Chair, 2001

Evolution Symposium Organizer – College of Science & Mathematics and PBS Television and Radio. September, 2001

Evolution Video Conference Co-organizer – College of Science & Mathematics and PBS Television and Radio - 6 audiences across state of North Dakota - October, 2001

Darwin's Birthday Celebration Panelist, February, 12, 2009.

Faculty-Student Relations Committee, College of Science & Mathematics, 2001-2007

College of Science & Mathematics Scholarships/Awards Committee 2003-present

Advisor – Environmental & Conservation Sciences Graduate Student Association, 2009-2013

Advisor – Student Chapter of the Wildlife Society, 1998-2007 and 2011-2013

Advisor – Biological Sciences Graduate Student Association, 2005-2006

Hosted Biological Sciences Department seminar speakers (26 total speakers) 1998-present

PROFESSIONAL SOCIETIES

American Society for Advancement of Science
American Fisheries Society
Desert Fishes Council
Society for Conservation Biology

PROFESSIONAL SERVICE

Scientific Panelist – Devils Hole Pupfish Genetics Panel. Organized by National Park Service, Fort Collins, CO, September 2007.

Scientific Panelist – Devils Hole Panel Review. Organized by National Park Service, Death Valley, CA, 2007-2009

Workshop Invited Speaker - Assessment and Evaluation of Reintroducing Native Fishes, Oregon Chapter – American Fisheries Society, February 2007

Scientific Advisor - White Sands Pupfish Conservation Team, 1999-2006

Scientific Panelist - Conservation genetics of an endangered species, the bull trout, June, 2000

Symposium Lead-off speaker - Evolution on Ecological Time Scales, Ecological Society of America, 2005

Symposium organizer - Translocations as a tool in the conservation of native desert fishes. Desert Fishes Council, Reno, NV, November, 1995

Symposium organizer - Organismal biology of the Northern Plains. North Dakota – South Dakota-Minnesota Academy of Sciences meeting, Moorhead, MN, April 2000.

Red River Zoo Board Member 2011-2014

Red River Zoo Education Committee Chair 2011-2014

Red River Zoo Buildling Committee 2011-2013

EDITORIAL AND REFEREE ACTIVITIES

Associate editor – *Transactions of the American Fisheries Society*, 2015-

Associate editor – *Transactions of the American Fisheries Society*, 2001-2003

Assigning editor - *Conservation Biology* 1998, 2002, 2003, 2010, 2012

Referee Activity - (1997-present) – National Science Foundation, Sea Grants, Ambio, Animal Conservation; Behaviour; Biological Invasions; Biodiversity and Distributions; Biological Letters - Royal Society; Conservation Biology; Conservation Genetics; Copeia; Evolution; Evolutionary Applications; Genetica; Great Basin Naturalist; Journal of Animal Ecology; New Zealand Journal of Marine & Freshwater Research; North American Journal of Fisheries Management; Reviews in Fish Biology and Fisheries; Transactions of the American Fisheries Society; Trends in Ecology & Evolution

COURSES DEVELOPED AND TAUGHT

North Dakota State University

Biological Research Principles (Graduate)
Conservation Biology (Undergraduate / Graduate)
Advanced Conservation Biology (Graduate)
Wildlife & Fisheries Management Techniques (Undergraduate / Graduate)
General Biology (Undergraduate)
Ichthyology (Undergraduate / Graduate)
Senior Seminar (Undergraduate)
Graduate Seminar (Graduate)

University of Nebraska, Cedar Point Biological Station

Prairie Ecology – summer course 1999 & 2000

TEACHING ACTIVITIES AND TRAINING

Co-Developed new Ph.D. program in Environmental & Conservation Sciences 2002-2003
Workshop participant; Curricular and Pedagogical Development of a Conservation Biology Program —Reform for the 21st Century – Session I. May, Session II, July 2001
Biological Sciences Senior Seminar mentor: 2000-2010
Advised undergraduates (30-45 students each year) 1999-2014
Graduate Advisory Committee member (~10 students each year including 2-4 students in my laboratory, see list of graduate students below) 1998-2014
Attended Faculty Institute for Excellence in Learning (FIEL) Luncheons 2001-2002
Participated in *Peer-Review-of- Teaching* Program, 2002-2003

FUNDING (Extramural funding: $1,359,700)

2012 – Ecological Responses to Regional Climate Change. USGS Northern Prairie Wildlife Research Center - $167,700.
2011 – Investigation of refugial fish genetic structure and local adaptation for the Pahrump poolfish. Nevada State Wildlife Grant – $100,000
2010 – Population status of the Northern Leopard Frog in North Dakota. North Dakota State Wildlife Grant - $100,000.
2009 - 2013 Reciprocal predation and co-persistence of non-native and native fishes Western National Parks Association - $14,000
2008-2010 Hybridization of endangered Mohave tui chub and non-native arroyo chub Western National Parks Association - $7,500
2006-2009 Lake ecology and population dynamics of the Endangered Mohave tui chub (*Siphateles bicolor mohavensis*). National Park Service - $150,000.
2005-2007 Conserving Integral Units of Chihuahuan Desert Biodiversity. Phase V. Department of Defense Legacy Grant -- $98,000
2004-2005 Conserving Integral Units of Chihuahuan Desert Biodiversity, Phase IV. Department of Defense Legacy Grant -- $157,718.
2003-2004 Conserving Integral Units of Chihuahuan Desert Biodiversity, Phase III. Department of Defense Legacy Grant -- $134,784.
2001-2002 Conserving Integral Units of Chihuahuan Desert Biodiversity, Phase II. Department of Defense Legacy Grant -- $126,000.
2000-2002 Conserving Integral Units of Chihuahuan Desert Biodiversity-Supplemental Department of Defense Legacy Grant - $18,364
2000-2001 Conserving Integral Units of Chihuahuan Desert Biodiversity, Phase I. Department of Defense Legacy Grant -- $87,500.
1995-1998 Population genetic structure and life history of the White Sands pupfish (*Cyprinodon tularosa*). Holloman Air Force Base, NM -- $200,000.
1991-1992 Rapid evolution in recently established populations of mosquitofish (*G. affinis).* Sigma Xi Scientific Research Society (two grants) -- $845.00.
1984 Environmental Conservation Fellowship. National Wildlife Federation -- $1,000.00.
1984-1986 Effects of helicopter overflights on desert bighorn foraging behavior at Grand Canyon National Park. Grand Canyon Natural History Association, Grand Canyon, AZ -- $13,800.00.

NDSU INTERNAL GRANTS (~$207.000.00)

2010-2011 Experimental approach to the study of the constraining effects of gene flow on evolutionary divergence. North Dakota EPSCoR - $24,000.

2003 Automated Sequencing Analysis Facility, ND EPSCoR Infrastructure Improvement Program (IIP) – Equipment Grant. -- $92,567.58.

2003 Environmental & Conservation Sciences Book Acquisition Grant for NDSU Library. CoPI -- $4,000.00

2002-2004 Development and application of microsatellites for the genetic management of a protected species, the White Sands pupfish (*Cyprinodon tularosa*). ND EPSCoR – EPA – STAR grant -- $40,000.00

1999 Molecular assessment of hybridization between western mosquitofish (*Gambusia affinis*) and the Endangered Clear Creek gambusia (*G. heterochir*). NDSU Development Foundation -- $2,000.00

1998-1999 An experimental assessment of the costs of parasitism in the White Sands pupfish (*Cyprinodon tularosa*). Grant-in-Aid, North Dakota State University, Fargo, ND -- $12,845.

1998 Gene Expression and Genome Analysis Center, National Science Foundation. EPSCoR. CoPI -- $32,000.00

PUBLICATIONS

Purcell, K. and **C. A. Stockwell.** 2015. Species in a bucket: rapid expansion and genetic structure of an invasive species in New Zealand. *Biological Invasions. In press.*

Henkanaththegedara, S.M.,, J. Fisher, D. McEwen and **C.A. Stockwell**. 2015. The impacts of recently established fish populations on invertebrate communities in desert springs and potential conflict in setting conservation goals. *Diversity Special Issue Global Freshwater Diversity (invited). Diversity* 7:3-15.

Reed, J.M. and **C. A. Stockwell.** 2014. Evaluating an icon of population persistence: The Devil's Hole pupfish. *Proceedings of Royal Society of London Series B*. 281: 20141648.http://dx.doi.org/10.1098/rspb.2014.1648.

Henkanaththegedara, S.M. and **C.A. Stockwell**. 2014. Intraguild predation mediates co-existence of native and non-native fish: Insights from a mesocosm experiment. *J. Applied Ecology* 51:1057-1065; doi: 10.1111/1365-2664.12285

Fisher, J. D., D. M. Mushet and **C. A. Stockwell**. 2014. Potential for parasite-induced biases in aquatic invertebrate population studies. *Hydrobiologia* 722:199-204.

Mushet, D. M., N. H. Euliss, Jr., and **C.A. Stockwell**. 2013. Complex spatial dynamics maintain northern leopard frog (Lithobates pipiens) genetic diversity in a temporally varying landscape. *Herpetological Conservation and Biology* 8:163–175.

Mushet, D.M., K. McLean and **C.A. Stockwell.** 2013. Salamander colonization of chase lake, Stutsman County, North Dakota. *Prairie Naturalist* 45:106-108.

Stockwell, C.A., J.S. Heilveil and K. Purcell. 2013. Estimating divergence time for two Evolutionarily Significant Units of a protected fish species. *Conservation Genetics* 14:215–222

PUBLICATIONS (continued)

Henkanaththegedara, S. M. and **C.A. Stockwell**. 2012. The role of gape-limitation in intraguild predation between native and non-native fish. *Ecology of Freshwater Fishes* 22: 11–20

Purcell, K.M., Ling, N. and **C.A. Stockwell** 2012. Evaluation of the introduction history and genetic diversity of a serially introduced fish population in New Zealand. *Biological Invasions.* 14:2057-2065; DOI 10.1007/s10530-012-0213-1

Mushet, D. M., N. H. Euliss, Jr., and **C.A. Stockwell**. 2012. Mapping anuran habitat suitability to estimate effects of grassland and wetland conservation programs. *Copeia* 2012: 321–330

Mushet, D. M., N. H. Euliss, Jr., and **C.A. Stockwell**. 2012. Conceptual model to facilitate amphibian conservation in the northern Great Plains. *Great Plains Research* 22:45-58.

Stockwell, C.A., K. M. Purcell, M.L. Collyer and J. Janovy. 2011. Effects of salinity on *Physa acuta*, the intermediate host for the parasite *Posthodiplostomum minimum*; implications for the translocation of the protected White Sands pupfish. *Transactions of the American Fisheries Society* 140:1370-1374.

Collyer, M. L., J. S. Heilveil and **C.A. Stockwell**. 2011. Contemporary evolutionary divergence for a protected species following assisted colonization. *PLoS ONE* 6(8): e22310. doi:10.1371/journal.pone.0022310

Henkanaththegedara, S. M. and **C.A. Stockwell**. 2011. Melanism in endangered Mohave tui chub *Siphateles bicolor mohavensis* Snyder 1918 (Cypriniformes: Cyprinidae). *Western North American Naturalist* 71:127-130.

Purcell K.M., S. L. Lance, K. L. Jones and **C.A. Stockwell**. 2011. Ten novel microsatellite markers for the western mosquitofish *Gambusia affinis*. *Conservation Genetics Resources* 3:361-363

Kinnison, M. T., A. P. Hendry and **C.A. Stockwell**. 2007. Contemporary evolution meets conservation biology II. Impediments to integration and application. *Ecological Research* 22:947-954. (Invited)

Collyer, M. L., **C.A. Stockwell**, D. C. Adams and M. H. Reiser. 2007. Unpredictable morphological divergence in refuge populations of a desert fish. *Ecological Research* 22:902-910. (Invited)

Rogowski, D., H. Reiser and **C.A. Stockwell**. 2006. Fish habitat associations in a spatially variable desert stream. *Journal of Fish Biology* 68:1473-1483.

Rogowski, D. and **C.A. Stockwell**. 2006a. Parasites and salinity: costly tradeoffs in a threatened species. *Oecologia* 146:615-622.

Rogowski, D. and **C.A. Stockwell**. 2006b. Assessment of the potential impacts of exotic species on populations of White Sands pupfish, *Cyprinodon tularosa*. *Biological Invasions* 18:79-87.

Moen, D. S. and **C.A. Stockwell**. 2006. Specificity of the monogenean *Gyrodactylus tularosae* Kritsky and Stockwell 2005, to its Natural Host, the White Sands Pupfish (*Cyprinodon tularosa* Miller and Echelle 1975). *Comparative Parasitology* 73:278-281.

Collyer, M. L., J. M. Novak and **C.A. Stockwell**. 2005. Morphological Divergence of Native and Recently Established Populations of White Sands Pupfish (*Cyprinodon tularosa*). *Copeia* 2005:1–11.

Kritsky, D. C. and **C.A. Stockwell**. 2005. New species of *Gyrodactylus* (Monogenoidea, Gyrodactylidae) from the White Sands pupfish, *Cyprinodon tularosa,* in New Mexico. *Southwestern Naturalist* 50:312-317.

PUBLICATIONS (continued)

Collyer, M. L. and **C.A. Stockwell**. 2004. Experimental evidence for costs of parasitism for a threatened species, White Sands pupfish. *Journal of Animal Ecology* 73:821-830.

Iyengar, A., **C. A. Stockwell,** D. Layfield and P. A. Morin. 2004. Characterisation of microsatellite markers in White Sands pupfish (*Cyprinodon tularosa*). *Molecular Ecology Notes* 4:191-193.

Stockwell, C. A. and M. V. Ashley. 2004. Rapid adaptation and conservation. *Conservation Biology* 18:272-273.

Epifanio J., G. Haas, K. Pratt, B. Rieman, P. Spruell, **C.A. Stockwell**, F. Utter and W. Young. 2003. Integrating conservation genetic considerations into conservation planning: a case study of bull trout (*Salvelinus confluentus*) in the Lake Pend Oreille – Lower Clark Fork River System. *Fisheries* 18:10-24.

Stockwell, C. A., A. P. Hendry, and M. T. Kinnison. 2003. Contemporary evolution meets conservation biology. *Trends in Ecology and Evolution* 18:94-101. ***Thomas Reuters Essential Science Indicators as the highest cited paper in the research area of rapid climate change. Reviewed in Science-Watch as "Fast Moving Front": http://sciencewatch.com/dr/fmf/2008/08julfmf/08julfmfSockwl/

Stockwell, C. A. and P. L. Leberg. 2002. Translocations as a tool in the conservation of native fishes: emerging research directions. *Western North American Naturalist* 62:32-38.

Stockwell, C. A. 2002. Threatened fishes of the world: *Cyprinodon tularosa* Miller & Echelle, 1975 (Cyprinodontidae). *Environmental Biology of Fishes* 63:404

Hershler, R., H-P. Liu and **C.A. Stockwell**. 2002. *Juturnia*, a new Genus of aquatic Gastropods (Rissooidea: Hydrobiidae) from the North American Southwest: Phylogenetic Relationships and Biogeography. *Proceedings of the Washington Biological Society* 115:171-188.

Stockwell, C. A. and G. L. Vinyard. 2000. Life history variation in recently established populations of western mosquitofish (*Gambusia affinis*). *Western North American Naturalist* 60:273-280.

Stockwell, C. A. and S. C. Weeks. 1999. Translocations and rapid evolutionary responses in recently established populations of the western mosquitofish (*Gambusia affinis*). *Animal Conservation* 2:103-110.

Stockwell, C. A. and M. Mulvey. 1998. Phosphogluconate dehydrogenase polymorphism and salinity in the White Sands pupfish. *Evolution* 52:1856-1860.

Stockwell, C. A., M. Mulvey and A. G. Jones. 1998. Genetic evidence for two evolutionarily significant units of White Sands pupfish. *Animal Conservation* 1:213-226.

Jones, A. G., **C.A. Stockwell**, D. Walker and J. C. Avise. 1998. The molecular basis of a microsatellite null allele from the White Sands pupfish. *Journal of Heredity* 89:339-342.

Stockwell, C. A., M. Mulvey and G. L. Vinyard. 1996. Translocations and the preservation of allelic diversity. *Conservation Biology* 10:1133-1141.

Stockwell, C. A. 1991. Behavioural reactions of desert bighorn sheep to avian scavengers. *Journal of Zoology (London)* 225:253-256

Stockwell, C. A., G. C. Bateman and J. Berger. 1991. Conflicts in National Parks: A case study of helicopters and bighorn sheep at Grand Canyon. *Biological Conservation* 56:317-328.

BOOK CHAPTERS / REPORTS

Stockwell, C. A. and S. M. Henkanaththegedara. 2011. Conservation biology of poeciliids. **Invited book chapter**, Editors, I. Schlupp, A. Pilastro and J. Evans, *The evolutionary ecology of the Livebearing Fishes*". University of Chicago Press

Stockwell, C. A. and M. L. Collyer. 2006. Rapid adaptation and conservation. Pages 192-194 *in* F. Allendorf and G. Luikart, editors, ***Conservation and the Genetics of Populations***. Blackwell Press.

Stockwell, C. A., M. T. Kinnison and A. P. Hendry. 2006. Evolutionary Restoration Ecology. Pages 113-138 *in* D. A. Falk, M. A. Palmer and J. B. Zedler, Editors, ***Foundations of Restoration Ecology,*** Island Press.

Stockwell, C. 1994. The biology of Walker Lake. Report to University of Nevada, Biological Resources Research Center, Reno.

Stockwell, C. A. 1994. Current nomenclature and status of fishes of Nevada. Pages 5-6n *in* I. LaRivers, ***Fishes and Fisheries of Nevada.*** University of Nevada Press, Reno, NV.

Matschke, G. H., P.L. Hegdal **and C.A. Stockwell**. 1986. Gophers. Pages 60-65 *in* S. Barry and D. R. Houghton. ***The 6th International Biodeterioration Symposium.*** C.A.B. International.

BOOK REVIEWS

Stockwell, C. A. 2004. Conservation biology for biologists. *Conservation Biology* 18:284-285.

INVITED SEMINARS

Stockwell, C. A. 1997-2015; Twenty-three invited seminars

SYMPOSIA

2013 Symposium Organizer - *Evolutionary Ecology of Protected Species: Refuges & Restoration* – Desert Fishes Council, Death Valley, CA.

2005 Symposium Lead-off Speaker - *Evolution on Ecological Time Scales*, Ecological Society of America, Montreal.

2001 Symposium Speaker – *Conservation, biology, genetics and management of freshwater fish in the Southwest and Mexico.* American Fisheries Society, Phoenix, AZ

2000 Symposium Organizer - Organismal biology of the Northern Plains. North Dakota – South Dakota-Minnesota Academy of Sciences meeting, Moorhead, MN

1995 Symposium Organizer - Translocations as a tool in the conservation of native desert fishes. Desert Fishes Council, Reno, NV, November, 1995

PROFESSIONAL PRESENTATIONS

American Fisheries Society

2010 - **2** presentations (Minnesota Chapter)
2008 – **1** presentation (Minnesota Chapter)
2007 – **1** presentation (**Invited**; Oregon Chapter)
2001 – **1** presentation (**Invited;** National Meeting)
1998 – **1** presentation (Dakota Chapter; **Best Paper**)

Society for Conservation Biology

2014 – **4** presentations
2012 – **4** presentations

PROFESSIONAL PRESENTATIONS (continued)

2011 – **2** presentations
2008 – **1** presentation
2006 – **1** presentation
2003 – **3** presentations
2000 – **3** presentations (Student won graduate student competition)
1991 – **1** presentation

Desert Fishes Council

1992 – 2014 - **24** presentations
2003 Graduate student won best presentation
2012 Undergraduate student - Best student poster – including graduate students

The Wildlife Society

2013 – **1** presentation
2013 – **2** presentations (North Dakota Chapter; students best paper & best poster)
2012 - **1** presentation (North Dakota & Minnesota Joint meetings; student won graduate student competition)
2011 – 1 presentation (North Dakota Chapter)
2010 - **2** presentations (North Dakota Chapter)
2009 – **1** presentation (North Dakota Chapter)
2002 – **1** presentation

Society of Wetland Scientists

2014 – **1** presentation
2013 – **1** presentation
2008 - **1** presentation
2010 - **1** presentation
2011 - **1** presentation

American Society of Ichthyologists and Herpetologists

2011 – **4** presentations
2009 – **1** presentation
2007 **– 1** presentation
2002 – **1** presentation
1996 – **1** presentation

North American Benthological Society

2006 – 1 presentation

Ecological Society of America

2013 - **3** presentations
2005 – **1** presentation (Invited)
1995 – **1** presentation

EcoTAS – Joint meeting of the New Zealand & Australian Ecological Societies

2013 – **1** presentation (Invited)

Society for the Study of Evolution

2008 - **1** presentation
1999 – **1** presentation (Invited)
1998 – **1** presentation
1997 – **1** presentation

AWARDS / INVITATIONS / RECOGNITION

James A. Meier Junior Professorship Award, 2008-2012

University of Manitoba, George A. Lubinsky Featured Seminar Speaker – invited by UM graduate students, March, 2009

Invited Speaker - Summer School in Conservation Genetics of Marine Organisms, Chioggia Italy, July 2012

IN THE MEDIA

Discover Magazine (2014)
http://blogs.discovermagazine.com/science-_sushi/2014/09/30/unexceptional-devils-hole-pupfish/#.VGzcX8leJNh

Nature News (2014)
http://www.nature.com/nature/journal/v513/n7519/full/513462a.html

Phys Org (2014)
http://phys.org/news/2014-09-biological-sciences-professor-publishes-pupfish.html

PLoS Blog (2012) –
http://blogs.plos.org/toothandclaw/2012/01/16/the-alicia-patterson-fellowship-and-a-two-minute interview-with-craig-stockwell/

Earth Times (2011)
http://www.earthtimes.org/scitech/evolution-measured-decades-centuries/1366/

News Wise (2011)
http://www.newswise.com/articles/evolution-not-as-long-as-you-think

Phys Org (2011)
http://phys.org/news/2011-09-contemporary-evolution-published.html

Science Direct (2008)
Stockwell et al. 2003 paper recognized as one of most cited papers by Science Direct
http://archive.sciencewatch.com/dr/fmf/2008/08julfmf/08julfmfSockwl/

Global Public Media (2008)
http://old.globalpublicmedia.com/the_rate_of_evolution_an_interview_with_dr_craig_stockwell

Amy B. Welsh

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West Virginia University
Morgantown, WV 26506
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EDUCATION

University of California – Davis, *2001-2006*
Graduated with a Ph.D. in Ecology; Area of Emphasis: Conservation Biology
Dissertation title - Lake Sturgeon Conservation in the Great Lakes: Scaling it Up from Genetics to Policy

The George Washington University, *Washington, DC, 1997-1999*
Graduated with a Master of Forensic Sciences

University of Maryland at College Park, *1992-1996*
Graduated with a Bachelor of Science in Zoology and Psychology

WORK EXPERIENCE

West Virginia University

Assistant Professor (2011-present)

- Develop a research program in conservation genetics
- Teach an undergraduate and graduate course in conservation genetics
- Mentor M.S. and Ph.D. students
- Advise undergraduate students

State University of New York – Oswego

Assistant Professor (2006-2011)

- Taught courses in Evolution, Conservation Genetics, Introductory Biology lab, Zoology seminar, and Biological Conservation
- Designed laboratory class in genetics
- Mentored students on senior honors thesis projects related to genetics, ecology, or zoology
- Developed a genetics research program
- Collaborated with faculty on research projects involving ecological genetics
- Advised undergraduates on course selection and career goals

University of California – Davis

Post-doctoral Researcher (2006)
Graduate Research Assistant (2001-2006)

- Designed primers to target disomic microsatellite loci.
- Coordinated microsatellite standardization among nine genetic laboratories.
- Assess population genetic structure of 21 lake sturgeon populations throughout the Great Lakes using microsatellites and mitochondrial DNA (mtDNA), and visualizing results on an MJ Research BaseStation.

- Assign non-spawning individuals to most likely natal site of origin.
- Develop a genetics-based management plan for lake sturgeon throughout the Great Lakes basin.
- Assisted in microarray project examining whirling disease resistance in rainbow trout.
- Conducted policy analysis of state versus federal legislative protection of lake sturgeon.
- Write proposals and reports for funding agencies.
- Present results to managers and biologists at various meetings.

United States Fish and Wildlife Service, Sacramento, CA
Fish and Wildlife Biologist, Student Trainee (SCEP) (2004-2006)

- Conduct interagency consultations authorized by Section 7 of the Endangered Species Act on projects within the San Joaquin Valley, affecting species such as the San Joaquin kit fox and valley elderberry longhorn beetle.
- Review Habitat Conservation Plans for the issuance of incidental take permits.
- Provide technical assistance to nonfederal projects.
- Provide genetic assistance on listing decisions, candidate evaluations, and recovery projects.
- Guide projects that impact the riparian brush rabbit and assist in implementation of their recovery strategy, while serving as a member of the recovery team.

Great Lakes Fishery Commission, Ann Arbor, MI
Three-Month Detail (February 2005-May 2005)

- Interacted with managers and biologists in the Great Lakes region to obtain input on lake sturgeon management issues.
- Developed genetic management guidelines addressing lake sturgeon stocking throughout the Great Lakes basin.
- Observed the coordination of interjurisdictional fisheries management by attending committee meetings at various hierarchical levels.

Armed Forces DNA Identification Laboratory, Rockville, MD
DNA Analyst (2000-2001); DNA Technician (1999-2000)

- Extracted, amplified, sequenced, and analyzed mtDNA from the bloodstains of family references of missing soldiers to be used in the development of a database.
- Validated a high-throughput laboratory method for the sequencing of DNA, fine-tuned the system, and trained team members on the proper utilization of the technique.

National Fish and Wildlife Forensics Laboratory, Ashland, OR
Forensic Biology Intern (Summer 1998)

- Extracted, amplified, sequenced, and analyzed mtDNA of sturgeon to determine the frequency of mislabeled caviar and to develop a database containing the sequences of different species of sturgeon.

Walter Reed Army Institute of Research, Forest Glen, MD
Research Assistant (1995-1999)

- Performed microsleep and spectral analyses on EEG data collected from sleep deprivation studies and trained students in microsleep analysis.
- Conducted statistical analyses on actigraphy and oculomotor data.
- Mapped PET data onto MRI.
- Managed a sleep dose-response study involving human subjects, which included supervising shift workers and overseeing proper data collection.

TEACHING EXPERIENCE

Assistant Professor (2011-present)
West Virginia University
Classes taught: Conservation Genetics (undergraduate & graduate courses); Conservation Ecology

Assistant Professor (2006-2011)
State University of New York – Oswego
Classes taught: Evolution; Conservation Genetics; Zoology Seminar; Laboratory in Genetics; Introductory Biology Laboratory; Biological Conservation

Teaching Assistant, Introduction to Biological Sciences – Zoology (2004)
University of California – Davis
Prepare and present lecture for laboratory sections. Assist students with laboratory exercises. Grade quizzes and assignments.

Guest Lecturer, Conservation Genetics Seminar (2003)
University of California – Davis
Presented lecture on the maintenance of genetic diversity in small populations.

PEER-REVIEWED PUBLICATIONS

(underlined authors: student authors)

Submitted:

Marranca, J.M., **Welsh, A.B.,** and Roseman, E. Genetic effects of habitat restoration in the Laurentian Great Lakes: an assessment of lake sturgeon origin and genetic diversity. Submitted to Restoration Ecology (Status: Minor revisions submitted)

Published:

Buckner, J., **Welsh, A.B.,** and Sime, K.R. (2014) Evidence for population differentiation in the bog buckmoth of New York State. Northeastern Naturalist 21(4): 506-514.

Welsh, A. and Jackson, J.R. (2014) The effect of multi-year versus single-year stocking on lake sturgeon genetic diversity. Journal of Applied Ichthyology 30: 1524-1530.

Welsh, A.B., Baerwald, M.R., Friday, M., and May, B. (2014) The effect of multiple spawning events on cohort genetic diversity. Environmental Biology of Fishes DOI 10.1007/s10641-014-0309-9.

Welsh, A. (2014) Genetic considerations in the restoration of small forest populations: perspectives from fish and wildlife genetics. Journal of Sustainable Forestry 33: s66-s92.

Welsh, A. (2013) Recognizing the genetic population structure of lake sturgeon. In: N. Auer & D. Dempsey (eds) The Great Lake Sturgeon. Michigan State University Press, Michigan, pp. 79-92.

Questel, J., Walsh, M., Smith, Jr., R., and **Welsh, A.** (2012) New data on mitochondrial diversity and origin of *Hemimysis anomala* in the Laurentian Great Lakes. Journal of Great Lakes Research 38: 14-18.

Welsh, A.B. and Mohamed, K.I. (2011) Genetic diversity of *Striga hermonthica* populations in Ethiopia: evaluating the role of geography and host specificity in shaping population structure. *International Journal of Plant Sciences* 172: 773-782.

Brooking, T., Rudstam, L.G., Krueger, S.D., Jackson, J.R., **Welsh, A.B.,** and Fetzer, W.W. (2010) First occurrence of the mysid *Hemimysis anomala* in an inland lake in North America, Oneida Lake, NY. *Journal of Great Lakes Research* 36: 577-581.

Welsh, A. and McLeod, D. (2010) Detection of natural barriers to lake sturgeon (*Acipenser fulvescens*) movement within the Namakan River, Ontario. *Canadian Journal of Zoology* 88: 390-397.

Welsh, A.B., Elliott, R.F., Scribner, K.T., Quinlan, H.R., Baker, E.A., Eggold, B.T., Holtgren, J.M., Krueger, C.C., May, B. (2010) Genetic guidelines for the stocking of lake sturgeon (*Acipenser fulvescens*) in the Great Lakes basin. Great Lakes Fishery Commission Miscellaneous Publication 2010-01.

Welsh, A., Hill, T., Quinlan, H., Robinson, C. and May, B. (2008) Genetic assessment of lake sturgeon population structure in the Laurentian Great Lakes. *North American Journal of Fisheries Management* 28: 572-591.

Baerwald, M.B., **Welsh, A.B.**, Hedrick, R.P., and May, B. (2008) Discovery of genes implicated in whirling disease infection and resistance in rainbow trout using genome-wide expression profiling. *BMC Genomics* 9:37.

Welsh, A. and May, B. (2006) Development and standardization of disomic microsatellite markers for lake sturgeon genetic studies. *Journal of Applied Ichthyology* 22: 337-344.

Welsh, A. (2004) Factors influencing the effectiveness of local versus national protection of migratory species: a case study of lake sturgeon in the Great Lakes, North America. *Environmental Science and Policy* 7(4): 315-328.

Welsh, A., Blumberg, M., & May, B. (2003) Identification of microsatellite loci in lake sturgeon, *Acipenser fulvescens*, and their variability in green sturgeon, *A. medirostris*. *Molecular Ecology Notes* 3(1): 47-55.

Thomas, M.., Sing, H., Belenky, G., Holcomb, H., Mayberg, H., Dannals, R., Wagner, Jr., H., Thorne, D., Popp, K., Rowland, L., **Welsh, A.**, Balwinski, S. & Redmond, D. (2003) Neural basis of alertness and cognitive performance impairments during sleepiness. II. Effects of 48 and 72 h of sleep deprivation on waking human regional brain activity. *Thalamus and Related Systems* 2(3): 199-229.

Thomas, M.., Sing, H., Belenky, G., Holcomb, H., Mayberg, H., Dannals, R., Wagner, Jr., H., Thorne, D., Popp, K., Rowland, L., **Welsh, A.**, Balwinski, S. & Redmond, D. (2000) Neural basis of alertness and cognitive performance impairments during sleepiness. I. Effects of 24 hours of sleep deprivation on waking human regional brain activity. *Journal of Sleep Research* 9(4): 335-352.

PRESENTATIONS & ABSTRACTS

Oral Presentations: (students underlined)

Wood, D. (presenter), and **Welsh, A.** (2014) Lake sturgeon on the move? Identification of lake sturgeon migrants into a genetically deficient area. Oral presentation at the American Fisheries Society meeting, Quebec City, QC

Wood, D. (presenter) and **Welsh, A.** (2014) Restoring the connection between brook trout populations within an Appalachian Watershed. Oral presentation at the American Fisheries Society meeting, Quebec City, QC

Welsh, A. and Quinlan, H. (2014) Homebodies or roamers? Genetic assignment of lake sturgeon in Lake Superior. Oral presentation at the American Fisheries Society meeting, Quebec City, QC – **INVITED SPEAKER**

Whitaker, J. (presenter)**, Welsh, A.,** and King, T. (2014) Refining management units through genomics. Oral presentation at the American Fisheries Society meeting, Quebec City, QC

Welsh, A. (2014) The use of population genetics to inform management: a case study of lake sturgeon in the Great Lakes. Oral presentation during the Ecology and Evolutionary Biology Seminar Series at Virginia Tech – **INVITED SPEAKER**

Welsh, A. (2013) Creating genetic management plans in the face of uncertainty: a case study of lake sturgeon in the Great Lakes. American Fisheries Society, Little Rock, AR ***Invited speaker**

Wood, D. (presenter) and **Welsh, A.** (2013) The effects of culverts on brook trout genetic diversity. American Fisheries Society, Little Rock, AR

Schreier, A. (presenter), **Welsh, A.,** and May, B. (2013) Improving sturgeon management and conservation with genetic management plans: case studies from both coasts. Western division of the American Fisheries Society.

McDougall, C. (presenter), **Welsh, A.**, Peake, S.J., and Anderson, G. (2013) An inter-reservoir contribution of lake sturgeon: unforeseen consequences of survived downstream passage? International Sturgeon Symposium, Nanaimo, BC.

Welsh, A. and Jackson, J.R. (2013) The effect of multi-year versus single-year stocking on lake sturgeon genetic diversity. International Sturgeon Symposium, Nanaimo, BC.

Welsh, A., Jackson, J.R., and Sloss, B. (2012) Effects of stocking on the genetic diversity of lake sturgeon. Great Lakes Lake Sturgeon Coordination Meeting, Sault Ste. Marie, MI.

Welsh, A., Scribner, K., Stott, W., and Walsh, M. (2012) Genetic identification of the origin of the Lake Ontario deepwater sculpin population. American Fisheries Society meeting, St. Paul, MN. ***Invited speaker**

Welsh, A., Scribner, K., Walsh, M., and Stott, W. (2012) Genetic identification of the origin of the Lake Ontario deepwater sculpin population. Northeast Association of Fish and Wildlife Agencies meeting, Charleston, WV.

Welsh, A., Questel, J., Smith, R., Walsh, M., Bowen, K., and Schaner, T. (2010) Genetic determination of the invasion pathway of *Hemimysis anomala* throughout the Great Lakes. International Association of Great Lakes Research Meeting, Toronto, ON, Canada.

Welsh, A., Scribner, K., Elliott, R., Quinlan, H., Baker, E., Eggold, B., Holtgren, J.M., Krueger, C., and May, B. (2010) Population genetic structure of lake sturgeon in the Great Lakes and its implications for management. Lake Sturgeon Research and Recovery Workshop, Winnipeg, MB, Canada. ***Invited speaker.**

Welsh, A., Scribner, K., Elliott, R., Quinlan, H., and May, B. (2009) Lake sturgeon population genetics. Great Lakes Fishery Commission Lake Committee Meeting, Ypsilanti, MI. ***Invited speaker.**

Welsh, A. (2009) Human-induced evolutionary changes in lake sturgeon. Darwin 200 event, SUNY-Oswego.

Welsh, A. (2009) The use of population genetics for the conservation of lake sturgeon in the Great Lakes. Aquabreak seminar series, SUNY- Environmental School of Forestry. ***Invited speaker.**

Welsh, A., Baerwald, M., Friday, M., and May, B. (2008) Hydropower facilities and sustainable sturgeon: a conservation genetic approach to understanding lake sturgeon on the Kaministiquia River. American Fisheries Society, Ottawa, ON.

Welsh, A., Quinlan, H., Mohr, L., and May, B. (2008) Genetic assignment of lake sturgeon in Lake Superior and Lake Huron. American Fisheries Society, Ottawa, ON. ***Invited speaker.**

Welsh, A. (2008) Lake sturgeon conservation genetics: not just another fish tale. Science Today talk series, SUNY-Oswego. ***Invited speaker.**

Welsh, A. (2008) Conservation genetics: undergraduate research that makes a difference. Sigma Xi dinner, SUNY-Oswego. ***Invited speaker.**

Questel, J., Back, R., and **Welsh, A.** (2008) Genetic Determination of the Origin of *Hemimysis anomala* in Lake Ontario. International Association of Great Lakes Research, Peterborough, ON. ***Undergraduate student presenting.**

Welsh, A.*, DeHaan, P., Scribner, K., Elliott, R. (presenter), Krueger, C., Quinlan, H., & May, B. (2007) Genetic structuring of remnant populations and related conservation and stocking guidelines. Great Lakes Fishery Commission Lake Committee Meetings, Ypsilanti, MI. ***Invited speaker; needed to decline due to illness.**

Welsh, A.B. & Sloss, B. (2007) Proposal to study the effects of lake sturgeon mating strategies on the maintenance of genetic diversity at the major histocompatibility complex. Board of Technical Experts for the Great Lakes Fishery Commission, Ann Arbor, MI.

Welsh, A.B.*, Elliott, R., Krueger, C., Quinlan, H., & May, B. (2006) Development of lake sturgeon genetic stocking guidelines. Great Lakes Lake Sturgeon Coordination Meeting, Sault Ste. Marie, MI. ***Also participated as a panelist.**

Bott, K., Scribner, K. (presenter), Elliott, R., Ragavendran, A., Rosa, G., and **Welsh, A.** (2006) Genetic assignment of open water stocks to rivers of origin and comparative analyses of recruitment in lake sturgeon. Great Lakes Lake Sturgeon Coordination Meeting, Sault Ste. Marie, MI.

Welsh, A.B.; C. Krueger, & B. May (2006) Development of genetic stocking guidelines for conservation of lake sturgeon in the Great Lakes. American Fisheries Society meeting, Lake Placid, NY.

Baerwald, M.R. (presenter), **Welsh, A.B.**, Hedrick, R.P., & May, B. (2006) Discovering genes associated with whirling disease resistance using microarray analysis. American Fisheries Society meeting, Lake Placid, NY.

Welsh, A.B.; C. Krueger, & B. May (2006) Genetic stocking guidelines for lake sturgeon conservation in the Great Lakes. Society for Conservation Biology meeting, San Jose, CA.

Welsh, A.B. (2005) Lake sturgeon conservation in the Great Lakes: scaling it up from genetics to policy. Animal Science Seminar Series, University of California-Davis.

Welsh, A.B.; T. Hill, & B. May (2005) Population genetic structure of lake sturgeon in the Great Lakes and implications for management. American Fisheries Society meeting, Anchorage, AK.

Welsh, A.; T. Hill, P. DeHaan, K. Scribner, & B. May (2004) Spatial population genetic diversity of lake sturgeon throughout the Great Lakes. Great Lakes Lake Sturgeon Coordination Meeting, Sault Ste. Marie, MI.

Welsh, A.* & B. May (2004) Standardization of microsatellite loci in lake sturgeon. American Fisheries Society, Madison, WI. ***Invited Speaker; Panelist.**

Welsh, A. (2004) Effectiveness of state management of migratory species: a case study. World Fisheries Congress, Vancouver, BC.

Welsh, A.; T. Hill & B. May (2002) Development of a lake sturgeon management plan: Status of molecular markers and sampling. Great Lakes Lake Sturgeon Coordination Meeting, Sault Ste. Marie, MI.

Welsh, A.; M. Blumberg, C. Lowie & B. May (2002) Standardization of microsatellite markers for lake sturgeon, *Acipenser fulvescens*. American Fisheries Society, Baltimore, MD.

Poster Presentations: (students underlined)

Price, L. and **Welsh, A.** (2014) Genetic differentiation of lake sturgeon in the St. Lawrence River. Poster presentation at the American Fisheries Society meeting, Quebec City, QC

Wood, D.**, Welsh, A**., and Crum, J. (2014) Landscape attributes affecting the spread of chronic wasting disease in West Virginia. Poster presentation at The Wildlife Society meeting, Pittsburgh, PA

Frantz, M.**, Welsh, A.,** and Wood, P. (2014) Epigenetic (DNA methylation) variation in the Louisiana waterthrush due to shale gas development in West Virginia. Poster presentation at The Wildlife Society meeting, Pittsburgh, PA

Marranca, J. (presenter), **Welsh, A.**, and Roseman, E. (2013) Genetic assessment of lake sturgeon origin following reproduction on an artificial reef. International Sturgeon Symposium, Nanaimo, BC.

Whitaker, J. (presenter), Welsh, A., Boase, J., and Hondorp, D. (2013) Morphometric analysis of lake sturgeon. International Sturgeon Symposium, Nanaimo, BC.

Questel, J., Smith, R., Walsh, M. (presenter), and **Welsh, A.** (2011) Genetic determination of the origin of *Hemimysis anomala* in the Laurentian Great Lakes. American Fisheries Society meeting, Seattle, WA.

Baerwald, M.R.; R. Hedrick, **A. Welsh**, & B. May (2005) Identifying genes associated with whirling disease resistance in rainbow trout using microarray analysis. American Fisheries Society meeting, Anchorage, AK.

Welsh, A. & B. May (2004) Patterns of population genetic diversity in lake sturgeon of the Great Lakes. American Fisheries Society, Madison, WI.

Welsh, A & B. May (2003) Potential role of genome duplication to impede gene pool erosion in sturgeon of the genus *Acipenser*. American Fisheries Society, Quebec City, QC.

Welsh, A.; N. Jimerson, D. Herman, S. Kodsi, M. Holland & T. Parsons (2000) Implementation of a 96-well high-throughput method for mitochondrial DNA databasing. International Symposium on Human Identification, Biloxi, MS.

Jones, S.; J. Irwin-Ross, F. Love, **A. Welsh**, M. Holland & T. Parsons (1999) Development of an efficient, high-throughput strategy for sequence analysis of the entire human mitochondrial DNA control region. 10th International Symposium on Human Identification.

Welsh, A.; M. Thomas, D. Thorne, H. Sing, L. Rowland, D. Redmond, R. Peters, E. Wagner & G. Belenky (1998) Effects of 64 hours of sleep deprivation on accidents and sleep events during a driving simulator test. *Sleep* 21(Suppl. 3): 234.

COMPETITIVE FELLOWSHIPS & GRANTS

Competitive Grants Funded:

Welsh, A. (2014-2017) Landscape genetics of white-tailed deer in West Virginia. West Virginia Division of Natural Resources - $175,477

Anderson, J. and Welsh, A. (2014-2018) Population study of bobcats in West Virginia. West Virginia Division of Natural Resources - $268,600

Welsh, A. (2014-2015) Genomic analysis of a freshwater mussel *Actinonaias ligamentina*. WVU ADVANCE Center - $15,000

Welsh, A. (2014-2015) Genomic differences between urban and rural hawks. Daniel C. & Elizabeth D. Brown Faculty Development Fund - $10,000

Welsh, A., Katzner, T., and Anderson, J. (2013-2016) Distribution, differentiation, and hybridization of king and clapper rails in eastern VA. U.S. Fish and Wildlife Service - $419,368

Welsh, A. (2013-2014) Mitogenomic analysis of the phylogenetic relationships among North American sturgeon. WVU ADVANCE Center - $15,000

Welsh, A. (2012-2014) Genetic study of lake sturgeon in the St. Clair-Detroit River system. USGS - $65,000

Welsh, A. (2012-2013) Lake sturgeon migratory genomics. WVU ADVANCE Center - $15,000

Welsh, A. and Petty, J.T. (2012-2013) Effects of culverts on the genetic diversity of brook trout. WVU Faculty Senate Research Grant - $18,880

Welsh, A., Walsh, M., Stott, W., Scribner, K., Connerton, M., Keir, M., and Hoyle, J. (2010-2012) Evaluating genetic relationships between the Lake Ontario deepwater sculpin population and upper Great Lakes populations. Great Lakes Fishery Commission - $62,822

Welsh, A., Back, R., Bowen, K., Schaner, T. & Walsh, M. (2009-2010) Tracing the invasion pathway of *Hemimysis anomala* into Lake Ontario and beyond. Great Lakes Protection Fund (through the Great Lakes Research Consortium) - $6,120

Mohamed, K. & Welsh, A. (2008) Genetic diversity of *Striga hermonthica* populations in Ethiopia. Scholarly and Creative Activities Committee, SUNY-Oswego - $2,750

Welsh, A. & Sloss, B. (2008-2010) A comparison of genetic diversity at the major histocompatibility complex in hatchery-produced and wild lake sturgeon. Great Lakes Fishery Commission - $10,000

Welsh, A., Scribner, K., Boase, J., Elliott, R., Quinlan, H., Thomas, M., Mohr, L., Baker, E., Donofrio, M. & Lenart, S. (2007-2009) Genetic identification of non-spawning lake sturgeon in the Great Lakes. Great Lakes Fishery Trust - $170,871

Welsh, A., Rosenbaum, P., Pursel, K., & Volny, M. (2007-2008) Ecological genetics of two native New York species. SUNY-Oswego Student Faculty Collaborative Challenge Grant - $2,500

May, B., Welsh, A., Hill, T., Haas, R., Bruch, R., Krueger, C. (2004-2008) Development of genetic management guidelines for lake sturgeon. Great Lakes Fish and Wildlife Restoration Act - $84,600
May, B. & Welsh, A. (2005-2008) Assessment of the population genetic structure of lake sturgeon. Great Lakes Fishery Commission - $79,681

Fellowships:

University of California – Davis Dissertation Year Fellowship (2005-2006) – Stipend, tuition, $500 research funds, $500 travel funds
James Wright Scholarship – American Fisheries Society (2004) – Travel funds to national meeting
University of California Graduate Student Travel Award (2004) – $1000 travel funds to attend World Fisheries Congress
Jastro Shields Research Award (2003, 2004) – $4000 research funds
Hart, Cole, Goss Fellowship (2002-2004) – Summer stipend for each year
University of California – Davis Block Grant Fellowship (2001-2005) – Stipend and tuition

CONTRACTED PROJECTS

Welsh, A. (2013-2016) Source population assignment of Lake Superior lake sturgeon. U.S. Fish and Wildlife Service - $125,182
Welsh, A. (2010-2012) Genetic investigation of downstream passage by lake sturgeon at a generating station on the Winnipeg River. University of New Brunswick - $30,000
Welsh, A. (2009-2011) Genetic assessment of the hatchery-produced lake sturgeon population in the Oswego River basin. New York State Department of Environmental Conservation - $42,102
Welsh, A. (2007-2008) Population structure of lake sturgeon within the Namakan River, Ontario. Ontario Ministry of Natural Resources - $14,203

PROFESSIONAL SERVICE

Chair, Division of Forestry and Natural Resources Undergraduate Research Committee (2014-present)
Initiated and led the committee to encourage undergraduate research in the Division; managed the development of award guidelines and selection of award recipients

Secretary/Treasurer, American Fisheries Society, Genetics Section (2014-present)
Manage funds for the section, take meeting minutes, manage section membership.

Faculty advisor, WVU student chapter of Society for Conservation Biology (2012-present)
Formed a new chapter of this international professional society. Assist in the coordination of events and activities.

Chairperson, Wright Award, American Fisheries Society, Genetics Section (2013-present)
Reviewed student applications for the Wright Award, which provides a graduate student with travel funds to the national meeting. Coordinated reviews of other committee members to select a winner.

Manuscript review (2003-2014)
Journals: Conservation Genetics, Molecular Ecology, PLoS One, Environmental Biology of Fishes, North American Journal of Fisheries Management, Transactions of the American Fisheries Society; Journal of

Applied Ichthyology, Aquaculture Research, Fish Physiology and Biochemistry, Journal of Great Lakes Research, Canadian Journal of Fisheries and Aquatic Science

Project proposal review (2002; 2005-2014)
Great Lakes Fishery Commission; National Fish and Wildlife Foundation; New York Sea Grant; Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative; Minnesota Sea Grant; NOAA-Fisheries; South Carolina Water Resources Center

Phelps Award Committee, American Fisheries Society, Genetics Section (2013)
Reviewed all genetics paper published in 2012 in the four American Fisheries Society journals to select the winner of the Phelps Award.

Department of Biological Sciences service, SUNY-Oswego (2007-2011)
First-Year advisor; Member of the Curriculum committee; Chair of the Awards committee (2007-2008); Member of the Molecular Biologist Search Committee (2008-2009); Representative on the Campus Technology Advisory Board (2007-2008); Representative on Faculty Assembly (2008-present); Member of the Provost's Committee on Scientific and Quantitative Literacy (2008-2009); Member of the Personnel Committee (2009-present); Chairperson of the Provost's Committee on Biotechnology Planning (2009-present)

Expert Participant (2009)
Department of Fisheries and Oceans Canada Lake Sturgeon Recovery Workshop
Provided peer review, guidance, and feedback on agency efforts to assess the recovery potential of lake sturgeon in Hudson Bay.

Guest Speaker (2006)
U.S. Department of State International Visitor Leadership Program
Hosted a group of sturgeon biologists and managers from Azerbaijan at our genetics laboratory. Described the use of genetics in the management of North American sturgeon species.

Genetic Support (2004, 2005)
Lake Michigan Lake Sturgeon Task Group; Lake Superior Lake Sturgeon Task Group
Presented genetic data and answered questions about implications of the data at meetings where members were making lake sturgeon management decisions.

Treasurer (2004-2005)
Society for Conservation Biology – UC Davis Student Chapter
Work as a team with other officers to organize and motivate chapter for the 2004-2005 school year. Manage chapter funds and membership dues.

Graduate student representative (2003-2005)
Conservation Biology Area of Emphasis, Ecology Graduate Group, UC Davis.
Represent needs and interests of graduate students in the Conservation Biology Area of Emphasis to the parent graduate group. Assist in planning graduate student seminar with conservation focus.

Chairperson, Educational Outreach Committee (2002-2005)
Society for Conservation Biology – UC Davis Student Chapter
Coordinate educational outreach to children about local endangered species.

APPENDIX D

Comment Matrix

Expert Peer Review of the Middle Rio Grande Endangered Species Collaborative Program's Rio Grande Silvery Minnow Genetics Project

U.S. Bureau of Reclamation

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
1	Executive Summary	ii	35-37	last sentence uses "assess" three times; maybe change to "assessing quantitative traits over year classes in the hatcheries to evaluate changes"…	Price	USACE	Corrected.
2	Executive Summary (also relates to Question 16)	ii	28-29	"using one female-one male breeding pairs (or assessing genetic contributions in offspring of 10 x 10 pairings)"- Please provide, somewhere in the document, an evaluation of the pros/cons of paired matings vs. 10x10 matings with genetic assesssment. Does 10x10 group mating allow a more "natural" spawn and is this advantageous compared to paired mating?	Price	USACE	The genetics group has already published a paper showing differential contributions of parents in the 10 x 10 pairings currently used. These differential contributions lower the effective population size of the stocking population. The degree of dimunition of Ne has not been calculated. Mate choice and increased chances of egg fertilization are the principal advantages of 10 x10 matings. While 1 x 1 pairings remove mate choice, broadcast/multiple-participant spawining species do not appear to be exercising mate choice. Reduced fertilization of any lot of eggs will be readily compensated by more equitable contributions of individual broodstock. It could be argued that combining many males and females in close proximity during spawning more readily reflects what occurs in nature, the problem is this practice in a hatchery does not reflect the large number of these events that occur in nature. The biggest difference is that in the hatchery one is decreasing loss from fertilzed egg to juvenile as a compensation for using a smaller number of broodstock. In other words, differential individual and family contribution in nature is compensated for by a larger number of broodstock and selection.
3	1.0	1	Para 2	The term "population bottlenecks" is jargon that perhaps all readers may not understand, please clarify for those readers.	Mike Marcus	APA	Added to glossary, sentence slightly revised. See comment #34.
4	1.0	1	Para 3	The program has funded the Genetics program since 2004 with a critical gap in funding in 2013. Prior to 2004, funding came from UNM (Turner start-up and seed grants), NM Department of Game and Fish, and the Bureau of Reclamation.	Osborne & Turner	UNM	Added language to paragraph.
5	1.0	1	Para 3, 3rd sentence	We define augmentation as the beginning of planned augmentation activities by the USFWS SNARCC and do not include the experimental augmentation activities that occurred in 2000 where fish were spawned and larval fish were released (survival of larval fish is predicted to be low). Releases from 2002-2003 primarily comprised fish reared from wild-caght eggs (natural spawning). See comment #116 below.	Osborne & Turner	UNM	See comment #16
6	1.0	1	Para 3, last line	Please clarify, here and elsewhere the term "wild population of RGSM" is used. Yet on page 10, first full para after Objective 1 is stated, "... there is likely no remaining wild population in the Middle Rio Grande because most captured fish and eggs likely had hatchery rearing in its lineage." Perhaps instead of "wild" here and elsewhere, as indicated in additional comments below, some other term could be used ... perhaps, "instream populations"?	Mike Marcus	APA	See glossary for definition of 'wild vs. captive' for the purposes of this report.

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
7	1.0	1	Para 3, Line 3	Sentence 3 is not entirely correct. It states that “augmentation consists primarily of capturing eggs from the Middle Rio Grande and rearing them to a larger size and then releasing them back into the river (e.g., Archdeacon 2015)”. While this is the stated goal of the Service-run augmentation program, due to the numbers of captured eggs from the wild for every year but one, augmentation actually has consisted of spawning fish in the hatchery that were from captured eggs and stocking their offspring in the river. This has implications, as you later describe, on the genetic management for both propagation and augmentation that may not have been considered by the Service in the early 2000’s. We would appreciate the discussion of augmentation be clarified in this paragraph to provide the difference in the goal vs. the actual occurrence.	NM ISC	NM ISC	Revised sentence.
8	1.0	2	Para 3	Blake et al 2014, is not correct and should be Carson et al. 2014	Osborne & Turner	UNM	Corrected
9	1.0	2		In the middle of this page, the report references "Blake et al. 2014" as one of the annual reports for the RGSM Genetics Project. This should be Carson et al. 2014. Also, in Appendix A (page A-1) the same correction is needed.	Bachus	BOR	Corrected in both places.
10	1.0	2		The reviewers state that “The ongoing Genetics Project provides a genetic sampling and assessment program, which refers to the estimation of population genetics parameters, such as gene diversity, heterozygosity, allelic richness, and genetic effective size of RGSM (e.g., Osborne et al. 2012)”. The report would be well served if a synopsis for the parameters stated in this sentence is provided that explains each, assumptions for each, and their use for conservation genetics/ species preservation and management? This would set the stage for the report and provide details that are not known by readers who are not geneticist or biologists.	Gonzales	BOR	Added to glossary, see comment #34
11	3.0, Question 1	3	Bullet 1	We explicitly did this in our 2012 paper (Osborne) where we looked at pre and post-augmentation time periods to examine the effects of environmental conditions (ie flow), demography (population abundance, catch-per-unit-effort) and augmentation of metrics of genetic diversity. We could restate null hypotheses - i.e no change in diversity/effective population size or increase/decrease in these metrics in future reports.	Osborne & Turner	UNM	No comment from panel.
12	3.0, Question 1	4	Bullet 2	Logistic regression might be a better way to assess an exponential decay function. We have tested a number of hypotheses using time series data and in a comparative context related to life-history differences among species with different egg characterisitics (Turner et al. 2006, Proceeding of the Royal Society of London B, 273:3065-3075)	Osborne & Turner	UNM	No response from panel.
13	3.0, Question 1	4	Bullet 2	With all due respect to the reviewers, suggestions such as this tend to oversimplify a complex time-series. Like any model (including split plot regressions) there should be well founded underlying biological reasons to choose it. We have adopted simulation approaches to disentagle hatchery effects, dispersal and retention, and other effects on the system. These results will be made available to the Program, along with interpretations grounded in genetic and demographic theory and sensitivity analysis.	Osborne & Turner	UNM	This bullet has been modified somewhat. The panel's inclusion of this point was a suggestion only, as an additional approach to assessing genetic change over time

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
14	3.0, Question 1	4	Bullet 3	Could you provide an example of how genome-wide variation could be negatively affected but not detected via the nine microsatellites loci being evaluated?	Gonzales	BOR	This bullet has been tweaked to be more explicit. However, the examples provided are only included here as a reply. Here are two examples of how genome-wide variation could be affected but not at the nine microsatellite loci being screened. The important underlying point in each example is that nine small repeats of DNA will very unlikely reflect genome-wide trends due to small sample size/sampling variance. Example 1) All genetic diversity in the genome is selectively neutral, but by chance, the nine microsatellite loci have lower allelic richness relative to the average of other similar loci across the genome (uncertainty in how well these nine loci represent all others): whenever founder effects, nonrandom sampling of RGSM or genetic drift occur (etc.), loss of rarer alleles will occur in the non-sampled loci but such losses of genetic diversity will be less likely detected with the nine loci currently being screened for monitoring (loci with more common alleles do not lose these as quickly through drift). 2) Other parts of the genome either encode for functional traits associated with fitness/survival in RGSM, or are closely linked to other loci that are of functional significance for the species: in this case, we might easily detect no differences over time in 'genetic diversity' with the nine microsatellite loci, even though significant, selective changes were occurring elsewhere in the genome at loci of functional importance. In RGSM, such changes to function genetic variation are most likely to arise via hatchery manipulation at any step, as discussed elsewhere.
15	3.0, Question 1	4	Bullet 3	In light of the page 10 statement, referenced in my comment 2, is this recommendation relevant related to "genetic diversity of the natural spawning population", if all RGSM in the MRG have their origins with hatchery stocks?	Mike Marcus	APA	See glossary term and notes under 'wild vs. captive'
16	3.0, Question 1	4	Bullet 3	Larval fish were released in 2000 as part of experimental breeding that was conducted by Stephen Platania. No augmentation activities occurred in 2001. Experimental augmentation activities in which eggs from natural spawning (of wild fish) were reared and released in 2002 and 2003. Hence, we refer to the preaugmentation period as 1987, 1999-2003. We will (and have in the past) clarified the distinction between experimental and management oriented and purposeful augmentation. We could define preaugmentation very strictly and only include samples from 1987 (n=43) and 1999 (n=46) but there are very few samples in those collections so they may not provide a representative sample of the wild population.	Osborne & Turner	UNM	Although the augmentation was experimental and not part of the formal augmentation program, it still represents supplementation that could have had an effect on the population's genetic diversity. The fact that it was not part of the genetic management program means the released offspring could actually reflect even lower genetic diversity than those released as part of the genetic management program. Sample sizes of n=43 and n=46 should be sufficient to provide an idea of pre-augmentation genetic diversity.
17	3.0, Question 1	4	Bullet 4	We will prepare a table of standard genetic metrics and interpretations to include in future reports.	Osborne & Turner	UNM	None.
18	3.0, Question 1	4	Bullet 5	Could you provide a list of those conclusions that the panel thinks have been overstated within published and unpublished reports? If what is included in parentheses is exhaustive then please ignore the comment.	Gonzales	BOR	Sentence revised; the example provided is the conclusion that has been overstated.
19	3.0, Question 1	4	Bullet 5	Overstated with respect to what?	Osborne & Turner	UNM	See comment #18
20	3.0, Question 1	4	Bullet 6	Would development of barcode markers address this comment?	Porter	USACE	Text revised.

Comment #	The comment refers to the			Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
	Section	Page	Line				
21	3.0, Question 1	4	Bullet 6	The draft report states that microsatellite loci may not be the most effective markers for the purpose. What would be? And how does the panel view the trade-off between having a long-term dataset using consistent techniques and changing (or adding?) whatever you might be recommending for more effective markers? This response should also state what is recommended here as more effective markers and whether that replaces or is done concurrently (added to) the existing methods for long-term dataset maintenance. Or if this is addressed at length elsewhere in the report, restate a summary here and refer reader to that section elsewhere.	Bachus	BOR	Sentence revised and cross-references to other questions that discuss this have been added.
22	3.0, Question 1	4	Bullet 6	Microsatellite loci may not be the most effective markers for the purpose because…….. Could you please list reasons why microsatellite loci may not be effective for the needed purpose?	Gonzales	BOR	See comment #21
23	3.0, Question 1	4	Bullet 6	Regarding "Microsatellite loci ….", can a recommendation be included here or a reference to another point in the report to suggest markers that might be more effective? If Bullet 7 is the recommendation, (but does not seem directly to be the recommendation) then perhaps these two bullets should be merged?	Mike Marcus	APA	See comment #21
24	3.0, Question 1	4	Bullet 6	When the genetic monitoring program for RGSM commenced in 1999 the techinques/genetic loci (ie microsatellites) developed from RGSM were the markers of choice for genetic monitoring studies and have been for most species in which there are time-series data. In the published literature there are very few genetic monitoring time series that employed SNPs, this is because the technology has only recently become a cost effective way of screening individuals for genetic variation across large numbers of SNPs. We acknowledge that development of single nucleotide polymorphism (SNPs) for RGSM would provide additional insight not afforded by microsatellites. However, Hoban et al (2014) show that microsatellites do a fairly good job of identifying declines in genetic diversity. It would be helpful to readers of the report (who are not geneticists) to explictitly provide some historical context for the use of microsatellites.	Osborne & Turner	UNM	See comment #21
25	3.0, Question 1	4	Bullet 6	Use of microsatellite is addressed in the cover letter and below	Osborne & Turner	UNM	See comment #21
26	3.0, Question 1	4	Bullet 7	The reviewers idea of using 95% Cis for genetic diversity is a good suggestion and we will explore this further.	Osborne & Turner	UNM	None.
27	3.0, Question 1	4		We concur with the peer review panel's listed recommendations for improvements. The error range associated with Ne's and the different values that are generated make it difficult to assess the actual Ne. We also agree that far more loci need to be assessed.	NM ISC	NM ISC	None.
28	3.0, Question 2	4	Para 1	"… not sure…" Reference is included to Question 11. Would additional reference to Question 3, Page 6, Line 7 also be relevant here? --> "Simulations or analysis using known families from the hatchery …."	Mike Marcus	APA	Modified text. Referenced line for suggested additional reference doesn't match. The reference to "simulations using known families" addresses a different question (i.e., accurately identifying sibling relationships) and is not relevant to developing a genetic diversity threshold.
29	3.0, Question 2	5	3	"live longer in captivity."?	Porter	USACE	Corrected

Comment #	The comment refers to the			Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
	Section	Page	Line				
30	3.0, Question 2	5	Para 2	2nd paragraph. We agree with this assessment and are well placed to develop, design, ground-truth and implement this strategy (use of SNPs). It is also critical to maintain continuity with previous monitoring and we have the historical material to help establish a chain of continuity. These development activities should be initially funded outside of the standard genetic monitoring until they can be developed, tested and implemented in high-throughput and near real-time fashion. It is important that the reviewers acknowledge in their review that these methods and sequencing platforms have only recently become well developed and cost effective enough for high throughput screening of 100's to 1000's of individuals per year.	Osborne & Turner	UNM	Added text.
31	3.0, Question 2	5		Concur with breeding strategy	Porter	USACE	None.
32	3.0, Question 2	5		We concur with the panel's comments. Spawning 3- and 4-year-old hatchery-raised fish introduces both domestication and inadvertent selection. When fish are cultured, all aspects of management lead to both domestication and the fish are subjected to inadvertent selection because those that survive and reproduce are those that responded best to management. We agree that a better approach to maximizing Ne and minimizing loss of alleles and inbreeding would be to make paired matings fish and equalizing family size. Additionally, this mating technique would enable us to produce the desired Ne every year and one that could be precisely enumerated. Finally, we also agree that the monitoring program should take advantage of new technologies and assess loci that are expressed and are subject to selection.	NM ISC	NM ISC	None.
33	3.0, Question 3	5	25	"1) The key relevant life history parameter is Ne"- should this be "The key genetic parameter that is relevant to life history is Ne"? At least some of us in the Workgroup think of life history as traits like timing and location of spawning; larval, juvenile and adult habitats; response to events like river drying or cold winter temperatures, etc.	Price	USACE	Text revised
34	3.0, Question 3	5	36-37	Wahlund effect- Some readers won't be familiar with this. Suggest providing a glossary of genetics terms; the report will be read by non-geneticists and even non-scientists in the Collaborative Program. Provide brief definitions/explanations for this and other tems like null alleles, Ryman-Laikre effect, H-W equilibrium, genotyping-by-sequencing, etc.	Price	USACE	Added glossary in Section 6. Clarified in text. Reference to Wahlund effect has been eliminated and can be removed from the glossary.
35	3.0, Question 3	5	Bullet 3	The draft report refers to the possibility of a Wahlund effect. The audience for this report includes biologists and managers not directly familiar with all terminology in the genetics field. For clarity, recommend this sentence provide a definition explaining the Wahlund effect. E.g., "Additionally, many of the loci are out of Hardy-Weinburg equilibrium, which may indicate a Wahlund effect, where [explain what might be happening in the population genetically]."	Bachus	BOR	See Comment #34.
36	3.0, Question 3	5	Bullet 3	Could you please briefly explain the Wahlund Effect after it is introduced?	Gonzales	BOR	Added to glossary, see comment #34.
37	3.0, Question 3	5	Bullet 3	For general reader, please define "Hardy-Weinberg equilibrium" (add "(HWE)" here?) and "Wahlund effect"	Mike Marcus	APA	Added to glossary
38	3.0, Question 3	6	Bullet 3	The suggested analyses could be accomplished by updating the genetics dataset in the DBMS and working through analysis with R statistical software. This would increase transparency and educate the workgroups on the analysis and results.	Porter	USACE	Text revised.

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
39	3.0, Question 3	6	Bullet 3	This draft report suggests possible analyses on family structure (e.g., STRUCTURE, COLONY, FLOCK). What is the benefit of doing these analyses? Especially since "augmentation has likely homogenized the population." Wouldn't you need data from a time without augmentation? What would this tell us about the genetics of the population that we don't already know and which is management-relevant?	Bachus	BOR	Paragraph revised
40	3.0, Question 3	5-6	Bullet 3	I suggest this discussion could benefit from clarifying thoughts or deletion. Specifically, the first sentence suggests that fragmentation could affect "population structure" but then the first line on the next page suggests that "augmentation has likely homogenized the population." This last quote seems to be a repeating theme through the report. As such, the need for such analysis as proposed here would seem to have relatively low potential value. As such, is this recommendation even warranted?	Mike Marcus	APA	See comment #39
41	3.0, Question 3	5-6	Bullet 3	We have considered the effects of fragmentation by dams on Rio Grande silvery minnow in a number of publications (e.g. Turner et al. 2006) and routinely use F-statistics to examine whether there is population structure. Values of F_{ST} are typically very low over the time series (-0.001-0.01), though occassionally a value is significant. We selected two years of our time series with the highest F_{ST} values (2002 and 2007) and analysed these years with the program STRUCTURE using K=1 (to reflect a panmictic population) to 3 (to reflect the three river reaches [Angostura, Isleta and San Acacia]). Unsurprisingly, K=1 is the best supported model for both years suggesting a high degree of gene flow in the population including in 2002 (before the commencement of large scale population augmentation). This is consistent with the life-history of RGSM, in which the pelagic nature of RGSM eggs facilitates genetic mixing despite the presence of dams. Additionally, augmentation practices allow for mixing across reaches. It is also worth noting that prior to the augmentation program,RGSM had effectively disappeared from the upstream reaches (Angostura) and were in very low abundances in the Isleta reach.	Osborne & Turner	UNM	This information is very useful. However, it still raises the fundamental question: why so many HWE deviations? Biological or technical? Furthermore, STRUCTURE is well known to not adequately portray biologically-meaningul substructure at low FST (<0.02-0.03), particularly when the genotypic throughput is modest in terms of numbers of loci and alleles per locus. Additional analyses have been suggested in the text of the report to confirm/refute the presence of multiple populations. Significant FST values could also be observed among reaches due to related individuals being released in certain reaches. Family reconstruction will help to determine if observed deviations from HWE and significant FST values are due to family structure.
42	3.0, Question 3	6	Bullet 4	Please provide a citation to explain Null Alleles	Porter	USACE	Added to glossary
43	3.0, Question 3	6	Bullet 4	Could you explain the concept of a null allele and how they can introduce substantial errors into empirical assessments of specific mating events by leading to high frequencies of false parentage exclusions (Dakine and Avise 2004)?	Gonzales	BOR	Null allele added to glossary. Null alleles represent genotype errors that introduce bias that is often not included when estimating parameters
44	3.0, Question 3	6	Bullet 4	.Perhaps "(HWE)" should be included on page 5 (see my comment 6) where the concept is first mentioned.	Mike Marcus	APA	Added to glossary
45	3.0, Question 3	6	Bullet 4	We have acknowleged and investigated departures from HWE in a number of our peer reviewed papers. SNP's may help to avoid these issues and we are eager to embrace these approaches as funding becomes available.	Osborne & Turner	UNM	None.
46	3.0, Question 3	6	Bullet 5	Yes. The data for floodplain spawning indicates differential connectivity based geomorphology and hydrology. This would be a good question for Adaptive Management.	Porter	USACE	None.
47	3.0, Question 3	6	Bullet 5	This is an interesting question. We propose that natural spawning might be defined as spawning, rearing, retention and recruitment, thus closing the loop on demographic and genetic processes.	Osborne & Turner	UNM	Text revised.

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
48	3.0, Question 3	6	Bullet 5 and 6	The draft report is asking questions rather than providing responses from the panel. This is not informative unless the panel also includes for these responses # 5 and 6 some statement of why or how this would matter for the genetics monitoring and assessment effort. For example, #5 asks "Do different reaches have more natural spawning than other reaches"? Why does this matter and - if yes or if no - what would this mean for the appropriateness of genetic parameters being monitored (the purpose of Question 3)? You don't need to have that answer to assess "if - then" scenarios for the genetics parameters being used. Similarly for response #6, which asks "Did the wild fish % vary among reaches within year?" Why does this matter and - if yes, or if no - what would this mean for the appropriateness of genetic parameters being monitored?	Bachus	BOR	Text revised.
49	3.0, Question 3	6	Bullet 6	Did the 'wild' fish % vary among reaches within years. Do the reviewers mean the % of wild fish with respect to marked fish or are they referring to the abundance of wild fish only?	Osborne	UNM	We were wondering if the percentage of unmarked fish varied among reaches within years. We were interested in knowing whether the amount of natural reproduction varied spatially and temporally.
50	3.0, Question 3	6	Bullet 6	"wild" fish … refer to my comment 2	Mike Marcus	APA	See glossary
51	3.0, Question 3	6	Bullet 6	The short answer is yes, the abundance of unmarked fish ('wild') can vary by orders of magnitude among reaches within years and this is likely related to habitat differences between reaches as well as the extent of summer drying (primarily effects Isleta and San Acacia reaches).	Osborne & Turner	UNM	Text revised.
52	3.0, Question 3	6	Bullet 8	This again asks questions and points out there was insufficient information. The panel should also indicate here how this issue (collection of data) might affect the appropriateness of genetic parameters being used. If it would not, then the response here should indicate why this is important to know - how is it management-relevant.	Bachus	BOR	We have modified the text here to emphasize why more detailed infirmation is critical for assessing how genetic diversity is being monitored over time.
53	3.0, Question 3	6	Bullet 8	We provide details of our wild fish sampling strategy in reports and publications. Sampling of hatchery fish is somewhat out of our control but we attempt to sample at least 50 fish per captive lot. We will endeavor to provide additional detail in future reports.	Osborne & Turner	UNM	None.
54	3.0, Question 3	6	Bullet 9	What information is missing that precludes reproduction of the methods?	Osborne	UNM	In some of the annual reports the methods are pretty slim, but in other reports there is good detail. Perhaps the specific methodology that does not change should be included with each report.
55	3.0, Question 3	6	Bullet 9	Would the panel be available to review a compilation of the methods to verify completeness?	Porter	USACE	Not applicable as Bullet 9 has been deleted.
56	3.0, Question 3	6	Bullet 9	Could you elaborate on what information is missing by providing examples or a list? A list of methodological deficiencies is important but may be unknown to much of the audience for the Program without explicitly being stated.	Gonzales	BOR	This section was revised and should now address this comment.
57	3.0, Question 3	6	Bullet 9	In addition to reports to the program, we have published 20 papers in peer reviewed journals,and this information was provided. Recent reports include the methods that were provided in Osborne et al. 2012. We anticipate inclusion of a standard set of genetic metrics and a brief description and intepretation of each in future reports.	Osborne & Turner	UNM	None.

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58	3.0, Question 3	6		We concur with the panel's findings. We believe that management of Ne must become the primary concern in the breeding program. The monitoring program needs to establish the minimal Ne that will be produced annually in the hatcheries. While river fragmentation could have an effect on population structure,the genetic monitoring data do not support this as a primary and urgent concern. As stated by the peer review, the augmentation program has probably created a uniform hatchery-based population in all three reaches. The questions posed by the peer review panel in responses 3.5, 3.6, and 3.8 are particularly important and should be investigated. We are very concerned that the peer review panel could not utilize the reports to reproduce the methods.	NM ISC	NM ISC	None.
59	3.0, Question 4	7	Bullet 1	This discussion should include the Science workgroup and Adaptive Management technical team.	Porter	USACE	Added 'and others' to the text.
60	3.0, Question 4	7	Bullet 1	Could this be because precision is too low at the current sample sizes? Could a power analysis be done to determine optimal sampling sizes? Does the group have any recommendation for the association between sample size and the estimate of effective population size?	Gonzales	BOR	No response from panel.
61	3.0, Question 4	7	Bullet 1	Sampling is necessarily affected by abundance and distribution of wild fish and abundances can fluctuate by orders of magnitude from one year to the next. Our ideal sampling strategy is to sample 50 individuals from at least three localities in each of the three river reaches. In many years it is not possible to meet these goals, in which case less samples are collected or more localities are sampled. Years when sample sizes are low reflect years when abundances are also extremely low, and these years likely also will have the lowest genetic effective size. To mitigate the potential effect of sample size on genetic effective size we conducted a ressampling exercise. We resampled (five replicates) the empirical data at four different sample sizes reflective of the four smallest temporal collections (n=45, n=121, n=145, n=161). These results were compared to the estimates obtained using the full empircal dataset. With the exception of one replicate run at n=45, all estimates (~90-1200) were in the same ball-park as the estimates obtained using the full dataset (115-462). Also, it shold be emphasized that our genetic diversity estimates are corrected for differences in sample size as certain metrics such as allelic/haplotypic diversity are impacted by sample size. See appendix 2.	Osborne & Turner	UNM	No response from panel.
62	3.0, Question 4	7	Bullet 2	We will include a table of metrics, definitions and interpretations in all future reports including decriptions of different estimators of Ne. Additionally we are using simulation studies to examine the differences between NeV and NeI and their interpretation. This is new research that capitalizes on some theoretical expectations of differences in these metrics in non-equilibrium conditions such as those experienced by RGSM in the wild.	Osborne & Turner	UNM	Genotyping the broodstock will directly measure number of individuals measures contributing.

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63	3.0, Question 4	7	Bullet 3	We have routinely used F-statistics to look at changes in allele frequencies between years and between river reaches and sample sites. In almost all instances, values of FST are small to zero (ie indistinguishable from a panmictic population). We have used the computer program Structure to evaluate the presence of genetic differences between reaches/ years etc and these results show the population to be panmictic. This result is unsurprising because of the pelagic nature of RGSM eggs which allow for large amounts of genetic mixing. Additionally, augmentation practices facilitate genetic mixing. Family reconstruction using COLONY is unlikely to provide meaningful results because of the nature of silvery minnow population dynamics. Population abundance likely ranges from the 100-1000s in bad years to millions of individuals in a good year. We know that our sample reflects only a subset of the population. We will explore the use and incorporation of the relatedness statistics (as implemented in the program COANCESTRY) in the future.	Osborne & Turner	UNM	The consistent lack of HWE across many loci suggests that the composition of the gene pool may not be consistent across generations. Added text.
64	3.0, Question 4	7	Bullet 4	Could you provide examples of the type of bias(es) that may exist when estimating the relevant parameters?	Gonzales	BOR	The bias(es) depend on the estimator used. The report(s) should just clearly state the bias for any estimator.
65	3.0, Question 4	7	Bullet 4	We agree that the augmentation will affect variance effective population size. A simulation study is near completion that explicitly considers this issue.	Osborne & Turner	UNM	See comment #62
66	3.0, Question 4	7		It appears that the answer to this question, while not stated as such, is no. The question of whether the experimental design and sampling methodology is appropriate and did the methods have sufficient power to detect the trends and findings that were reported was addressed by the peer reviewers in a manner that indicates to us a critical need for the geneticists to take a hard look at the goals and sampling strategies.	NM ISC	NM ISC	None.
67	3.0, Question 5	8	10-12	"it is unlikely the population will become self-sustaining without hydrological changes"- Would the Panel consider including habitat restoration efforts to restore floodplain connectivity as a measure that may contribute to the population's ability to sustain itself, or become less dependent on augmentation? Any suggestions for how to evaluate population sustainability when fish are augmented each year?	Price	USACE	We concur that habitat restoration efforts may positively influence RGSM viability, but because river hydrology is beyond the scope of our review and expertise, we are electing not to make formal recommendations of this sort in the summary report. Certainly, however, a consistently available floodplain of sufficient size would go a long way towards a sustained wild population of RGSM that may not necessarily depend on as much augmentation
68	3.0, Question 5	8	12-13	Re: fragmentation, could the Panelists suggest additional measures to evaluate the extent of fragmentation and effects on the population genetics? Genetic reports so far suggest a single panmictic population, but the effects of augmentation are confounding.	Price	USACE	Additional analyses to test for the effects of habitat fragmentation have been added to Question 3, Bullet 3.
69	3.0, Question 5	8	Para 1 under Propagation Plan	Propagation plan: the reviewer suggest that genetic sample collection and characterization should be conducted well in advance of release. This idea will be discussed with the Captive Propagation and Genetics team. It may not be possible due to the narrow window between when fish are spawned (May-June) and have attained a sufficient size to allow non-destructive sampling and when the fish are released in October (the number of fish to be released is not determined until September when population monitoring data becomes available). With the development of high throughput techniques it may be more plausible.	Osborne & Turner	UNM	While high throughput analysis will give more information about the stocking population, changes in current mating protocols will have the greatest effect on the composition of the stocking population.
70	3.0, Question 5	8	Para under "Recovery Plan"	The draft water budget for the MRG recently produced by the NMISC projects a water supply short fall of >200 acre feet during drought years (another from UNM and SNL researchers have projected >500 AF short fall (both without considerations for ESA water needs). This is likely to increase with climate change. Given that information, would the review authors like to reconsider or expand on their last two sentences of this section regarding potential RGSM benefits from hydrological changes.	Mike Marcus	APA	Additional text added.

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71	3.0, Question 5	8	Paragraph 2	The literature reviewed for understanding silvery minnow habitat needs is incomplete.	Porter	USACE	This peer review did not focus on habitat use and, therefore, the literature review on habitat use is incomplete.
72	3.0, Question 5	8		"It is likely that, without the augmentation program, the species would have gone extinct in the MRG"- Given the discussin of the Ryman-Laikre effect under Question 7, would the Panelists suggest an appropriate level or % of augmentation relative to the wild population?	Price	USACE	It is extremely difficult to recommend appropriate levels or % of augmentation relative to the wild population for a host of reasons, including that modeling on this topic has not factored in all conditions that might influence demographic and genetic outcomes of augmentation jointly, and that empirical testing of modeling exercises have been very limited. With improved data on the relative number of RGSM produced in the wild vs. the hatchery, future recovery efforts could reduce augmentation inputs in years where a demographic stable number of RGSM were produced in the wild, as part of the balancing act of not constraining the RGSM population in nature with more maladapted augmentation fish, whilst giving a demographic boost to the population when necessary to avoid extirpation. These sentiments are now echoed in the summary.
73	3.0, Question 5	9		Under "B)" on this page (under Propagation Plan), the draft report response recommends the augmentation releases "NOT use any surplus fish." What does the panel see or define as the "surplus" fish? Criteria for identifying these?	Bachus	BOR	Text added explaining surplus fish.
74	3.0, Question 5	10	Objective 1	Under "Objective 1" (under Scope of Work for Genetics Project), the draft report states there is no likely remaining wild population in the MRG because hatchery rearing is in the lineage for most minnows. Please note that the "wild" population includes the minnows that occur in the MRG (in the wild) and not necessarily defined by hatchery rearing for parent generations. There are not multiple generations held in the hatcheries before release - the offspring are released (F1) from hatchery broodstock (wild-caught), or the eggs that are wild-caught are reared and then those fish are released. It sounds like the panel is using a specific definition here for "wild" that differs, and that should be explained. E.g., under the panel's definition is a fish never considered "wild" if it was spawned, hatched, and developed entirely in the wild, but had a hatchery-reared grandparent? or even multiple generations back? Where do you draw that line to distinguish? Especially since the "lineage" for hatchery-reared fish is consistent with and derived directly from wild-caught eggs?	Bachus	BOR	See glossary term and notes under 'wild vs. captive'. Text revised to better use these terms.
75	3.0, Question 5	10	Objective 2	For "Objective 2" (under Scope of Work for Genetics Project), the draft report states that "Implementation of the practices suggested in this review will help to maximize Ne." It is not clear here to the reader which suggested practices this is referring to. Please include a summary statement that identifies those practices suggested by the panel that would help maximize Ne.	Bachus	BOR	See the overall recommendations for suggested practices.

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76	3.0, Question 5	8-10		Thank you for your insightful comments on the current plans and operations concerning propagation and augmentation. Below are observations that support the review. A particularly concerning statement is that “there is likely no remaining wild population in the Middle Rio Grande because most captured fish and eggs likely had hatchery rearing in its lineage”(page 10 first paragraph). There should be a genetics adaptive management plan that guides the Program’s actions in response to genetic conditions that are revealed through the genetics monitoring. We agree that a weakness in the program is that the information cannot be used in a timely manner to inform breeding. A deficiency in the current program is that there is no targeted Ne based on genetic management goals (e.g., 500) that must be produced annually. The communal spawning technique makes it impossible to determine the exact Ne that was produced, and this is important if we are to conserve genetic variance. There is no way to know many females produced viable eggs or how many males spawned in each communal group. Furthermore, this technique makes it impossible to equalize family size, and variance of family size can dramatically lower Ne. The current breeding program likely produces an Ne far smaller than the Ne that is “guesstimated,” based on how many females are spent. The fish raised in the three facilities could easily be assessed to evaluate how differences in culture techniques affect domestication so that the facilities can begin to culture in a manner that produces fish that most closely resemble wild fish. Furthermore, the subsequent contribution of these fish during wild spawning should also be assessed. The collaboration among the facilities to create a more functional program would be beneficial and support the efforts of all the agencies and entities to recover this species. Different breeding programs are needed to maximize Ne. A critical component of this process is to equalize family size. The fish that are culled from the families to produce uniform family size, as the peer review suggests, cannot be used for augmentation. We suggest that these fish that cannot be used for augmentation are still valuable as they can be used to conduct research projects to better understand the life history of the species.	NM ISC	NM ISC	The panel agrees with these points and hope our recommendations address these issues.
77	3.0, Question 6	11	Bullet 1	In Bullet "1", there is a statement that although not meeting the assumptions is common in population genetics studies, it does not appear there are problems with the estimates. Bullet "2" is pretty short and does not provide this similar explanation - does this also apply to Item 2? and if so, please state that, or explain how it is different and what those concerns are.	Bachus	BOR	There may be problems with the estimates based on violations of genetic assumptions, e.g. various Mendelian assumptions about a genetic population such as no selection, no mutation, etc. One doesn't know if there are in fact problems because one doesn't know the degree of violation of the assumptions, such as the linkage of markers or linkage disequilibrium due to unequal family sizes in the stocking population. The same unknown effects of genetic assumption violations applies to Fst calculations in Bullet 2.
78	3.0, Question 6	11	Bullets 1 and 2	For responses 1 and 2 to Question #6, could the assumptions be listed that were needed for the anlayses that were discussed in this section?	Gonzales	BOR	See comments #50 and 51.
79	3.0, Question 6	11		No Comment	NM ISC	NM ISC	None.

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80	3.0, Question 7	11		There are 3 items which need some additional explanation so the reader can understand what the panel is suggesting: (1) The Ryman-Laikre effect is not clearly known by most readers of this panel report. Please provide a quick explanation - e.g., "The reports sometimes mention the Ryman-Laikre effect (which occurs when....[explain]), but more attention...." (2) For the following statement, please state what types of "analyses" the panel is recommending: "Analyses could be conducted to determine how environmental data, sample size, and hatchery releases affect Ne, and to determine which is the most likely explanation." (3) Again, for the following statement, please state what types of "analyses" the panel is recommending: "Additional analyses to determine the variance in family size of released offspring can also provide insight into the effects of hatchery augmentation on effective population size." These last 2 comments (2 and 3) also relate back to Page 10 Objective 3 for the Scope of Work for Genetics, so in order to move forward with any changes to the SOW (should the Program decide that) we would need to know what types of "analyses" we need to include in the scope related to this issue. Right now, the draft report is too vague to know that.	Bachus	BOR	These points have been clarified as requested.
81	3.0, Question 7	11		The peer review panel notes that, given the current monitoring program, the results that have been detected could be due to the sampling program, which means they could be confounded and that we really do not know with any accuracy what is actually occurring. If this is true, then the results will not be able to direct management towards recovery. This needs to be investigated. If the sample sizes must be increased to guarantee that these are decoupled, then the increase in sample sizes must be incorporated into future monitoring protocol.	NM ISC	NM ISC	Our comment focused on a noted correlation between Ne and sample size. These observations were made during the review, and we believe should be further evaluated, to assure that Ne estimates reflect biotic variation and not variation due simply to un-even sampling. See also Comment #88.
82	3.0, Question 8	12	Para 1	Please provide some references for this approach	Porter	USACE	Reference added
83	3.0, Question 8	12	Para 1	The first paragraph states "Instead, determination of the number of breeders through parentage analysis and/or sibship reconstruction may be more useful for management decisions." How so? Please explain both why this would be more useful for management decisions and how that information could be used.	Bachus	BOR	The analyses used to calculate Ne provide values with huge variances and do not provide a deterministic cause of any observed differences, and as such are of limited value in deciding on changes in management. Parentage analysis provides a more accurate measure of Ne for the stocking populations and can implicate differential parental contribution and family size as the cause of Ne fluctuation and permit changes in management, e.g. equalizing family or increasing the number of parents used as broodstock.
84	3.0, Question 8	12	Para 2	The report observes that "pre-augmentation [data] are limited by the few number of years available." Following the Question #8, are there any remedies to address this gap? If not, please specify that is the case.	Bachus	BOR	Without the availability of additional years prior to any augmentation, there is no remedy and the focus should instead be on maintaining remaining genetic diversity. Text has been added to the report to this effect.
85	3.0, Question 8	12	Para 3	The report recommends that broodstock also by genotyped, so that parental contribution can be assessed. Does the panel recommend genoptyping each individual from the broodstock or would a subset suffice?	Bachus	BOR	The genetics group already knows from their published work that there is differential contribution of parents used as broodstock and therefore also differences in family sizes. Further testing of the current practice of combining 10 males with 10 females would confirm this finding. This finding causes a significant decrease in Ne for the number of broodstock available. We recommend that management employ an alternate breeding scheme (e.g. one male one female crossing combined with equalizing family size mixing) that will inrease Ne.

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86	3.0, Question 8	12	Para 3	Sentence 3: Would every animal held as broodstock need to be genotyped? If not how many individuals would need to be genotyped to accurately depict broodstock genotypes and parental contribution?	Gonzales	BOR	Monitoring the contribution of each member of the broodstock to each of the 10 x 10 matings will allow one to canculate the effect of this practice on Ne. Switching to a 1 x 1 mating protocol and equalizing family size when mixed will make this unnecessary, except to test whether there is differential family survival up to release. Differential family survival is important to know, but currently it is far less of a problem than the current practice of 10 x 10 matings.
87	3.0, Question 8	12	Para 4	Two questions related to the last paragraph on Page 12: (1) The report recommends using next-gen sequencing (GBS) - is this in addition to maintaining the existing long-term dataset using microsatellite and mtDNA markers? (2) The paragraph mentions a "candidate gene approach" - please explain or otherwise define what this is and cite relevant reference.	Bachus	BOR	We have clarified this recommendation in the section to emphasize the recommendation that the RGSM recovery team will need to transition to new technologies in the coming few years.
88	3.0, Question 8	12	Para 4	The reviewers suggest conducting analyses to determine how environmental data, sample size and hatchery releases affect N_e. These analyses were done and reported in our 2012 paper published in Evolutionary Applications. We are also conducting a simulation study (not funded by the program) that looks specifically at the effect of hatchery augmentation on different measures of genetic effective size. Sample size is neccessarily tied to census size such that when abundance in the wild is low, sample sizes are also very low. All metrics of genetic diversity are currently adjusted to account for sample size differences.	Osborne & Turner	UNM	None.
89	3.0, Question 8	12	Para 4	The reviewers suggest conducting analyses to determine the effect of variance in family size of released offspring on effective population size. We would be willing to explore such analyses when sampling of all broodstock can be accomplished. Currently we are not funded to genotype broodstock but agree that it is prudent to do so in upcoming years. As the reviewers correctly point out, hatchery broodstock are now driving the gene pool of the species.	Osborne & Turner	UNM	None.
90	3.0, Question 8	12	Para 4	We have discussed the Ryman-Laikre effect in publications and reports and we are willing to revisit this issue in future reports. We are clearly aware that supportive breeding and enhanced survival of a segment of the overall population will increase the variance in family size and depress genetic effective population size. However, in the case of Rio Grande silvery minnow, the 'wild' population is no longer wild (as almost all fish are likely derived from a hatchery) because of unsuitable enviromental condition in the Rio Grande over recent years which have precluded/reduced successful spawning and recruitment in the wild. However, we recognize that it is important to maximize genetic effective size of the fish being produced in the hatchery and stocked into the river.	Osborne & Turner	UNM	None
91	3.0, Question 8	12		We agree that a major shortcoming is that the effect of hatchery breeding practices on Ne has not been thoroughly evaluated. Variance of family size could be a major liability and has probably reduced Ne dramatically every year. The effect of hatchery Ne on either loss of rare alleles (f = 0.01) and on non-neutral alleles or on inbreeding has not been evaluated. We agree that parents should be genotyped to assess genetic contribution. Genotyping parents and making paired matings could also minimize inbreeding. It is assumed that non-relatives are mated, but the way eggs are collected and differential family survival of these eggs/fish at the hatchery could result in inbreeding. We agree that far more loci need to be assessed. Monitoring non-neutral alleles could provide us with a better understanding of domestication and selection at the hatchery and during post-augmentation survival.	NM ISC	NM ISC	None.

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92	3.0, Question 9	13	Para 3	The draft report states that mtDNA ND4 does not seem to add any info beyond the microsatellites. It was my understanding that mtDNA is maternally-inherited for all individuals and tends to be highly conserved. So detecting changes in mtDNA could tell you something significant is occurring correct? Or is this not the case? Since others might have this misperception as well, please explain the rationale for this statement that mtDNA does not add anything additional, since this is a very different type of genetic data compared to microsatellites.	Bachus	BOR	It is indeed a genetic marker with different characteristics compared to microsatellites. However, because it is a coding gene and is highly conserved, it is better suited for detecting relationships between different species (i.e., phylogenetics). It would be a more efficient use of financial resources to pursue additional species-specific microsatellite loci or GBS. Clarifying text has been added to the report.
93	3.0, Question 9	13		We concur with the panel's recommendation to use SNP's and other genetic markers in the monitoring program. We also agree that the mtDNA marker is not providing us with management information.	NM ISC	NM ISC	None.
94	3.0, Questions 1 and 11	4	Bullet 7	The draft report states that if diversity falls below the CI, then more aggressive management actions may be warranted. What types of management actions was the panel envisioning here? This same question applies on Page 14 for Question 11, where more explanation is needed so the reader can be clear what is recommended by the panel and why.	Bachus	BOR	Text revised to focus less on management actions. A section was added discussing how "fortuitous production" of broodstock from an un-planned mating could undermine the attempts to equalize family sizes.
95	3.0, Question 10	13		We concur the panel's recommended expansion of monitoring, especially brood stock genotyping. This can be used to help maximize genetic variance and prevent inbreeding. We understand that a cost benefits analysis may be needed to prioritize additional monitoring but these options must be thoroughly evaluated.	NM ISC	NM ISC	None.
96	3.0, Question 11	14		We agree with the panel's concern that the major concern for drift is the loss of common alleles (f = 0.1). The program should be trying to prevent the loss of rare alleles where f = 0.01. Establishing this as the goal would make it far easier to retain common alleles. Also, by setting the goal to save rare alleles, we would establish the Ne that must achieved annually in the breeding program.	NM ISC	NM ISC	None.
97	3.0, Question 12	14		The panel recommends monitoring broodstock genetics every year, and also the "refugia populations" every two years at a minimum to ensure the gene pool remains robust. Please explain the difference between these two categories, as the broodstock are the refugia populations. Are not all of the broodstock used every year? Then perhaps state that as the distinction here so it is more clear.	Bachus	BOR	Added broodstock and refugia to the glossary.
98	3.0, Question 12	14		We agree with the panel's recommended sampling frequency. We suggest that this be expanded to assess the populations of fish are cultured at the three facilities—at both stocking and harvest. This should also be done for eggs that are collected to be used a brood fish. Each lot should be assessed annually to measure drift and domestication. Additionally, it would be helpful to assess the relative contributions from the three facilities annually in wild recruitment. We believe that an initial cost may be reduced once sufficient information is available to make scientific determinations. Expanding the genetic data that are monitored will provide valuable information that can be used to assess management and to aid in recovery.	NM ISC	NM ISC	None.
99	3.0, Question 13	15	Item 1, Para 3	Under "1)" the second paragraph refers to a "richer set of genetic markers." What is meant by "richer"? Please explain.	Bachus	BOR	Changed to 'larger, more diverse'.
100	3.0, Question 13	15	Item 1, Para 3	When the report states that MHC genes would supplement the adaptive genetic variation monitoring - is this a supplement to the existing suite of monitoring being conducted, or a supplement to the SNPs? Could MHC genes be used without SNPs to monitor and supplement the adaptive genetic variation, in combination with the existing markers?	Bachus	BOR	This could supplement the existing microsatellite work. Identification of SNPs through GBS will likely identify MHC variation as well as variation at other genes.
101	3.0, Question 13	15	Para 1	Minor edit that would be helpful - the intro to this response under Question 13 refers to 3 different avenues to improve the genetics program and then labels them (i), (ii), (iii). The content then uses (1), (2), (3) for the narrative text for each avenue. Please make the numbering scheme match up so it is consistent.	Bachus	BOR	Corrected.

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102	3.0, Question 13	16	Bullet 1	Report statement: "Conduct random sampling of annual egg collections from nature (e.g., current collections only come from the main channel of the Rio Grande River, not on floodplains)." Comment: We collect Rio Grande Silvery Minnow eggs from the downstream river channel (below San Marcial, NM) since they are doomed to reservoir predators, those eggs appear to be the most genetically diverse (Carson et al. 2014, Table 4), and some floodplain eggs survive. Eggs that are collected from the downstream river channel also likely contain some portion of those eggs that were deposited on the floodplain, were suspended into the water column, and re-entered the channel through hydrodynamic forces. Carson et al. (2014, page 8, tables 3 & 4) conducted a genetic comparison between eggs collected from the floodplain (sample ID = 2014_WCE_RGNC) and those collected nearly simultaneously from the nearby river channel (sample ID = 2014_WCE_RG). Carson et al. (2014, Page 8), "Twenty-three of significant tests occurred among wild caught eggs from the Rio Grande Nature Center, which is a small, contained backwater [in the floodplain] represented by few individuals for which non-random associations among loci might be expected in offspring; this is also supported by the low effective number of breeders (NeD = 46, Table 3) that contribute to WCE collected at the Rio Grande Nature Center. If the Genetics Peer Review Panel is recommending that we should collect eggs from the floodplain then we could use instructions as to how (where, how often, how many, how to balance families) to maximize the NeD and mtDNA haplotypes of all the collected eggs sent to the hatchery system.Collections of eggs from the downstream river channel is an attempt to maximize the number of eggs collected efficiently, maximize genetic diversity, as well as rescue eggs that are destined for predation (paraphrased, Dudley et al. 2015, spawning periodicity, page 4). In a long, continuous river channel with historic floods, there was adequate time and space for some RGSM eggs to hatch in the water column and larvae to thrive in a diverse array of flood created habitats. But under the current conditions, many eggs are now swept quickly downstream into a predator-rich reservoir. In the current river configuration, eggs that are swept onto the floodplain or into many of the other types of shallow, instream habitats (e.g., side	Lusk	SFWS-NME	Modified recommendation to include: Sampling of floodplains should be considered and included where feasible to ensure that the genetic characteristics of RGSM are adequately represented in egg collection samples. The panel's recommendation was made with the hope of reducing the likelihood of any undesirable consequences of non-random sampling (main channels only) from occurring. Several reports on the biology of RGSM emphasized how the species is likely specialized for a floodplain existence. If main channel sampling does not fully capture the spatio-temporal coverage of eggs drifting in the Rio Grande (based on reproductive timing of RGSM, abiotic conditions in different parts of the river etc.), then such non-random sampling is a potential issue from the standpoint of maintaining the adaptive genetic characteristics of the RGSM and what is propagated in subsequent captive generations. Mortality is high in many fishes from the fertilized egg stage to hatching, hence the potential for selection at this stage is high; what is surviving on the floodplain might not be identical to what survives the drift downstream. In the face of uncertainty of not knowing how much this matters, would it not be preferred to err on the side of caution and conduct more random sampling?
103	3.0, Question 13	16	Item 1, Last para	The report at the top of page 16 recommends "examining phenotypic variation for important life history traits." Examining how? This needs more specific recommendations for analyses to conduct, in order for the Program to move forward on this recommendation (should it choose to do so) including cited relevant references.	Bachus	BOR	Examples added of rapid evolution for traits that could be under selection in a hatchery environment.
104	3.0, Question 13	16	Item 2	The report under "2)" states that the high mortality of RGSM from egg to age4 seen in captivity was a considerable concern and this mortality "likely differs from mortality in nature." How so and why did the panel conclude this? RGSM are known to live longer in captivity than in the wild, thus the presence of age 4 broodstock to maintain the genetics of the population when this age class most likely no longer occurs in the wild. Mortality does differ compared to wild fish specifically because wild fish don't live as long. So the mortality of captive fish - in and of itself - is not the concern, but rather the drivers/causes of that mortality may differ from what causes mortality in the wild, correct? This paragraph has big implications for the captive management of RGSM and the panel needs to be exceedingly clear on what they are saying and try to minimize the chance of different readers having different interpretations of this paragraph. For example, page 22 states this well and could be copied back here as appropriate: "The use of four year fish as broodstock may compromise the maintenance of genetic diversity because of the possibility of non-random, differential survival of individuals in the hatchery."	Bachus	BOR	Text revised. The main point is whether the drivers of mortality in the captive environment differ from those in the wild environment, facilitating domestication selection.

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105	3.0, Question 13	16	Item 2	For response 2): This comment in the report is a good comment: "Conduct random sampling of annual egg collections from nature (e.g. current collections only come from the main channel of the Rio Grande River, not on floodplains)." To date we know that the genetic diversity of eggs collected from a single floodplain site was lower than genetic diversity of eggs collected from flowing water habitats of the main channel. Intuitively if the eggs on this floodplain site were a product of gradual entrainment of propagules from the main channel then their diversity should be approximately equal. What would the diversity of eggs be from 100 floodplain sites relative to those collected from the main channel? Perhaps within a single floodplain site the genetic diversity of eggs is lower and can be related to a few females and males mating there; however, when compared over multiple sites is the diversity similar or higher than the diversity of eggs collected from the main channel? Conversely, some single floodplain sites might have high egg diversity (many spawners) and some may have low diversity (few spawners).	Gonzales	BOR	The panel's recommendation was made with the hope of reducing the likelihood of any undesirable consequences of non-random sampling (main channels only) from occurring. Several reports on the biology of RGSM emphasized how the species is likely specialized for a floodplain existence. If main channel sampling does not fully capture the spatio-temporal coverage of eggs drifting in the Rio Grande (based on reproductive timing of RGSM, abiotic conditions in different parts of the river etc.), then such non-random sampling is a potential issue from the standpoint of maintaining the adaptive genetic characteristics of the RGSM and what is propagated in subsequent captive generations. Mortality is high in many fishes from the fertilized egg stage to hatching, hence the potential for selection at this stage is high; what is surviving on the floodplain might not be identical to what survives the drift downstream. In the face of uncertainty of not knowing how much this matters, would it not be preferred to err on the side of caution and conduct more random sampling?
106	3.0, Question 13	16	Item 2, Bullet 1	The report recommends conducting random sampling of annual egg collections from nature. Random sampling for genetic testing (in what way)? Or more random collections themselves (for rearing)?	Bachus	BOR	We were referring to the annual egg collections collected in nature for hatchery rearing and have modified this passage. But certainly, any genetic testing of eggs in the hatchery itself should involve random sampling.
107	3.0, Question 13	16	Item 2, Bullet 2	The report recommends rearing RGSM in environmental conditions that resemble natural environmental conditions as much as possible. Since this is done to some extent at all 3 facilities - what specifically does the panel recommend be done differently? What is not being done that could be, to better simulate these more natural conditions?	Bachus	BOR	The panel provides a few key ways that hatcheries could better resemble the natural environment of the RGSM. We could be mistaken, but we do not recall that all of these environmental conditions (including exposure to natural predators) were being practiced currently in all RGSM hatcheries. Some specific considerations added.
108	3.0, Question 13	16	Para 4, Bullet 1	USACE/ISC have the expertise for egg sampling on the floodplain. How many sites, samples, frequency should be collected?	Porter	USACE	We do not have a recommendation for frequency, only that floodplains are included in the sampling
109	3.0, Question 13	16	Para 4, Bullet 3	Concur. This will require a comprehensive effort for annual sampling of spawning adults and analyzing scale samples to estimate age.	Porter	USACE	None.
110	3.0, Question 13	17	Item 2, Bullet 7	The panel recommends minimizing duration in captivity as much as possible before release - does the panel have a recommendation for changing the existing timeframe? Or is that a general guiding principle that may already be met?	Bachus	BOR	Our understanding is that each cohort is held for 4 years prior to breeding. There is a need to understand if certain phenotypes/genotypes are more likely to survive to 4 years, and if these same patterns would hold over the first 3 years. Thus, our recommendation is generic, but we strongly advise that additional research be pursued to evaluate 1) is there evidence for relaxed/altered selection, and 2) does such altered selection accelerate over time.
111	3.0, Question 13	17	Item 2, Bullet 8	The panel recommends the Program "assess phenotypic variation for important phenotyopes…" How shoud this be assessed? Please refer to specific types of analyses and include cited references so the Program can be clear on what is being recommended here. Also how will such analyses tell us something different for management of captive fish?	Bachus	BOR	Examples are provided including citations.
112	3.0, Question 13	17	Item 3, Para 2	For item "3)" suggest minor edit for readability: "…would be release of several treatment groups..."	Bachus	BOR	Made a minor adjustment to make that more clear.

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113	3.0, Question 13	17	Item 3, Para 2	In item "3)" the panel suggests releasing treatment groups into several sampling sites for later resampling - preferably for assessing reproductive success in the next generation. What about cross-generational tagging techniques such as strontium? Did the panel consider and can they recommend those types of methods to assess reproductive success when monitoring the F1 generation? Other methods?	Bachus	BOR	The panel is not aware of the relative performance of strontium as a cross-generational tagging technique, nor does it have suggestions for alternative methods to assess reproductive success in the F1 (or later) generation. But the general context for how to assess/monitor fitness using an experimental approach could still be applied if the RGSM recovery team determines that an alternative such as strontium is possible.
114	3.0, Question 13	17	Last para	This proposed experiment could be designed as a component of spawning habitat monitoring. USACE/ISC have several sites with demonstrated inundation that could be used as sample sites. The stocking of minnows would need to be configured for this study design.	Porter	USACE	None.
115	3.0, Question 13	18	Item 3, Para 2	In item "3)" on the top of page 18, the report states that within two to three years we might learn if more naturalized hatcheries produce better survival. Did the panel consider the tag recapture data that are specific to source-hatchery? Those data go back to 2002 (see Archdeacon and Austring 2016 report - annual 2015 RGSM augmentation report, Appendix B). Also, did the panel have recommendations on what aspects of "naturalized" hatcheries they are focusing on here? Food? Across the 3 hatcheries there are many conditions the fish are exposed to that are quite similar, despite the nomenclature of "naturalized." Please be specific about potential factors that the panel is referring to here.	Bachus	BOR	The data referenced is currently not in a form that addresses the recommendation. Text revised in various places for recommendations relating to naturalizing hatcheries.
116	3.0, Question 13	18	Item 3, Para 3	The top of this page includes the following statement: "Monitoring of domestication selection could include DNA fingerprinting (GBS) of wild egg collection and see how they change." This sentence needs some clarity. How would the panel recommend those data be analyzed ("see how") and what types of changes would potentially be detected that would be informative? ("they change") What is the management-relevance? The Program isn't just investigating interesting changes in genetics, but ones that are management-relevant. Please explain this recommendation in the report in more detail.	Bachus	BOR	This statement has been clarified to be more explicit.
117	3.0, Question 13	18	Para 2	Would appreciate a short discussion with key references of differences / similarities of DNA fingerprinting (GBS), bar-coding (e-DNA), high through-put technologies, etc.	Porter	USACE	We had added to the document what we feel is the most pertinent and user-friendly review paper on GBS and related approaches for researchers unfamiliar with conservation genetics. A discussion of eDNA or bar coding is beyond the scope of the document and the panel's review.
118	3.0, Question 13	15-17		1) We concur and have provided some comments on implementing these recommendations. 2) General comment on the recommendations provided here and at the end of the report: Would the Panelists consider ranking or grouping these recommendations? While not necessary for the simple and no-cost improvements, others that would be costly or require extensive changes in procedure to implement will require time and won't all be able to be done right away. It would be helpful to have help prioritizing.	Price	USACE	Priorities added to the recommendations.

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119	3.0, Question 13	15-17		We agree with the panel's recommendations about improving the monitoring program by expanding the number and type of loci that are monitored. All of the panel recommendations were important to consider in our view: 1. how to minimize domestication and selection in the hatchery breeding program; 2. fish should be raised under conditions that mimic the wild as much as possible; 3. feeding the fish should be only used as a last resort as it is a form of management that can produce both domestication and inadvertent selection; and, 4. the length of time fish are under culture conditions must be minimized to minimize domestication and inadvertent selection. Consequently, a captive spawning program should be concentrated towards 1-year-old fish. We agree that non-neutral loci should be monitored to assess the effects of selection and domestication. We agree with their recommendation that the effect of raising fish under different culture conditions should be assessed. We agree that fish should be genotyped so the genetic effects of survival at the hatchery can be assessed.	NM ISC	NM ISC	None.
120	3.0, Question 13	16-17	Item 2, Bullet 3	The bullet point at the bottom of page 16 is not clear. Did the panel mean "captive" adults are favored for delayed maturation and/or higher iteroparity? Higher iteroparity (i.e., more spawning events over a lifetime) seems intuitive for older adults compared to younger adults. But what evidence or information does the panel have to support it's claim for delayed maturation - either in the wild or captivity? The species life history includes quick maturation to adult life stage in under 1 year, and spawning for those adults the next spring at 1 year of age. Also, the bullet point makes the distinction between "captive adults" living longer than "naturally-spawned adults." This is a false distinction, as most of the captive adults - especially those released in the fall back to the river - were naturally-spawned and collected from the river as eggs. Broodstock adults maintained in captivity were also wild-caught (spawned in nature not in captivity). Perhaps the panel meant adults in captivity live longer than adults in the wild? That would be correct, but the report is not currently worded that way. Also - the bullet point states that adults should be spawned according to the age structure of naturally spawned RGSM - but the bullet point never explains what that is or what that looks like. So should only Age-1 fish be spawned in captivity? (that is the predominant age class that spawns in the wild). And if so, what is the genetic benefit of doing it that way? Lastly, the last sentence in this bullet point (top of Page 17) states that older captive adults have higher fecundity and represent a greater proportion of released fish annually relative to younger adults (with lower fecundity) - is that bad, good, or? Please clarify what message the reader should get from this statement.	Bachus	BOR	Text revised.
121	3.0, Question 14	18		When the panel states that the genetic analyses should focus on exhaustive characterization of the potential and actual broodstock from the four year classes present in the hatchery, this is not at the expense of (i.e., elimination of) the genetic monitoring of RGSM in the wild correct? Perhaps that could be clarified in this response section for question 14.	Bachus	BOR	Yes that is correct.
122	3.0, Question 14	18		We agree that the program should be changed to one where large numbers of breeders are used and that that brood fish make an equal contribution to the next generation. This would increase Ne two ways: first, it would force us to spawn more fish; second, it would prevent unequal family size from lowering Ne.	NM ISC	NM ISC	None.

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123	3.0, Question 15	18		We agree that a more rapid monitoring program would be of value. That way the information would always be available before fish are spawned. This would help direct the breeding program. This means we must have an adaptive management program in place so that we know the changes that will be needed in the breeding program to respond to a specific set of genetic changes or genetic trends.	NM ISC	NM ISC	None.
124	3.0, Question 16	19		We agree that the monitoring program must be expanded for the hatchery fish. Genetic information needs to be available before fish are augmented.	NM ISC	NM ISC	None.
125	4.0	19-23		The Genetics Review Panel provided 16 recommendations following a number of conclusions that reflected many of the same concerns and issues that had been discussed by Program scientists. We appreciate the forthright and objective assessment of the current species management program that includes genetics monitoring. We believe that the Collaborative Program should incorporate these recommendations to include new technologies in the Genetics Monitoring Program.	NM ISC	NM ISC	None.
126	4.0, Conclusions	19	Bullet 1	Under "Conclusions" on Page 19, the first bullet point (1) is not clear. What is meant by the pre-augmentation period? This is the first time the report has referred to conclusions on the timing and duration of the pre-augmentation period - this is confusing to see it here in the conclusions for the first time. Perhaps try to better connect this back to report content.	Bachus	BOR	The pre- and post-augmentation periods are identified in the Introduction and discussed extensively in responses to Questions 1 and 8. No change.
127	4.0, Conclusions	19	Bullet 1	Under "Conclusions" on Page 19, the first bullet point (1) is not clear. What do you mean "whether larvae or adults are counted as augmentation"? Adults released in the fall are the augmentation totals used. What do you mean by referencing larvae here? This is confusing.	Bachus	BOR	Text revised.
128	4.0, Conclusions	19	Bullet 1	Conclusion #1 does not make sense as written. Do you mean stocked adults and the larvae that they produce? Currently RGSM larvae are not stocked. They have been in the past but only on a very limited basis.	Gonzales	BOR	See comment #127
129	4.0, Conclusions	19	Bullet 2	Conclusion #2 refers to counting larvae as an augmentation release - this does not make sense. Fish are released as adults or once reaching an adult length, larvae are not released as part of the RGSM augmentation effort.	Bachus	BOR	See comment #127
130	4.0, Conclusions	19	Bullet 2	For conclusion #2: It is not clear what is meant by "(if larvae count as a release)".	Gonzales	BOR	See comment #127
131	4.0, Conclusions	19	Bullet 3	See the population monitoring panel report. The fish that are sampled by population monitoring are mostly one year-old fish. There haven't been any scales (age-class data) collected from floodplain spawning minnows. The primary age class may shift based on recruitment success in the previous year(s).	Porter	USACE	None.
132	4.0, Conclusions	19	Bullet 5	For conclusion #5: Since diversity has not changed through time, then has the diversity for the species been maintained relative to the pre-augmentation period? Also this conclusion is not in agreement with the way the data are interpreted for the species recovery plan.	Gonzales	BOR	Text has been clarified in the report. Due to the limited number of sampling years before fish were released into the river, it is difficult to say whether the diversity has been maintained relative to pre-augmentation. Instead, remaining genetic diversity in the population has been maintained.
133	4.0, Conclusions	19		These observations are very insightful. Thank you.	Mike Marcus	APA	None.

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134	4.0, Conclusions	20	Bullet 6	Conclusion #6 recommends using broodstock genotypes and resultant progeny to gain more realistic estimates of Ne, rather than from individuals captured in the MRG. This assumes current conditions of significant releases from wild-caught, hatchery-reared fish back into the MRG. There are years where this level of augmentation has not been needed and the wild population (population that occurs in the wild) was a mix of augmented and 'wild'-reared fish. Or even in some years tag recapture rates were really low compared to wild fish captures. Thus, just evaluating the broodstock composition would not tell you what is happening for Ne in the river. Please account for this as well in your recommendations.	Bachus	BOR	No response from panel.
135	4.0, Conclusions	20	Bullet 7	Drought years with poor (almost 0) recruitment include 2002-2003, 2006, & 2011-2014. In 2004, there was significant recruitment that increased the October index.	Porter	USACE	Text revised.
136	4.0, Conclusions	20	Bullet 7	Conclusion #7 states that all the RGSM in the river today are descendants from fish that were produced for augmentation in the hatcheries. This is not entirely correct. Many of the fish released for augmentation were wild-caught as eggs or larvae - those were then supplemented with captive propagation from broodstock - and those combined individuals released for augmentation purposes back to the river. Particularly in drought years, where spring peak flows are reduced - we see our egg capture rates go up (less water volume means easier capture of eggs that are in the system). Those eggs are then transported to the hatcheries to rear and release as mature fish back to the river later that year. These are not hatchery produced fish in the sense that seems to be implied by the panel's conclusion (i.e., spawned in hatcheries). Also, this is an absolute statement in this conclusion, and we simply do not have the evidence to unequivocally state that there are no more "wild" RGSM in the MRG, or that if they are there that they do not spawn and contribute to the existing population. That is very difficult to 'prove.' We still detect non-tagged RGSM in the MRG, and without any cross-generational tagging, there is no way to affirm that these were 100% spawned from augmented fish. Please be careful with absolute statements that do not have the full support of the data. Changing "...fish in the river today are all descendants from..." to "...fish in the river today are more likely to be descendents from..." would help address this concern.	Bachus	BOR	Statements in the conclusion have been changed as requested to not come across as absolute. We have also provided definitions of 'wild' and 'captive' in our glossary. We recognize that the degree of captive/hatchery rearing may vary among RGSM individuals that are captured in the wild. According to our definition, any fish that experienced some degree of captive rearing in its lifecycle would constitute a captive/hatchery fish.
137	4.0, Conclusions	20	Bullet 7	For Conclusion #7: How can we tell that they are all descendants of hatchery fish? Just because the long term monitoring data shows zero fish in the river does not mean that there actually no fish. This also implies that the species is essentially extinct, which we know is not the case.	Gonzales	BOR	See Comment #136
138	4.0, Conclusions	20	Bullet 8	… during marginal spring pulses. Large numbers spawn on the floodplain during average spring runoff (2000+ cfs at Albuquerque), with few eggs drifting in the current.	Porter	USACE	None
139	4.0, Conclusions	20	Bullet 9	Clarify the relative importance of maintaining flow (cohort survival) versus a spring environmental flow that is sufficient for successful floodplain spawning and recruitment (produce new cohort).	Porter	USACE	None
140	4.0, Conclusions	20	Bullet 9	Bullet 1 under Conclusion #9: The resultant larvae - in the hatcheries - constitute that generation's gene pool. This is true only in the hatcheries (not in the river) and less so in years when the population in the wild is at higher densities and there is less augmentation (or with higher spring flows - less egg collection). We do assume those collected eggs are representative of that generation's gene pool - perhaps that type of wording would clarify.	Bachus	BOR	Added clarifying text.

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141	4.0, Conclusions	20	Bullet 9	Bullet 2 under Conclusion #9: "…there are essentially no eggs or adults recovered from the river…." Please note, adults are not recovered from the river for use in augmentation efforts. Eggs and larvae are. Even when adult fish are not detected during population monitoring, it is not a 100% detection probability so we cannot say there are no wild fish. Suggest referring to gene pool in terms of likelihood - i.e., we conclude it is most likely that the hatchery broodstock are driving the gene pool of this species in years where substantial augmentation efforts are required to sustain the MRG population. Or similar. (the report uses likelihood rather than absolute statements in other sections - on page 22 bullet #4 for example).	Bachus	BOR	Text revised.
142	4.0, Conclusions	20	Bullet 9	Bullet 2 under Conclusion #9: The typical pattern for silvery minnow augmentation is eggs from fish that spawn in the spring are harvested from the river and then placed back into the river after irrigation season and the threat of river drying is gone. When there is a significant drought and runoff is meager/low typically more eggs are harvested from the river, hatched, and then returned to the river than during non-drought years. The reason is because it is hard to harvest eggs when discharge is high and the need for stocking is lessened since we expect natural recruitment during these years to be high. My comment mainly pertains to the assertion that hatchery broodstock are driving the gene pool of the species which is likely not true but instead natural spawned eggs that are raised in the hatchery then released after irrigation season are likely driving the gene pool of this species. Broodstock would imply that only progeny from fish spawned and hatched in captivity are being stocked and this is not the case with the Rio Grande silvery minnow, but instead augmentation consists of 1) naturally spawned eggs (or sometimes larvae) harvested from the river, hatched and grown to juvenile size and then released after the threat of drying has passed (typically higher during droughts/low water years), 2) Broodstock spawned in captivity and their progeny released into the river (typically lower during droughts or low water years, except when egg collections are really low due to low population densities).	Gonzales	BOR	See comment #140
143	4.0, Conclusions	20	Bullet 9	Bullet 3 under Conclusion #9: please recall that effective population size may be assessed by examining captive stock (and wild caught eggs) in years like recent years where significant augmentation is required to sustain the numbers of RGSM in the wild. However, there have been years where this is not the case (minimal to no augmentation is needed; tagged fish represent a very small proportion of the RGSM in the wild) and in those years using just the hatchery genetics would not be reflective of Ne in the wild, correct?	Bachus	BOR	Agreed.
144	4.0, Recommendations	21	Bullet 2	For recommendation #2, when deviations in the methodology result in offspring - would the panel recommend genotyping those to determine if they could be used? Or is that too dificult to ascertain or not advisable, and if so why?	Bachus	BOR	These fish should be discarded (allowed to die naturally in the hatchery) unless there has been a disaster with those intentionally produced for stocking.
145	4.0, Recommendations	21	Bullet 3	For recommendation #3, there can be up to 400,000 fish to take fin clips of (to accomplish this recommendation). Would sampling a subset for genotyping still accomplish the goal? Why or why not?	Bachus	BOR	A subset of 2000 would be sufficient, though as stated elsewhere, changes in broodstock management will make this less relevant.
146	4.0, Recommendations	21	Bullet 3	For recommendation #3: Are you recommending that all the fish released annually be genotyped? Is this cost prohibitive when greater than 50,000 fish are to be released?	Gonzales	BOR	See Comment #145

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147	4.0, Recommendations	21		This report identifies a great many apparent short-comings regarding the past efforts included under this review. It also provides perhaps even more suggested recommendations and options to address and potentially correct these issues. But the overall number of recommendations is overwhelming, with many per most pages of this review, likely even exceeding the list incorporated in this section. Considering a limited budget exists, inadequate to address immediately every recommendation, it would be extremely useful if the reviewers would provide a priority list for the recommendations. at minimum itemizing recommendations that are "essential" to address versus other that "would be nice" or others somewhere between these extremes. If relative costs (even just orders of magnitude) to complete the recommendations could be provided, that also would be most beneficial to the Program's planning process. Thank you, again.	Marcus	APA	Priorities have been identified for the recommendations in Questions 1 and 13 and in the Overall Recommendations.
148	4.0, Recommendations	22	Bullet 12	Recommendation #12 refers to inclusion of candidate genes - please define or explain what is meant by this.	Bachus	BOR	Added to glossary.
149	4.0, Recommendations	22	Bullet 4	For recommendation #4: Is there a way to determine if Rio Grande silvery minnow are still present that do not have hatchery ancestry?	Gonzales	BOR	It cannot be ruled out that all RGSM in the wild are influenced by hatchery ancestry. However, the only way to determine if some RGSM do not have hatchery ancestry at present (in 2016) would depend on there being a different genetic signal underlying 'remnant purely wild individuals' from any individual with some degree of hatchery ancestry. The extensive annual genetic monitoring of RGSM consistently supports that one population of RGSM exists (i.e. no remnant individuals). However, if the RGSM recovery team conducts some NGS/GBS as part of future monitoring efforts, it is recommended that they re-assess population clustering (e.g. with STRUCTURE or equivalent) within the Rio Grande River and contrasted with hatchery fish: if remnant RGSM exist and have been non-randomly mating, such an analysis may have the statistical power to 'pull the needles out of the haystack', in which case recovery plans could be modified.
150	4.0, Recommendations	22	Bullets 6, 9, 10	For recommendations # 6, 9 , and 10: Could you provide more detail as to what the proposed studies entail and a ballpark of anticipated costs (or relative costs)?	Gonzales	BOR	We have added some approximate costs per individual in the text for the RGSM recovery team to consider. The cost per individual depends on the type of analysis and certain kinds of genotyping will only be feasible on very large numbers of individuals (e.g. parentage assignment of 1000s of hatchery offspring is best using microsatellites). Please note that in all cases the approximate costs noted do not include salaries for research associates to prepare and analyze samples.
151	4.0, Recommendations	23	Bullet 14	Could recommendation #14 be combined with recommendation #7?	Gonzales	BOR	We have maintained these as separate recommendations since #14 can also apply to group spawning. Clarifying text has been added.
152	4.0, Recommendations	23	Bullet 3	We concur that it is prudent to genotype all broodstock used. However, genotyping ALL pre-release juveniles as suggested is unrealistic (logistically and financially and in the timeframe suggested ie before release) even with high-thoughput techniques given that 100,000-300,000 fish are released annually.	Osborne & Turner	UNM	See comment #86.
153	4.0, Recommendations	24	Bullet 6	We agree that a study that uses next gen sequencing technology that uses historical material to examine how the RGSM genome has changed over time is important. We are well positioned (ie. access to archived material, next ge sequencing and data analysis capabilities at UNM) to execute such a study should funding be available.	Osborne & Turner	UNM	None.

Comment #	*The comment refers to the* Section	Page	Line	Comment	Name of Reviewer	Office of Reviewer	Response from Panel (or Action Taken to Address the Comment)
154	4.0, Recommendations	21-23		Concur with recommendations. Be more explicit identifying studies, and priortize studies into must-do, opportunitistic (floodplain spawning), long-term value versus short-term needs, other.	Porter	USACE	Priorities have been identified for the recommendations in Questions 1 and 13 and in the Overall Recommendations.
155	Appendix B, Meeting Attendees	B-3		Joel Lusk is not a member of the Genetics Workgroup, but only the Science Subcommittee, and therefore, subscript 2 should be removed	Lusk	SFWS-NME	Corrected.
156	General	n/a		When recommending analyses or procedures, please cite relevant references so it is clear what the specific procedure is being recommended. For the Program to move forward on a given recommendation, we would need to develop a Scope of Work for these activities (should the Program decide to do that), so we would need to know what specific types of analyses or procedures we need to include in the scope accordingly. Cited sources can be vital for this. (A good example of this is what the panel wrote for Question 9, page 13 - referencing Palti et al. 2015).	Bachus	BOR	It is beyond the scope of the panel to suggest specific procedures. Often, there needs to be some flexibility in this,especially since the tools are so rapidly changing. The Scopes of Work should be more question-based, allowing the researcher to use the most appropriate tool at that time.