

Science and Habitat Restoration Work Group Meeting
January 17, 2017

Meeting Materials:

Meeting Agenda

Meeting Minutes

RGSM Population Monitoring Results from December 2016 [report not included]

**Middle Rio Grande Endangered Species Collaborative Program
Habitat Restoration and Science Joint Workgroup Meeting
January 17, 2017
1:00-3:00 PM
at ISC**

HRW/ScW Agenda

1. Introductions
2. Approval of Agenda
3. Genetics Monitoring Presentation: Dr. Megan Osborne
4. Approval of September meeting notes
5. Announcements
6. Program Updates - EC/RIP/PASS status, Competitive Grant Process
7. Subgroup Report Outs:
 - (a) HR Project GIS subgroup;
 - (b) RGSM Life History subgroup;
 - (c) Genetics & Propagation joint group with ScW;
8. Discussion of habitat restoration measures in the BO
9. Discussion of habitat restoration monitoring- current efforts; any evaluation of monitoring data and effectiveness?

Action Items:

Next Meeting: February 21, 2017 from 1:00-3:00 PM at IScan SC

**Middle Rio Grande Endangered Species Collaborative Program
Science/Habitat Restoration Workgroup Meeting
January 17th, 2017 – 1:00pm to 3:00pm
ISC**

Decisions Items:

- The September 2016 ScW/HRW Joint Meeting notes were approved for finalization with no changes.

Action Items:

- ✓ After discussions on the Adaptive Management Minnow Technical Workshop agenda (Corps' contract), Debbie Lee will email the updated agenda to Dana Price for distribution to ScW/HRW members. Please note that the agenda is still under construction and could be further revised. – *completed*
- ✓ Anyone interested in attending the Adaptive Management Minnow Technical Workshop is encouraged to please RSVP to Debbie Lee as soon as possible since space is limited. – *completed*
- Ken Richard will email the draft HR GIS template(s) to ScW/HRW members for review, feedback, and verification.
- ✓ Dana Price will distribute the 2014 Habitat Effectiveness Monitoring Report to ScW/HRW members. – *completed 01/17/17*
- Members are encouraged to read the Habitat Effectiveness Monitoring Report, particularly the executive summary and recommendations sections, in preparation for discussions at the February meeting.
- Workgroup members are encouraged to propose different approaches (or systems) for naming restoration sites and addressing naming standardization.
- ✓ Dana Price and Alison Hutson will poll ScW members for the next meeting date for the ScW – Genetics Subgroup. The primary agenda item is to continue development of the Genetics Recommendations Flowchart. – *completed 01/17/17*
- ✓ Mike Marcus will update the Genetics Recommendation “Topical” Spreadsheet (with the 12/13/16 subgroup discussions and priorities). – *completed for 02/13/17 meeting;*
- Members are encouraged to read the BO, particularly sections related to habitat restoration, in preparation for discussions at the February meeting.
- Joel Lusk will ask Vicki Ryan to attend the February ScW/HRW meeting (if possible) to aid in discussion on flycatcher habitat and the new Reclamation BO.
- Justin Reale will email the Sandia Restoration citation information (from the Habitat Effectiveness Report) to Dana Price for distribution to the workgroup.
- ✓ Danielle Galloway will contact Matt Johnson to schedule a salt cedar beetle presentation for the February 21st ScW/HRW meeting. – *completed*
- ✓ Grace Haggerty will schedule a meeting room at ISC for the February 21st ScW/HRW meeting. – *completed*

Recommendations/Requests:

- Given the recent developments in the Program (newly released BO, Program Management, etc.) and the time constraints to get a scope in the next queue, ScW/HRW members recommended putting the RGSM Life History subgroup on indefinite hold.
- When available, the HR GIS templates/spreadsheets/data sets will be distributed to workgroup members. Agencies are encouraged to verify the shape files, polygons, metadata, etc.
- Workgroup members were encouraged to develop a list of projects and activities to inform the EC on the current status and for consideration of any restructuring. Why meet? What is done during meetings and between meetings?

Announcements

- A save-the-date for the BEMP (Bosque Ecological Monitoring Program) Crawford Symposium has been sent out. BEMP is celebrating 20 years and will highlight work done by students and professionals on March 7th, from 4:00pm to 8:00pm at UNM.
- The Adaptive Management (Corps' contract) Technical Minnow Workshop has been scheduled for February 1st and 2nd at the Tamaya. The draft agenda is still under construction. Space is limited so please RSVP to Debbie Lee as soon as possible. Please note that this workshop is to be very technical and not necessarily policy-driven. The expert panel will submit a recommendations report based on their findings from the workshop.
- Matt Johnson, Tamarisk Coalition, will be asked to present annual updates on the beetle at the February 21st ScW/HRW joint meeting.

Next Meeting: Tuesday, February 21st, 2017 from 1:00pm to 3:00pm at ISC

- Tentative February meeting agenda items: (1) Tamarisk Beetle Presentation – 2016 Update (Matt Johnson); (2) Update presentation and discussion on HR GIS; discuss assistance (contract?) in getting the data sets together; (3) EC report out – discussion on transition to AMT?; (4) Discussion of habitat restoration measures in the BO (carried over from 01/17/17); (5) Discussion of habitat restoration monitoring- current efforts; any evaluation of monitoring data and effectiveness? (carried over from 01/17/17); (6) Genetics Recommendations Flow Chart – report out/presentation from subgroup (?)

Meeting Summary

- Dana Price brought the meeting to order and introductions were made. The agenda was approved with no changes.
- Dr. Osborne presented on Genetic Monitoring and Status of Wild and Captive Stock for 2016.
- The September 2016 ScW/HRW Joint Meeting notes were approved for finalization with no changes.
- The HR Project GIS subgroup reported on the work completed to date. Example(s) of the work done will be distributed to workgroup members for feedback before the subgroup proceeds. Eventually, agencies will be asked to verify their project data (shape files, polygons, metadata, etc.).
 - It was suggested members consider how they might use the data sets and what specific questions they might attempt to address. Suggestions included: (1) where has there been physical, on-the-ground work?; (2) what projects have been completed? and (3) in what areas?; (4) what are elevations of inundation?; and (5) how many acres of restoration have been done? Where? What extent? Per reach?
- The Genetics Subgroup met several times to review the genetics peer review recommendations. The recommendations were reformatted into a spreadsheet allowing the attendees to assign priorities, make qualitative judgments on implementation time scales and cost, and insert comments. The group is in the process of developing a flow chart on implementation recommendations. They will probably need to meet one more time to finish the flowchart before presenting it to the larger group.
- The last two (2) agenda items (discussion of habitat restoration measures in the BO and discussion of habitat restoration monitoring) were both postponed until the February meeting. Members are encouraged to read habitat restoration sections in the BO and pertinent sections of the Habitat Monitoring Effectiveness Report (executive summary, findings, and recommendations) in preparation for these discussions.

Full Meeting Notes

Introductions and Agenda Review: Dana Price brought the meeting to order and introductions were made. The agenda was reviewed and approved with additional discussion under the HR GIS Subgroup report out.

Presentation: Rio Grande Silvery Minnow (RGSM) Genetics Monitoring

- Dr. Megan Osborne, with UNM, presented *Genetic Monitoring of the Rio Grande Silvery Minnow: Genetic Status of Wild and Captive Stocks in 2016*.
 - *Background*
 - Genetic monitoring is the tracking of genetic diversity metrics over a contemporary time scale using multiple time points and consistent methodologies across that time series.
 - The genetic monitoring of the Rio Grande Silvery Minnow (RGSM) has been ongoing since 1999 allowing for comparison of the population through time.
 - The diversity metrics include:
 - Mitochondrial DNA (mtDNA) which provides information on the female contribution to the population; and
 - Microsatellites (estimates gene diversity, allelic richness, heterozygosity, etc.) are used to track trends in genetic diversity from generation to generation.
 - From these metrics, variance effective size can be calculated. Please note that “effective population size” refers to the number of individuals that are making reproduction contribution to the population.
 - *Allelic Diversity*
 - Number of alleles per locus is dependent on sample size. So the number of alleles/haplotypes per microsatellite/mtDNA locus is corrected for unequal sample size.
 - Bottlenecks and allelic/haplotype diversity – depends on the number of alleles and their frequencies. Rare alleles are the most likely to be lost.
 - *Genetic Effective Size*
 - “Genetic Effective Size” refers to the “ideal” size of a population that would experience the same degree of genetic drift as the observed population.
 - Genetic Effective Size is important because it determines the amount of variation that is translated from one generation to the next.
 - Please note that in general, the larger the population size the more diversity (in terms of number of alleles) can be expected. (For example, a large population can be expected to have large amounts of genetic drift – making it hard to tell the difference between a big population and a really big population. But in small populations, diversity is lost more quickly through drift than in larger populations.)
 - The genetic effective size and effective population size estimates are likely to be equal when a population is stable. When a population is supplemented by hatchery fish, these numbers will not be the same.
 - Assumptions shared for both genetic effective size and effective population size include:
 - Mutation is not important;
 - Alleles selectively neutral;
 - Alleles not in linkage disequilibrium with loci under selection;
 - Samples are drawn randomly no immigration from neighboring populations.
 - Additionally, it is assumed that for effective population size there is random mating.
 - Please note that in a majority of populations, the assumptions are very rarely met.
 - *Why Conduct Genetic Monitoring?*
 - Genetic monitoring of the RGSM is important because this is a short-lived species with Type III survivorship (meaning they produce a lot of gametes but very few survive). The environmental conditions are extremely variable and result in dramatic population

- fluctuations. Additionally, this is a highly managed system and management actions affect how diversity is distributed.
- Captive propagation and augmentation may increase or decrease diversity and genetic effective size.
- *General Sampling Procedure*
 - Fin-clip samples are taken from adult fish (considered non-destructive sampling).
 - Ideally, samples are collected from 3 locations within each river reach (Angostura, Isleta, and San Acacia) as well as representative captive stock released to the Middle Rio Grande (MRG) and Big Bend.
 - Cumulative for the duration of the monitoring program, a total of 4,979 wild fish (not tagged) and 3,987 hatchery origin fish have been sampled; 420 being from the 2016 efforts.
 - *Additional Analysis Based On Peer Review*
 - Last year, a Genetic Program Peer Review was completed. Additional analyses were conducted in response to some of the peer review recommendations, including:
 - *Recommendation:* Are there thresholds of genetic diversity where management actions should be taken?
 - *Response:* Create 95% thresholds of diversity over space and time to determine if diversity has fallen below a critical thresholds
 - *Recommendation:* Assess the effective sample size of genetic effective size?
 - *Response:* Use random resampling set to the smallest sample sizes and recalculate N_e
 - *Recommendation:* Pooled hatchery sample diversity metrics
 - *Project Objectives*
 1. Collect samples from 'wild/naturally spawned' RGSM population and captive stocks;
 2. Establish benchmarks of diversity using existing data (newly added in response to recommendations);
 3. Determine levels of genetic variability and compare to evaluate temporal trends;
 4. Evaluate genetic effects of captive propagation/augmentation on wild stocks;
 5. Estimate contemporary genetic effective size (N_{ev} & N_{el}) in the wild population to evaluate temporal trends;
 6. Evaluate the association between sample size and genetic effective population size (newly added in response to recommendations).
 - *Objective 1: 2016 Samples*
 - Ideally, there will be 50 samples per each reach every year (for a total of 150 samples). However, there are years where the number of samples is much less (for example, 2014).
 - For the 2016 monitoring, there was a total of 420 unmarked fish sampled:
 - 171 in the Angostura Reach;
 - 121 in the Isleta Reach; and
 - 128 in the San Acacia Reach.
 - *Objective 2: Establish Benchmarks Of Diversity*
 - To address the recommendation of establishing diversity benchmarks using existing data, all *wild fish were pooled into one large population (of about 5,000).
 - *Please note that "wild" refers to unmarked fish, spawned in the river. It is acknowledged that with the stocking and augmentation program there is a hatchery pedigree for the entire population.
 - From that grouped population of 5,000, 43 samples were randomly selected (43 being the smallest sample size) for 10,000 iterations to estimate diversity statistics.
 - Because our primary interest is maintaining genetic diversity, the one-tailed benchmark corresponds to the lower 5% of the resampled distribution (as opposed to lower 2.5% for a two-tailed).
 - The distribution contained above the benchmark corresponds to a conservative null hypothesis of no loss of diversity.

- *Objective 3: Estimate Genetic Diversity In The Wild Population To Assess Temporal Trends*
 - Assessing the temporal trends (benchmarks) has only been completed for microsatellites; the mtDNA analysis is in process.
 - *Microsatellites:*
 - An increase in haplotype diversity and allelic richness was observed in 2016. Two (2) rare haplotypes were detected for the first time since 2012. This is likely due to the increased number of samples (more samples means greater detection opportunities). The rare haplotypes can be traced back to the hatchery use of 2012 broodstock. The haplotypes were detected in the Angostura Reach in 2012.
 - But the genetic diversity basically remains the same since 2015.
 - For clarification, the 2016 genetic monitoring reflects data on fish collected from December 2015 through April 2016 - thus reflective of the 2015 breeding. Fish augmented in the fall of 2014 contributed to breeding in 2015 and whose offspring are now being detected as wild fish in 2016.
 - Comparing the reaches, Angostura has remained “genetically” stable. All metrics in the Isleta Reach declined while all metrics in San Acacia increased. Changes in San Acacia aren’t unexpected as the lower reach see the most influence from the other reaches. It is also subject to the most drying, etc. so its metrics can “bounce around” the most.
 - *Mitochondrial*
 - mtDNA increased at reach level and is likely attributed to stocking efforts.
- *Objective 4: Genetic Diversity Of Captive Stocks 2016*
 - If taken individually, the BioPark and the Los Lunas Silvery Minnow Refugium (LLSMR) are below benchmark; but the 2016 “global” is above the estimated benchmarks. Sample size is the same across the lots.
 - In response to a question on the April 2016 stocking, it was clarified that the 2016 individuals will not be reflected in this monitoring. However, if/as they reproduce in spring 2017 then they will contribute genetically. There are samples from those stocked fish so their haplotypes can be tracked.
- *Objective 5: Inbreeding Genetic Effective Size*
 - The inbreeding genetic effective size tracks the allele frequency from one year to the next and the active number of breeder available for the next spawn. In other words, it measures the number of parents for the current generation. The inbreeding genetic effective size is estimated using linkage disequilibrium (non-random association of alleles at different loci).
 - Variance Effective Population Size measures loss of genetic variation from genetic drift. It is estimated with allele frequency changes. For 2016, there was an increase over previous estimates but that is not surprising given the 2 years of no/poor sampling (2013 and 2014).
 - Female Variance Effective Population Size (mitochondrial) has less power (than microsatellites) since there is a single locus, fewer alleles, and one dominant haplotype (which is found in 50-70%). In the 2016 monitoring, the Female Variance Effective Population Size went from “big” to “very, very small” – small values that were seen at the start of the genetic monitoring program.
 - Please note that this could be an artifact of the “new” haplotypes. Since the frequency in change is being measured, the addition of the 2 rare haplotypes indicates a “large” change for this time period and will artificially drop the number.
 - It was also noted that there is one really common haplotype found in ~70% of individuals and the power of detection for changes is not that great for the rest (which are rare alleles). The microsatellites have better power to detect the changes.

- *Objective 6: Resampling Size Exercise*
 - Effective size estimates obtained using smaller sample sizes than the actual N results in estimates which are very similar and within the 95% CI's obtained by resampling.
 - The genetic effective size was “recalculated” using a resampling at the lowest number of 45 individuals. Recalculations were also completed for sample sizes of 127, 143, and 161 for comparison.
 - All the results are very similar. However, as expected, there can be periodic estimate “blips” when the sample size is very small (<45).
- *Conclusions*
 1. Genetic diversity is stable since 2015;
 2. Genetic diversity in 2016 remains above the benchmarks;
 3. Global hatchery diversity is above benchmarks;
 4. N_{eV} estimated from microsatellites has increased over previous estimates (2012-2015);
 5. Female N_e has declined from previous estimates; and
 6. Sample size has little impact on genetic effective size estimates.
- *Questions:*
 - *Comment:* As describing these population genetics, it might be helpful to add, where appropriate, a terminology qualifier of “brood stock” or “breed stock” to help clarify references to the fish produced in 2015.
 - *Response:* The interest is in the fish that are contributing (reproducing) for the year. Samples are taken from December to April and there will occasionally be older fish in those collections.
 - *Questions:* There have been recent discussions (sparked from the peer review) regarding the genotyping of all fish before they are released to the river – including the parents and broodstock. The concern is that since we aren't using paired spawning, the genotyping is needed for tracking. What would it take to be able to know the genotypes of the fish being put into the river? Right now, there are several issues with getting samples of the offspring – including size and time constraints.
 - *Response:* There is a very tight timeframe from production to sufficient growth in size to release. And we don't know until right beforehand what is going to be released. There would need to be methodology changes.
 - While genotyping broodstock is a good idea as it would provide opportunities for parentage analysis, without changes it is almost pointless to attempt it now. There is an extremely tight timeline in which to try to accomplish it and it will require several changes before it really becomes a feasible option.
 - *Question:* How big a concern is the parentage? If we move to paired spawning, what are the concerns that drive the need for genotyping?
 - *Response:* A lot depends on what the hatcheries do. With a very orchestrated hatchery program, genotyping the broodstock is a good first step.
 - Genetic diversity has been maintained in the minnow produced in the wild. And they are an aggregate spawner. Paired spawning requires more intervention and is less like natural conditions. Hatchery fish are breeding in the river and given the data, we are accomplishing the “charge” in terms of maintaining genetic diversity.
 - However, we don't know to what extent we may be selecting traits for domestication; we are monitoring neutral variation. There are programs for small-bodied fish that do have paired spawning.
 - Attendees briefly discussed the standard use of microsatellites since the 1990s. Next generation models have been and are being developed but those are not trivial, especially for “non-model” species. There have been studies in other taxa (ie. not RGSM) or using simulations that have compared genetic effective sizes calculated from SNP data to those obtained using microsatellite data. These studies show similar estimates but with narrower confidence intervals for SNP data (because you are looking at many more loci). And there are cost considerations.

- Dr. Osborne later clarified that using next generation sequencing to develop SNP markers for RGSM would allow many more loci to be screened including those potentially under selection in addition to neutral loci, would facilitate more rapid screening of individuals and would help to transition the program away from microsatellites before this technology becomes obsolete.
 - *Question:* It was mentioned that the detection of 2 rare alleles could be from two (2) potential sources. Would (could) genotyping the broodstock help solve that type of uncertainty in the future? And it is important?
 - *Response:* It is useful to know which hatchery fish are contributing offspring. There are methods in diversity statistics that can emphasize relationship to/from the hatchery.

Approval of September 2016 Meeting Notes

- The September 2016 ScW/HRW Joint Meeting notes were approved for finalization with no changes.

Announcements

- A save-the-date for the BEMP (Bosque Ecological Monitoring Program) Crawford Symposium has been sent out. BEMP is celebrating 20 years and will highlight work done by students and professionals on March 7th, from 4:00pm to 8:00pm at UNM.
- The Adaptive Management (Corps' contract) Technical Minnow Workshop has been scheduled for February 1st and 2nd at the Tamaya. The draft agenda is still under construction. Space is limited so please RSVP to Debbie Lee as soon as possible. Please note that this workshop is to be very technical and not necessarily policy-driven. The expert panel will submit a recommendations report based on their findings from the workshop.
- Matt Johnson, Tamarisk Coalition, will be asked to present annual updates on the beetle at the February 21st ScW/HRW joint meeting.

Program Updates

- The EC is scheduled to meet tomorrow (Thursday, January 18th). Program updates will be shared at the February ScW/HRW joint meeting.

Subgroup Report Outs

- *HR Project GIS Subgroup:*
 - Several members have met and are working to put together a “clean data set” of all the restoration sites. Part of the challenge is dealing with non-standardized nomenclature. There is a desperate need for terminology and reference standards.
 - The subgroup members propose sending the GIS and Excel spreadsheet table(s) to everyone in order to have agencies verify and populate the data for their projects.
 - The intent is to eventually have “useable” and easily-accessible data for analyses and not just a repository. And hopefully the Program will be confident in the final data set since both the workgroup and agencies will be contributing and verifying everything. If done correctly, this dataset could eventually be used to help select restoration sites.
 - Right now, the subgroup is just trying to collect the data but there will need to be future discussions on where the GIS is hosted.
 - Workgroup members are encouraged to think about specific questions and how the GIS dataset might be used. This will better allow the subgroup to make sure it is set up to be able to address those types of questions.
 - Suggestions:
 - date/year completed;
 - imbed the metadata;
 - ownership in counties;
 - Z-score/elevation;
 - Agreement on descriptors of restoration feature types - fewest possible;

- Site construction information including elevation surveys;
 - Identify sensitive sites (wetlands, mouse population, etc.) for use as a planning tool;
 - Not limit to Program work, but all agency work that contributes needs to be in one place.
- One of the first steps the subgroup is addressing is compiling one large shape file for layering. The DBMS has multiple shape files. The subgroup is also working through all the synonyms and trying to establish naming protocol.
 - The subgroup was referred to the SWCA Effectiveness Monitoring Report that might assist as a starting point for consistency.
- Possible questions for consideration:
 - Where has ground been touched? Specifically, how many acres of restoration have been done?
 - What projects have been completed? Where?
 - What are the elevations of inundation?
- A possible suggested approach could be to take a test area with restoration construction and build the GIS for this one particular site and test how it answers questions on that project/area/mile. Then, build the database outward from there.
- Another suggestion was to use a spreadsheet join for agencies to update fields - rather than trying to have multiple people editing shape files. It is a “cleaner” editorial process to export/merge with the master file and reduces error rates for updates.
- Workgroup members are encouraged to suggest protocol for standardizing site names.
 - While Reach and River Mile might be the simplest approach, it was cautioned that the River Miles can get reassessed and then change. And there would be a need to reference left or right bank. Certain data could be included in the metadata.
- *RGSM Life History Subgroup:*
 - Given the recent developments in the Program (newly released BO, Program Management, etc.) and the time constraints to get a scope in the next queue, ScW/HRW members recommended putting the RGSM Life History subgroup on indefinite hold.
- *Genetics & Propagation Joint Group With ScW:*
 - The Genetics Subgroup met several times to review the Genetics Peer Review Recommendations.
 - The recommendations were reformatted into a spreadsheet allowing the attendees to assign priorities, make qualitative judgments on implementation time scales and cost, and insert comments.
 - The group is in the process of developing a flow chart on implementation recommendations. They will probably need to meet one more time to finish the flowchart before presenting it to the larger group.

Discussion on Habitat Restoration Measures in the BO

- The Service issued a Final BO to Reclamation and partners in early December. The EC will be discussing the role of the Program.
 - In a very brief summary, it was shared the “majority” of habitat restoration mentioned in the BO is for the San Acacia Reach as proposed by the state and others. There are 2 large activities planned for the Ft. Craig and Bosque del Apache areas. There are also associated “plumbing” changes with the MRGCD and how ditches receive water. Other restoration involves suitable and moderately-suitable flycatcher habitat and how to address potential loss. The BO considers riparian and aquatic habitat but the main focus is really on the lower reaches.
- Workgroup members are encouraged to BO in preparation for discussing the future of the Program’s habitat work.
- Attendees briefly discussed the possible re-organization into an Adaptive Management Team (AMT). While being proactive can be a good thing, it was cautioned that the EC will be discussing the role of the Program tomorrow and any restructuring should come at the EC’s direction. And the CC requested WEST devise recommendations on if/how the Program could restructure.

- Attendees briefly shared the evolution of the standing workgroups and the decision to meet jointly for the time being - loss of funding (so the groups had fewer projects and less work) combined with the lack of direction from the EC (since the Program was basically on-hold until the BO was issued).
- It was suggested the workgroup develop a list of projects and activities to inform the EC on the current status and for consideration of any restructuring. Why meet? What is done during meetings and between meetings?

Discussion of Habitat Restoration Monitoring- Current Efforts; any evaluation of monitoring data and effectiveness?

- Members are encouraged to read the Habitat Effectiveness Monitoring Report, particularly the executive summary and recommendations sections, in preparation for discussions at the February meeting.
 - SWCA consolidated a lot of raw monitoring data. The fish monitoring section has clear conclusions but the available data on the riparian habitat was very “helter-skelter”. The bulk of the report goes site-by-site through the deficiencies in the riparian monitoring. The introductions, findings, executive summary, and recommendations would be the most useful.
 - Additional information can also be found in the 404 Compliance Monitoring reports from Tetra Tech. These reports documented the changes in riparian vegetation cover over time. That monitoring did not include flycatcher monitoring just vegetation monitoring. These reports should be in the DBMS.

Next Meeting: Tuesday, February 21st, 2017 from 1:00pm to 3:00pm at ISC

- Tentative February meeting agenda items: (1) Tamarisk Beetle Presentation – 2016 Update (Matt Johnson); (2) Update presentation and discussion on HR GIS; discuss assistance (contract?) in getting the data sets together; (3) EC report out – discussion on transition to AMT?; (4) Discussion of habitat restoration measures in the BO (carried over from 01/17/17); (5) Discussion of habitat restoration monitoring- current efforts; any evaluation of monitoring data and effectiveness? (carried over from 01/17/17);

**Science/Habitat Restoration Workgroup Meeting
January 17, 2017 Meeting Attendees**

	NAME	AFFILIATION	PHONE NUMBER	EMAIL ADDRESS	Primary, Alternate, Other
1	Dana Price	USACE	505-342-3378	dana.m.price@usace.army.mil	P – ScW Co-Chair
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3	Michael Porter	USACE	505-342-3264	michael.d.porter@usace.arm.mil	A - ScW
4	Justin Reale	USACE	505-342-3138	justin.k.reale@usace.army.mil	A - HRW
5	Grace Haggerty	ISC	505-383-4042	grace.haggerty@state.nm.us	P - HRW
6	Ken Richard	ISC	505-383-4057	kenneth.richard@state.nm.us	A
7	Brian Hobbs	Reclamation	505-462-3564	bhobbs@usbr.gov	O
8	Joel Lusk	FWS	505-761-4209	joel_lusk@fws.gov	P - ScW
9	Malia Volke	NMDGF	505-476-8160	malia.volke@state.nm.us	P - ScW
10	Mike Marcus	For APA	505-379-6891	mdmenv@gmail.com	P - ScW
11	Kim Eichhorst	BEMP	505-277-0758	kimde@unm.edu	P - HRW
12	Kathy Lang	COA/BioPark	505-848-7174	klang@cabq.gov	P - ScW
13	Megan Osborne	UNM	505-277-3234	mosborne@unm.edu	O
14	Tyler Pilger	UNM	505-277-3234	tjpilger@unm.edu	O
15	Debbie Lee	WEST	505-492-2239	dlee@west-inc.com	O
16	Marta Wood	Alliant Env.	505-259-6098	mwood@alliantenv.com	O – note taker