

Date and Time: 04/03/2012 at 9:30am – 12:00pm

Meeting Location: New Mexico Ecological Services Field Office

Attendees: Melissa Mata-NMESFO, Susan Oetker-NMESFO, Steve Chambers-USFWS R2 RO, Thomas Turner and Megan Osborne-University of New Mexico, Thomas Dowling-Arizona State University

Purpose: Discuss the genetic status of Zuni bluehead sucker in New Mexico and Arizona. To identify all populations that should be within the subspecies name of *Catostomus discobolus yarrowi*.

Meeting Notes:

Is the Zuni bluehead sucker a valid subspecies?

Yes, the scientific community agrees that this is a subspecies and is no longer in question, based on work conducted by Smith et al. and Crabtree and Buth in the 1980s. Validity of the subspecies is based on both morphological and biochemical characters.

The main purpose of this meeting was to go over a PowerPoint that we received from Tom Dowling regarding genetic analysis based on bluehead suckers that were collected on Navajo Nation at several locations in 2000, 2001 and 2004. This work is nearly complete and will be submitted for publication within the next year.

Tom Dowling presented this information and both Tom Dowling and Tom Turner provided explanation of the analysis.

Based on mtDNA data, Dr. Dowling has identified several groupings that have been established well before any intervention of humans in these areas. Where *Catostomus plebeius* in the Rio Grande is distinct from the *C. plebeius* markers found in the Rio Nutria area in New Mexico. Evidence for evolutionary significance of this group are the branch lengths in the mtDNA phylogeny tree and that these haplotypes are not found within the Rio Grande has different haplotypes. This is consistent with previously published work.

Otherwise, these fish would not be distinct and share the haplotypes with other populations. For example, if we said that man contributed to this distinction, this would have occurred in the 1800s and if man had any part in the *C.d. yarrowi* creations; there would still be evidence of the Rio Grande *C. plebeius* form. But, because of the branch lengths mentioned above and the distributions of mtDNA types, these forms most likely reflect geological events that predate human influence, which is postulated in other publication as well.

In addition, mtDNA analysis identified a unique cluster that has been well established in time within the Canyon de Chelly area. This is more closely related to *C. discobolus* compared to *C.*

plebeius, as described in the literature. If you move across a gradient from southeast to the northwest the form favors (in terms of morphology) more *C. plebeius* to *C. discobolus*.

The most interesting finding with the mtDNA analysis is that there is a unique form of *C. discobolus* in the headwaters of the Little Colorado River (LCR), which is unique from any blueheads found within the mainstream of the Colorado River. This appears to be evolutionary significant and quite old, but does not clearly fall into the category with what we see in the Rio Nutria or Canyon De Chelly area.

Then a second analysis was done, using 2H2 allele distribution, which is an anonymous nuclear DNA based marker. This analysis is more fine-tuned by identifying the distribution of allele in the area samples and pinpointed areas of bluehead suckers that contain material from both *C. discobolus* and *C. plebeius* (i.e. Zuni bluehead sucker). Based on the literature it has been argued that *C. d. yarrowi* is only present in the LCR, but information from this analysis shows a few locations within the San Juan drainage that should be considered as *C. d. yarrowi* based on the presence of alleles from *C. plebeius*. The explanation for this is that there may have been a second geological event that allowed fish from the LCR and San Juan to mix, which also occurred before the intervention of man. This event possibly occurred 50,000 years ago or later (no good estimates of dates at this point), but well before the influence of man. It is suggested that streams located within the Canyon de Chelly are part of a closed system and may only flow into the San Juan during large flood events and therefore we don't see any *plebeius* markers in the major portion of the San Juan drainage. Note that Wheatfields Creek is the only creek that contains traits of *C. plebeius*, but it is highly likely that Tsaille and Whiskey, should be included in this grouping because they are within reasonable distance of each other and may be contributing genetic material to each other.

The most surprising information from this 2H2 analysis is that within the headwaters of the LCR it did not reveal any information *C. plebeius*. One explanation that was offered is that maybe the female parent was *C. discobolus* most of the time and therefore *C. plebeius* may have dissipated over time. It is quite clear that this form of *C. discobolus* has been established for quite some time now. This should be investigated further to explain what's going on here.

Comment [ted1]: To be specific, there are lots of *plebeius* alleles in the headwaters of the LCR, including Rio Nutria and Kinlichee, but not in the uppermost portion of the drainage (Nutrioso Creek) or the other tributaries on the southern side of the drainage

In addition, the Service asked if the geneticist had any recommendation regarding collecting more specimens for their analysis. They did identify that there is a gap, between geographically areas between Zuni River area and North to Fort Wingate. If we were able to find bluehead sucker and sample, it would contribute to their analysis and potentially identify other populations.

I (Melissa Mata) mentioned that we are trying to plan a sampling effort on Navajo Nation and that they have identified two locations that have never been sampled and believe to have bluehead suckers in the area. These two locations were Bonita Creek in Arizona west of Fort Wingate and Bowl Canyon in Arizona northeast of Fort Wingate, which could provide

Zuni Bluehead Sucker

Note to File

information. If we can get the samples, they would be willing to re-run the mtDNA and 2h2 allele test on these sample and add to their work.

End of Meeting Notes.