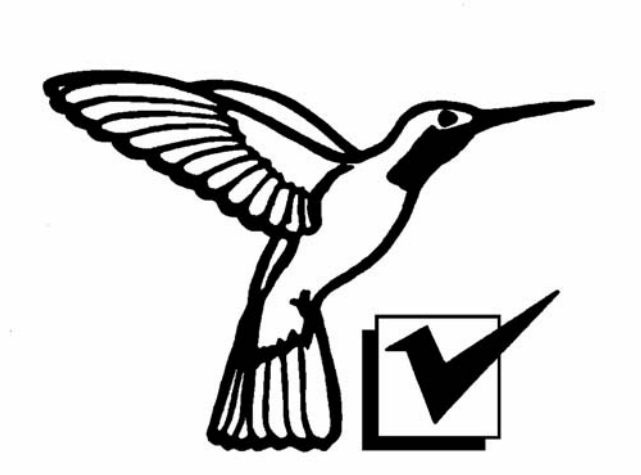
ANNUAL PERFORMANCE REPORT

Share with Wildlife Projects

T-32-P-1



New Mexico Department of Game and Fish

May 2009

ANNUAL PERFORMANCE REPORT

State Wildlife Grants

State: New Mexico Grant Number: T-32-P-1

Project Title: Share with Wildlife Projects

Performance Period: February 22, 2008 To: February 21, 2009

A. Objective

To establish better status information and understanding of conservation needs of endangered, threatened and nongame wildlife in New Mexico, and determine those that may be in need of additional management or conservation efforts.

B. Need

Share with Wildlife was created by the New Mexico state legislature in 1981. The program was established to "provide additional wildlife funds to perpetuate the renewable wildlife resource of New Mexico that gives so much pleasure and recreation to all New Mexicans." Share with Wildlife is a program of the New Mexico Department of Game and Fish (Department) that is particularly committed to helping those species that do not receive funding from any other sources, including many endangered and threatened species. The means established for collecting these additional funds was a "check-off" on the state income tax form for those who receive a tax refund. Share with Wildlife receives much of its funding through the state income tax check-off, but also accepts mail-in contributions, and receives revenues from the sale of New Mexico wildlife license plates.

Many species of nongame wildlife are unprotected under New Mexico state law, unless they are listed as threatened or endangered under the New Mexico Wildlife Conservation Act (WCA). Examples of unprotected wildlife include nongame mammals, nongame fishes, and mollusks or crustaceans that are not listed under the WCA. Many species of nongame wildlife receive little management attention unless they are listed under the WCA, or are being considered for listing. Sources of funding for these species are limited. Work on nongame mammals and birds can be supported by Federal Aid in Wildlife Restoration Act funds. Endangered Species Act Section 6 funds support much of the Department's work on endangered, threatened, or rare wildlife. However, Section 6 funds are insufficient to support work on all 118 New Mexico threatened and endangered species, much less the total of 452 Species of Greatest Conservation Need identified in the Comprehensive Wildlife Conservation Strategy for New Mexico. In many cases, additional status information is necessary before a determination can be made as to whether a species requires additional management or protection. Share with Wildlife helps to meet this need of fulfilling conservation and information gaps identified within the Comprehensive Wildlife Conservation Strategy.

C. Expected Results and Benefits

During the grant period, the Share with Wildlife program is expected to fund anywhere from 6-20 contracted projects annually, for work on a variety of wildlife that are lacking funding from other sources for obtaining information that may be important for

conservation. Data and knowledge gained through this grant will be used to determine which species or subspecies of wildlife in New Mexico are in greatest need of additional management and conservation efforts.

Share with Wildlife will help to meet the New Mexico Department of Game and Fish's objective to recover threatened and endangered wildlife. Share with Wildlife helps to achieve this by providing support for some "lower profile" species on the state list of threatened and endangered wildlife. The Department does maintain a very active program for monitoring of many of the state-listed species, and this program provides detailed and current information on the biology and ecology of these species. However, due to the limitations of resources within the Department's Game Protection Fund and General Fund appropriations, and available federal matching funds, not all of the state-listed species can be monitored at this level. For those species that would otherwise receive less attention, often because they are less imperiled or appear to be faced with fewer changes to their populations and habitats, Share with Wildlife provides a mechanism for obtaining some valuable information. In addition, Share with Wildlife helps to meet this objective by supporting studies of nongame wildlife that might otherwise be suspected by some parties as needing to be considered for inclusion within the state's list of threatened and endangered wildlife. In this way, Share with Wildlife provides one of the only Department sources of funds for nongame wildlife work.

D. Approach

Each year, Share with Wildlife obtains input from a variety of Department biologists to determine priority needs, which are then conveyed to potential contractors through a request for proposals (RFP). Project proposals are received in response to the RFP, and are selected by an interagency and interdisciplinary review panel. Selected proposals are implemented through Department contracts to the various proposers. Projects may be from 1-4 years in length, but must be reapplied for each year. Because funding decisions for individual projects are made on a year-by-year basis, it is impossible to list all of the projects that will be funded under this grant. However, the list below contains some of the projects that have been selected for funding.

E. Results

1. **Habitat and Diet of the Threatened New Mexico Meadow Jumping Mouse**: This project was deleted under an amendment in May 2005, due to the proposed contractor being unable to perform the required duties. No work or charges under this project were initiated.

2. **A Key to the New Mexico *Rodentia***. The contractor (Dr. Jennifer K. Frey) created and expanded the detailed key for the identification of selected New Mexico rodents. A final report containing a key for all New Mexico rodents was completed and submitted with the T-32-P-1 2008 annual performance report.

3. **Habitat Fragmentation and Shrub Encroachment on Avian Community Dynamics in Chihuahuan Desert Grasslands**. Contractor Dr. Martha Desmond of New Mexico State University submitted a completion report for this project in June 2006. This report was submitted with the 2007 annual performance report.

4. **Winter Ecology of New Mexico Bats**. This project was completed by Dr. Keith Geluso, and the completion report was included within the T-32 performance report submitted in 2006.

5. **Coexistence between Two Species of *Gambusia* (*G. nobilis* and *G. affinis*).** Contractor Daniella Swenton-Olson of the University of New Mexico provided a final report for all work under this project. This report was submitted with the 2008 annual performance report. Additional work on this project is continuing under a different grant segment (T-32-P-2).

6. **Data Synthesis of 10 Years of Data on the Greenthroat Darter and Bigscale Logperch in New Mexico**. This project was completed in January 2008, and a final project report was included within the 2008 annual performance report.

7. **Levels and Patterns of Morphological and Molecular Variation in the Zuni Bluehead Sucker**. Contractor Dr. Thomas Dowling of Arizona State University completed all work regarding morphological variation of Zuni bluehead sucker in 2006. A final project report on this work was provided with the May 2006 T-32 performance report.

8. **Prairie Rattlesnake Denning Project**. Contractor Dr. Andrew Holycross provided a completion report for this project in July 2005, which was included within the T-32 performance report submitted in 2006.

9. **Documentation of Current Presence/Absence and Activity Level of the Gunnison's Prairie Dog at Colonies Known from Historic and Past Records in New Mexico**. Contractor Bob Luce provided a completion report for this project in June 2005, which was included with the 2006 T-32 performance report.

10. **Gray Vireo Population Monitoring in Otero County.** Contractor Mike Stake of Hawks Aloft, Inc. provided a final report for this project in January 2006, which was included within the 2007 T-32 performance report.

11. **Remote Sensing of Prairie Dogs.** Natural Heritage New Mexico (at the University of New Mexico) completed a final report for this project in January 2006, which was included with the 2006 T-32 performance report.

12. **Food Habits of Chiricahua and Plains Leopard Frogs.** Contractor Bruce Christman provided a final report, along with a listing of all previously-collected leopard frog specimens examined, in June 2005 to complete this project. This project completion report was included within the 2006 T-32 performance report.

13. **Bats and Bridges.** Contractor Dr. Keith Geluso provided a completion report for this project in February 2006, which was included in the 2006 T-32 performance report.

14. **Re-establishment of Gunnison's Prairie Dogs to the Sevilleta National Wildlife Refuge.** Gunnison's prairie dogs were removed from the city of Santa Fe's railyard area, and 362 Gunnison's prairie dogs were relocated to Sevilleta National Wildlife Refuge from May-June 2005. Wildlife monitoring was

conducted during spring and summer of 2005 and 2006, and documented use of the prairie dog relocation area by raptors, and immediate presence of burrowing owls, followed by owls nesting in 2006 at the newly established prairie dog burrows. Prairie dog monitoring from 2006 indicates a 40-50% survival rate, and no significant differences in vegetative characteristics have yet been documented between the treatment (relocation) and control areas. A completion report for this project was included with the 2007 performance report.

15. **Dispersal and Radio Tracking of the Sand Dune Lizard.** This project was implemented through a contract to Lee A. Fitzgerald, Texas A & M University. Results of pitfall trapping and radio-telemetry monitoring were included in the final report, which was completed June 2007, and submitted with the 2008 annual performance report.

16. **Baseline Genetic Survey of the threatened Pecos Bluntnose Shiner (*Notropis simus pecosensis*).** This projected has been implemented through a contract with Dr. Thomas F. Turner and Dr. Megan J. Osborne of the University of New Mexico for this work. A 2008 report describing the results of genetic analyses, estimates of effective population size, levels of genetic variation, indications of gene flow among populations, and recommendations to assist bluntnose shiner recovery is attached (Appendix A). This represents a final report for this grant segment. Work on this project is continuing under T-32-P-2.

17. **Density and Habitat Use of Gray Vireo (*Vireo vicinior*) in northwestern New Mexico**. A contract was initiated with Ecosphere Environmental in December 2005 for this work. A final report was included with the 2008 annual performance report.

18. **Investigation of the status and distribution of the Blotched Water Snake (*Nerodia erythrogaster transversa*) and the Rio Grande Cooter (*Pseudemys gorzugi*).** This project is being implemented through a contract with Bruce Christman and Larry Kamees. A completion report was provided June 2007, and was submitted with the 2008 annual performance report.

19. **Life History of Southern Redbelly Dace in New Mexico.** This project is being implemented through a contract to Steven P. Platania. An annual progress report report was provided in 2007, and a final project report is attached (Appendix B).

20. **Recurrence, Seasonal Activity, Summary of Captures of the Spotted Bat and Allen's Big-eared Bat in New Mexico.** A contract was initiated with Dr. Keith Geluso in March 2006 for this work. Bats were surveyed via mist-netting and audible echolocation calls in May-August 2006. A total of 1751 bats representing 20 species were captured. Spotted bats were documented at 2 new sites, and Allen's big-eared bats were documented at 2 new sites, one of which represented a new county record. A report describing the complete results of this project was provided with the 2007 annual performance report for this grant.

21. **Development of an Immunological Approach to Determining Host Fishes of the Texas Hornshell (*Popenaias popeii*).** A contract for this work with Miami University (Ohio) was implemented in 2005. An annual report describing results

of laboratory and field research to determine host fishes of Texas hornshell glochidia was submitted in June 2007, and the final project report is attached (Appendix C).

22. **Linking People with New Mexico's Amphibians and Reptiles.** A contract for this work was initiated with Howard L. Snell and J. Tomas Giermakowski, Museum of Southwestern Biology, University of New Mexico. The contractors created a digital bibliography of 2,368 references related to New Mexico herpetology, and included full-text PDF documents of 380 of these references. The contractors also created predicted distribution maps for all native New Mexico reptiles and amphibians. A project completion report was provided with the 2007 annual performance report.

23. **Boreal Toad (*Bufo boreas*) habitat assessment and chytridomycosis investigation**. A contract for this work was initiated with Bruce Christman in February 2006. Sampling of potential boreal toad habitats for amphibians and chytrid fungus was performed May-July 2006. No boreal toads were found at Canjilon, Lagunitas, or Trout Lakes. Two positive chytrid fungus tests were received from samples taken at Canjilon Lakes, one from a northern leopard frog and one from a tiger salamander. A completion report for this project was provided with the 2006 annual performance report.

24. **Compilation of Literature on New Mexico's Native Fishes**. This project was deleted during 2007. No work on this project occurred in 2007 or 2008, and no expenses were incurred or charged. This project should now be deleted from the list.

25. **Grant Administration**. During the reporting period, the project coordinator administered 6 individual projects being conducted during the reporting period for this grant segment (T-32-P-1). Grant administration involved project monitoring and supervision, report review, dissemination of results, and selection of new projects.

26. **Colonial Waterbird Rookery Survey—Rio Grande Valley.** This project was implemented through a professional services contract to Eagle Environmental, Inc. Colonial waterbird nesting sites were observed from aerial surveys conducted twice during the breeding season of 2007, and from follow-up ground surveys. A final report for this project was submitted with the 2008 annual performance report.

27. **Native Fish and Desert Invertebrates in Desert Sinkholes.** This project was implemented through a professional services contract with Dr. Wiebke Boeing of New Mexico State University. A report describing results of fish sampling and water quality measurements at Bitter Lake National Wildlife Refuge was provided in June 2008, and is attached (Appendix D). The attached report represents the final deliverable under this grant segment. Work on this project is continuing under T-32-P-2.

28. **Morphology and Genetics of the New Mexico Jumping Mouse.** This project was implemented through a professional services contract to Frey Biological

Research. It includes use of novel techniques to morphologically identify different species and subspecies of jumping mouse. One of the tooth identification methods is currently undergoing genetic confirmation through work outside of the scope of this grant. Information regarding this single morphological technique is currently blocked out within the attached report, pending confirmation of the accuracy of the methodology. All other findings are considered final, and meet the requirements under this grant. A final project report is attached (Appendix E).

29. **Chiricahua Leopard Frog Distribution, Abundance, and Prevalence of Chrytrid Fungus.** This project was implemented through a professional services contract to Turner Endangered Species Fund. Population surveys and chytrid fungus assays were conducted for leopard frogs on and around the Ladder Ranch in Sierra County, New Mexico. A completion report for this project was included within the 2008 annual performance report.

30. **Distribution of New Mexico's Reptiles and Amphibians.** This project was implemented through a professional services contract issued to Dr. Howard L. Snell and J. Tom Giermakowski at the University of New Mexico. The contractors have worked to improve distribution maps created under a previous grant project through expert review, reptile and amphibian community surveys at selected locations, and additional analyses of distributions. A final report for this project is attached (Appendix F).

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Appendix A

Genetic Survey of the Threatened Pecos Bluntnose Shiner (*Notropis simus pecosensis*)

Megan Osborne and Thomas Turner

2008

Baseline Genetic Survey of the Threatened Pecos Bluntnose Shiner (*Notropis simus pecosensis*)

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Funding provided by New Mexico Department of Game and Fish
Share with Wildlife Program

Interim Report submitted to Chuck Hayes
New Mexico Department of Game and Fish
16 th June 2008

Executive Summary

Genetic monitoring is the analysis of genetic diversity in space and time, with emphasis on the temporal dimension to understand trends in genetic diversity in contemporary populations. In 2004, we began a genetic monitoring program of the federally threatened Pecos bluntnose shiner (*Notropis simus pecosensis*) and have continued to sample the population annually since. In addition, we have obtained samples and genetic data from 107 samples that were collected from three localities on the Pecos river in 2002 to serve as a refugial population. This data set, representing seven generations, provides unique information regarding trends in genetic diversity and genetic effective size that can be interpreted with reference to trends revealed by population monitoring. We report on the genetic status of Pecos bluntnose shiner sampled in 2007-2007 in addition to the refugial population representing the wild 2002 population. In 2008 we sampled 252 wild fish from eight localities on the Pecos river.

Major Findings for 2008:

(1) Genetic diversity, as measured by observed heterozygosity (microsatellites) and average gene diversity (mitochondrial DNA), was marginally lower in 2007 and 2008 than in 2006. Mitochondrial DNA allelic richness was higher in 2007 and 2008 than in 2006.

(2) Genetic diversity of the refugial population established in 2002 was comparable to the wild population.

(3) A significant portion of genetic variation was explained by differences among years rather than localities.

(4) Microsatellite genetic effective size estimates corrected for overlapping generation have increased from 58 in (2005 – 2006) to about 150 (2007-2008). Mitochondrial DNA reveals the same trend between 2006-2007 (N_e=310) and 2007-2008 (N_e=2648).

Introduction

The Pecos bluntnose shiner (*Notropis simus pecosensis*) is a subspecific form of the bluntnose shiner (Chernoff *et al*. 1982). The only other subspecies, the Rio Grande bluntnose shiner (*Notropis simus simus*), is presumed extinct with the last collection made in 1964. The Pecos bluntnose shiner was once relatively abundant in the Pecos river but has suffered significant declines and a reduction in its range following habitat changes caused by the installation of mainstream dams (Platania 1995; Hoagstrom 2003; Hoagstom et al. 2008). As such, the Pecos bluntnose shiner was listed as threatened by the State of New Mexico in 1976 and under the Endangered Species Act in 1987 (U.S. Department of the Interior, Federal Register 1987). The species is also listed as endangered in Texas (Campbell 1995) and by the Republic of Mexico. The Pecos bluntnose shiner is now restricted to a 333 kilometer reach of the Pecos River from downstream of Sumner Reservoir to above Brantley Reservoir, New Mexico (Brooks *et al*. 1991; Platania 1995).

Since the species was federally listed there have been several dramatic population fluctuations in the Pecos bluntnose shiner population. Pecos bluntnose shiner mean annual densities and percent species composition were low in 1992 due to streamflow intermittence that occurred during between 1989 and 1991 (USFWS, 1992; Robertson 1997). Densities increased gradually between and 1991 and 2002; a time of perennial streamflow and relatively high and stable mean discharge (Hoagstrom et al. 2008). The core Pecos bluntnose shiner population crashed between 2002 and 2005 reaching very low densities by 2005 (Hoagstrom et al. 2008; Davenport et al. 2007). Since 2005, the population has begun to rebound. Extreme population fluctuations, like those observed in recent times for the Pecos bluntnose shiner, are expected to cause losses of genetic diversity. Allelic diversity is more sensitive than heterozygosity to contemporary impacts and will be eroded more rapidly through the process of genetic drift.

In 2004, we began genetic monitoring of the Pecos bluntnose shiner population. We follow Swartz *et al*. (2007) and define genetic monitoring as the case where two or more temporally-spaced genetic samples are taken from the same population. Temporal sampling allows changes in measures of genetic diversity including allelic richness, heterozygosity and genetic effective size to be tracked in the population. This data can then be interpreted in light of population trends apparent from routine monitoring.

In summary, the project has five objectives:

1. Obtain genetic data from Pecos bluntnose shiner population sampled annually.

2. Develop genetic markers to track changes genetic diversity measures.

3. Use genetic data to estimate the genetic effective population size.

4. Calculate the population's allelic diversity and heterozygosity and compare this to data collected between 2002 and 2008 to establish temporal trends in these measures.

5. Provide data to resource managers to assist in recovery efforts for the Pecos bluntnose shiner.

We present data collected from the Pecos bluntnose shiner population in 2008 and compare this data to that collected in previous years.

Methods

Sampling

Fin clips of Pecos bluntnose shiners were collected from eight sites on the Pecos river throughout the species' current that extends from Sumner to Brantley Dam, New Mexico (Table 1) between December 2007 and March 2008. In addition, samples collected between 2004 and 2008 were screened for variation using four new microsatellite primers (see below).

Molecular Methods

Genomic DNA was isolated from air-dried fin clips using standard proteinase-K digestion andphenol-chloroform methods (Hillis *et al.* 1996). Genotype data from eleven microsatellite loci: *Lco1*, *Lco6*, *Lco3*, (Turner *et al.* 2004) *Ca6*, *Ca8* (Dimsoski *et al.* 2000), *Ppro*118 and *Ppro*126 (Bessert & Orti, 2003), Nme208, Nme174, Nme232, Nme93 (Gold et al. 2004) and a 318 base pair region of the mitochondrial gene ND4 were obtained for all individuals. Microsatellite loci were amplified using multiplex PCR (1x PCR buffer, 2mM $MgCl_2$, 125μM dNTPS, 0.4μM of each primer and 0.375 units of TAQ polymerase) with the following cycling conditions: one denaturation cycle of 93°C for 3 minutes, 30 cycles of 90°C for 20 sec, 49 °C for 20 sec (*Lco1* and *Ca6*; *Lco3* and *Lco6*; and *Ca8*) or 58°C (Nme174; Nme232 and Nme93) 60°C (*Ppro118* and *Ppro126*; Nme208) and 72°C for 30 sec followed by a final extension step of 72°C for 30 minutes. PCR product (1 μL) was mixed with 10 μL of formamide and 0.3 μL of size standard (ABI HD400 or ROX350) and denatured at 90°C for 5 minutes. All samples were run on an ABI3100 automated DNA sequencer and analyzed using GeneMapper software (Applied Biosystems).

Individuals were screened for variation in the mitochondrial ND4 gene using single stranded conformational polymorphisms (SSCP) analysis following the procedures outlined in Aló & Turner (2005) and Sunnucks *et al.* (2000). A proportion of individuals from each gel were

Table 1. Pecos bluntnose shiner collection localities, County, UTM coordinates and number of individuals sampled per site. Sample for 2002 are a mixed refugial population that were collected at three localities.

Collection Locality	County	UTM Coordinates	2002	2004	2005	2006	2007	2008
Willow Creek Confluence	Chaves	13S 0567061 3754818		20	4	17	45	5
Six-Mile Draw	Chaves	13S 0567090 3746757		26	1	37	24	46
Crockett Draw	Chaves	13S 0565213 3742022		24	0	0	66	56
Bosque Draw	Chaves	13S 0564139 3735299		0	0	11	41	58
Cortes Gasline	Chaves	13S 0563811 3737265		12	5	6	11	1
Gasline Crossing	Chaves	13S 0559701 3722493		13	0	15	26	12
Hwy 70 Bridge Crossing	Chaves	13S 0558355 3714591		24	0	23	19	49
Acme Gage	Chaves	13S 0557699 3711107		0	7	0	58	0
Bitterlake NWR- Scout Camp	Chaves	13S 0555831 3694992		3	0	7	0	27
Hwy 380 Bridge Crossing	Chaves	13S 0555831 3694992		3	2	6	37	0
Sallee Ranch	Chaves	13S 0559656 3686890		28	1	0	0	0
Dexter Bridge	Chaves	13S 0556250 3686910		0	0	6	4	0
Lake Arthur Falls	Chaves	13S 0563820 3650142		15	0	0	7	0
Brantley Inflow	Eddy	13S 0560837 3606540		0	0	2	0	0
TOTAL			107	168	22	138	338	252

sequenced using ABI Big Dye kit to confirm sequence designations. Unique haplotypes were sequenced in the forward and reverse direction. For haplotypes identified in single individuals, PCR amplification and sequencing were repeated to confirm haplotype designations. Representatives of several other Pecos river cyprinids (*Hybognathus placitus*, *Notropis girardi*, *N. jemezanus*, *N. stramineus*) were also sequenced to provide references that would allow mis-identified samples to be identified to species. DNA sequences were visualized using Sequencher Version 4.2 and aligned manually.

Data Analysis

Genetic Diversity

Microsatellite allele frequencies and descriptive statistics, including allelic richness (A_R), average inbreeding co-efficients (F_{IS}) and Nei's (1987) unbiased gene diversity (H_E), were obtained using FSTAT Version 2.9.3.1 (Goudet 1995). Allelic richness was calculated using the methods described Petit *et al.* (1998). This method allows the number of alleles to be compared among populations independently of sample size (Leberg 2002) and is based on the smallest number of individuals typed for any locus. FSTAT was also used to conduct global tests of linkage disequilibrium among all pairs of loci and to test for departures from Hardy-Weinberg expectations (HWE). The computer program MICROCHECKER 2.2.1 (van Oosterhout *et al.* 2004) was used to investigate the possible cause of deviations from HWE, including mis-scoring due to stuttering, presence of null alleles and large allele dropout. For mitochondrial DNA, data estimates of unbiased gene diversity (*h*) and nucleotide diversity (π) were obtained using ARLEQUIN Version 3.0 (Excoffier *et al*. 2005). FSTAT was used to obtain measures of allelic richness for mtDNA. Percent sequence divergence was estimated using Kimura-two parameter method implemented in PAUP. The computer program TCS (Clement *et al.* 2000) was used to construct a statistical parsimony network among mitochondrial DNA haplotypes using the method of Templeton *et al*. (1992).

Spatial Structure

We tested for spatial genetic structure by calculating Weir and Cockerham's (1984) *F*-statistics, as implemented in the computer program ARLEQUIN (Schneider *et al.* 2000). Hierarchical analysis of variance (AMOVA) (Excoffier et al.1992) partitions the total variance into covariance components due to differences among groups of populations (F_{CT}), between populations within groups (F_{SC}) and among all populations (irrespective of groups) (F_{ST}). F_{ST} is the standardized variance in allele frequencies between populations and is the most commonly used measure of genetic distance between populations. Φ-statistics were calculated from mt-DNA data (Excoffier et al. 1992). Φ-statistics are equivalent to F-statistics; however, they incorporate allele frequencies and evolutionary distances between haplotypes. Significance of results was tested using a bootstrapping procedure. For Pecos bluntnose shiner, we tested whether a significant

proportion of genetic variance could be explained by differences among years (2002, 2004-2008) and whether a significant proportion of variance could be explained by collection locality (only for 2007 and 2008 samples).

Contemporary Genetic Effective Size

The temporal method (Pollack 1983; Waples 1989; Wang & Whitlock 2003) was used to estimate the variance effective population size from microsatellite and mt-DNA data collected from samples representing 2002, 2004, 2005, 2006, 2007 and 2008. This method assesses the change in allele frequencies across generations. Estimates of N_{eV} (referred to as contemporary N_e) accurately follow current variations in effective population size and are not greatly affected by historical events such as population bottlenecks (Avise 1994). For estimates based on Mt-DNA data, contemporary N_e is only estimated for the female portion of the population, as mtDNA is maternally inherited. Moments-based estimates of N_e and 95% confidence intervals were estimated, using the method of Waples (1989), for both Mt-DNA and microsatellites using the program NeEstimator (Peel *et al.* 2004).

Estimates of N_e were corrected for effects of overlapping generations using a model described in Jorde & Ryman (1995; 1996). The model requires a basic life table with information on age-specific survival rates (l_i) and birth rates (b_i). Survival rate (S) was estimated from age-structured catch data for *N. simus pecosensis* (Hoagstrom et al. 2008; U.S. FWS unpublished data). Age-specific survivorship, l_i, is equal to S^{i-1} where $l_0 = 1$. Average reproductive contribution was estimated as modal body length at age i raised to the third power (Charnov et al. 1999). This value was multiplied by l_i to obtain the proportional contribution of each age class to the offspring pool (p_i) and then p_i values were summed over k age classes. Birth rates at each age class were divided by $\sum_{i=1}^{k} p_i$ to produce a standardized birth rate (b_i), corrected to reflect a non-growing population with stable age structure, i.e., $\sum_{i=1}^{k} l_i b_i = 1 = \mathrm{R}_0$. We assumed that males and females had identical mortality and reproduction schedules. Resulting life tables were used to calculate a correction factor (C) for overlapping generations by using 100 iterations of Equation 5 in Jorde & Ryman (1996). The value C accounts for variance due to mortality as a cohort passes from one year class to the next and for genetic covariance among cohorts (because individuals from multiple age classes are the parents of a given cohort). The mean generation length in years (G) was calculated using Equation 10 in Jorde & Ryman (1996). The correction can be applied to effective size estimates for adjacent cohorts obtained from both mitochondrial and microsatellite data.

Results and Discussion

Genetic Diversity- Microsatellites

In 2008 we collected 252 Pecos bluntnose shiner from eight localities on the Pecos river, New Mexico. Genetic variation was assessed using eleven microsatellite loci. These markers were moderately to highly polymorphic. Lco1 was the most polymorphic marker with 46 alleles detected across all samples (Appendix 1). Allelic richness was slightly lower in 2007 and 2008 than in 2006 (Table 2) (2005 sample was not included in calculations of A_R because of the small sample size). The lowest allelic richness was seen in 2002 but this sample is the refugial population that was originally derived from only three collection localities. Nei's (1987) unbiased gene diversity (H_E) and observed heterozygosity (H_O) also declined slightly during the same period. There were 44 deviations (from a total of 66 tests) from Hardy-Weinberg equilibrium after Bonferroni correction for multiple comparisons. These were explained by heterozygote deficiency and are reflected in the values of the average inbreeding co-efficients (F_{IS} = 0.192-0.241). MICROCHECKER showed that there was no evidence of large allele dropout or of scoring errors. Null alleles were the most likely cause of homozygote excess. There were seven instances of linkage disequilibrium that were significant after Bonferroni correction.

Genetic Diversity- Mitochondrial DNA

A 318 base pair fragment of ND4 was sequenced. Across all years, 49 unique haplotypes were identified. In both 2007 and 2008 29 haplotypes were observed. Four haplotypes were identified in the 2002 sample that have not been seen subsequently. ND4 haplyotypes were separated by one to eight base pairs (0.315 to 2.25 % sequence divergence, Kimura-two parameter distance). The majority of substitutions were transitions, but several transversions were also observed. Two haplotypes (B and A) were present at moderate to high frequencies (A- 12% - 44% and B- 38.9% and 69.2%). The remainder of the haploypes were considered rare, i.e. present in fewer than 5.0% of individuals (Table 3). In 2008 four new haplotypes were identified. Haplotype diversities in 2007 and 2008 were marginally lower than in 2006.

The statistical phylogenetic network was star-like and revealed that all sequences were closely related to the most frequently encountered and presumably ancestral haplotypes A and B (Figure 1). Past rapid population growth following a bottleneck leaves a characteristic signature in which DNA sequences form the star-like pattern and there is an excess of rare sequence variants that are closely related to the most common allele (ancestral).

Population comparisons- Microsatellites

Pairwise F-statistics were calculated to determine whether there were significant differences in allele frequencies among samples collected between 2002 and 2008 (Table 4). There were

Table 2. Summary of diversity statistics for microsatellite and Mt-DNA data. Abbreviations are N- number of individuals, A_R- allelic richness, H_E- Nei's unbiased gene diversity, H_O - observed heterozygosity, *h*- gene diversity.

	2002	2004	2005	2006	2007	2008
Microsatellites						
N	107	172	22	139	338	252
H_E	0.840	0.849	0.849	0.859	0.843	0.843
H_O	0.670	0.645	0.657	0.694	0.679	0.664
A_R	20.699	21.313	-	22.557	21.753	21.312
F_{IS}	0.204	0.241	0.231	0.192	0.195	0.212
Mt-ND4						
N	105	168	18	132	332	248
Number of Haplotypes	16	20	4	20	29	29
h	0.544	0.614	0.673	0.658	0.509	0.554
A_R	16.000	18.596	-	19.540	21.278	23.855
Nucleotide Diversity	0.003	0.003	0.003	0.004	0.002	0.003

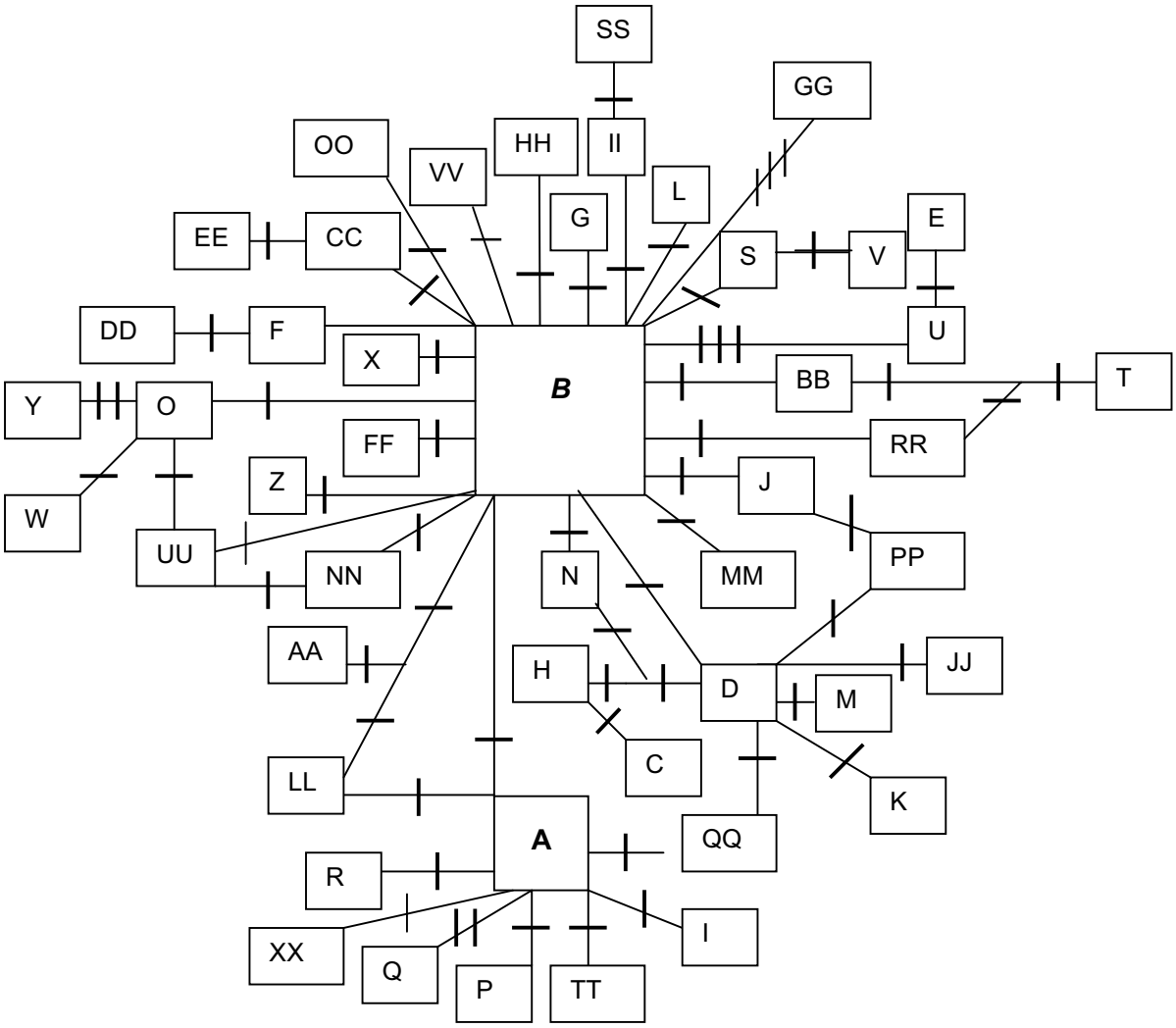

Figure 1. Statistical phylogenetic network of mitochondrial ND4 sequences for Pecos bluntnose shiner. Bars indicate a nucleotide change.

Table 3. ND4 haplotype frequencies by year.

	2002	2004	2005	2006	2007	2008
A	0.162	0.218	0.444	0.250	0.120	0.117
B	0.657	0.582	0.389	0.530	0.690	0.657
C	0	0.006	0	0	0.003	0.004
D	0.010	0.006	0	0.008	0.006	0
E	0	0.012	0	0	0	0
F	0.019	0.018	0	0.008	0.009	0.012
G	0	0.006	0	0	0.015	0.004
H	0	0.012	0	0.008	0.003	0.004
I	0	0.018	0	0	0.006	0.008
J	0	0.006	0	0.015	0.012	0.008
K	0	0.006	0	0.008	0.003	0
L	0	0.018	0	0	0.003	0.016
M	0.019	0.018	0	0.030	0.027	0.024
N	0.010	0.029	0.111	0.008	0.024	0.020
O	0.029	0.012	0.056	0.015	0.006	0.004
P	0	0.006	0	0	0.003	0
Q	0	0.012	0	0	0	0.004
R	0	0.006	0	0.008	0	0
S	0	0.006	0	0.008	0.006	0.004
T	0.010	0.006	0	0.008	0	0.008
U	0.010	0	0	0.008	0.003	0.016
V	0.010	0	0	0.023	0	0
W	0	0	0	0.015	0	0.004
Y	0	0	0	0.015	0	0
X	0	0	0	0.023	0	0
Z	0	0	0	0.008	0	0
AA	0	0	0	0.008	0	0.008
BB	0.010	0	0	0	0.006	0.012
CC	0	0	0	0	0.009	0.012
DD	0	0	0	0	0.003	0
EE	0.010	0	0	0	0	0
FF	0.019	0	0	0	0	0.008
GG	0	0	0	0	0	0.004
HH	0.010	0	0	0	0	0
II	0.010	0	0	0	0	0
JJ	0	0	0	0	0.006	0
KK	0	0	0	0	0.003	0.004
LL	0.010	0	0	0	0	0
MM	0	0	0	0	0	0.008
NN	0	0	0	0	0.003	0.004
OO	0	0	0	0	0.003	0
PP	0	0	0	0	0.003	0.012
QQ	0	0	0	0	0.003	0
RR	0	0	0	0	0.009	0
SS	0	0	0	0	0.006	0
TT	0	0	0	0	0.006	0
UU	0	0	0	0	0	0.004
VV	0	0	0	0	0	0.004
XX	0	0	0	0	0	0.004

Table 4. Pairwise F_{STs} calculated from microsatellite allele frequencies among samples collected between 2002 and 2008 (below diagonal). Associated P-values are given above the diagonal. Significant values are shaded.

	2002	2004	2005	2006	2007	2008
2002	*	0.0000	0.0000	0.0000	0.0000	0.0000
2004	0.0162	*	0.0000	0.0068	0.5918	0.9951
2005	0.0414	0.0191		0.0000	0.0000	0.0000
2006	0.0145	0.0023	0.0212	*	0.0088	0.5088
2007	0.0138	0.0003	0.0231	0.0015	*	0.0000
2008	0.0200	-0.0006	0.0182	0.0005	0.0022	*

Table 5. Pairwise values of F_{ST} (below diagonal) calculated from microsatellite data among 2007 and 2008 samples from collection localities on the Pecos River. Associated P-values are given above the diagonal.

	Acme 2007	Bosque 2007	Cortez 2007	Crocket 2007	Gasline 2007	Hwy 70 2007	Hwy 380 2007	Six-mile 2007	Willow 2007	Bosque 2008	Crocket 2008	Gasline 2008	Hwy 70 2008	Bitterlake 2008	Six-mile 2008
Acme 2007	*	0.001	0.061	0.000	0.688	0.005	0.000	0.948	0.000	0.003	0.000	0.122	0.000	0.027	0.000
Bosque 2007	0.009	*	0.064	0.306	0.687	0.067	0.000	0.087	0.022	0.002	0.414	0.218	0.013	0.486	0.006
Cortez 2007	0.014	0.012	*	0.029	0.800	0.002	0.000	0.719	0.134	0.057	0.002	0.019	0.013	0.113	0.002
Crocket 2007	0.008	0.002	0.014	*	0.993	0.146	0.000	0.563	0.142	0.045	0.060	0.286	0.012	0.052	0.032
Gasline 2007	0.001	0.001	-0.001	-0.004	*	0.216	0.007	0.925	0.659	0.918	0.698	0.242	0.995	0.956	0.901
Hwy 70 2007	0.013	0.008	0.028	0.006	0.006	*	0.000	0.032	0.016	0.000	0.010	0.226	0.010	0.030	0.001
Hwy 380 2007	0.017	0.016	0.024	0.013	0.011	0.021	*	0.000	0.001	0.000	0.000	0.002	0.000	0.000	0.000
Six-mile 2007	-0.001	0.006	-0.001	0.001	-0.004	0.011	0.015	*	0.466	0.922	0.332	0.008	0.039	0.661	0.006
Willow 2007	0.008	0.006	0.009	0.003	0.001	0.010	0.009	0.002	0.000	0.039	0.065	0.017	0.002	0.023	0.000
Bosque 2008	0.007	0.007	0.013	0.004	0.000	0.015	0.013	-0.001	0.005	*	0.463	0.169	0.053	0.029	0.022
Crocket 2008	0.011	0.002	0.019	0.004	0.001	0.011	0.014	0.003	0.004	0.002	0.000	0.250	0.187	0.063	0.045
Gasline 2008	0.010	0.007	0.024	0.007	0.008	0.010	0.023	0.020	0.014	0.009	0.008	*	0.543	0.514	0.252
Hwy 70 2008	0.009	0.006	0.018	0.006	-0.003	0.012	0.021	0.008	0.008	0.005	0.003	0.005	0.000	0.526	0.221
Bitterlake 2008	0.008	0.002	0.014	0.006	-0.002	0.013	0.028	0.002	0.008	0.007	0.007	0.006	0.003	*	0.285
Six-mile 2008	0.012	0.007	0.021	0.005	-0.001	0.015	0.022	0.011	0.011	0.005	0.005	0.008	0.003	0.004	*

eleven significant differences from 15 total comparisons after Bonferroni correction. The 2002 sample differed significantly from all subsequent samples, as did the 2005 sample. In 2005 the sample size was very small. Pairwise F-statistics were calculated among samples collected at different localities in 2007 and 2008. Significant values of F_{ST} were observed in 18 of a total of 105 comparisons after Bonferroni correction (Rice 1989) was applied. Eleven of these involved the collection made at Hwy 380 in 2007 (Table 5). For AMOVA analysis, samples were grouped by populations across years. F_{SC} was significant (F_{SC}=0.0085, P=0.001), indicating that some variation could be attributed to differences within localities between years. Significant variation could not be ascribed to differences among localities across years (F_{CT}=-0.00046, P=0.3431).

Population comparisons- Mitochondrial DNA

Pairwise Φ_{ST}'s were calculated to determine if there was significant divergence among samples collected in different years. From fifteen pairwise comparisons five were significant after Bonferroni correction for multiple comparisons. The other significant comparisons, were between both 2007 and 2004-2006 collections and between the 2008 and 2004, and 2008 and 2006 collections (Table 6). For AMOVA analysis, samples were grouped by populations across years. F_{SC} was significant (F_{SC}=0.0033, P<0.0001), indicating that some variation could be attributed to differences within localities between years. The large difference in sample sizes between some localities between years probably explains this significant result. Significant variation could not be ascribed to differences among localities across years (F_{CT}=-0.0094, P=0.7321).

Contemporary Effective Population size- Microsatellites

Using microsatellite data, fifteen temporal comparisons were used to estimate the contemporary effective population size. Contemporary effective size estimates ranged from a low of 57.3 (95% confidence intervals 39.4 to 85.6) to a high of 467.2 for the 2004 to 2008 comparison (95% CI 330.8 - 687.9) (Table 7). To account for overlapping generations in Pecos bluntnose shiner, the equations of Jorde and Ryman (1995) and life table data were used to estimate a correction factor (C) and generation time (G). The model accounts for the effects of genetic drift as a cohort passes from one age class to the next and for the contributions of parents in multiple age clases to progeny in a non-growing population. Estimates of N_e obtained using NeEstimator were multipled by the ratio C/G. For Pecos bluntnose shiner, the generation time was estimated to be 1.36 and a correction factor of 2.145 was obtained, hence C/G was 1.5772. Corrected N_e estimates from adjacent cohorts reveal an increase in effective size from 70.82 (2004-2005) to 151.57 (2007-2008).

Contemporary Effective Population size- Mt-DNA

The effective size estimate (N_{ef}), based on mitochondrial DNA data for 2007 and 2008 was

Table 6. Pairwise F_{STs} calculated from Mt-DNA haplotype frequencies among samples collected between 2002 and 2008 (below diagonal). Associated P-values are given above the diagonal. Significant values are shaded.

	2002	**2004**	**2005**	**2006**	**2007**	**2008**
2002	*	0.1133	0.0088	0.1572	0.4014	0.7578
2004	0.0051	*	0.2090	0.4971	0.0000	0.0029
2005	0.0724	0.0132	*	0.1699	0.0010	0.0039
2006	0.0035	-0.0009	0.0143	*	0.0010	0.0029
2007	-0.0002	0.0146	0.0967	0.0162	*	0.7393
2008	-0.0022	0.0130	0.0810	0.0141	-0.0012	*

Table 7. Temporal estimates of N_e for microsatellite and mitochondrial DNA data (N_{ef}) and associated 95% confidence limits. The number of generations separating the sampling periods are given.

Generations	Temporal Comparison	N_e	-95%	95%	N_{ef}	-95%	95%
1	2004-2005	70.8	26.5	96.5	infinity	89.0	Infinity
1	2005-2006	58.8	23.2	70.3	infinity	55.5	Infinity
1	2006-2007	152.2	70	137	310.4	99.68	Infinity
1	2007-2008	151.6	73.22	12702	2648	279.16	Infinity
2	2002-2004	81.1	61.6	107.3	637.3	62.3	Infinity
2	2004-2006	286.5	182.7	513.1	413.9	61.1	Infinity
2	2005-2007	90.2	55.1	178.7	infinity	82.1	Infinity
2	2006-2008	152.6	55.1	211.4	193.9	59.1	Infinity
3	2002-2005	57.3	39.7	86.4	infinity	86.3	Infinity
3	2004-2007	381.2	271.7	556.4	785.1	149.9	infinity
3	2005-2008	114.3	71.9	209.4	infinity	101.6	Infinity
4	2002-2006	166.2	124.8	223.8	1481.9	110.8	Infinity
4	2004-2008	467.2	330.8	687.9	776.3	141.4	Infinity
5	2002-2007	381.2	271.7	556.4	14302.2	275.0	Infinity
6	2002-2008	223.9	173.4	289.1	infinity	361.7	infinity

2648 (Table 7). This is a substantial increase from the estimate based on the preceding cohort (2006-2007 N_{ef} = 310.4). The harmonic mean across temporal comparisons (excluding estimates of infinity) was 560.7.

Conclusions

The low densities of Pecos bluntnose shiner population that occurred between 2002 and 2005 were accompanied by a decrease in the genetic effective size in 2005 and 2006. Recent population monitoring data for the Pecos bluntnose shiner indicates that the population is gradually rebounding (USFWS unpublished data) and this is reflected in the large increases in the genetic effective population size. Population fluctuations are predicted to erode allelic diversity, however high levels of genetic variation particularly at the mtDNA ND4 gene persist in Pecos bluntnose shiner. To date we have identified 49 distinct mitochondrial DNA haplotypes in around 1000 individuals. This can be compared to Rio Grande silvery minnow, in which we have detected only 14 haplotypes in the same fragment of DNA in roughly 5000 individuals screened over the past decade. The genetic effective size of the remaining Rio Grande silvery minnow population also appears to hover around 100, even in years when there are huge increases in density. In Rio Grande silvery minnow early life-history and river fragmentation and drying of substantial regions act to erode genetic variation and to depress the genetic effective size of the population (Turner et al. 2006). In the Pecos bluntnose shiner, high levels of diversity may persist because the river reach where the species persists is not fragmented, allowing at least some individuals to move to refugia when conditions are adverse. These individuals are then able to recolonize the formerly desiccated regions. However Hoagstrom *et al*. (2008) found that fluvial species like Pecos bluntnose shiner do poorly during river intermittence, possibly due to declining water quality (Ostrand & Marks 2000; Ostrand & Wilde 2004) or poor reproductive success (Durham and Wilde 2006).

The genetic effective size, estimated from eleven microsatellite DNA loci, shows the same trend as mitochondrial DNA data with increasing values from 2004-2005 to 2006-2008. However, effective size estimates are considerably lower for microsatellite DNA. These estimates are all below the theoretical benchmarks set out in the conservation genetics literature that are required to maintain both neutral and adaptive genetic variation. It has been proposed that N_e should exceed 500 to preserve variation at selectively neutral loci (Frankham 1995) while N_e should exceed 5000 if a species is to maintain sufficient variation for quantitative traits such as fecundity, spawning time and body size (Lande 1995).

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Appendix 1. Summary statistics for microsatellites tabulated by locus and year. Abbreviations are N- number of individuals, total number of alleles, A_R- allelic richness, H_E- Nei's unbiased gene diversity, H_O - observed heterozygosity.

Year	Locus	N	Total Alleles	A_R (n=18)	H_E	H_O	F_{IS}
2002	118	107	32	18.335	0.949	0.738	0.223
	126	107	9	4.544	0.289	0.262	0.091
	Lco1	103	34	19.667	0.957	0.709	0.260
	Ca6	107	9	7.824	0.846	0.925	-0.094
	Lco3	104	13	8.511	0.798	0.644	0.193
	Lco6	95	24	12.521	0.861	0.600	0.304
	Ca8	98	26	17.648	0.949	0.582	0.388
	Nme232	103	18	12.846	0.899	0.893	0.007
	Nme93	105	24	15.771	0.939	0.781	0.169
	Nme208	107	24	12.973	0.864	0.664	0.234
	Nme174	103	21	13.471	0.892	0.573	0.359
2004	118	172	30	17.238	0.943	0.802	0.150
	126	172	12	5.009	0.375	0.326	0.123
	Lco1	169	39	20.413	0.959	0.769	0.199
	Ca6	172	10	7.930	0.855	0.814	0.048
	Lco3	168	13	8.436	0.726	0.714	0.016
	Lco6	169	25	13.358	0.890	0.550	0.382
	Ca8	158	29	17.537	0.948	0.475	0.500
	Nme232	146	20	12.546	0.879	0.808	0.081
	Nme93	148	24	14.850	0.925	0.750	0.190
	Nme208	172	32	15.425	0.917	0.576	0.373
	Nme174	163	23	14.323	0.916	0.509	0.445
2005	118	21	17	16.318	0.950	0.810	0.151
	126	22	10	9.027	0.661	0.636	0.078
	Lco1	20	20	18.680	0.960	0.727	0.247
	Ca6	22	9	8.599	0.769	0.750	0.026
	Lco3	21	9	8.533	0.714	0.619	0.136
	Lco6	21	13	12.120	0.870	0.333	0.623
	Ca8	18	15	15.000	0.895	0.500	0.449
	Nme232	18	14	14.000	0.895	0.833	0.071
	Nme93	21	16	14.960	0.927	0.810	0.129
	Nme208	21	11	10.876	0.854	0.524	0.392
	Nme174	22	12	10.998	0.848	0.682	0.199
2006	118	135	32	16.694	0.932	0.711	0.237
	126	138	12	5.708	0.425	0.391	0.105
	Lco1	132	38	20.438	0.961	0.788	0.181
	Ca6	136	13	8.170	0.851	0.897	-0.055
	Lco3	137	12	8.480	0.743	0.708	0.048
	Lco6	132	26	14.657	0.912	0.636	0.303
	Ca8	132	31	19.138	0.955	0.568	0.406
	Nme232	108	22	13.362	0.907	0.880	0.031
	Nme93	114	25	15.436	0.936	0.754	0.194
	Nme208	133	30	15.878	0.927	0.617	0.336
	Nme174	122	22	13.757	0.903	0.689	0.239

Year	Locus	N	Total Alleles	A_R (n=18)	H_E	H_O	F_{IS}
2007	118	331	35	18.934	0.954	0.767	0.196
	126	334	13	5.173	0.347	0.320	0.080
	Lco1	301	39	20.325	0.961	0.761	0.208
	Ca6	312	13	8.236	0.841	0.840	0.001
	Lco3	314	12	8.040	0.693	0.654	0.056
	Lco6	291	30	13.999	0.892	0.577	0.353
	Ca8	314	31	18.620	0.955	0.557	0.417
	Nme232	311	25	12.893	0.898	0.875	0.026
	Nme93	326	29	14.840	0.929	0.779	0.162
	Nme208	335	33	15.049	0.916	0.737	0.195
	Nme174	320	25	13.800	0.893	0.606	0.321
2008	118	253	34	17.841	0.944	0.787	0.167
	126	252	8	4.233	0.319	0.298	0.040
	Lco1	248	39	20.457	0.961	0.722	0.249
	Ca6	251	12	7.779	0.844	0.869	-0.030
	Lco3	249	11	7.607	0.682	0.671	0.017
	Lco6	251	30	13.585	0.887	0.542	0.390
	Ca8	243	28	18.429	0.954	0.547	0.427
	Nme232	253	25	13.190	0.899	0.830	0.076
	Nme93	252	25	14.691	0.928	0.762	0.179
	Nme208	252	30	15.797	0.928	0.667	0.278
	Nme174	249	24	15.159	0.926	0.614	0.337

Appendix B

Life History of Southern Redbelly Dace, *Phoxinus erythrogaster*, an Imperiled New Mexico Cyprinid

Steven P. Platania, Lee E. Renfro, and Robert K. Dudley

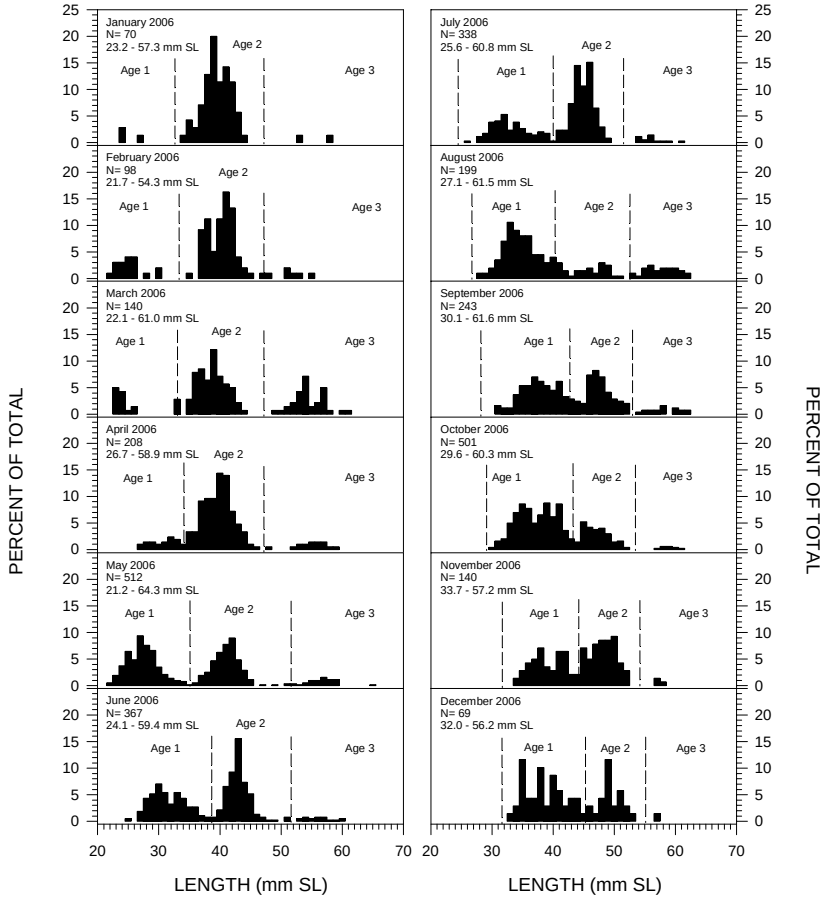
2008

Life history of Southern red bellied dace, Phoxinus erythrogaster, an Imperiled New Mexico Cyprinid

2006 - 2007 Final Report

A New Mexico Game and Fish
Share with Wildlife Funded Project

RFP: 50-516-07-04406



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15 July 2008

Project Title:

Life history of southern redbelly dace, *Phoxinus erythrogaster,* an imperiled New Mexico cyprinid

RFP: 50-516-07-04406

submitted to:

Share with Wildlife Coordinator
New Mexico Department of Game and Fish
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15 July 2008

INTRODUCTION

Southern redbelly dace, *Phoxinus erythrogaster*, is unique among native fish in New Mexico because of its extremely limited relictual distribution. Although this species has been protected in New Mexico as an endangered species (19 NMAC 33.1) since 1975, it is common and widespread throughout much of the rest of its range in the Mississippi River basin. The New Mexico population of southern redbelly dace is confined within the headwaters and tributaries of the Mora River, especially Coyote Creek. Records at the Museum of Southwestern Biology-Division of Fishes (University of New Mexico) also indicate that a small population may persist in Jarosa Creek (a tributary of Coyote Creek). The New Mexico population of southern redbelly dace is thought to be a relict from the Pleistocene (Sublette et al., 1990) when cooler ambient temperatures allowed a more widespread distribution of dace throughout lower elevation streams in New Mexico. Elevated ambient and water temperatures, in the Post-Pleistocene, likely restricted southern redbelly dace to limited areas with suitable habitat conditions and resulted in the loss of dace from lower elevations. Other relictual populations are known from Colorado (Sublette et al., 1990) and portions of Mississippi and Tennessee (Starnes and Starnes, 1980). In general, populations of southern redbelly dace are disjunct and often widely separated (Propst, 1999) likely as a result of Post-Pleistocene warming.

The most commonly occupied habitats of southern redbelly dace appear to be spring and small stream areas with cold clear water and abundant aquatic vegetation (Becker, 1983). These habitats also provide the necessary cover (e.g., undercut banks, fallen terrestrial vegetation, larger substrata) and spawning habitat (moderate water velocity with clean gravel) utilized by southern redbelly dace (Ross, 2001). In New Mexico, southern redbelly dace are known to be relatively common in deep pools associated with undercut banks.

The spawning season of southern redbelly dace ranges from May to July in higher latitude states, such as Wisconsin (Becker, 1983), but begins in April and ends in July in Tennessee (Etnier and Starnes, 1993). The timing and duration of the spawning season in New Mexico is likely intermediate between Wisconsin and Tennessee because of the high elevation (ca. 2,500 m) of populations in New Mexico. Males become intensely colorful during spawning season with golden-yellow fins and banded sides rivaled only by brilliant red of the lower pectoral and dorsal fins, chin, lower head, and abdomen (Becker, 1983). Spawning occurs as numerous males (Greenfield, 1973) compete to fertilize the eggs expelled by the ripe female (Smith, 1908; Etnier and Starnes, 1993). Total number of mature eggs at any time during spawning season is estimated to be about 300 (Settles and Hoyt, 1978). Fertilized eggs are demersal and quickly settle into the gravel where they develop (Smith, 1908).

The conservation status of southern redbelly dace in currently occupied habitats in New Mexico is largely unknown. However, the highly restricted range of this species should be cause for some concern. The limited distribution and abundance of southern redbelly dace increases the likelihood of extirpation in a relatively short time period if local environmental conditions degrade. The relict population of southern redbelly dace in New Mexico is thought to be diminishing (Sublette et al., 1990), but it appears to be faring better in spring and spring-run habitats compared with riverine habitats (J.S. Pittenger, pers. comm.). Southern redbelly dace has been reported to hybridize with central stoneroller, *Campostoma anomalum,* (Cross and Minckley, 1960) and creek chub, *Semotilus atromaculatus*, (Trautman, 1957) and could be an issue in portions of their New Mexico range where these species frequently co-occur. Nonnative species likely to pose a predatory threat to southern redbelly dace include brown trout, *Salmo trutta,* and rainbow trout, *Oncorhynchus mykiss*, as they occupy similar elevations and habitats. These two trout species have been present in the same vicinity as southern redbelly dace in previous sampling efforts (unpubl. data) and could pose the most immediate threat to the continued persistence of dace. Other potential threats include groundwater pumping, which is thought to have led to declines of southern redbelly dace in Alabama (Boschung and Mayden, 2004), and sedimentation of spring and creek habitats.

Thorough research on the life history of southern redbelly dace is necessary for management of existing populations and recovery of the species in New Mexico. Little information on southern redbelly dace life history traits are available and to date no such comprehensive study has been undertaken in New Mexico. Some data are available on the food habits of southern redbelly dace

from other regions where they have been found to feed on diatoms and other microscopic aquatic plant material (Forbes, 1883; Philips, 1969), and may also feed on small insects (i.e., chironomids; McNeely, 1987). However, the relative composition of the diet of southern redbelly dace could be quite different from streams in Minnesota (Philips, 1969) where the most complete data is available. The growth, age-class structure, and life span of southern redbelly dace are also largely unknown for the unique New Mexico population.

Project Objectives and Needs

This study proposes to describe life history traits of southern redbelly dace in New Mexico. Life history information on the relictual population of southern redbelly dace in New Mexico will provide insight to factors that are necessary to sustain this population in perpetuity. A better understanding of the autecology of this imperiled species will also aid in the development and implementation of effective conservation strategies to protect this species from biotic and abiotic threats to its continued persistence. This information will help achieve the greater mission and goals of wildlife conservation which is the legislative mandate of the New Mexico Department of Game and Fish.

Materials and Methods

Personnel.—Field and Laboratory work will be completed solely by American Southwest Ichthyological Research, including Steven P. Platania, Robert K. Dudley, and Michael A. Farrington (see Section IV [E]: Specifications [Offeror Experience] for details).

Field.— A total of at least 24 monthly fish collections will be made in Coyote Creek, a tributary of the Mora River, at NM State Hwy 434, just downstream of Black Lakes, Black Lake, New Mexico (UTM Zone 13: 4014360N, 477713E) in 2006 and 2007 (Figure 1). This site was chosen because it supports an abundant population of southern redbelly dace (based on 2000 - 2001 sampling efforts). Adult and juvenile fishes will be collected with a 3.0 m x 1.8 m 4.8-mm mesh seine while larval fish will be taken with a 1.0 m x 1.0 m 0.8-mm mesh seine. Sampling for larval fish will begin annually in March and continue through August to ensure that any early or late spawning efforts are detected.

Sampling efforts will be directed towards collection of a representative sample of the ichthyofaunal community (as opposed to being focused exclusively on the capture of southern redbelly dace), in addition to ensuring that a sufficient number of southern redbelly dace will be taken to complete a life-history study. All available aquatic mesohabitats will be sampled independent of their relative abundance or any habitat preference exhibited by southern redbelly dace. Retained adult and juvenile fish will be fixed in the field in a solution of 10% formalin and subsequently returned to the laboratory where they will be processed prior to being transferred to 70% ethanol. Conversely, larval fish will be preserved and maintained in 5% buffered formalin. Field notes will be recorded for every collection and will include sampling effort, water depth and temperature, and information on changes in habitat availability. All retained specimens will be deposited in the Division of Fishes of the Museum of Southwestern Biology at University of New Mexico.

Laboratory.—Adult and juvenile southern redbelly dace will be measured to the nearest 0.1 mm standard length (SL) with electronic calipers while larval fish lengths will be measured (0.1 mm SL) under a stereomicroscope equipped with an ocular micrometer. Length-frequency histograms will be prepared for each sample date and will include all southern redbelly dace collected at that site on that date. Age of fish will be derived from histogram plots of SL and separation of age-classes verified, as necessary and if possible through scale analysis. These data will also be analyzed to determine growth-rates and survivorship of southern redbelly dace. Mean monthly size (mm SL) will be calculated by age class (independent of gender) and used to generate growth curves. Annual age class survivorship will be determined for each age class and adjusted for sampling effort.

Prior to determination of SL, a subsample of 20 southern redbelly dace (specimens $\geq$25 mm SL) was obtained from each sample and assigned a unique number. The subsample will be used to determine sample gender ratios, reproductive status, length-mass relationships, and dietary

composition of southern redbelly dace. The 20 individuals per sample will be measured (SL mm), viscera removed (assigned the same unique number as the body), and mass of both the body and ovaries determined. Adjusted gonadosomatic mass, defined as the mass of the body after extraction of all major internal organs (heart, liver, gonads, and gut), will be recorded for each member of the subsample. Eviscerated specimens and excised ovaries were blotted on tissue paper and mass of each determined (wet weight) to the nearest 0.001 g on an analytical balance. Excised male gonads were examined under a stereomicroscope and length and maximum width along the left testis determined to the nearest 0.01 mm with an ocular micrometer.

Stomach and intestinal tracts (=gut) removed from the subsample of adult southern redbelly dace in each collection will be dissected and contents examined for dietary composition and endoparasites. Material in the gut will be rinsed into a petri-dish and examined under a dissecting microscope. Dietary material will be identified to the appropriate taxonomic level and enumerated. Correlations between SL and eviscerated body mass will be generated from the cumulative dataset and segregated by gender. Analysis of covariance (ANCOVA) will be used to test for slope and elevation differences in length-mass linear regression relationships between genders and sample stations while a t-test will be employed to detect any statistical differences in SL of the sexes.

Summary of Results

Length frequency histograms indicate the presence of at least three age classes in the population (Figure 2, 3, 4). The 2004 year class (Age 2 fish) initially comprised the majority of the population through July 2006. Age 1 specimens (2005 year class) were the second most abundant cohort in the population and comprised the majority of post-July 2006 samples. Age 0 individuals (specimens < 20 mm SL) were not present in 2006 collections. If 2007 population dynamics follow those observed in 2006, the 2006 year class should be taken in January or February 2007. Concerted efforts will be made in 2007 to collect larval (Age 0) southern redbelly dace.

Both total length (TL) and standard length (SL) of southern redbelly dace were recorded and linear regression of the lengths plotted to provide a highly predictive (r^2=0.996; F=2,066,452; p<0.0001) model (Figure 5). The standard errors were 0.033 and $8.39*10^{-4}$ for the intercept and standard length terms, respectively. The mean value for the response variable (TL) was 47.3 mm. Southern redbelly dace in the samples ranged from 14.6 to 68.0 mm SL and 17.5 to 82.5 mm TL. Variation around the predicted regression was fairly uniform, indicating that there was relatively less percent variation in total length as a function of standard length for larger individuals (i.e., the range of variation in total length for a fixed standard length was about 5 mm regardless of the size of the individual). The large sample size (N=8,390) included a few outliers, especially for individuals that exceeded 50 mm SL.

A subsample of 50 individuals (when available) was selected from each of the 24 monthly collections and further analyzed to determine gender, length-mass ratios, and gonadosomatic index values. The total number of fish analyzed was 1,069 (as opposed to 1,200) because some months yielded less than the target number or yielded fish that were too small to analyze properly. Female southern redbelly dace comprised 67.3% (n=719) of the subsample with monthly ratios ranging from 33% to 96% (Figure 6). Female southern redbelly dace were more than 50% of the monthly sample on 17 occasions, were exactly 50% of the sample on one occasion, and were less than 50% of the sample on only five occasions. The largest percent difference between males and females occurred during May in both 2006 and 2007. With the exception of July 2006, females were more common in subsamples from March through November in both years. One sampling trip (January 2007) did not yield any fish because extremely thick ice prevented access to the water.

Mass (both whole body and eviscerated body) of southern redbelly dace was regressed against standard length (Figure 7). The resulting equations were highly predictive for both whole body mass (r^2=0.901; F=4,856.8; p<0.0001) and eviscerated body mass (r^2=0.893; F=4,450.3; p<0.0001). For whole body mass, the standard errors were 0.066, $1.27*10^{-3}$, and $1.52*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. For eviscerated body mass, the standard errors were 0.049, $9.28*10^{-4}$, and $1.12*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. The mean value for the response variable (mass) was 2.44 g for whole body and 1.83 g for eviscerated body.

Southern redbelly dace in the samples ranged from 29.9 to 68.0 mm SL. Variation around the predicted regression increased as a function of size, indicating that there was relatively similar percent variation in mass as a function of standard length.

In addition, mass-length relationships were determined by gender (Figure 8). Female whole body mass (r^2=0.877; F=2,553.6; p<0.0001) and eviscerated body mass (r^2=0.880; F=2,626.2; p<0.0001) equations were highly predictive. Similar predictive equations were calculated for males (whole body mass [r^2=0.896; F=1,491.0; p<0.0001] and eviscerated body mass [r^2=0.880; F=1,261.1; p<0.0001]). For female whole body mass, the standard errors were 0.112, $2.00*10^{-3}$, and $2.07*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. For female eviscerated body mass, the standard errors were 0.079, $1.40*10^{-3}$, and $1.44*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. For male whole body mass, the standard errors were 0.090, $1.97*10^{-3}$, and $2.77*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. For male eviscerated body mass, the standard errors were 0.081, $1.77*10^{-3}$, and $2.49*10^{-4}$ for the intercept, first SL, and second SL terms, respectively. For females, the mean value for the response variable (mass) was 2.74 g for whole body and 2.01 g for eviscerated body. For males, the mean value for the response variable (mass) was 1.82 g for whole body and 1.46 g for eviscerated body. Southern redbelly dace in the samples ranged from 29.9 to 68.0 mm SL for females and between 30.1 to 60.8 mm SL for males. The largest southern redbelly dace, in both length and body mass (either whole or eviscerated), were female.

Mean monthly gonadosomatic index values for females southern redbelly dace ranged from 3.66 (N=19; SE=0.27; range=1.80-7.01) in July, 2006 to 21.70 (N=29; SE=1.71; range=8.37-36.40) in April, 2006. Similarly, mean monthly gonadosomatic index values for females southern redbelly dace ranged from 3.76 (N=38; SE=0.18; range=0.33-6.41) in July, 2007 to 16.54 (N=40; SE=0.78; range=10.55-33.20) in April, 2007. Spawning period appeared to be April and May but might have included March and June (Figure 9). Besides containing the largest mean monthly GSI values, April and May generated the largest individual GSI values and the greatest standard deviation. Mean monthly GSI values were lowest during July but then appeared to increase slightly from August to October/November. The most rapid increase in GSI values occurred between February and April of both 2006 and 2007.

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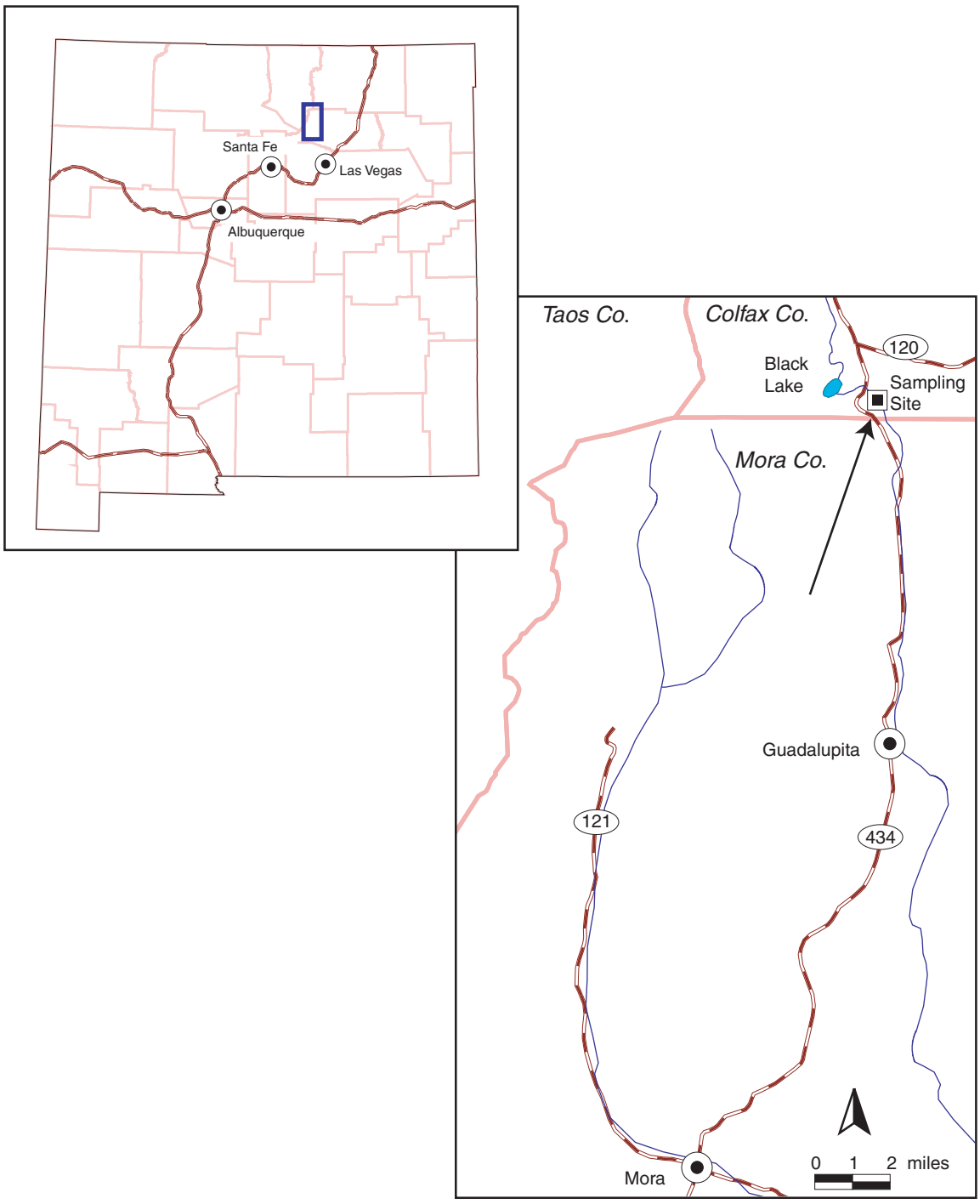

Figure 1. Coyote Creek (Mora River System, Canadian River Drainage) sampling locality for southern redbelly dace during 2006 (square).

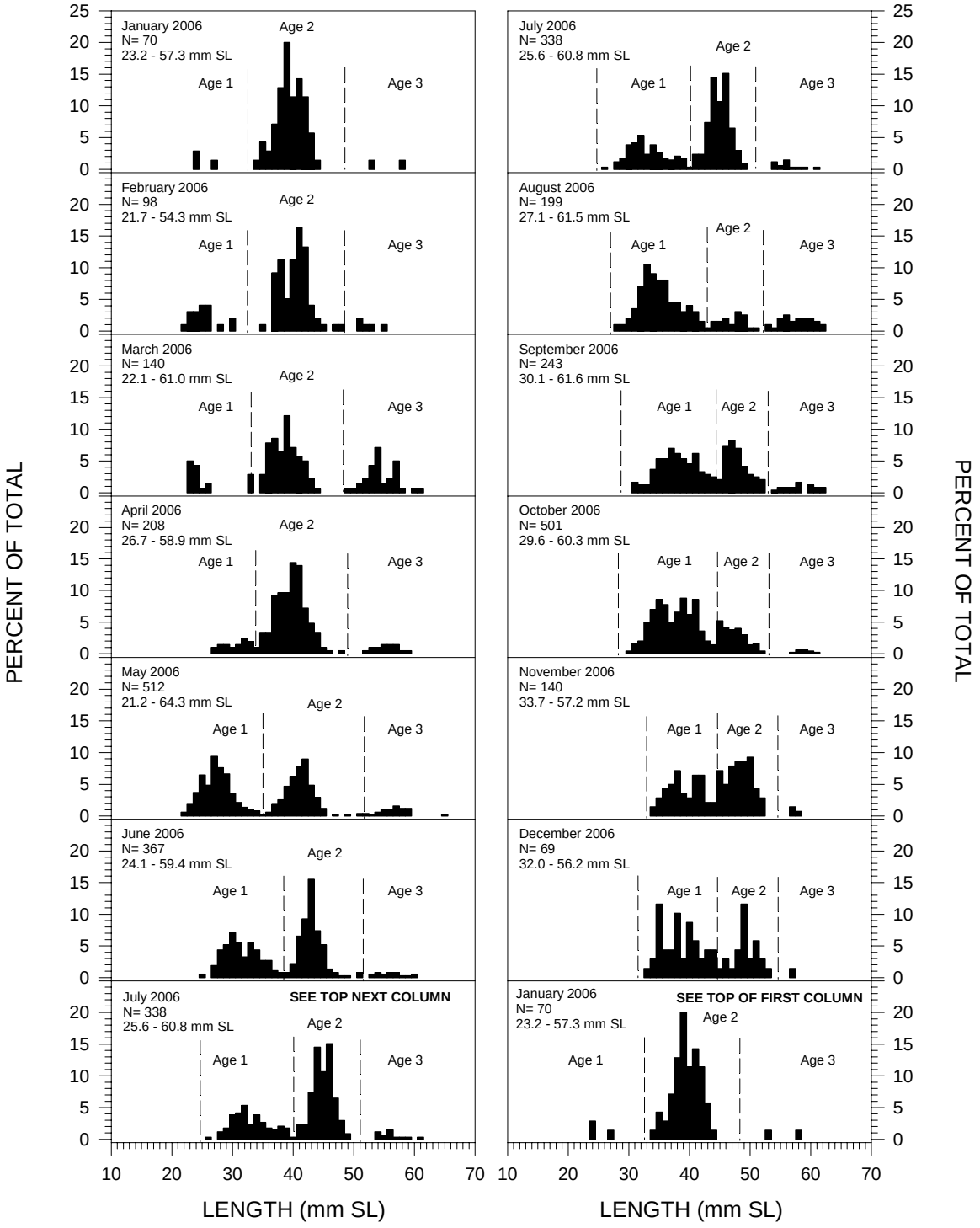

Figure 2. Length frequency historgrams of southern redbelly dace from January2006 through December 2006. Dashed vertical lines separate putative age classes.

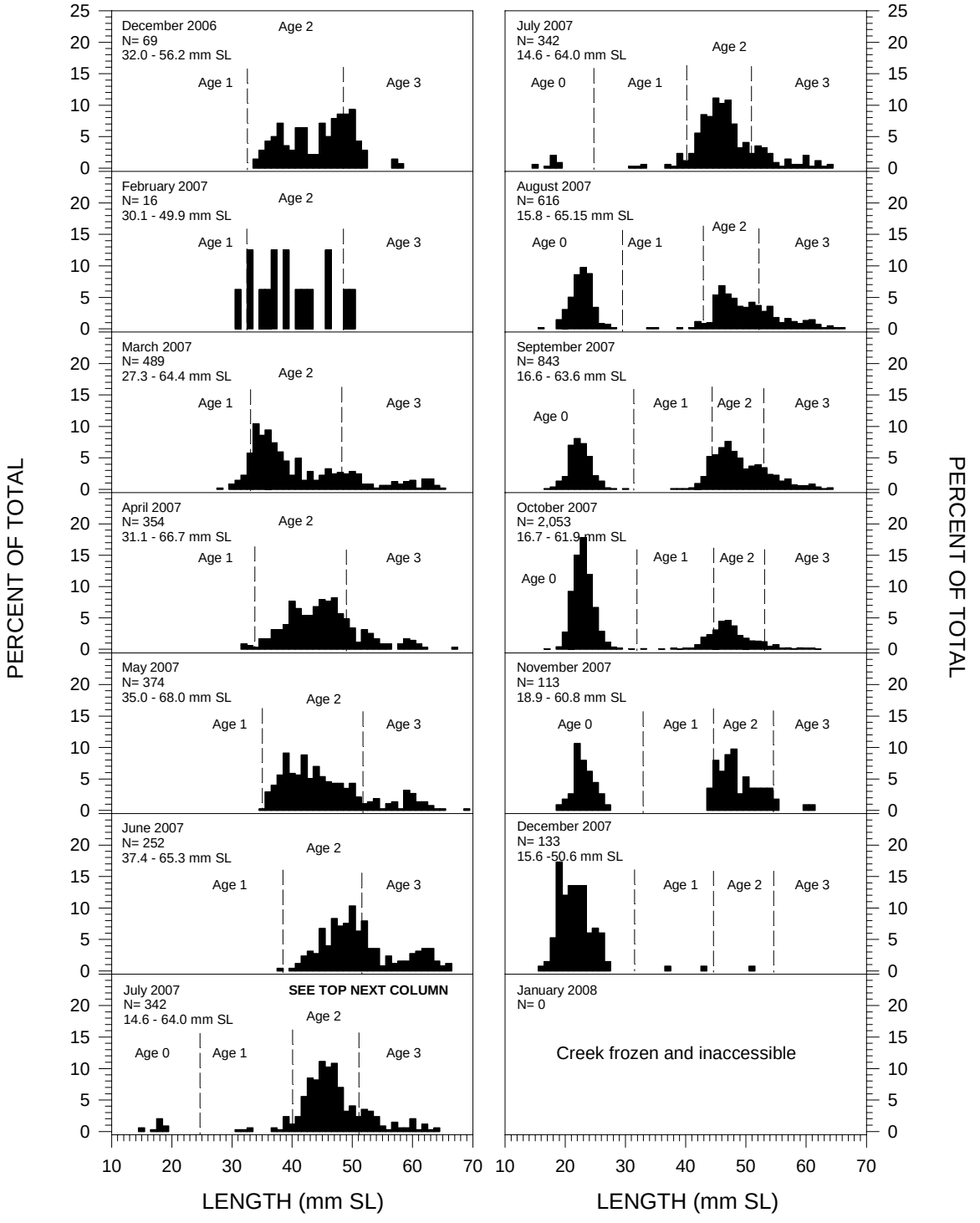

Figure 3. Length frequency historgrams of southern redbelly dace from December 2006 through December 2007. The site was frozen and inaccessible during both January 2007 and January 2008. Dashed vertical lines separate putative age classes.

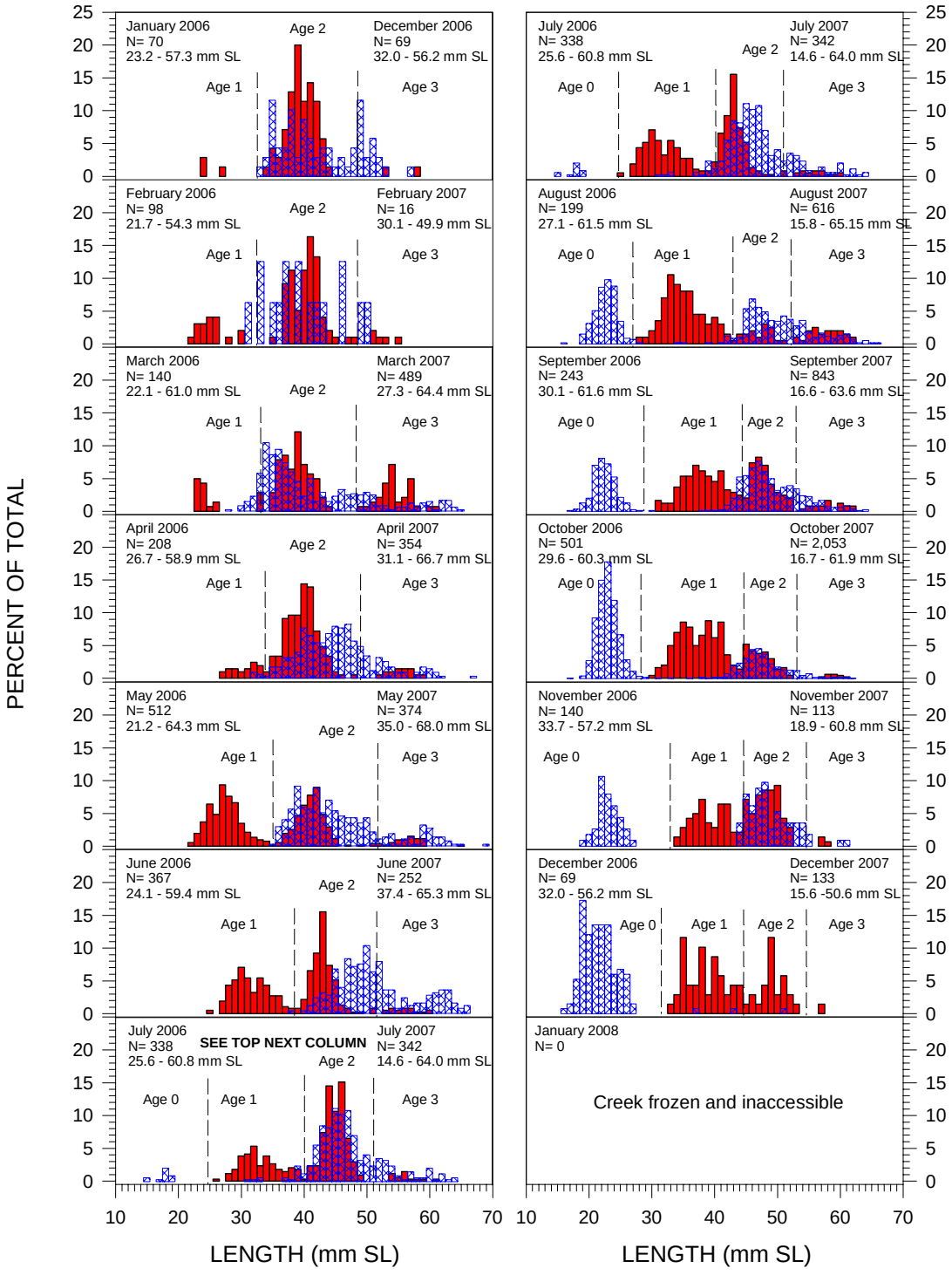

Figure 4. Overlay of 2006 (solid color-red) and 2007 (blue cross hatching) length frequency histograms to illustrate relative absence of the 2006 year class from 2006 samples (age 0) and 2007 samples (age 1).

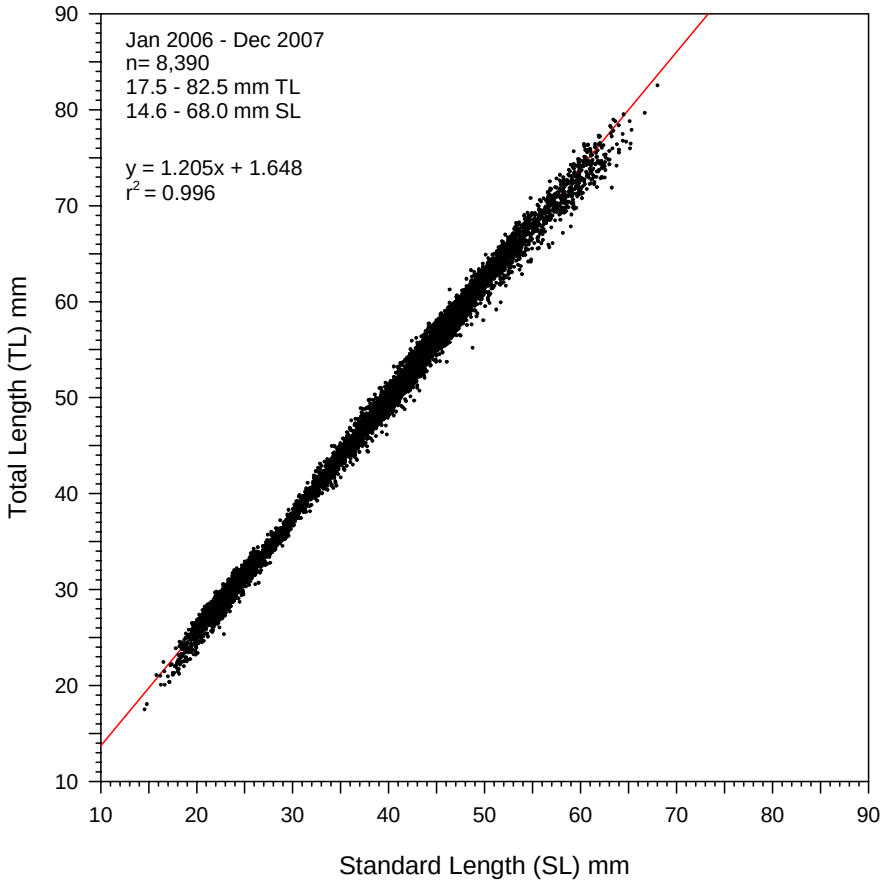

Figure 5. Correlation between total length and standard length in southern redbelly dace collected in Coyote Creek, New Mexico from January 2006 through December 2007.

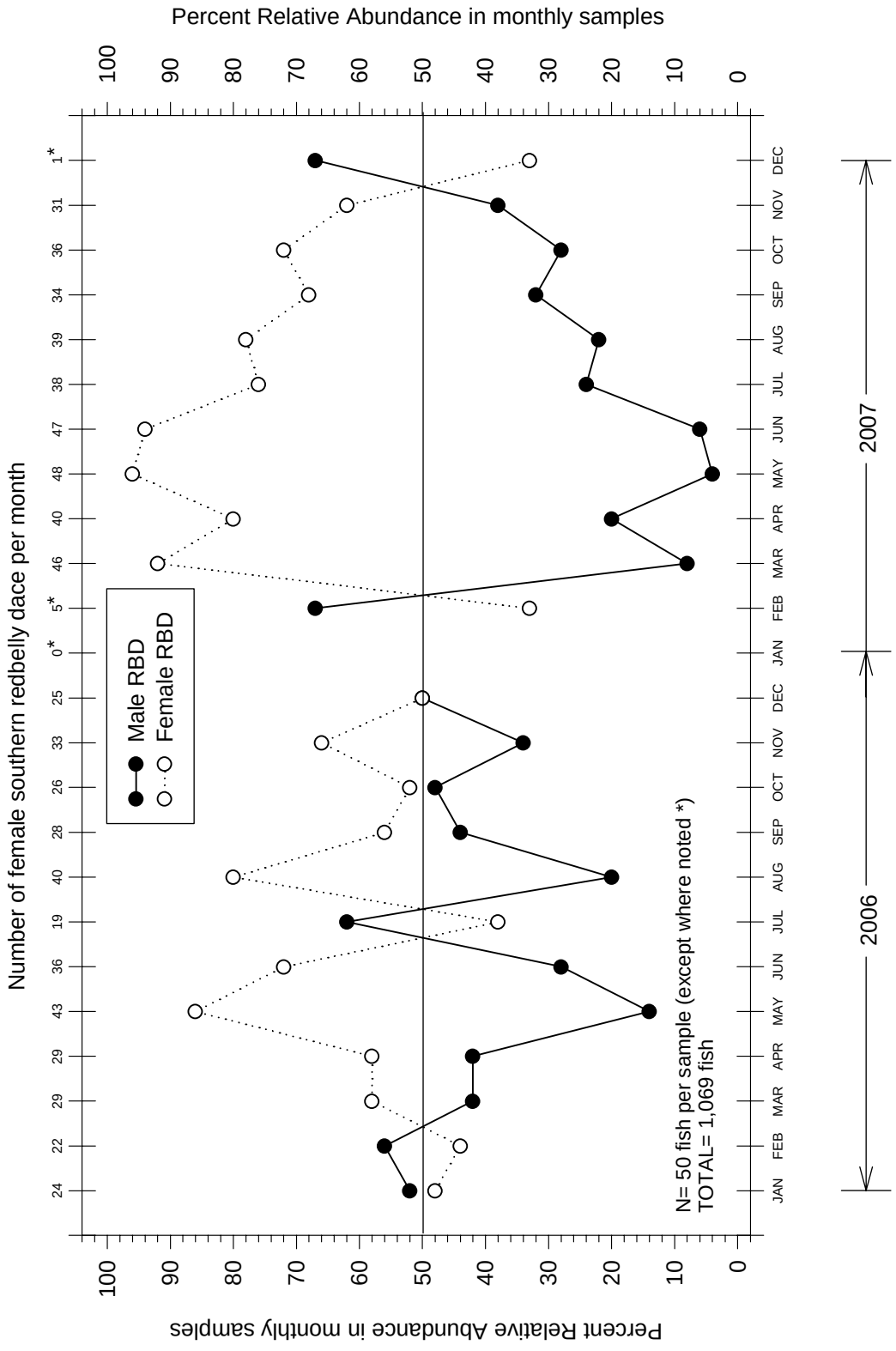

Figure 6. Southern redbelly dace monthly gender ratios from January 2006 through December 2007.

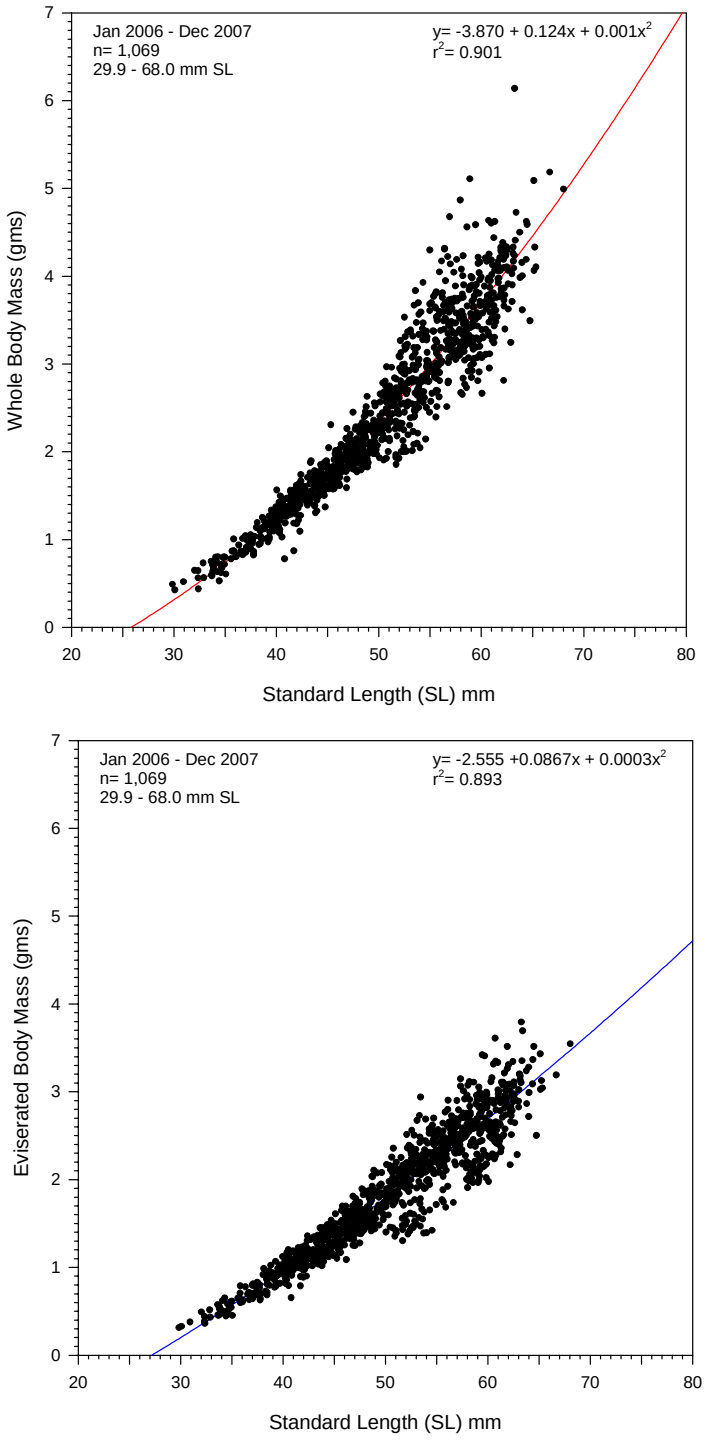

Figure 7. Body mass (whole and eviserated) length (standard) ratios of southern redbelly dace during 2006 and 2007.

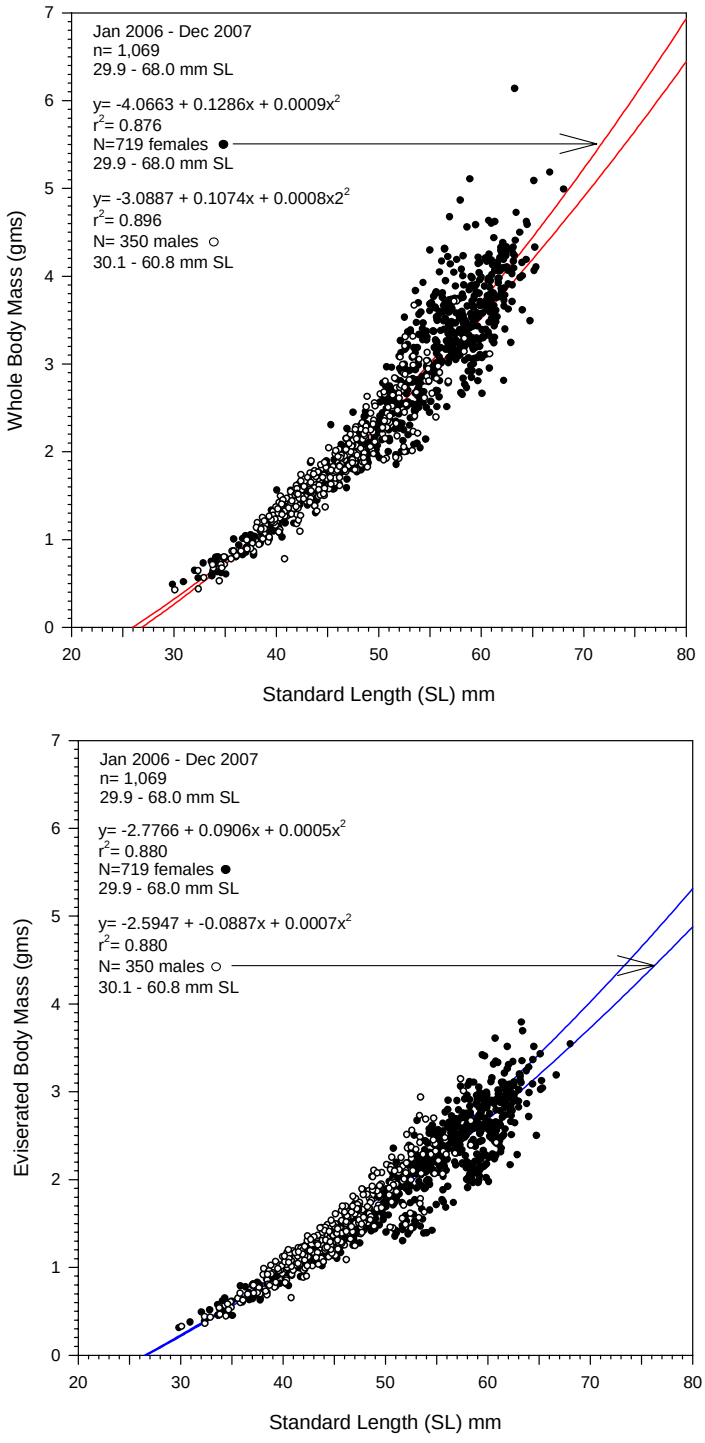

Figure 8. Body mass (whole and eviserated) length (standard) ratios of southern redbelly dace by gender during 2006 and 2007.

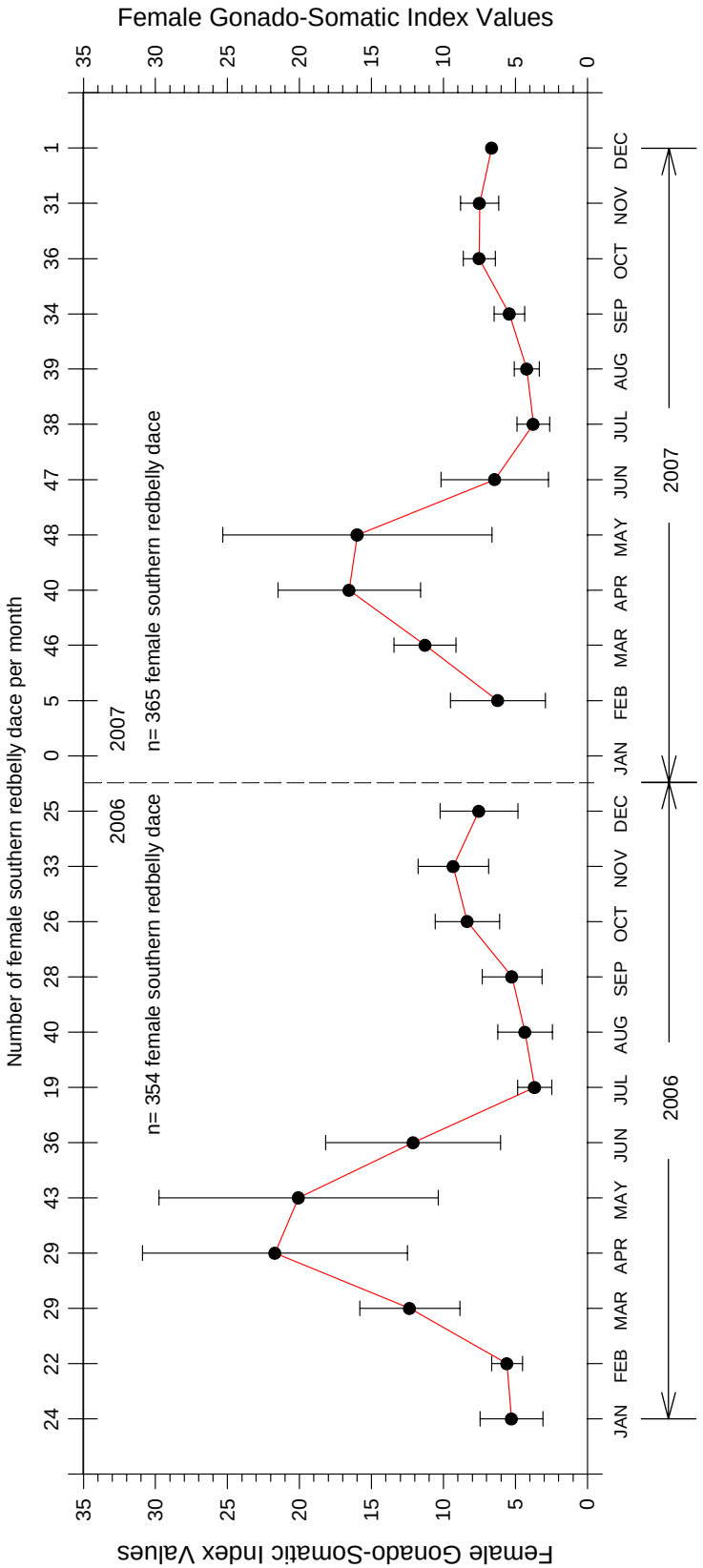

Figure 9. Mean monthly gonadosomatic index values of female southern redbelly dace. Capped bars indicate one standard error around the mean.

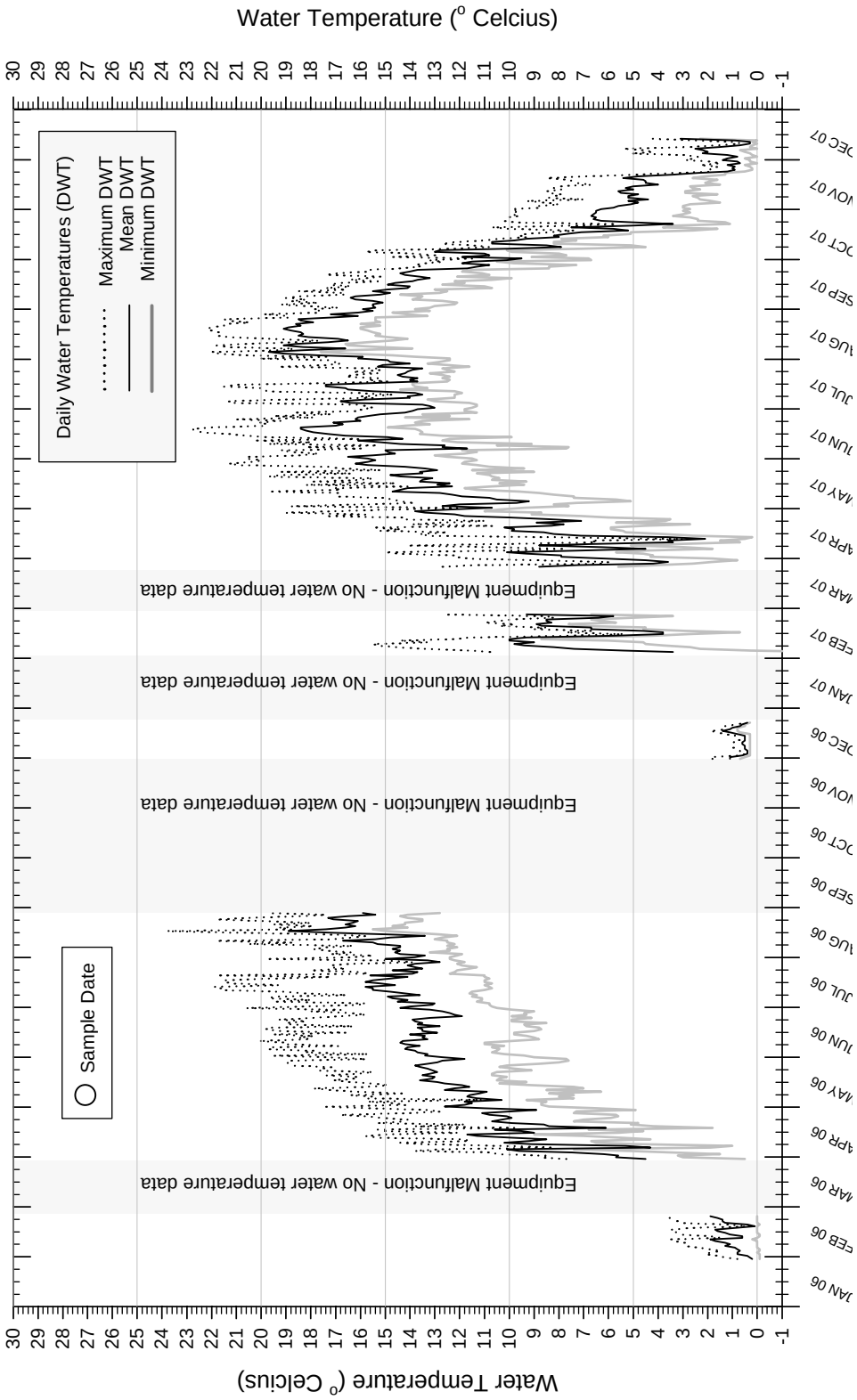

Figure 10. Minimum, maximum, and meand daily water temperatures during 2007 at the southern redbelly dace sampling site, Coyote Creek, Mora County, New Mexico. Water temperature data presented above are based on hourly temperatures. Hollow circles indicate sampling dates.

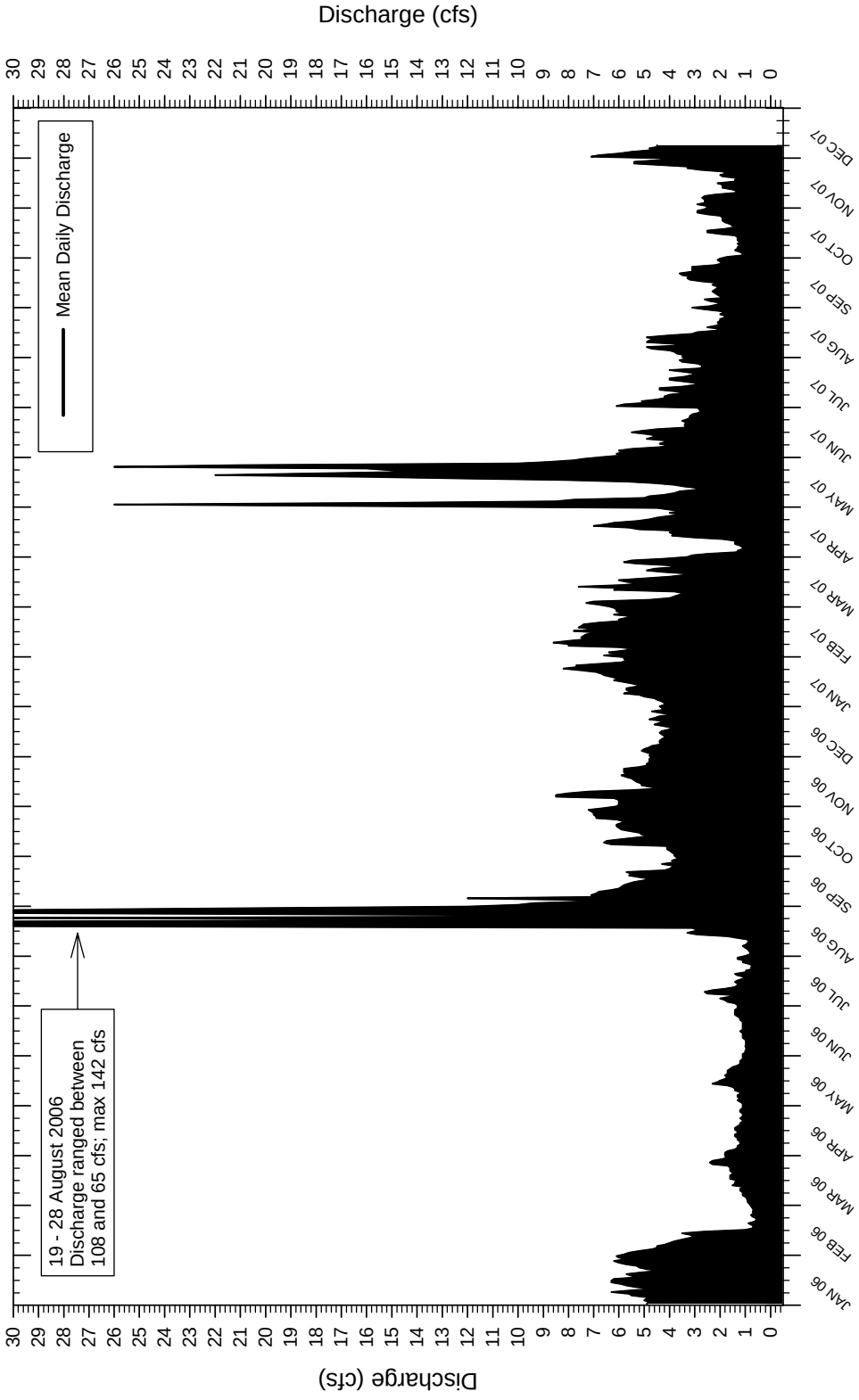

Figure 11. Mean daily discharge of Coyote Creek as recorded at the U.S. Geological Survey's gauging station (07218000; Coyote Creek near Golondrinas, Mora County, NM) located about 30 river miles downstream of the sampling site.

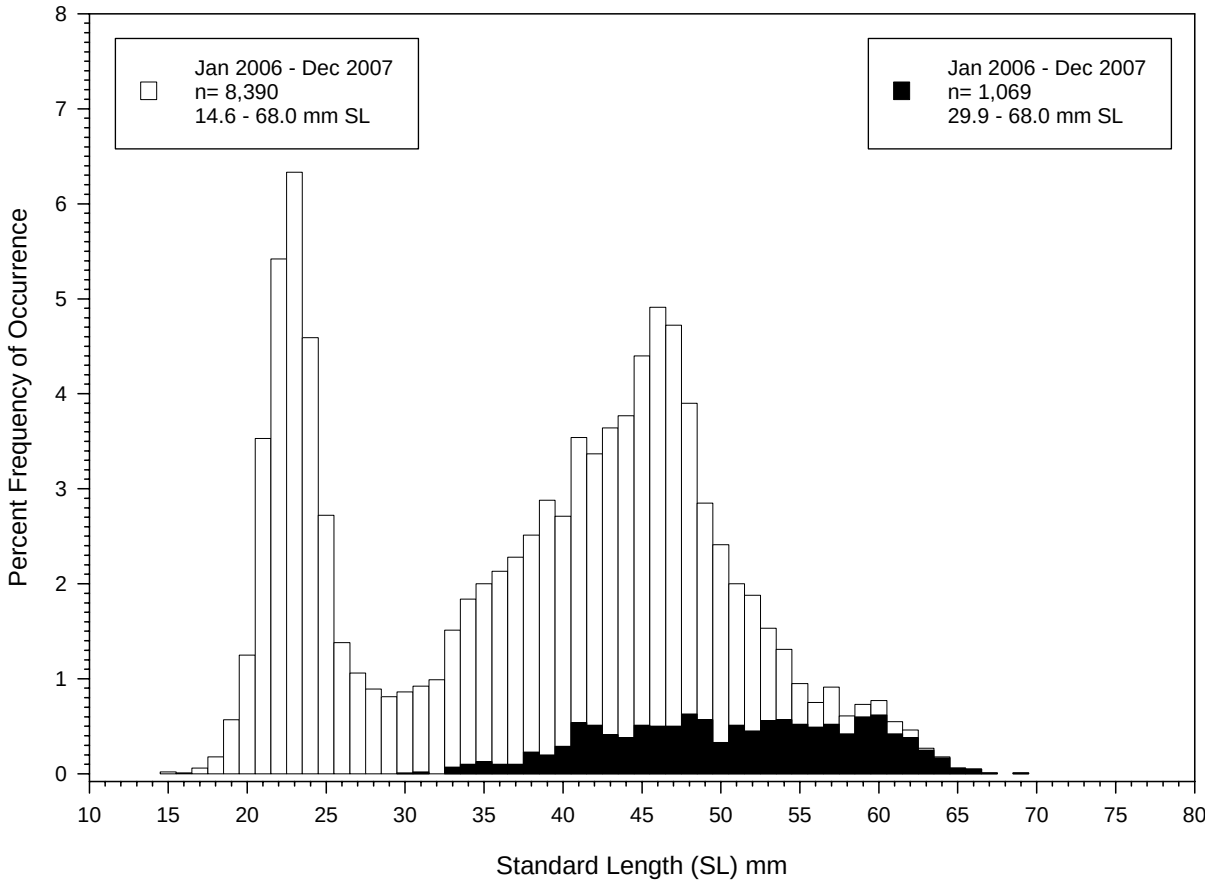

Figure 12. Length-frequency distribution of all southern redbelly dace collected during 2006 and 2007 (white or clear bars) and of the subeset of specimens examiined for life history attributes (black bars).

Table 1. Summary of dietary analysis of 1,069 southern redbelly dace collected during 2006 and 2007.

FOOD ITEMS	N	%
PLANT MATERIAL		
Fine	642	60.1
Coarse	165	15.4
Filamenteous Algae	245	22.9
Silica	179	16.7
Amphipods	377	35.3
Corixidae/Hemiptera	37	3.5
Diptera	351	32.8
Ephemeroptera	62	5.8
Trichopteran	53	5.0
Coleopteran	30	2.8
Odonate	34	3.2
Misc. Invertebrate	343	32.1
Fish: Scales/Fin rays	0	0
Parasites	54	5.1
Empty	102	9.54

N = presence/absence of a food item in gut of the 1,069 southern redbelly dace examined

% = percent frequency of occurrence of a food item in the gut of the southern redbelly dace examined (N/1,069 * 100)

Appendix C

Development of an Immunological Approach to Determining Host Fishes of the Texas Hornshell (*Popenaias popeii*):

Todd D. Levine and David J. Berg

2008

Final Report to the Share with Wildlife Program
For Contract No. 05-516.0000.0082
"Development of an Immunological Approach to
Determining Host Fishes of the Texas Hornshell (*Popenaias popeii*)"

Todd D. Levine & David J. Berg
Department of Zoology, Miami University
Oxford, Ohio

June 27, 2008

Background

The Texas hornshell, *Popenaias popeii*, is one of eight freshwater mussel species native to New Mexico, and the only one extant within the state (Lang 2001). Once found throughout the Rio Grande basin in New Mexico, Texas, and Mexico, the U.S. range of this species is now restricted to the Black River in Eddy County, New Mexico (Lang 2001), and a stretch of the lower Rio Grande in Texas (Robert Howells, TX Parks and Wildlife Dept., pers. comm.). Due to its reduced range and declining populations, the Texas hornshell is considered "endangered" under the New Mexico Wildlife Conservation Act and is a Priority 2 candidate for federal listing under the Endangered Species Act.

Freshwater mussels have a complex life history. Adult males release sperm that are filtered from the water column by females. Fertilization leads to production of larvae called glochidia that are brooded within the female gills. At the appropriate time in development, the glochidia are released and become obligate parasites on the gills of fishes (or very rarely, other freshwater vertebrates). After feeding on the host for several days-to-weeks, the glochidia transform into juvenile mussels and drop off of the host and settle in benthic habitats where they grow to adulthood. Because of the obligate nature of its relationship with its hosts, population viability of freshwater mussels is inextricably linked to viability of host fishes. In the case of the Texas hornshell, 23 of 30 fish species tested in laboratory trials were found to be suitable hosts (Gordon 2000). However in a natural setting, these so-called "physiological" hosts will only come into contact with glochidia if they are in proximity to a gravid female mussel.

Objectives

The objectives of this project are to:

1. Verify the presence of an immunological response to infection by Texas hornshell glochidia in fish species that are likely hosts for this mussel.

2. Collect blood samples from fishes located in proximity of Texas hornshell populations to determine which fishes serve as ecological hosts and to determine the proportion of individuals infected within these populations of host species.

3. Identify fishes infected with glochidia of the Texas hornshell.

Objective 1. Identification of host immunological response

1. Laboratory Experiment 1 (spring 2005)

We infested 5 channel catfish (*Ictalurus punctatus*), 2 carp (*Cyprinus carpio*) and 1 bullhead (*Ameiurus* sp.) with glochidia in aquaria at Bitter Lake National Wildlife Refuge during spring 2005. Glochidia were removed from the demibranchs of a female *P. popeii* and pipetted over the gills of the fish. We retained 5 channel catfish and 1 carp as an experimental control. Fish were bled 8 days post-infestation, and the serum was separated from the whole blood sample after coagulation of the cellular components, and preserved at -80^{o}C. Gills were removed from two fish that died during the experiment; these were cleared with 2% w/v potassium hydroxide and examined for encysted glochidia under a dissecting microscope (Fig. 1). Surviving fish were released to their point of capture.

Very few glochidia (≤ 3) were recovered from the gills of infected fish that died during the experiment and no sloughed nor transformed juveniles were recovered from the experimental tanks. We therefore believe that the infestations were not normal and may have been complicated by application of glochidia to surfaces that do not normally come into contact with the mussels or perhaps a pathogen, immune response or some other circumstance interfered with these infestations. This has been observed in the past with *P. popeii* (B. Lang pers. comm.) and other mussel species (D. Neves pers. comm.).

One female *P. popeii* held in captivity was observed releasing glochidia (Fig. 2-A). Viability of these glochidia was tested by exposing them to a saline solution daily after release. Most glochidia were responsive and classified as viable for the first three days after release, although some were viable up to five days after release.

2. Laboratory Experiment 2 (spring 2006)

We developed and submitted a plan to Dexter National Fish Hatchery to experimentally infest fish with glochidia in May and June 2006 (attached as Appendix 1) and, in conjunction with Brian Lang, we obtained naïve fishes for this experiment from outside of the range of *P. popeii* in the Black River. A total of 15 fish (5 *Moxostoma congestum*, 5 *Ictalurus punctatus*, and 5 *Lepomis* spp.) were exposed to glochidia via direct pipetting of glochidia to the face, gills and opercula, and by further exposing fish in an

aerated bath of glochidia. This allowed glochidia to come into contact with the external tissues and may have better mimicked normal routes of infestation. Approximately 3 pipettes of glochidia were applied to each fish, with subsamples preserved for enumeration and estimation of number of glochidia exposed to each fish. Infected fish were placed in individual aquaria with false bottoms. All material recovered from tanks were sieved to preserve all particles with a size similar to glochidia, i.e. >180 um (similar to Lang 2002). Samples were concentrated by settling and preserved in formalin. All fish were bled after about 14 days. Additionally, 5 fish of each species were maintained as controls and blood samples were taken for use as negative controls in laboratory tests.

Similar to the previous year, we observed natural releases of glochidia in captivity. With slightly increased flow, due to a different aeration system, we observed suspension of the mucus mass containing the glochidia in a net-like "conglutinate" mass (Fig. 2-B). As far as we know, this is the first evidence of a mechanism of infestation in *P. popeii* and may explain the pattern of infestation that we have observed in field studies. Based on the shape of the conglutinate, i.e. a net, it seems likely that glochidia will be delivered to the surface of fishes, rather than gills (the typical location of infestation of other mussels). Such routes of infestation are known for some mussel species such as *Strophitus undulatus*, which produces a net-like conglutinate (Watters 2002). Similarly, species of *Anodonta* have been known to infect their hosts on the outer surfaces of their bodies (Jansen and Hanson 1991), in contrast to the many mussel species known to infest gill tissues.

3. Laboratory and Immunological Procedures

General procedures for observing antibody/antigen reactions followed methods of O'Connell and Neves (1999) and other sources (J. Stevenson, Miami University; M. O'Connell, University of New Orleans; pers. comm.). We screened these procedures using 152 samples run against antibodies and developed a standard operating procedure (attached as Appendix 2) consistent with O'Connell and Neves (1999).

Equivocal results required that we continue to revise the procedures used to detect antibody formation in infested fishes. Through additional discussions with experts (M. O'Connell) and review of newer literature, such as Dodd *et al.* (2006), we reconsidered our techniques. During the spring of 2008, we attempted a suite of methodological modifications for the detection of antibody production against *P. popeii* antigens by fishes. We modified the original procedure, by varying staining and washing techniques. We varied the wash, stain, and destain periods, but still saw no evidence of antibody-antigen interaction on positive control samples from either experimental infestations nor in blood collected from wild, infested fishes.

Objectives 2 and 3: field sampling

1. *Field Sampling 1 (spring/summer 2005)*

We collected 30 fish from the Black River in 2005, but observed only one infestation by glochidia: on the face and opercula of a blue sucker (*Cycleptus elongatus*). Blood samples were taken from the caudal fins of 15 fishes. Sampling sites are plotted in Figure 3.

Glochidia were collected from 3 females for use in immunological tests. Gills from these females were excised and glochidia were removed from them by mechanical destruction of the gill tissue. The females were preserved and two are retained with Brian Lang at NMDGF; one female is archived at Miami University.

2. Field Sampling 2 (spring/summer 2006)

Using a variety of fishing techniques (i.e., hoop and trammel nets, seining, electroshocking), we collected 299 fishes representing 14 species (Figure 4-a), from the Black River between May 8 and June 15. We measured total and standard lengths, and weight for almost all fishes and tagged 161 individuals. Fishes were not tagged if tagging was likely to represent a substantial threat to their health. Glochidia were observed on 20 individuals from 6 species, and 7 additional fish (including 2 additional species) may have been infested. Glochidia on fishes were observed throughout the sampling period. River carpsucker (*Carpiodes carpio*) and gray redhorse (*Moxostoma congestum*) were most frequently infested. Eight of 10 river carpsucker (80%) and eight of 64 (12.5%; with one more possibly infected) gray redhorse were infested (see Fig. 4-A). All other species of fishes were either infested at very low rates (< 10% and never more than 1 individual and/or 2 possible individuals), or were rarely caught. We obtained blood samples from 215 fish. All blood samples are currently archived at -80^{o} C at Miami University. Small fishes such as minnows were preserved and examined in the lab.

5. Field Sampling 3 (spring/summer 2007)

Fish sampling, using similar techniques and methods described above, throughout the inhabited range of *P. popeii* was continued during the summer of 2007. We observed 447 fishes, representing15 species, from the 14 km stretch of the Black River between May 26 and June 20. Glochidia were observed on 18 individuals from four species, and three additional gizzard shad may have been infested (Fig. 4-B). Because it was difficult to determine whether cysts and other bumps on the skin of shad were glochidia, we preserved these individuals and collected blood samples. Although it is unlikely that shad are hosts, because they would be susceptible to secondary infection and when feeding in benthic areas are typically in open water, we examined individuals with skin conditions similar in appearance to glochidial infestation to ensure accurate reporting of infestation. Glochidia on fishes were observed throughout the sampling period. River carpsucker (*Carpiodes carpio*) and gray redhorse (*Moxostoma congestum*) were most frequently infested. Eight of 29 river carpsucker (30%) and five of 118 (4.0%) gray redhorse were infested. Additionally, it is possible that a gizzard shad and a single bass were infested, but infestation could not be confirmed. We obtained blood samples from over 300 fishes. All blood serum samples are archived at -80^{o} C at Miami University. Small fishes such as minnows were preserved separately and were not counted in the totals above, but were examined for presence of glochidia.

6. Overall analysis of field samples 2005-2007

Field sampling locations are plotted in Figure 3. We tested the entire dataset for differences in infestation rates between species, based on the results from field surveys.

We used a chi-square contingency table to test for differences in infestation rates between species, using data from the entire project ($\chi^2 = 144.240$, df=17, $p < 0.001$). Many potential hosts are fairly rare in the current range of *P. popeii*, therefore we were unable to preserve a large number of individuals to examine in the laboratory for infestation intensity (number of glochidia attached to a given host). However, in the samples that could be enumerated, the difference in infestation intensity between host species was large (Fig. 5). We used a graphical approach to examine the value of different host species toward recruitment of mussels (Fig. 6). As abundance, prevalence, and intensity of infestations on hosts increase, the importance of that host species to the recruitment of mussels increases. The most important hosts will have values that lie in the far, upper, right corner of the three-dimensional plot. Hosts that have values in other parts of the plot will be limited in the proportion of individuals infested (low prevalence), the number of glochidia per infestation (low intensity), and/or the number of fish present (low abundance).

For example, a parasite might take advantage of an abundant species of host and infest a large proportion of them (i.e. attain high prevalence), despite being unable to infest individuals of that host species at high intensities. This would plot in the far, lower, right corner and could lead to production of a large number of offspring in the next generation. Alternatively, a parasite could efficiently infest (attaining high prevalence) hosts that occur in low numbers (low abundance), but carry large numbers of the parasite (high intensity). In this case, the host would plot at the far, upper, left corner. The outcomes of these scenarios may be equivalent in terms of number of mussels recruited.

In the Black River, fishes with the highest infestation intensity and prevalence were catostomids (sucker family), namely *C. carpio*, *C. elongatus*, and *M. congestum*. However, none of these species occurred in high numbers compared to other species (Fig. 6). Because these catostomids likely contributed the most to recruitment of *P. popeii*, we believe that they represent ecological hosts, a distinct subset of fishes that are exploited more efficiently than other physiological hosts (Lang 2001). All other host species likely represent insignificant contributions to the recruitment of *P. popeii*.

Infestation rate within species did not differ between individual sampling sites (*C. carpio* $\chi^2 = 23.84$, df = 15, $p = 0.068$; *C. elongatus* $\chi^2 = 4.87$, df = 3, $p = 0.18$; *M. congestum* $\chi^2 = 37.00$, df = 33, $p = 0.29$), nor did infestation rates differ between sites, when species were pooled ($\chi^2 = 58.21$, df = 44, $p = 0.061$). Some of these tests approached significance and might exhibit real differences which are obscured by small sample size. Pooling sites nearby one another or by habitat type may change these results. However, the proportion of fishes encountered that were ecological hosts differed by site ($\chi^2 = 145.00$, df = 44, $p < 0.001$), with ecological hosts having greatest frequency at sites scattered along the sampled stretch of the river.

These ecological hosts are generally benthic-feeding, highly vagile catostomids. There was no effect of fish size (*C. carpio*, χ^2=0.5304, df=1, p=0.467; *C. elongatus*, χ^2 = 0.107, df = 1, p = 0.743; *M. congestum*, χ^2 = 0.146, p=0.703). Additionally, the length-weight relationship between infested and uninfested fishes did not differ within species (*C. carpio* F = 1.399, df = 1, p=0.245; *C. elongatus* F = 1.85, df = 1, p = 0.25; *M. congestum* F = 0.377, df = 1, p = 0.540; Fig. 7), suggesting that fish body condition did not differ between infested and uninfested fishes. When pooled together, infested fishes were larger compared to other fishes in the survey (F = 67.38, df = 729, p < 0.001). Ecological hosts had larger average body size than the other species sampled (F = 527.63, df = 1,739, p < 0.0001).

Although several species became infested at low prevalence and intensity, only a few species were infested consistently and at high prevalence and/or intensity. While these species are not the most abundant in our surveys, they represent the largest potential contribution to recruitment of *P. popeii* of all the fishes surveyed. If the number of glochidia infested on these fishes reflects the number of transformed juveniles, then these results demonstrate a clear disparity among fish species' potential to contribute to recruitment of juvenile mussels. These three species have subterminal mouths, are benthic feeding and may process large quantities of material from the bottoms of rivers (Pflieger 1997). It is likely that use of these environments predisposes them to incidental contact with mussels and their glochidia. The pattern of external and, typically, facial infestation sites suggests that a passive mechanism may be responsible. The feeding motions of these fishes are likely to increase their exposure to the net-like masses produced by *P. popeii*. Smaller-bodied fishes, e.g. *Lepomis* spp. and *Cyprinella lutriensis*, were all infested on the gills. This discrepancy in the location of attached glochidia suggests that smaller and more pelagic fishes are more likely to become infested by ingesting drifting glochidia, which would lead to much lower infection intensity.

Using large-bodied hosts may have important ecological and evolutionary consequences for *P. popeii*, because large-bodied hosts offer opportunities for parasite species to ameliorate environmental uncertainty. Large-bodied hosts may represent a more valuable resource than small-bodied hosts because of the larger surface area for glochidia attachment. This may be especially important in mussel species that have few opportunities to deliver their offspring to appropriate hosts. Because the ecological hosts of *P. popeii* are not the most abundant fishes in the river, the mussel may be trading off high host prevalence for the more predictable resource offered to them by large-bodied hosts which are more likely to survive long enough for glochidia to transform into juveniles. These large-bodied hosts are also likely to better tolerate high infestation intensity. Desert rivers are notoriously unpredictable with both short, high-intensity, scouring floods and periods of low-flow or complete drying. Large fishes are often more vagile and may provide better opportunities for recolonization where local mussel populations have been extirpated. Although *P. popeii* likely used mainstem

habitats, use of large-bodied hosts might allow them to exploit smaller tributaries, or reestablish mainstem sites after catastrophic events.

Conclusions

We were unable to develop an effective method for measuring immunological response of host fishes to infestation by Texas hornshell. Reasons for this negative result might include: weak response of fishes to glochidial attachment due short attachment periods, or known methods (i.e. O'Connell and Neves 1999) being unsuitable for this mussel-host system. We will maintain the blood samples at -80°C in case a refined method is developed.

We feel, however, that our field approach allowed us to identify most accurately the ecologically relevant hosts of *P. popeii*: river carpsucker, blue sucker, and gray redhorse. A total of more than 700 fishes were observed in the wild, but few were observed to have encysted glochidia and, of these, the overwhelming majority were large-bodied, benthic feeding catostomids. Glochidia of *P. popeii* appear to attach largely to the face and opercula of fish hosts. This is consistent with our observations of the shape of released glochidial masses and habitat use patterns and feeding ecology of this suite of catostomids.

Catfishes were occasionally observed to have cysts that were superficially similar to those caused by glochidial attachment, but these did not appear to be glochidia when viewed with a microscope. Few other species appear to be consistently or intensely exploited by *P. popeii*. Interestingly, while early lab studies (Gordon 2000) indicate a broad range of physiologically relevant host fishes, our field data point to only a few of those species as being ecologically relevant.

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Appendix 1:

STUDY PLAN
U. S. Fish and Wildlife Service
Dexter National Fish Hatchery and Technology Center

Study Number: DX-06-001

Title: Development of an Immunological Approach to Determine Host Fishes of the Texas Hornshell (*Popenaias popeii*)

Principal Investigators: Brian Lang, New Mexico Department of Game and Fish, and Todd Levine, Miami University, Oxford, Ohio

Co-Invest./Cooperators: Dexter National Fish Hatchery and Technology Center, Dexter, NM 88230

Background and Justification:
The Texas hornshell, *Popenaias popeii*, is one of eight freshwater mussel species native to New Mexico, and it is the only one currently extant within the state. Once found throughout the Rio Grande basin in New Mexico, Texas, and Mexico, this species is now restricted to the Black River in Eddy County, New Mexico, and the lower Rio Grandenear Laredo, Texas. Due to its reduced range and declining populations, the Texas hornshell is considered "endangered" by the state of New Mexico and is a Priority 2 candidate for federal listing under the Endangered Species Act.

Freshwater mussels have a complex life history. Adult males release sperm that are filtered from the water column by females. Fertilization leads to production of larvae called glochidia that are brooded within the female gills. At the appropriate time in development, the glochidia are released and become obligate parasites on the gills of fishes (or very rarely, other freshwater vertebrates). Because of the obligate nature of its relationship with its hosts, population viability of freshwater mussels is inextricably linked to viability of host fishes.

Objectives:
We propose to develop and test a method for determining ecological hosts of the Texas hornshell. Because infection of host fishes by glochidia can trigger an immune response in fishes (O'Connell and Neves 1999), we will use immunological techniques to determine which fishes in the Black River are serving as, or have previously served as,

hosts for the Texas hornshell.

Our objective is to:

Verify the presence of an immunological response to infection by Texas hornshell glochidia in fish species that are likely hosts for this mussel.

Material and Methods:

We will use an immunological approach to determine the ecological hosts for the Texas hornshell. The "immunological responses" that we will measure are antibody-antigen reactions between antibodies contained in host fish blood serum and antigen proteins present in ground tissues of glochidia.

We will conduct laboratory experiments to demonstrate the presence of an antigen-antibody reaction in several species of fishes infected with glochidia of the Texas hornshell. Target species will include 1) bullhead (*Ameiurus* sp.), 2) gray redhorse (*Moxostoma congestum*),3) channel catfish (*Ictalurus punctatus*) and 4) sunfish (*Lepomis* sp.). These species are from three separate families and represent a broad taxonomic range.

We will obtain naïve (never infected) fish from outside the Black River watershed and bring them to Dexter National Fish Hatchery and Technology Center, where the experiments will be conducted.

A bank of 29 gallon tanks will be set up, and walled off from the rest of the facility with heavy gauge black plastic on 2x4 frames. This will serve two functions, containment and privacy for wild specimens acclimating to culture conditions. Entry to the study area will be limited only to personnel actively involved in the study.

Standard water quality parameters will be monitored and recorded daily. These should include at a minimum: dissolved oxygen, nitrates, nitrites, ammonia, pH, temperature, and conductivity.

Four gravid female Texas hornshell will be collected and maintained in the lab for collection of viable glochidia. All glochidia remaining after fish inoculations will be flash frozen in liquid nitrogen. Up to **10** fish of each species will be infected with glochidia following Gordon and Layzer (1993) method as described in Lang (2001). This group of fishes will constitute the treatment group. Up to 10 additional members of each fish species will be held under identical conditions, but will not be exposed to glochidia. This group will serve as the control fishes.

Fish will be maintained until glochidia transform into juveniles and detach from their hosts (approximately 6-14 days post-infection). Once glochidia have detached, blood will be drawn from each fish (experimental and control groups) for future analysis at Miami University, Oxford, OH.

Containment protocols:

This study will be conducted using the *Guidelines for the Use of Fishes in Research* (Nickum et al. 2004) for containment protocols and acclimation to laboratory conditions.

Specifically 1) "Prior to bringing fish into a laboratory, facilities and plans should be in place to ensure that the fish cannot escape from the facility, especially species not native to the watershed, and that the introduced fishes can be isolated physically from fishes already present.

2) Each holding unit should have its own set of nets and other equipment. Facilities and equipment used for previous studies should be disinfected prior to use in new studies, typically with a chlorinated disinfectant (300 ppm). If the introduced fishes may carry disease agents, especially pathogens or parasites that are not endemic to the area, quarantine-level facilities should be used.

3) Effluents from units used to hold newly introduced fishes should, at a minimum, pass through screens with openings sufficiently small to retain any escaped fish, followed by mechanical grinding devices and, in turn, chemical or other treatment sufficient to kill all pathogens and parasites that can be expected to be present."

<u>This policy shall be stepped down to daily standard operating procedures for the study location at Dexter to:</u>

<u>Transportation to facility</u>

Vehicle Shipments:

Exterior of vehicle should be disinfected with a 200-ppm solution of Quaternary Ammonium Compound in the designated area. The solution should be liberally applied with a garden sprayer on all external surfaces and be allowed to sit for 15 minutes before moving about the station. Operators should use eye protection and protective gloves.

Vehicle should be moved immediately to the quarantine area. All

acclimation water should be released into the underground containment tank for disinfection. When fish are acclimated to ambient conditions they should be netted from the transport tank and placed into the culture vessel. Care should be taken to avoid spilling and dripping water from the transport tank.

When fish are removed from the tanks chlorine should be added to a concentration of 300-ppm. Walls of the tank should be scrubbed with a brush and held for one hour. Water from the tanks should be discharged into the underground containment tank. Safety glasses and protective clothing should be worn when handling the chlorine solution. All equipment, boots and nets should be cleaned and disinfected. The ground between the truck and the holding facility should be disinfected with a 200ppm solution of Quaternary Ammonium Compound.

Hands should be washed thoroughly after handling the fish and shoes disinfected in a footbath before moving to other parts of the hatchery.

Box Shipments:

Animals should be delivered to the quarantine area for acclimation. Bags are floated in the culture vessel until acclimation is completed. Fish are removed from the bags with as little water as possible. The remaining water in the bag is poured down the drain to the underground containment tank for disinfection. The bag should be placed in a bucket and sprayed down with a 300 ppm chlorine solution or autoclaved. Hands should disinfected before moving away from the quarantine area.

Facility protocols:

1. Hands and arms should be washed with a disinfectant soap upon entering and leaving the study area. Hands and arms should be washed before moving from one tank to another during daily cleaning operations.

2. The study area will have a footbath containing a 200-ppm Quaternary Ammonium Compound solution. Staff should step in the solution when entering and leaving the facility. Footbath solution should be maintained at an adequate level and be changed daily. To prevent damage to personal clothing, rubber boots may be worn when entering the study area. Boots should be sprayed with 200-ppm Quaternary Ammonium Compound and stored at the entrance to the study area.

3. Prior to entering the study area, a labcoat or other protective clothing (raingear or coveralls) should be worn. A locker will be provided for storage of protective wear outside the entrance to the study area. Protective clothing should be removed and stored when leaving the area.

4. Records should be updated daily. Any problems or conditions out of the ordinary should be brought to the attention of the principal investigator AND the fish health representative. No treatments or alterations should be made without written direction of the fish health representative.

5. Any mortality that may occur during the course of the study period should be documented and immediately transported in a sealed zip lock bag to the fish health unit for evaluation. Moribund fish shall remain in the system and brought to the attention of the fish health representative to determine the disposition of the animal. Any animals to be removed shall be euthanized in the facility and transported as outlined above.

6. Materials taken into the quarantine facility may not be removed from the facility for any reason unless there has been adequate disinfection. Adequate disinfection can only take place when animals have been removed from the facility and the entire facility can undergo decontamination. For this reason it is necessary that only essential items be brought into the quarantine area.

7. Refuse generated within the facility should be sealed in biohazard bags and brought to the fish health center to be autoclaved.

8. The study facility will be dismantled and sterilized upon study completion by Game and Fish personnel, with assistance from center staff.

Acclimation to Laboratory Conditions

"Fish should be given time to acclimate to new environments, feeds, and routine activities before being used in studies. Slow acclimation to change often is critical. It is not uncommon for fish to exhibit acute health problems 48 to 72 hours following transfer. A commonly used acclimation period is 2–4 weeks." For this reason, NMDGF personnel will attempt to bring in sufficient study specimens at least a month prior to

onset of study so that fish can be treated for stress and disease, and acclimated to a feeding regime before the study. This is particularly important to this study, as the immunological response to glochidial attachment is unknown, and any stress response could mask the desired unknown.

Disposition of study animals: All study animals will be euthanized with the exception of the gray redhorse. If a suitable location such as a public aquarium is identified, these fish may be donated to a public facility. No fish should be released to the wild after the study concludes.

Schedule: Sampling for study specimens will begin in May, so study facility will be operational by May 1, 2006 to allow the biofilters and system to be tested prior to bringing in fish. Study will begin in May 2006 and terminate by July 2006.

Estimated Costs:

Supplies:	
setup of the containment area and the study tanks:	$400
Labcoats, boots, chemicals for decontamination	$200
Labor:	
Setup ($15.00/hourly/40 hours)	$600
Daily maintenance and water quality ($15/1.5 hours/15 days)	$400
Utilities for 1.5 months	$600
Miscellaneous related costs	$300
Total estimated cost to facility:	*$2500*

Intended Method of Information Dissemination:
Technical information bulletin, in conjunction with NMDGF to be completed by September 30, 2006.

Reference Literature:

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Appendix 2: Antibody Detection

Glochidia preparation

Materials:

Lab notebook
Glochidia (frozen)
Secure container for counting glochidia
1.5 mL microcentrifuge tube
Blue Sharpie
Volumetric pipette
TBS (Tris-buffered saline)

Procedure:

1) Remove glochidia from the freezer and monitor them as they thaw. Work with them as soon as they are thawed.
2) Place glochidia on the plankton net sieve and rinse with distilled water and then TBS.
3) Rinse the glochidia out of the plankton net sieve and into a Petri dish.
4) Begin counting the glochidia by using the suction tubes and the microscope, transferring glochidia to a 1.5 mL microcentrifuge tube.
5) Dilute glochidia to 1 glochidium per microliter of TBS by adding TBS with a volumetric pipette.
6) Use pestle to grind the glochidia, by pressing down and twisting handle.
7) Label glochidia vial with date, number of glochidia and identify which TBS solution was used; record these data in the lab notebook as well.
8) Store in refrigerator for maximum of 1 week, preferably use the same day as preparation.

Ouchterlony Double Diffusion Method

Materials:

Lab notebook
1or more small Petri dishes
Balance
Disposable weigh boat
50 mL flask
0.25 g Seachem Agarose

Known antigen solution (e.g. Ovalbumin)
Known antibody solution (e.g. serum against albumin-AntiOvalbumin)
Samples:
    Prepared glochidia
    Fish serum
Disposable transfer pipet
Pipet (20 uL)
Yellow pipet tips
Buffer (current buffer TBS – Tris-buffered saline)

Procedure:

1) Record the samples that you are planning to use and the controls and their location on the gel and in the lab notebook.
2) Weigh 0.25 g of agarose in a weigh boat and place in flask by folding the weigh boat in half and placing tip into flask and tapping boat.
3) Add 20 mL of buffer solution to flask.
4) Cover flask with plastic wrap (leave, or make, a small hole) and microwave for 50 sec.
5) Allow the gel to cool to room temperature (you may run the flask under tap water to cool it faster).
6) Pour the gel into the smaller of the 2 parts of the Petri dish.
7) Allow the gel to set up until it is slightly whitish and solid.
8) Squeeze the bulb of the pipet and insert pipet tip into the gel.
9) Turn the pipet back and forth about ¼ - ½ turn in the gel and release bulb.
10) Remove the pipet and repeat to make enough wells in the gel.
11) Turn the dish over and label all wells.
12) Transfer 20 uL to each pair of wells, filling one with antigen (Ovalbumin or glochidia) and the other with test solution (antiOvalbumin or fish serum); make sure that each well containing antigen is next to a well containing test solution.
13) Carefully place the dish in the 37^{o} C incubator (24 hours) or on a shelf (somewhere safe and unlikely to be disturbed, 72 hrs)
14) Observe for banding between antigen and antibody wells. Bands are half-moon shaped and are an opaque, white color.

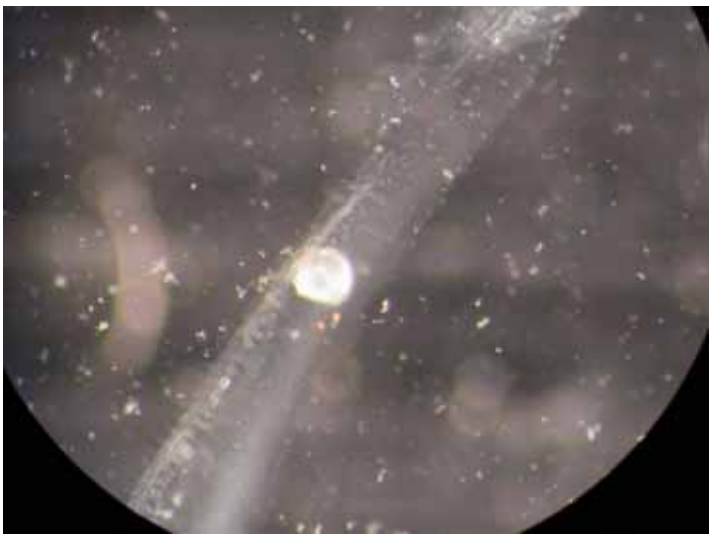


Figure 1. Microscopic view of a mussel gill with encysted glochidium from the first laboratory infestation. Gill was cleared with KOH.

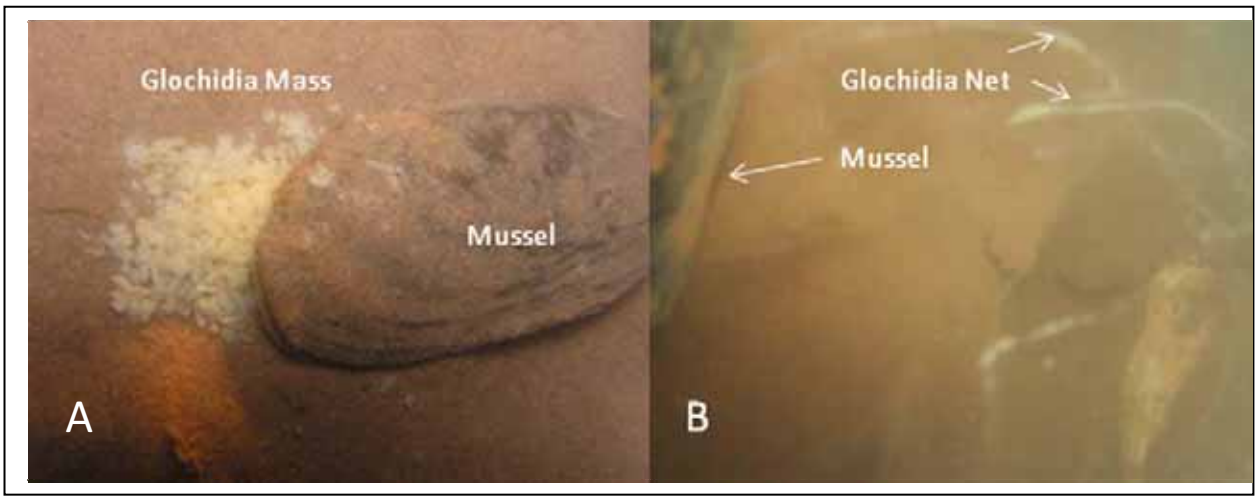


Figure 2-A. First glochidial mass observed in captivity
Figure 2-B. Example of glochidial mass observed in 2006

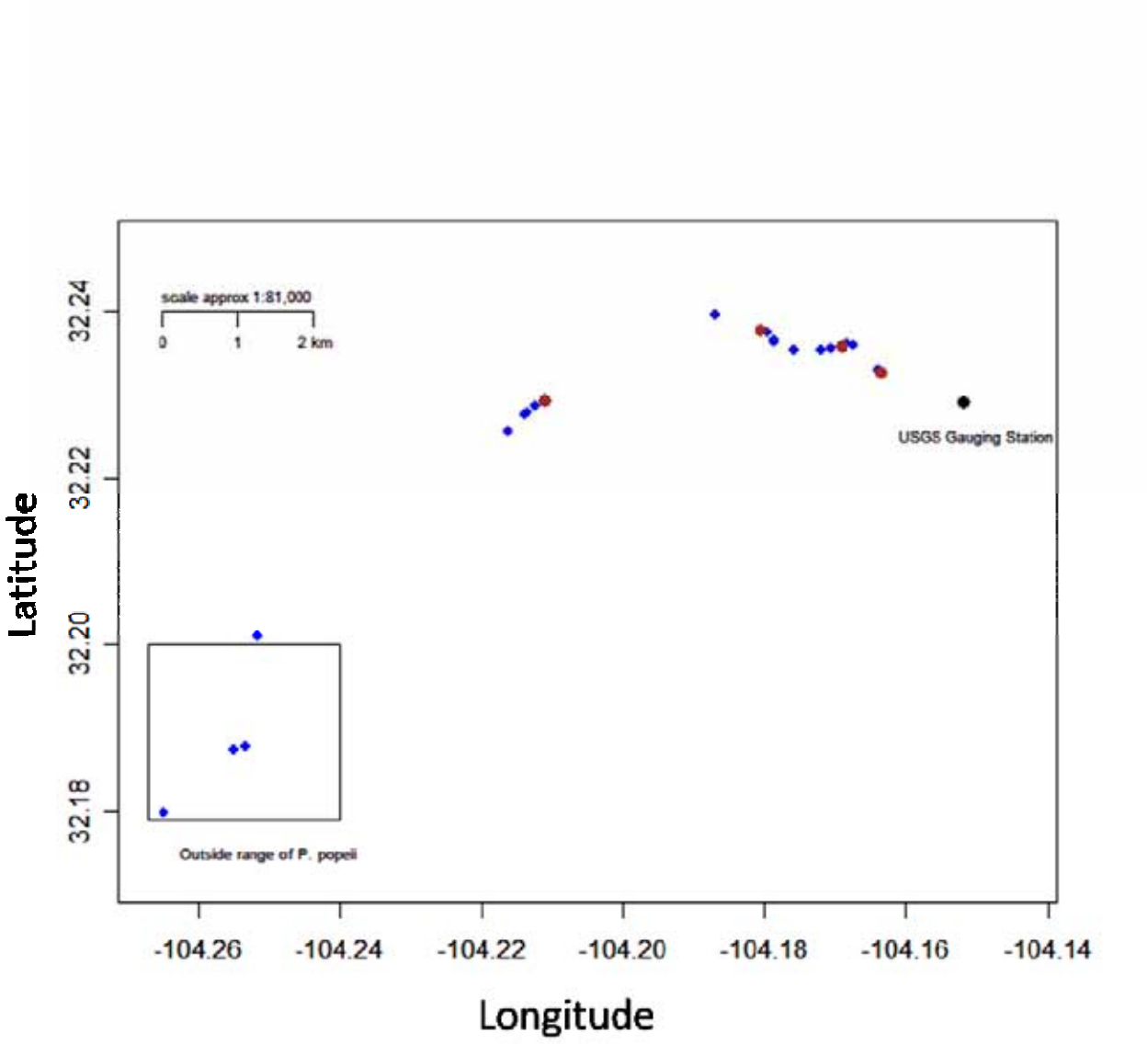


Figure 3. Fish were sampled throughout the portion of the Black River inhabited by *P. popeii* (blue dots). Data were retained from fish sampled outside of the range of *P. popeii* (box) that were used as controls during laboratory trials. Life history sites, where mussel demography data are collected are marked in brown. The three most western sites are still active and the most eastern (downstream) site was destroyed by flooding in 2000. The USGS gauging station ("Above Malaga") is marked in black for reference.

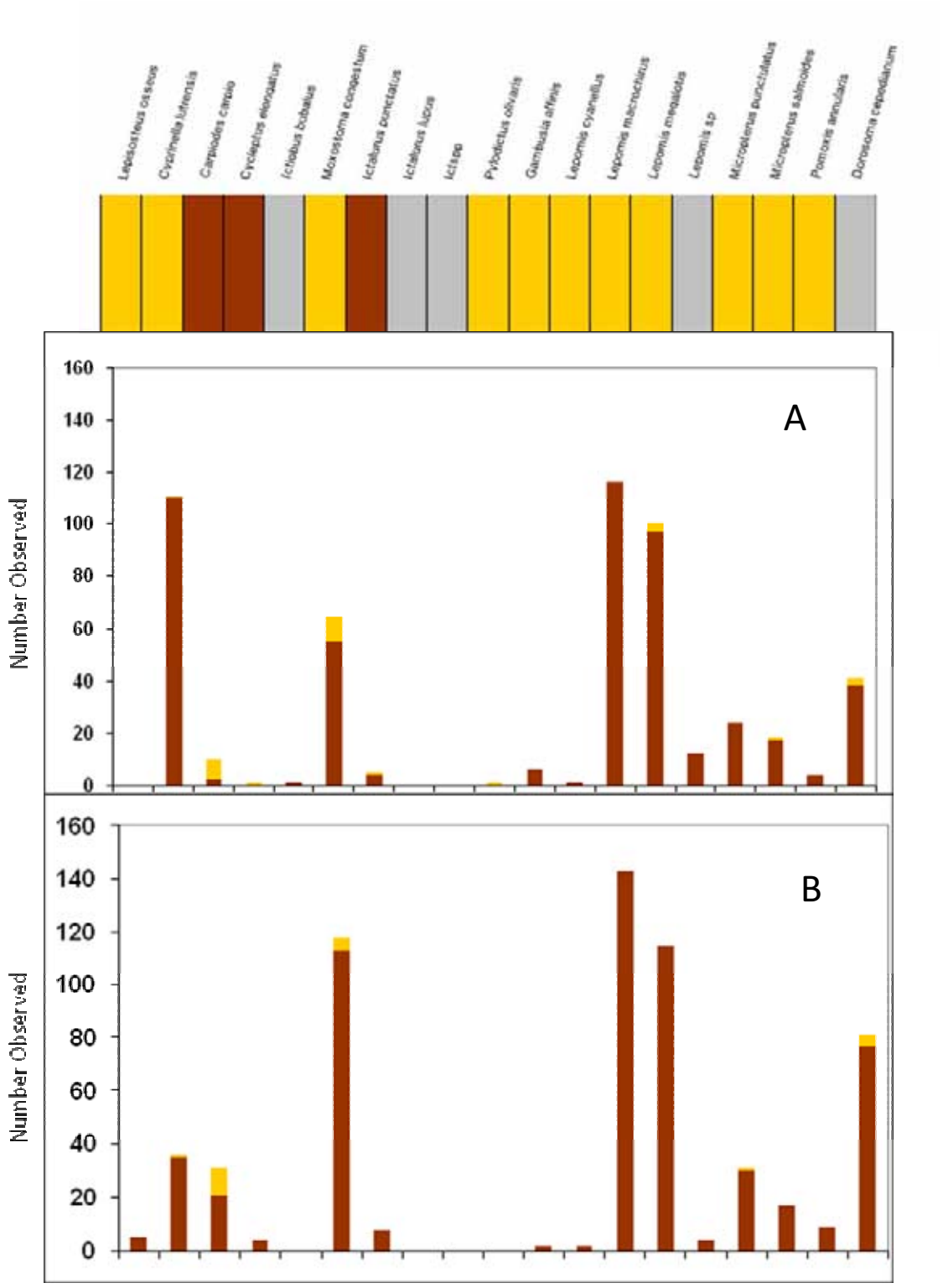


Figure 4-A. Top panel – physiological host/non-host determinations (Gordon 2000), Middle panel – 2006 fish data
Figure 4-B. Lower panel – 2007 fish data

Red = nonhost species; yellow = host species; gray = not tested by Gordon (2000)

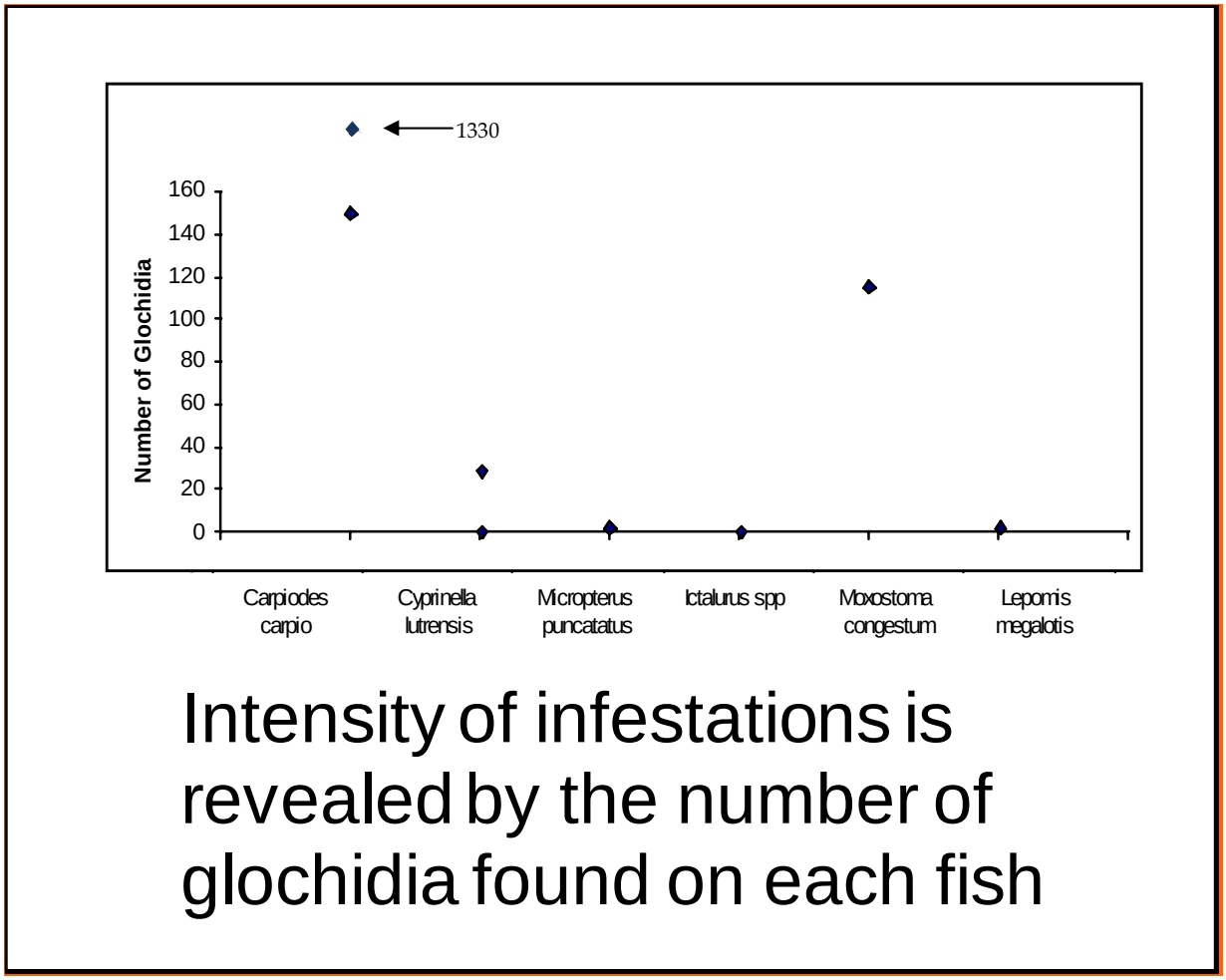


Figure 5. Infestation intensity differed between species.

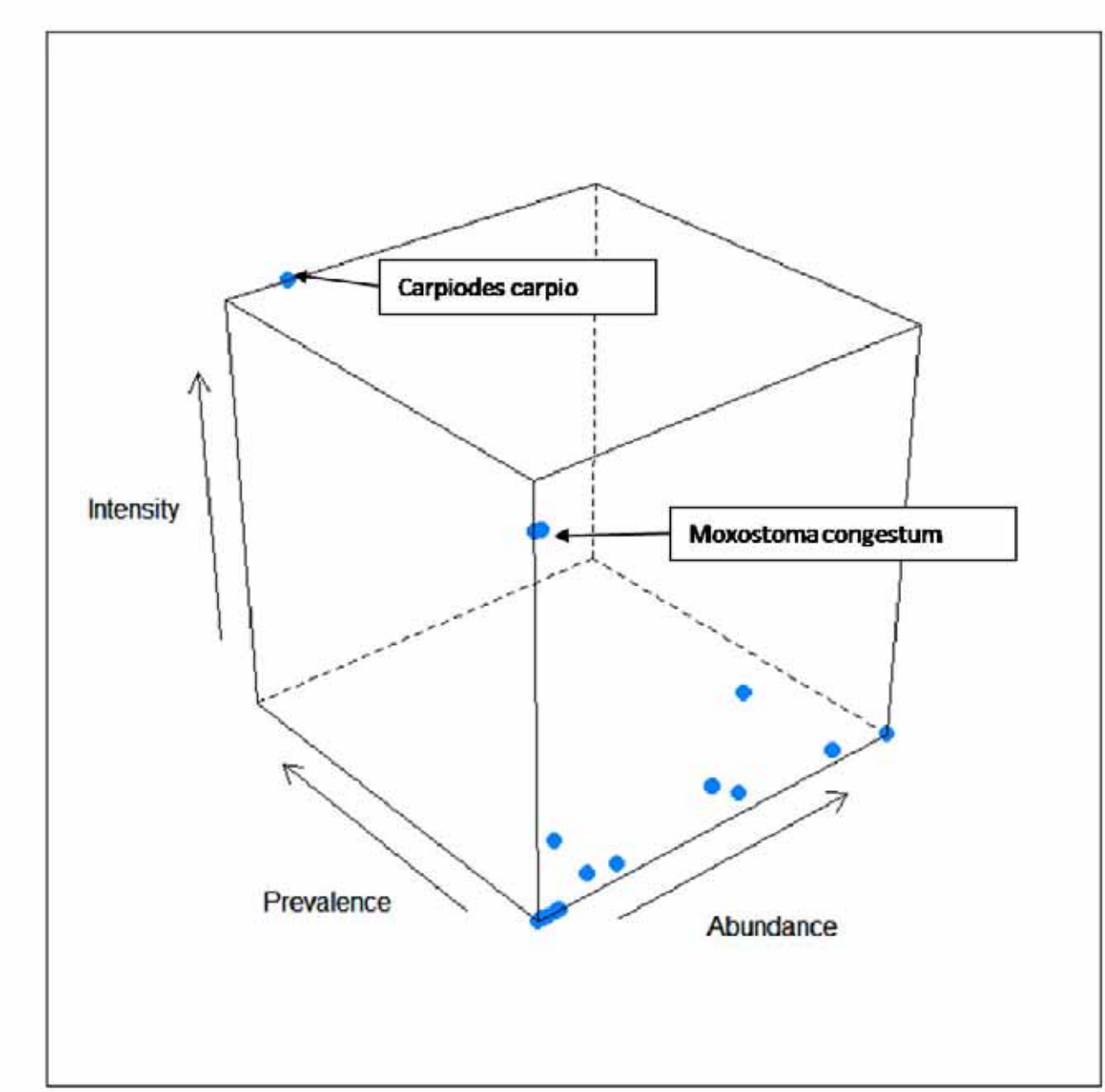
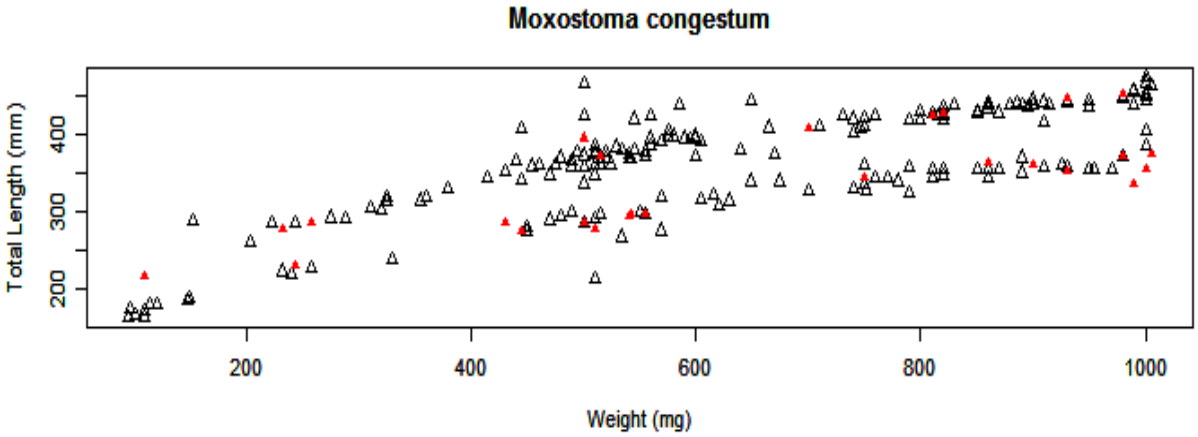
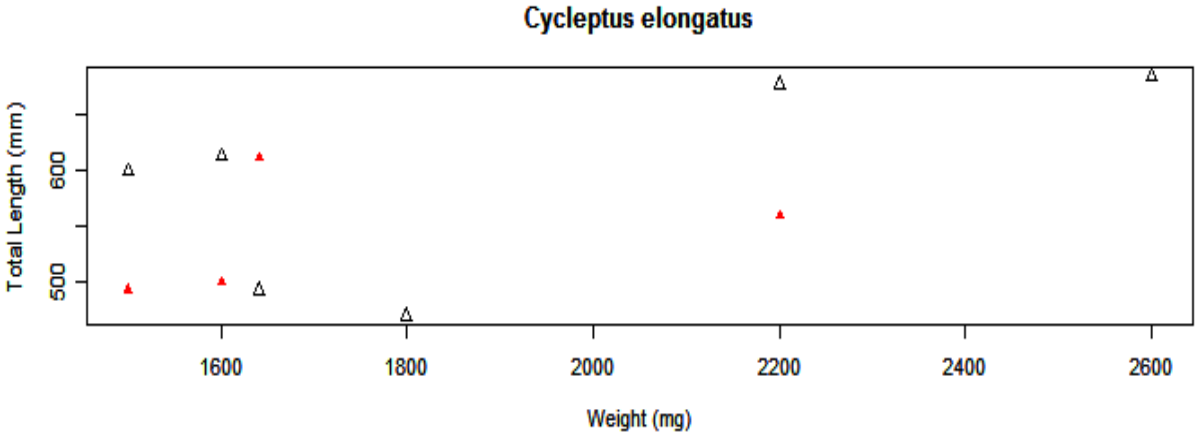


Figure 6. Data from all species encountered in field sampling with values averaged across years. Because blue sucker were returned live to the Black River, infestation intensity was not estimated.


Moxostoma congestum
Total Length (mm)
200
300
400
200
400
600
800
1000
Weight (mg)


Cycleptus elongatus
Total Length (mm)
500
600
1600
1800
2000
2200
2400
2600
Weight (mg)

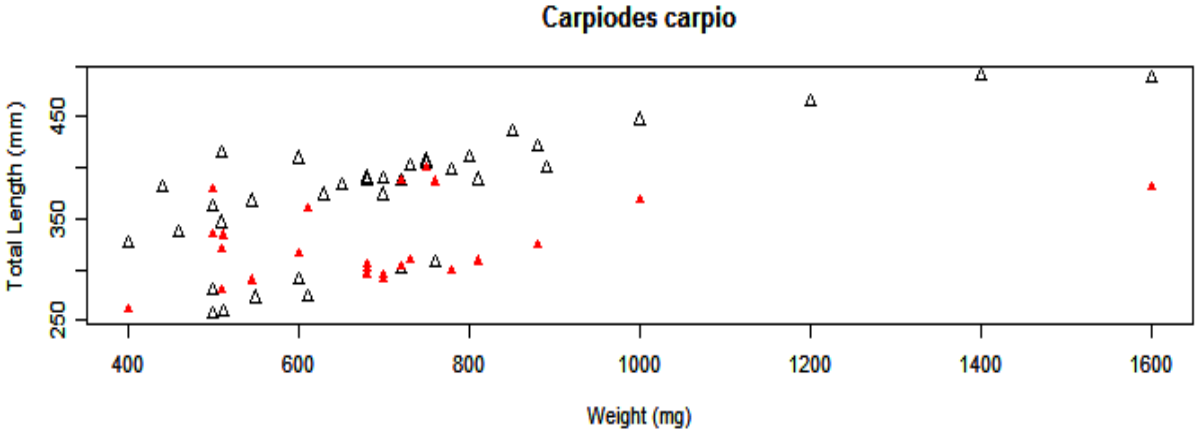

Carpiodes carpio
Total Length (mm)
250
350
450
400
600
800
1000
1200
1400
1600
Weight (mg)

Figure 7. Length and weight of infested (red triangles)and uninfested (open triangles) fishes from the three ecological host species. The interspersing of the open and red triangles indicates no difference in condition of infested and uninfested fish.

Appendix D

Relating Fish Abundance and Condition to Environmental Factors in Desert Sinkholes

Kristin W. Swaim and Wiebke J. Boeing

2008

Relating Fish Abundance and Condition to Environmental Factors in Desert Sinkholes

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2008 Annual Progress Report
New Mexico Department of Game and Fish
Share with Wildlife

Abstract

The relationships between fish assemblages and environmental factors have frequently been investigated. Often the focus has been on increasing or predicting yield or production for sport fisheries. Fish assemblages have also been studied to see if they show evidence of non-random patterns and, if so, what processes regulate those patterns. When relating fish communities to environmental variables, numerous studies have utilized a multiple-lake approach. These studies have largely been performed in north-temperate locations and little information is available about warmwater fish communities, like desert species. We studied native fishes in a sinkhole complex in New Mexico in the summers of 2006 and 2007 to determine if biotic, abiotic, or a combination of these factors influenced fish abundance and body condition. We investigated abundance using mark-recapture techniques and calculated population and catch-per-unit-effort estimates. Body condition was studied using the relative weight index. Abundance and condition were correlated with physical, chemical, and biological factors using regression analyses. Results showed that Pecos pupfish abundance was significantly lower in sinkholes where it occurred with other species. This was unexpected because all species were native and have potentially existed together for thousands of years. Pupfish body condition was also negatively influenced by the presence of other species. We suggest that low pupfish abundance and body condition is due to the presence of Pecos gambusia because it occurred in much greater numbers. Both predation and competition could be the means by which pupfish and gambusia interact. While pupfish and gambusia

do not compete for food or reproductive space, it appears likely that gambusia is in some way affecting pupfish reproduction. Abiotic factors like temperature, chlorophyll a, and salinity were significantly correlated with abundance and body condition, but the relationships varied between years, suggesting that either more data is necessary or that abiotic conditions in deserts are so variable that detecting patterns is difficult. This research contributed to multi-lake studies by providing information about desert systems and has serious management implications for the species studied since both Pecos pupfish and Pecos gambusia are species of concern.

Introduction

The relationships between fish assemblages and environmental factors have frequently been investigated. Often the focus has been on increasing or predicting yield or production for sport fisheries (see Hinch 1991). Fish assemblages have also been studied to see if they show evidence of non-random patterns and, if so, what processes regulate those patterns (see Jackson et al. 2001). When relating fish communities to environmental variables, numerous studies have utilized a multiple-lake approach. That is, several lakes are used as experimental units and environmental variables are correlated to fish assemblage structure (which can include species richness and presence/absence), biomass, production, yield, or abundance. For example, fish biomass has been correlated with total phosphorus (Moyle 1956), lake depth (Prepas 1983), and a macrobenthos biomass-mean depth ratio (Hanson and Leggett 1982). Fish production has been associated with lake depth (Rawson 1952) and total phosphorus and primary productivity (Downing et al. 1990). Hanson and Leggett (1982) further related their macrobenthos biomass-mean depth ratio to fish yield and also found a relationship with total phosphorus. Matuszek (1978) found individual correlations with yield and macrobenthos biomass and lake depth. Oglesby (1977) related yield to phytoplankton biomass and Ryder (1965) developed the morphoedaphic index (MEI), which related total dissolved solids-mean lake depth ratios to fish yield. The MEI was both commended and criticized for its simplicity (Ryder 1982) and its use of ratios has been deemed inappropriate due to spurious self-correlations (Jackson et al. 1990).

Perhaps most commonly studied are the associations between environmental variables and fish assemblage structure. Assemblage structure has been linked to pH (Rahel and Magnuson 1983, Rahel 1984, Rago and Weiner 1986, Persson 1997, Jackson et al. 2001), dissolved oxygen (Jackson et al. 2001), conductivity (Persson 1997), lake depth (Robinson and Tonn 1989, Rodriguez and Lewis 1997, Tejerina-Garro et al. 1998), lake area (Eadie and Keast 1984, Robinson and Tonn 1989, Rodriguez and Lewis 1997), Secchi depth (Rodriguez and Lewis 1997, Tejerina-Garro et al. 1998), lake connectedness (Tonn and Magnuson 1982, Olden et al. 2001), and winter oxygen concentration (Tonn and Magnuson 1982, Rahel 1984).

Abundance is possibly the least studied of the fish "indices" that are related to environmental factors, due to the difficulty in obtaining accurate estimates. Instead, relative abundance has been used and has been correlated with lake depth (Marshall and Ryan 1987), lake size (Hinch et al. 1991), and macrophyte cover and primary productivity (Hinch and Collins 1993).

The previous examples may cause one to conclude that abiotic variables are more important in structuring fish communities and abundances than biotic factors like competition and predation. However, in several of these same studies predation was also considered highly influential (see Tonn and Magnuson 1982, Rodriguez and Lewis 1997, Jackson et al. 2001, among others). Competition likely plays a role, although it is less understood, particularly in structuring fish assemblages (Jackson et al. 2001).

Can one set of environmental variables override another, e.g., can the effects of predation be negated by favorable temperature regimes? Quist et al. (2003) hypothesized that favorable abiotic conditions will be superseded by biotic variables when predator/competitor densities are high. Persson (1997) reanalyzed data from Sumari (1971 as cited in Persson 1997), finding that while his analysis agreed with Sumari's conclusion that biotic factors influence fish community structure, abiotic factors were also important (also discussed in Quist and Hubert 2005). It is likely environmental factors interact to some degree (Hinch 1991, Rodriguez and Lewis 1997, Jackson et al. 2001) and the importance of biotic variables may be habitat-specific (Hinch 1991).

Further complicating this issue is the matter of scale. Hinch's (1991) review of fish ecology research on small lakes stated that most studies are conducted on either a large or small scale. Small-scale studies have small taxonomic and environmental scales, that is, fewer species are present (median number of species was 2.5) and there is little variation in abiotic variables among lakes. Small-scale studies are often conducted for less than one year and frequently estimate species abundance. Large-scale studies are conducted on lakes with more species (median number of species was 24) and the magnitude of variation of abiotic variables among lakes is much larger. Large-scale studies occur over longer periods and usually focus on fish assemblage structure, as obtaining abundance estimates can be quite difficult. Since, by their design, small-scale studies cannot assess how abiotic variables affect abundance, biotic interactions are usually proposed to drive abundance patterns. By

contrast, large-scale studies typically conclude that abiotic variables influence assemblage types (Hinch 1991 and further discussion by Jackson et al. 2001). Clearly, the scale of the study can determine what questions are asked and researchers may unwittingly infer patterns that are more a product of the study design than of the data.

Multi-lake studies have largely been performed in north-temperate locations such as Wisconsin, Ontario, and Alberta. Consequently, studies have focused on cold- and coolwater fish communities and little information is available about warmwater fish communities (Hinch 1991). Studies have been conducted on species in tropical lakes (Rodriguez and Lewis 1997, Tejerina-Garro et al. 1998) and solution holes in Florida (Kobza et al. 2004) but information on desert species is limited by scarce water resources and the rarity of multiple lakes within a relatively confined geographic region. Yet, some groupings of water bodies in deserts exist, such as springs and sinkholes, and they support fish communities (see Kodric-Brown and Brown 1993 for a study of desert springs). Desert fish communities tend to be depauperate; springs and small streams may contain a single species (Soltz and Naiman 1981). What is lacking is more data regarding fish abundance as related to environmental factors in desert systems. While desert fishes do not have the same level of economic importance that sport fishes do, studying their patterns of abundance is important because they are some of our most endangered species.

Desert lentic habitats can be considerably varied, from the relative constancy of thermal, chemical, and discharge characteristics of springs to more wide-ranging

conditions of temperature, turbidity, and salinity in lakes (Deacon and Minckley 1974). Perhaps not surprisingly, desert fishes tend to have wide physiological tolerances to abiotic factors: they can withstand high temperatures, low dissolved oxygen levels, and high salinities (Barlow 1958, Lowe et al. 1967, Lowe and Heath 1969, Brown and Feldmeth 1971). Alternately, low species diversity would seem to indicate that biotic interactions are minimized as there are fewer species competing for resources. There are few predaceous fishes in desert habitats (Meffe 1985) and segregation into different niches is apparent (Deacon and Minckley 1974). How abiotic and biotic factors might interact in desert systems is unclear, but the generalist nature of species with respect to their tolerances for extreme conditions may make it difficult to discern competitive interactions (Deacon and Minckley 1974). It would seem likely that highly tolerant species could easily move into different niches, camouflaging evidence of competition.

We studied a sinkhole complex in New Mexico, in which sinkholes inhabited by fish primarily contain a single native species, but several contain two to three native species; no non-native fish species are present. Abiotic conditions vary greatly among sinkholes (unpublished data). Obviously, biotic interactions are minimal in sinkholes with just a single species (although intraspecific competition should be considered). In these sinkholes we investigated which abiotic variables were most associated with abundance and body condition. In sinkholes containing multiple species both abiotic and biotic factors were assessed. Because this research could be

considered both small- and large-scale, results should not be limited by study design and should add to the body of knowledge that multi-lake studies provide.

Materials and Methods

Study Area

Bitter Lake National Wildlife Refuge (BLNWR, Fig. 1) comprises approximately 23,350 acres (36 square miles) in southeastern New Mexico (Brooks and Wood 1988). The geology of this region is limestone—formed by layers of marine organisms, sand, and mud from the ancient Permian Sea—overlain by gypsum (Land 2003). Within the limestone and underneath the city of Roswell and BLNWR lies an aquifer, part of the Roswell Artesian Basin (Barroll and Shomaker 2003). Groundwater from the aquifer slowly dissolves the overlying layers of gypsum and forms caverns and sinkholes. The middle tract of BLNWR contains several dozen sinkholes. Most are circular and often steep-sided with a small littoral zone, although others are more lake-like. The substrate is silt/limestone bedrock and vegetation consists mostly of *Chara* and *Potamogeton* (Hoagstrom and Brooks 1999). Rolling tumbleweed (*Salsola*) can line the shore in large numbers and in smaller sinkholes nearly fills them.

Fish Community

Twenty-three sinkholes on the middle tract of BLNWR support native fishes. The Pecos pupfish (*Cyprinodon pecosensis*) occurs in twenty sinkholes. The Pecos

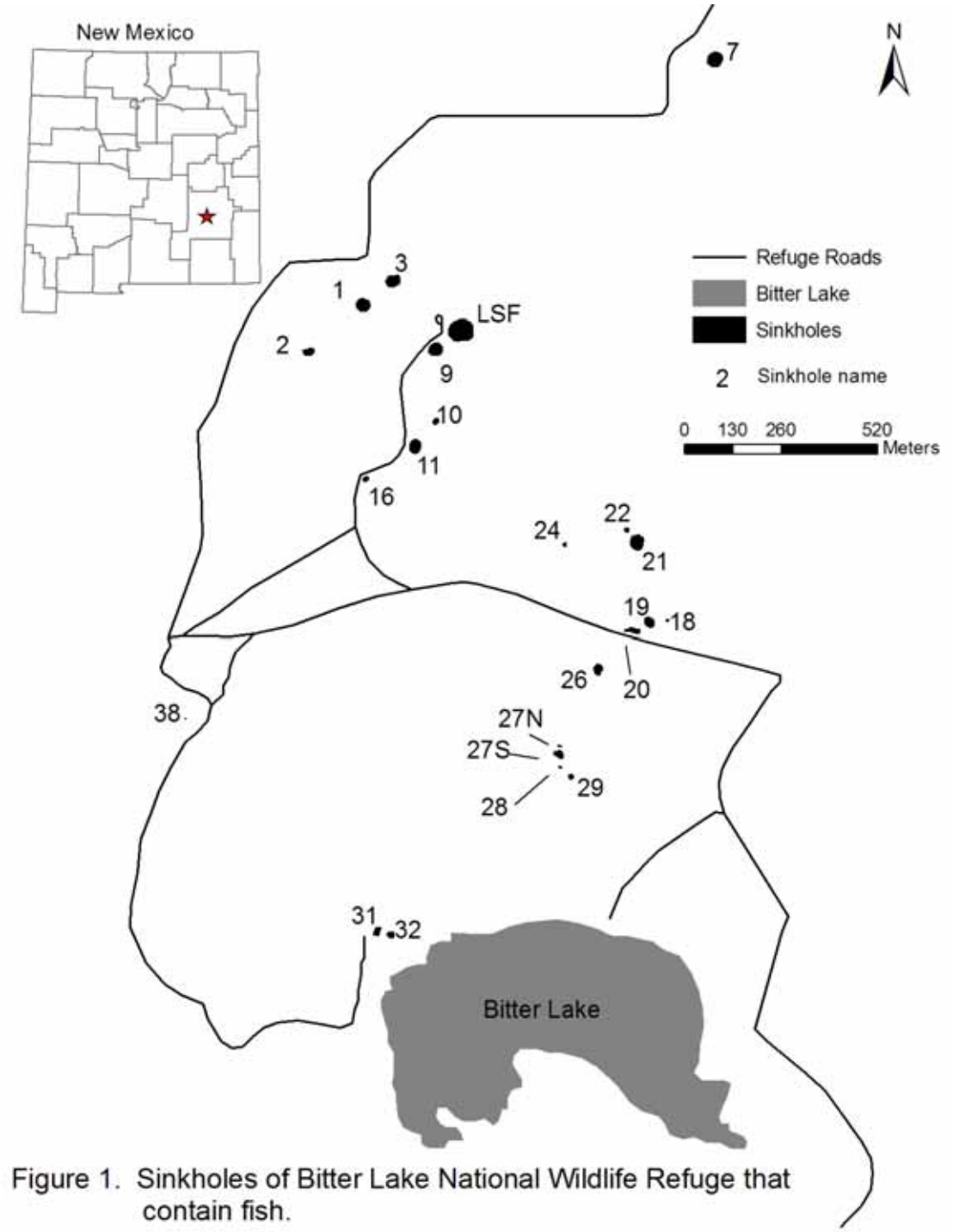


Figure 1. Sinkholes of Bitter Lake National Wildlife Refuge that contain fish.

gambusia (*Gambusia nobilis*) occurs in six sinkholes. The plains killifish (*Fundulus zebrinus*) occurs in five sinkholes and the red shiner (*Cyprinella lutrensis*) is present in one sinkhole. For a list of species per sinkhole see Table 1.

The establishment of the native fish community is unknown. The nearby Pecos River occasionally inundated the refuge (Brooks and Wood 1988) and could have been a potential source of fish, as could have Bitter Creek (Hoagstrom and Brooks 1999). In the 1930s many sinkholes were connected via a system of canals dug to harness water for the creation of waterfowl areas (Brooks and Wood 1988) and fish could have moved amongst the sinkholes (the canals have since been filled in). Several sinkholes were at one time stocked with game fish and native species could have accidentally been introduced (Brooks and Wood 1988). Finally, native species have been intentionally introduced to supplement populations but records are incomplete (Gordon Warrick, personal communication). These uncertainties greatly limit hypotheses concerning how the fish community may have evolved. One final note: although several sinkholes are in close proximity to each other, it is believed that subterranean movement of fishes among sinkholes is not likely (Gordon Warrick, personal communication).

Fish Sampling

Jackson and Harvey (1997) stated that small-bodied fish species (which comprise all species in sinkholes at BLNWR) are most effectively captured with minnow traps. From this information, combined with the fact that the steep-sided

nature of the sinkholes eliminated the possibility of using seines, we concluded that minnow traps would most successfully capture fish. We conducted a pilot study in April 2006 to establish the appropriate number of minnow traps to set in each sinkhole. We decided to set vertical arrays of minnow traps so that a considerable portion of the water column could be sampled. One trap was set 0.5 meters from the bottom, one at mid water-column depth, and one 0-0.5 meters from the surface. Traps were attached to rope that was anchored to the bottom by a brick and secured at the top with an empty milk jug to ensure proper placement in the water column. In shallower sinkholes (those with perimeter depths of 2 meters or less) we removed the middle trap. Arrays were set approximately 2.5 meters from shore (nearshore) and further offshore. After an initial trial in which offshore traps caught few fish, we continued the pilot study with traps set only on the nearshore. We predicted that setting arrays in the nearshore every 5 meters around the perimeter of a sinkhole would allow me to capture a sufficient number of fish to effectively estimate population size. We tested this prediction on two sinkholes. Estimated population sizes were 405 ± 59 and 7486 ± 1305 (95% confidence interval) adult pupfish, which we thought were reasonable estimates. Because of the small number of fish captured in the middle traps in 2006, we eliminated them from my sampling protocol in 2007.

Full data collection began at the end of July and lasted approximately 2.5 weeks in both 2006 and 2007. This time period was selected because fish are most active in warmer months and it also coincided with the end of the pupfish spawning season. Aside from not wanting to hinder reproduction, male Pecos pupfish establish

and defend territories during the spawning season and there was concern that sampling during this time could result in lower catch rates because males may not move far from their territories. All sinkholes that contained fish (n = 23) were sampled. Due to its connection to a small spring, sinkhole 31, while sampled for fish and environmental variables, was excluded from statistical analyses.

Mark-recapture methods were used to estimate abundance of adult (≥20 mm standard length) pupfish. Baited minnow traps (0.32-0.64 cm mesh) were set in late afternoon / early evening, and retrieved the following morning. Traps were set from 13 to 20 hours. Captured fish were marked by clipping the upper portion of the caudal fin with scissors.

Due to the smaller caudal fin of Pecos gambusia, mark-recapture methods were not possible. Instead, catch-per-unit-effort (CPUE) was calculated to determine relative abundances of gambusia. In 2006, the mesh size of the minnow traps was too large to reliably capture gambusia and therefore CPUE was not calculated. In 2007, the traps were lined with window screening (0.1 cm mesh) that enabled juvenile and adult gambusia to be captured. Juvenile pupfish were also captured with the smaller mesh size. We kept separate counts of juvenile and adult pupfish so that comparisons could be made between years.

Standard lengths (tip of snout to posterior end of vertebral column, in mm) and weights (g) of up to fifty adult individuals per species were measured as an index of body condition. The diet of Pecos pupfish was also examined. Several unbaited traps were set for approximately 30 minutes and five captured adults were sacrificed

per sinkhole for the majority of sinkholes in which they occurred. Fish were preserved in 10% formalin until they could be processed in the lab. Once in the lab, fish were dissected under a microscope. Length was measured, sex was determined, and amount of fat (high or low) was recorded. Gut length was measured, as was relative fullness of the gut. Items in the gut were ranked according to abundance. Pecos gambusia diet was not analyzed.

Environmental Factors – Abiotic

Two morphometric variables, total depth and diameter, were measured with metered rope. To measure total depth, the rope was attached to a brick and dropped in the center of each sinkhole; depth was measured to the nearest tenth of a meter. The rope was then strung across the diameter of each sinkhole and measured to the nearest half-meter. For the few non-circular sinkholes, the long and short axes were measured and then averaged.

A Hydrolab (Hach Environmental) measured temperature, salinity, dissolved oxygen, pH, and turbidity at 1-m depth intervals and average values for each sinkhole were also calculated. A horizontal water sampler collected water samples at 1-m depth intervals. The samples from each meter were mixed in a bucket. Two 125-mL water samples were obtained in 2006: one for the analysis of total phosphorus and the second for calcium carbonate. Both samples were kept at 4°C until they were handed over to NMSU's Soil, Water, and Agricultural Testing (SWAT) Lab for analysis. Total phosphorus and calcium carbonate were not measured again in 2007.

Secchi depth, a measure of lake transparency, was measured with a Secchi disk. Abiotic variables were collected from forty-one sinkholes (twenty-three with fish and eighteen fishless) in both years.

Environmental Factors – Biotic

Aside from competition and predation, there are a few other biotic variables to consider. From the water sample collected in the manner described above, chlorophyll a was measured, giving an estimate of phytoplankton biomass. 100-500 mL of the water sample was filtered with a hand pump onto a GF/C filter. The filters were wrapped in aluminum foil and kept frozen until they could be processed. Filters were ground in a foil-covered test tube with an aqueous acetone-magnesium carbonate solution and allowed to sit overnight. The following day the samples were centrifuged and the extract decanted. The extract was acidified with hydrochloric acid and chlorophyll a was measured with a spectrophotometer (Thermo Spectronic 20D+) according to APHA standards (Clesceri et al. 1998). Chlorophyll a was calculated as follows:

$$\text{Chlorophyll a, mg/m}^3 = \frac{26.7\,(664_b - 665_a) \times V_1}{V_2 \times L}$$

where: V_1 = volume of extract, liters

V_2 = volume of filtered sample, m^3

L = width of cuvette, cm

664_b, 665_a = optical densities of extract before and after acidification, respectively.

Zooplankton samples were collected via vertical tows with a zooplankton net (Ø 20 cm, 110-µm mesh). Two samples were collected and pooled per sinkhole in 2006 and preserved in 95% ethanol. One sample per sinkhole was collected in 2007. Samples were processed in the lab. A subsample was taken and at least 100 individuals of the most abundant species were counted using a dissecting microscope.

A petite ponar was used to collect two benthic samples per sinkhole in 2006. Samples were taken from the nearshore where minnow traps were set. Approximately two cups from each sample were taken from the ponar, transferred to plastic containers, and preserved in 95% ethanol. Upon returning to the lab, samples were washed through a 4760-µm sieve to separate larger particles and then a 500-µm sieve. All invertebrates were sorted under a dissecting microscope, preserved in 70% ethanol, and then identified to family. Biotic variables were collected from forty-one sinkholes.

Data Analyses

Fish abundance – The modified Lincoln-Petersen method was used to estimate adult pupfish abundance (Ricker 1975, with Chapman's modification that provides less bias).

$$\text{Population size, } N, = \left[\frac{(M+1)\times(C+1)}{R+1}\right] - 1$$

where: M = number of fish marked on first day

C = number of fish captured on second day

R = number of fish captured on second day that are recaptures.

Variance of N, with a modification from Seber (1970) for less bias, can be estimated as:

$$\text{Var}\,(N) = \frac{\left[(M+1)\times(C+1)\times(M-R)\times(C-R)\right]}{\left[(R+1)^2\times(R+2)\right]}$$

For a few sinkholes, when capture rate was very low, traps were set for an extra night and the Schnabel method was then used to estimate abundance (Ricker 1975, with Chapman's modification).

$$\text{Population size, } N, = \frac{\sum(M_t \times C_t)}{\left(\sum R_t\right)+1}$$

where: C_t = total number of individuals caught in sample t

M_t = number of marked animals in the population just before the tth sample is taken

R_t = number of individuals already marked (recaptures) when caught in sample t.

The variance can be calculated by inverting the following:

$$\text{Var}\,(1/N) = \frac{\sum R_t}{\left(\sum\left(M_t \times C_t\right)\right)^2}$$

CPUE was computed as fish per trap per day. For each trap, the number of fish captured was divided by the number of hours the trap was set (fish/hour). This was summed together for all traps in the sinkhole, and then divided by the number of traps set and multiplied by 24.

Body condition – I chose to look at body condition because it can indicate the general health of a fish. The weight of a fish relative to its length suggests its physiological condition and examination of condition may provide information about its habitat (Murphy et al. 1990, Blackwell et al. 2000). We used relative weight (Wege and Anderson 1978) as an index of body condition. Relative weight (W_r) is:

$$W_r = W / W_s \times 100$$

where W = the observed weight of an individual fish

W_s = a length-specific standard-weight value.

75^{th} percentile weights are used to calculate standard weights because they represent fish in better-than-average condition (Wege and Anderson 1978). No standard optimal relative weight exists and some researchers contend that relative weight target ranges depend on the species and management objectives (Murphy et al. 1991). Nonetheless, ranges of 90-100, 95-100, and 95-105 have been suggested (see Murphy et al. 1990, Murphy et al. 1991). Anderson and Neumann (1996) stated that relative weight values well above 100 for a species may indicate that the species is not under enough predation pressure and that other species are not taking advantage of a surplus in this species and that this is undesirable from a management perspective. Since we

was not concerned with this scenario, we decided that a relative weight ≥95 indicates a fish in good condition.

To develop a standard weight equation we used the regression-line-percentile (RLP) technique (Murphy et al. 1990), which is a popular method for the development of standard weight equations (Blackwell et al. 2000). Equations are developed from several populations of the species of interest. The procedure is as follows (from Murphy et al. 1990): Mean fish weight in 1-cm length intervals is predicted for each population by regressing log weights against log lengths. The 75th percentile of the mean weights (from all populations) in each 1-cm interval is identified. The 75th percentile weights are then regressed against length and this determines the parameters for the standard weight equation. Because the species studied here were small (approximate adult size range 20-40 mm), we used 1-mm length intervals. Unlike Murphy et al. (1990), instead of calculating mean weights for each population (sinkhole), we decided to pool data from all sinkholes to develop a standard weight equation. We felt this was necessary because we wanted to compare relative weights among sinkholes. Equations were developed for both pupfish and gambusia; in 2007 a second equation was developed for pupfish to compare it to the equation from 2006. A concern with standard weight equations is that they may be length-biased, that is, relative weight increases or decreases with length (Murphy et al. 1990). The RLP technique removes any length-related biases (Neumann and Murphy 1991, although this is disputed by Gerow et al. (2004)). As long as length-related trends are not present in a large number of sinkholes, indicating a general

pattern of bias, then any trends within a sinkhole can be indicative of environmental conditions (Murphy et al. 1990, Neumann and Murphy 1991). We checked for length-related trends by regressing mean relative weights against length intervals as suggested by Murphy et al. (1990), which can also reveal other patterns across size classes. An average relative weight was then calculated for each sinkhole.

Standard weight equations are primarily used in fisheries management and have been mostly developed for centrarchid game species (Blackwell et al. 2000), though equations have recently been developed for some nongame species (Bister et al. 2000, Didenko et al. 2004). It may seem inappropriate to develop standard equations for such small species in which the range of size classes is narrow and may not be as ecologically significant as compared to larger fish. However, the objective was to develop a metric for body condition that could be regressed against environmental factors.

Fish abundance and body condition vs. environmental factors – Multiple linear regression analyses were used to discern associations between abundance and body condition and environmental factors. Separate regressions were done for both years and both dependent variables. Analyses were further divided into sinkholes containing just pupfish and sinkholes containing multiple species (herein referred to as "Pupfish-only Group" and "Multi-species Group", respectively) because pupfish abundance was mainly influenced by the presence/absence of other species. To account for multiple species, a dummy variable was created where sinkholes containing only pupfish were given a value of 0 and those containing multiple species

given a value of 1. It was not possible to calculate pupfish population estimates in some sinkholes. As a result, CPUE was used because it gave a more accurate picture of pupfish abundance among sinkholes and allowed for all sinkholes to be used in the regression analyses. Data for gambusia was included in 2007. Sinkhole 27N, which contained only gambusia, was included in gambusia regression analyses to increase sample size, although close attention was paid to its role in results. This sinkhole was not included in the analyses that combined all sinkholes since it did not have pupfish. Fourteen total regression analyses were performed using SAS (SAS Institute 2003). Collinearity among variables, which can create misleading models, was first examined by calculating Pearson correlation coefficients, plotting variables, and examining variance inflation factors. Some variables were removed from further analysis if their correlations, $|r|$, were greater than or equal to 0.9, which indicates severe collinearity. Most often Secchi depth, diameter, and calcium carbonate were removed, but this depended on the analysis. The following model selection methods were applied: forward (entry level $\alpha = 0.10$), backward (stop level $\alpha = 0.10$), stepwise (entry level $\alpha = 0.15$, stop level $\alpha = 0.10$), r-square, adjusted r-square, and Akaike's Information Criterion (AIC). Ideally, all techniques would result in the same model, but this was never the case. Instead, the best one-, two-, three-, and four-variable models provided by the selection techniques were evaluated based on overall model p-value, parameter p-values, and adjusted r-square value. Rather than specify a particular α level for significance, the model with the lowest overall and parameter p-values was chosen and its p-values reported. Once a model was chosen,

residual diagnostics were performed, in which studentized residuals and potential influential observations and outliers were examined. The assumption of normality was tested with the Shapiro-Wilk test. Equal variances were checked by plotting residuals against predicted values. Any observations deemed to be outliers for several of the diagnostics were removed and the data were re-analyzed to see if a different model was more appropriate.

Diet – Once food items were ranked for each of the five fish sacrificed per sinkhole an average rank of food items per sinkhole was calculated. For example, diatoms were ranked 4, 4, 3, 5, and 6 in the five fish collected from Sinkhole 22, giving an average of 4.2. After each food item had been averaged as such, the averages were re-scored to provide rankings on a per-sinkhole scale so comparisons could be made among sinkholes. For example, if the diatom average score for sinkhole 22 was 4.2, detritus average score was 2.8, and dinoflagellate average score was 5.6, these would be re-scored as 2, 1, and 3, respectively. We used cluster analysis (SAS Institute 2003) to evaluate whether sinkholes could be meaningfully grouped based on pupfish diet. We standardized food items to zero mean and unit variance to limit those variables with larger variances from having more of an effect on cluster formation. Euclidean distance was used as the measure of dissimilarity and average linkage was the fusion strategy used to form clusters (McGarigal et al. 2000). Significant differences between cluster means for each food item were tested using Wilcoxon rank-sum tests.

Results

Fish Abundance

In 2006, pupfish CPUE was significantly higher in the Pupfish-only Group than the Multi-species Group (Wilcoxon rank-sum test, $p = 0.0002$, Fig. 2a). The same result was present in 2007 (Wilcoxon rank-sum test, $p = 0.0001$, Fig. 2b). Gambusia CPUE was not significantly different from pupfish CPUE where they co-occurred (Wilcoxon rank-sum test, $p = 0.1320$, Fig. 2b). This has largely to do with the very low catch rate for gambusia in two sinkholes. Obviously, with the exception of those two sinkholes, catch rate was much greater for gambusia. While gambusia CPUE included both adult and juvenile stages, no juvenile pupfish were caught in the sinkholes where they occurred with gambusia with the exception of two juveniles from Sinkhole 7; this allowed for direct comparisons to be made. Plains killifish CPUE (mean = 1.88) was not significantly different from pupfish CPUE (Wilcoxon rank-sum test, $p = 0.2159$, not shown). Significant differences in CPUE were not present between years in the Pupfish-only Group (Wilcoxon rank-sum test, $p = 0.3064$, Fig. 3a). The same was true for the Multi-species Group (t-test, $p = 0.5969$, Fig. 3b). Catch rate did vary among sinkholes. Within the Pupfish-only Group, sinkholes that had few pupfish in 2006 had higher catch rates in 2007 and vice versa (Figure 3a). Overall more pupfish were captured in 2007. Table 1 provides greater detail of CPUE for all species and population estimates for pupfish.

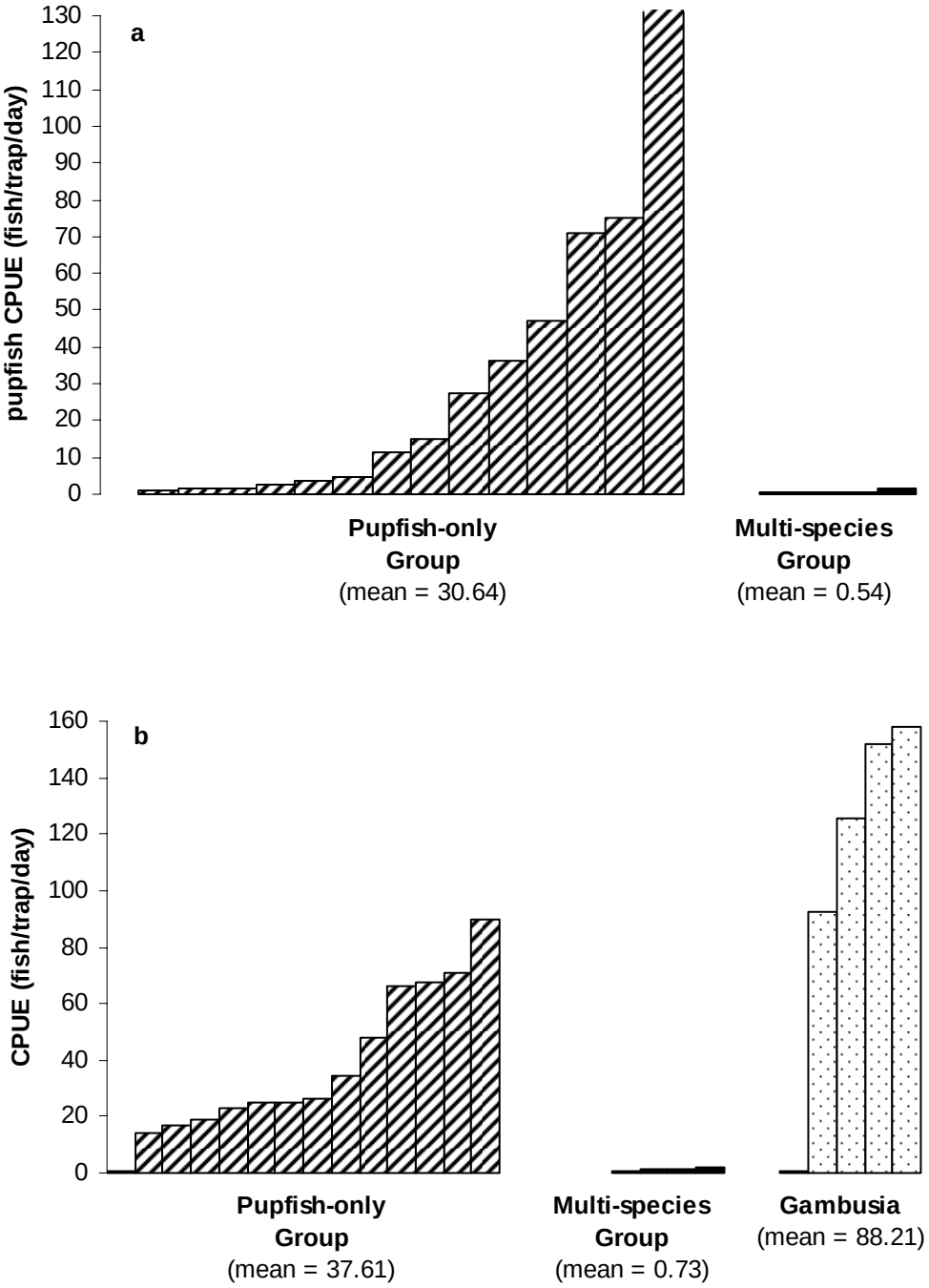


Figure 2. Pecos pupfish CPUE for 2006 (a) and 2007 (b), with data included for Pecos gambusia in 2007. Each bar represents a sinkhole.

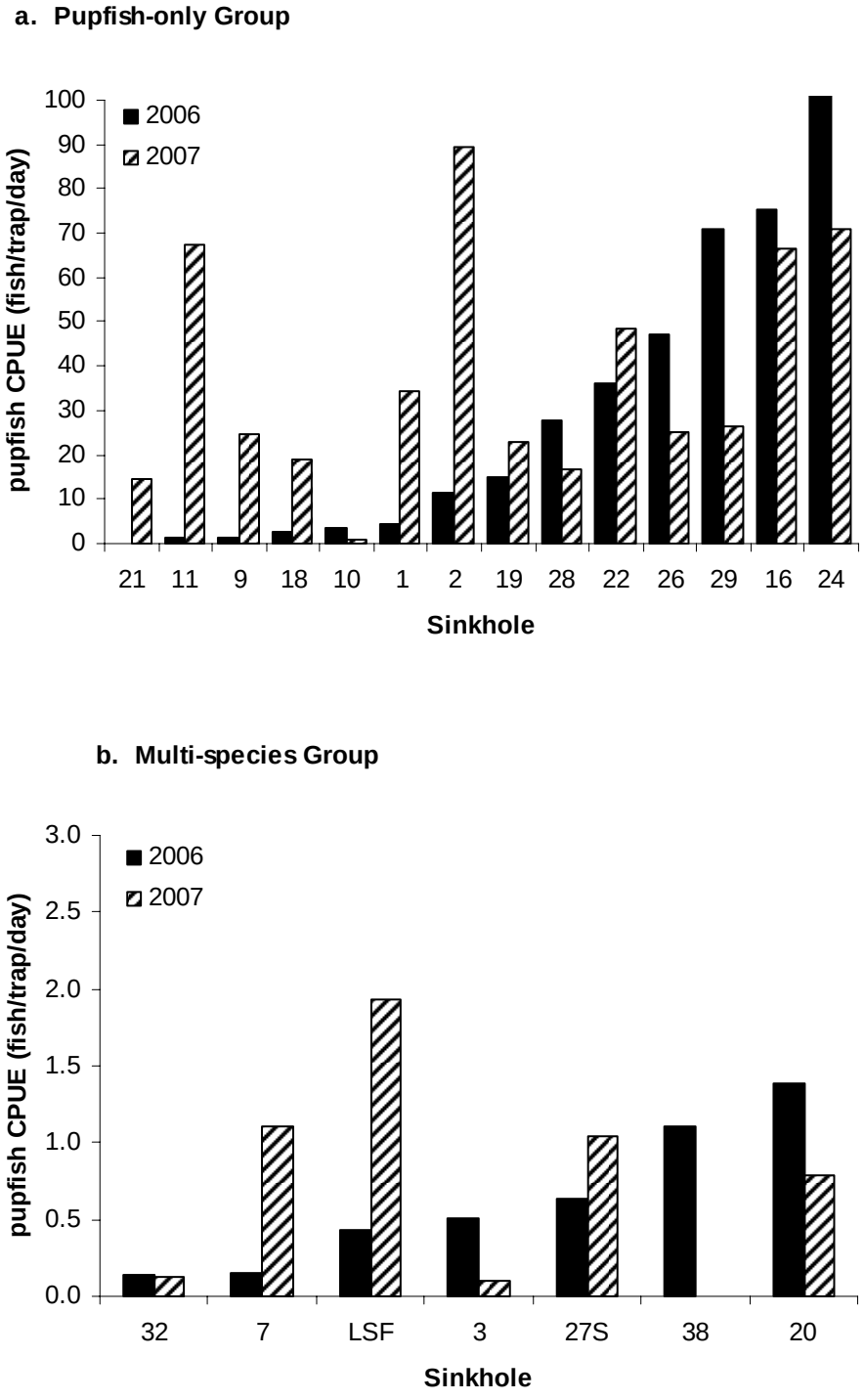


Figure 3. Yearly comparisons of Pecos pupfish CPUE for the Pupfish-only Group (a) and the Multi-species Group (b). Note the different scales on the Y-axes.

Table 1. Catch-per-unit-effort (CPUE), average relative weight, and population estimates for sinkholes of Bitter Lake NWR, 2006 and 2007. 95% confidence intervals for population estimates are given in parentheses. Pupfish CPUE is for adults only. An 'x' indicates the variable was not calculable or the estimate was poor; population estimates are for adult pupfish only. Pup = Pecos pupfish; Gam = Pecos gambusia; Killi = plains killifish; Shiner = red shiner.

Sinkhole	Species	CPUE (fish/trap/day)		Population Estimate		Avg. Relative Weight (%)	
		2006	2007	2006	2007	2006	2007
1	Pup	4.59	34.37	3524 (3265-3829)	5290 (4628-5951)	102	101
2	Pup	11.30	89.51	2656 (1786-3526)	7890 (7199-8581)	99	88
3	Pup	0.50	0.10	x	x	95	107
	Gam	x	92.82	x	x	x	84
7	Pup	0.15	1.11	x	116 (85-147)	82	94
	Gam	x	158.10	x	x	x	88
	Killi	0.66	0.28	x	x	x	x
9	Pup	1.49	24.68	3386 (3061-3787)	3454 (2980-3927)	83	85
10	Pup	3.37	0.84	664 (617-718)	x	101	88
11	Pup	1.32	67.22	x	5224 (4692-5755)	93	91
16	Pup	75.23	66.30	4657 (4076-5238)	4955 (3813-6096)	89	86
18	Pup	2.47	18.91	x	313 (236-391)	87	94
19	Pup	14.79	22.93	1850 (1537-2162)	1458 (1314-1601)	123	92
20	Pup	1.39	0.78	x	x	85	94
	Gam	x	0.74	x	x	x	111
	Shiner	7.84	1.44	x	x	x	x
21	Pup[a]	x	14.40	x	2721 (2275-3168)	x	101
22	Pup	36.06	48.26	x	991 (836-1146)	99	92

[a] Not captured in 2006.

Table 1 (continued)

Sinkhole	Species	CPUE (fish/trap/day)		Population Estimate		Avg. Relative Weight (%)	
		2006	2007	2006	2007	2006	2007
24	Pup	131.43	70.85	2462 (2235-2689)	1502 (1397-1608)	94	98
26	Pup	47.21	25.31	4871 (4321-5420)	2237 (2054-2421)	88	97
27N	Gam	x	185.61	x	x	x	91
27S	Pup	0.64	1.05	x	77 (69-86)	86	88
	Gam	x	151.75	x	x	x	80
	Killi	2.09	2.66	x	x	x	x
28	Pup	27.58	16.78	1458 (1168-1748)	826 (661-991)	98	89
29	Pup	71.02	26.22	4677 (3848-5507)	1278 (1103-1453)	93	86
32	Pup	0.14	0.12	x	x	92	x
	Gam	x	0.30	x	x	x	x
	Killi[a]	x	0.12	x	x	x	x
LSF	Pup	0.43	1.93	329 (36-622)	315 (299-333)	79	82
	Gam	x	125.57	x	x	x	88
	Killi	0.45	1.41	x	x	x	x
38	Pup[b]	1.11	0.00	x	x	90	x
	Killi[a]	x	4.92	x	x	x	x

[a] Not captured in 2006.
[b] Only one juvenile was captured in 2007

Body Condition

In 2006, the standard weight equation for pupfish was:

$$log(W_s) = 3.3599 * log(Length) - 4.9423$$

where W_s = the length-specific standard weight and *Length* = standard length in mm. In 2007, this equation was:

$$log(W_s) = 3.0749 * log(Length) - 4.5104$$

The standard weight equation developed for gambusia in 2007 was:

$$log(W_s) = 3.0259 * log(Length) - 4.6561$$

The equations were not length-biased. With the exception of a few sinkholes, only weak correlations existed between length and relative weight (Appendix A).

In 2006, pupfish relative weight was higher in the Pupfish-only Group than the Multi-species Group (Wilcoxon rank-sum test, p = 0.0242, Fig. 4a). Results are still significant if the sinkhole with the highest relative weight is removed. In 2007, there was no difference in relative weight (t-test, p = 0.7737, Fig. 4b). There was no difference in relative weight of pupfish and gambusia where they co-occurred (t-test, p = 0.6919, Fig 4b). For the Pupfish-only Group, a significant difference in relative weight between years was not present (Wilcoxon rank-sum test, p = 0.2689, Fig. 5a). The same was true for the Multi-species Group (t-test, p = 0.1936, Fig. 5b), although relative weight increased on a per-sinkhole basis. Table 1 gives exact average relative weights for each sinkhole.

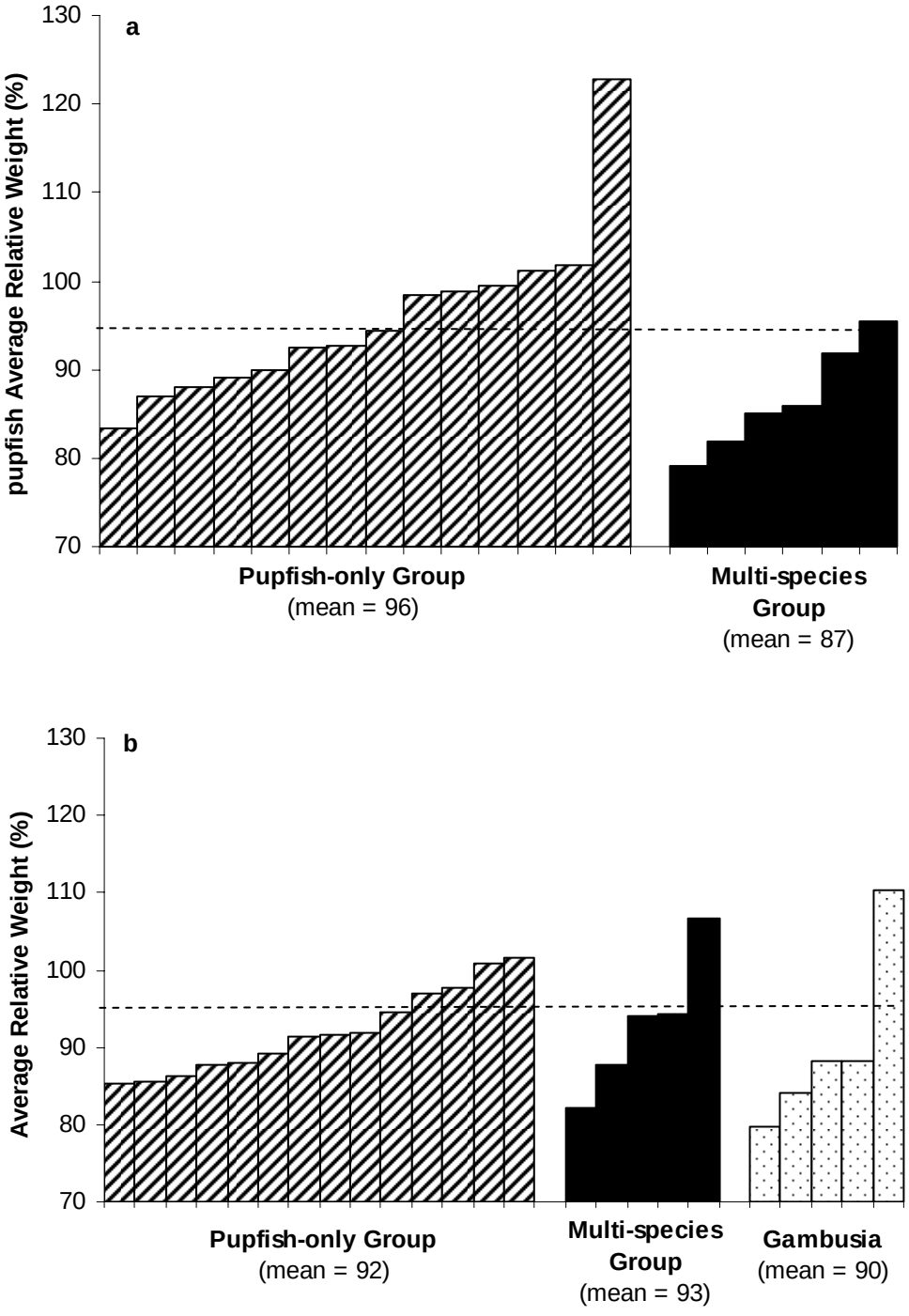


Figure 4. Pecos pupfish relative weight for 2006 (a) and 2007 (b), with data included for Pecos gambusia in 2007. Each bar represents a sinkhole. Values above the dashed line indicate fish in good condition.

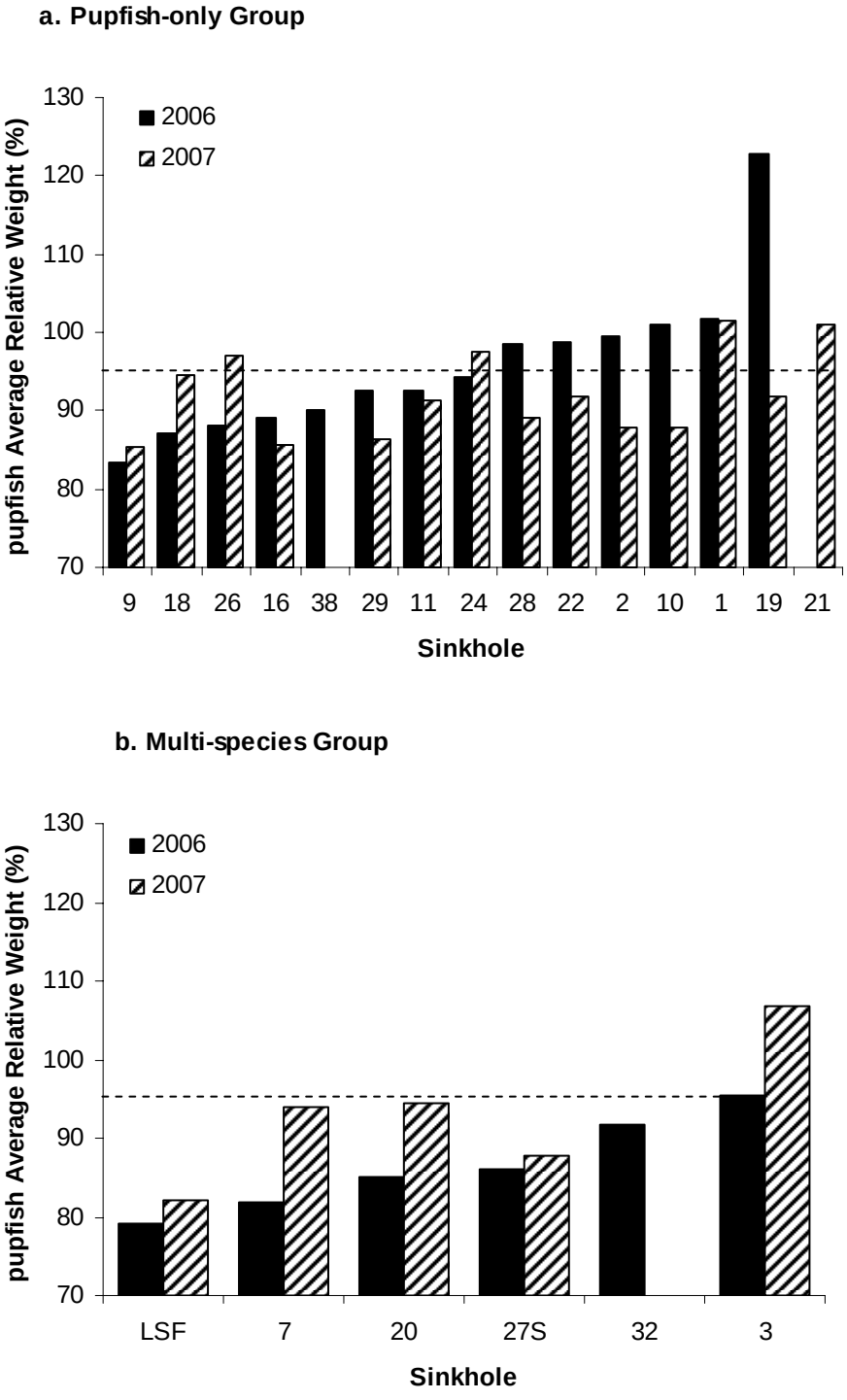


Figure 5. Yearly comparisons of Pecos pupfish relative weight for the Pupfish-only Group (a) and the Multi-species Group (b). Values above the dashed line indicate fish in good condition.

Environmental Factors – Abiotic and Biotic

Appendix B lists average values of the environmental variables for each sinkhole. Calcium carbonate was so highly correlated with salinity ($r = 0.92$) that it was not measured in 2007. Total phosphorus resolution was too poor to be useful for the regression analyses and also was not measured in 2007 (we used total phosphorus data collected by W. Boeing from 2005 but it was ultimately not significant in any regression models). Zooplankton and benthic samples are still being processed and thus were not part of the analysis. Averaged from all forty-one sinkholes, there were significant increases from 2006 to 2007 for total depth ($p = 0.0471$) and turbidity ($p = 0.0005$) and chlorophyll a was nearly significant ($p = 0.0531$). Salinity significantly decreased from 2006 to 2007 ($p = 0.0220$; all tests were Wilcoxon rank-sum tests). Between the two groups of sinkholes, salinity was significantly higher in the Pupfish-only Group (Wilcoxon rank-sum test, $p = 0.0101$) and oxygen was significantly lower (t-test, $p = 0.0311$) in 2006. In 2007, salinity was again significantly higher in the Pupfish-only Group (Wilcoxon rank-sum test, $p = 0.0013$), as was temperature (t-test, $p = 0.0052$) and chlorophyll a (Wilcoxon rank-sum test, $p = 0.0285$). Of note was sinkhole 21: in 2006 this sinkhole had almost no dissolved oxygen and a salinity of 122 ppt, nearly four times saltier than the ocean. Yet this sinkhole contained pupfish. Although no pupfish were captured in the traps, we observed a few swimming at the surface, likely obtaining oxygen from the air. We were able to catch one fish with a small dip net and found it to be emaciated. In 2007, salinity had decreased to 87 ppt and we estimated the pupfish population to be at least 2500.

Abundance and Body Condition vs. Environmental Factors

Figures 6-9 show the results of the fourteen regression analyses. Figure 6 illustrates the results for CPUE in 2006. When all sinkholes were included, the negative effect of other species on pupfish abundance was confirmed (Fig. 6a). In the Pupfish-only Group, CPUE was associated positively with oxygen and chlorophyll a and negatively with total depth (Fig. 6b). In the Multi-species Group, abundance was positively associated with temperature and negatively associated with chlorophyll a, but this model was not significant (Fig. 6c). Results were different for pupfish abundance in 2007. The effect of other species on pupfish abundance was still apparent (Fig. 7a). However, in both groups of sinkholes, CPUE was associated with temperature: positively in the Pupfish-only Group (Fig. 7b; note that the model was not significant), but negatively in the Multi-species Group (Fig. 7c). Temperature was highly correlated with total depth ($r = -0.86$) in the Multi-species Group. Gambusia abundance was related positively to salinity and negatively to oxygen and chlorophyll a, but the model was not significant (Fig. 7d).

Figure 8 shows the results for relative weight in 2006. When all sinkholes were included, the negative effect of other species on pupfish relative weight was recognized (Fig. 8a), yet it appeared to be driven by the same high relative weight as in Figure 4a. If this sinkhole is removed then pupfish relative weight was negatively associated with total depth (Fig. 8b). Again, this model appeared to be driven by a single point. If this sinkhole is also removed, then pupfish relative weight was once

again negatively associated with the presence of other species (not shown). There was a positive relationship between relative weight and temperature in the Pupfish-only Group, but the relationship is poor and may be due to a single observation (Fig. 8c). If this sinkhole is removed then no factors correlate with relative weight and this may be a more appropriate conclusion. In the Multi-species Group relative weight was positively associated with salinity and chlorophyll a (Fig. 8d). In 2007, the presence of other species did affect pupfish relative weight when all sinkholes were analyzed together, as did temperature (Fig. 9a). In this case, species presence is positively related to relative weight, yet there was no difference in relative weight among the two groups of sinkholes (Figure 4b) and Fig. 9a shows little difference between the two groups. When sinkholes are split into their respective groups both are positively associated with temperature (Figs. 9b and 9c). In the Pupfish-only Group, temperature was highly correlated with salinity ($r = 0.87$). The strength of this model appears to be influenced by one observation, as does the correlation with salinity. When this sinkhole is removed the best model is still one with temperature as a predictor but the p-value becomes much larger ($p = 0.3985$) and there is no longer a strong correlation with salinity. Again, it may be more appropriate to conclude that no variables explain relative weight for this group. In the Multi-species Group temperature was highly correlated with total depth ($r = -0.85$). Gambusia relative weight was negatively associated with total depth and salinity (Fig. 9d) but the model was not significant. Results are summarized in Table 2.

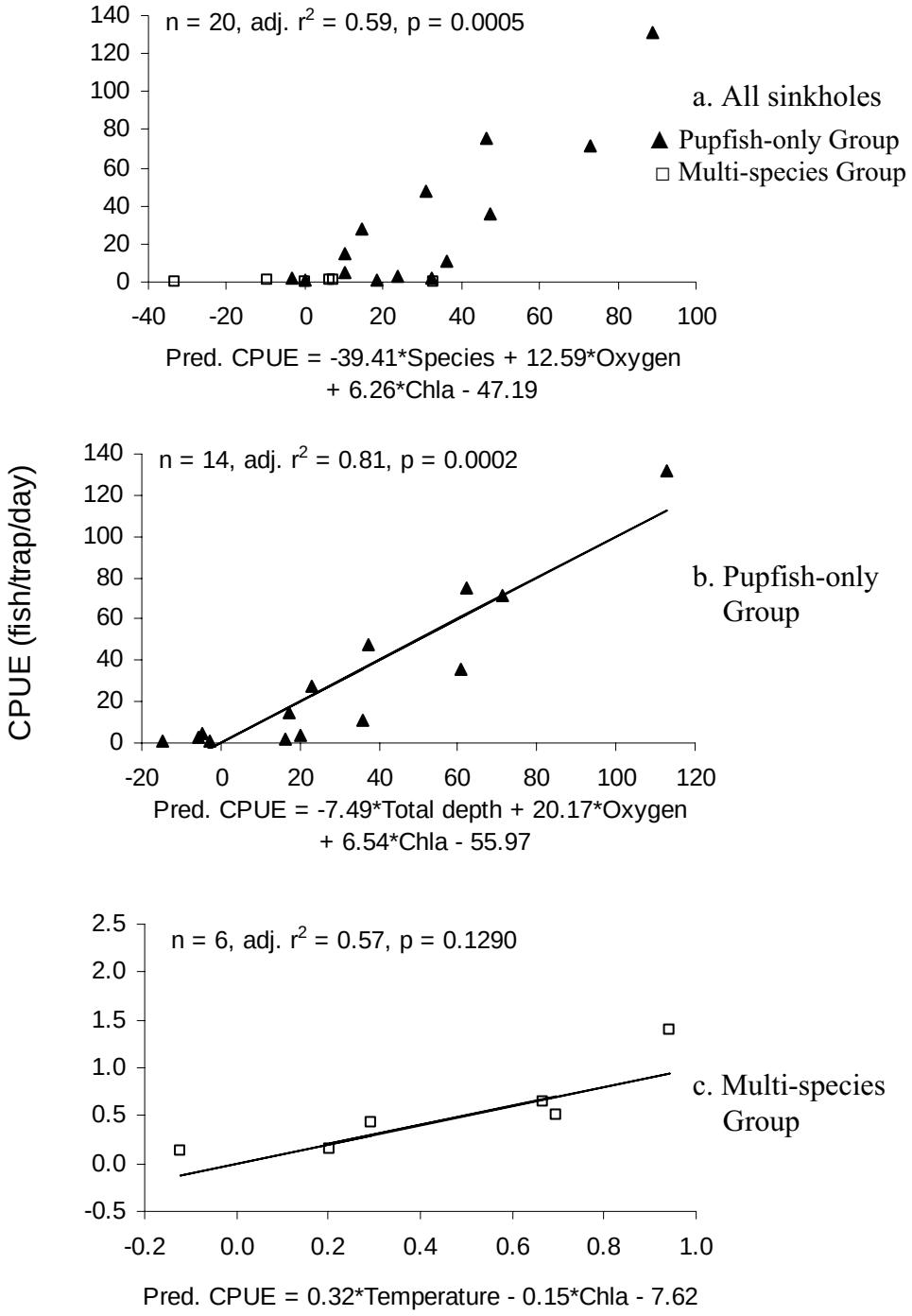


Figure 6. Predicted regression models for pupfish CPUE, 2006. Where there are two or more predictors, the x axis becomes a combination of the predictors so that results can be displayed graphically.

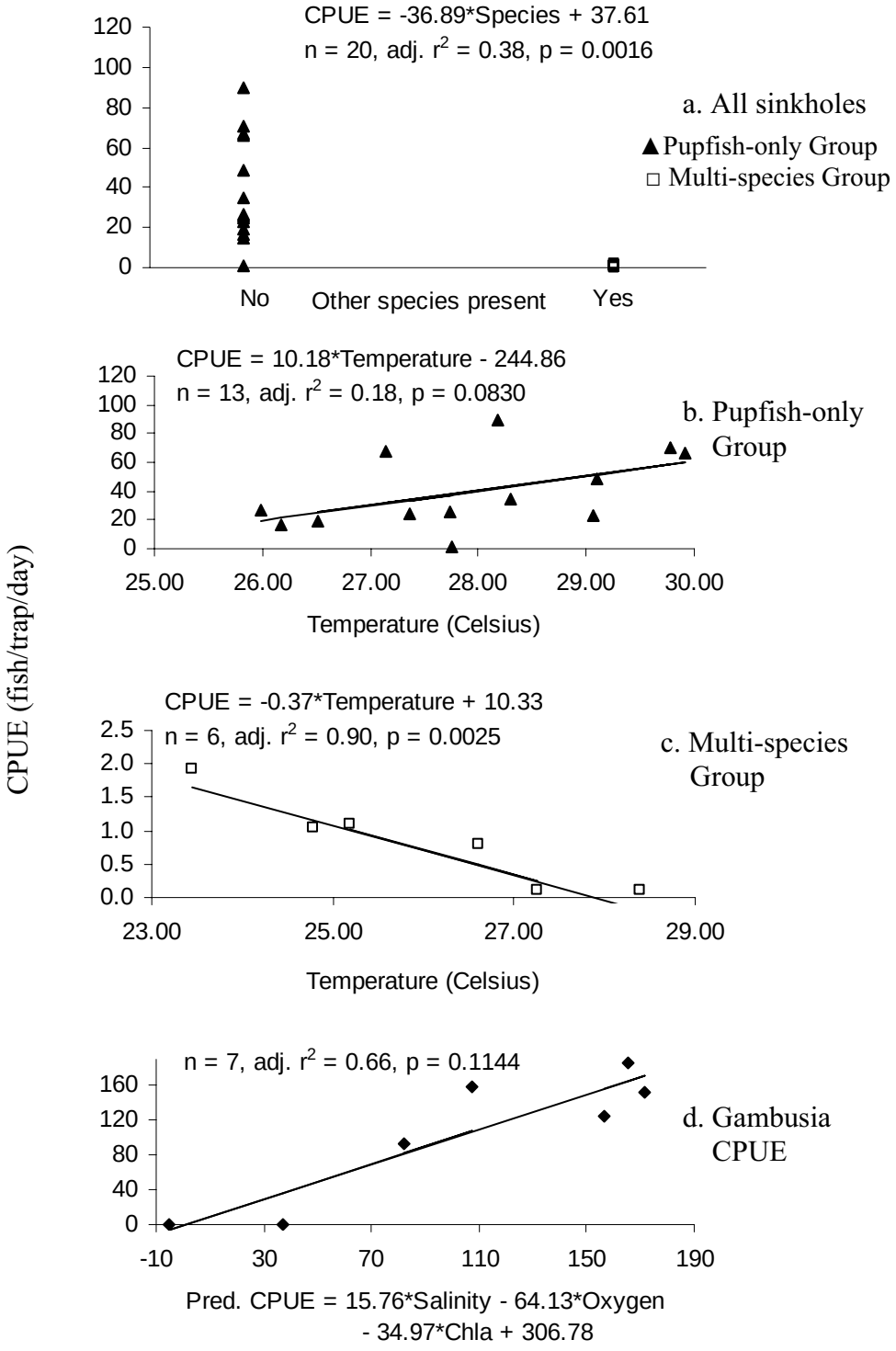


Figure 7. Predicted regression models for pupfish CPUE, 2007. Where there are two or more predictors, the x axis becomes a combination of the predictors so that results can be displayed graphically. Gambusia CPUE is also included.

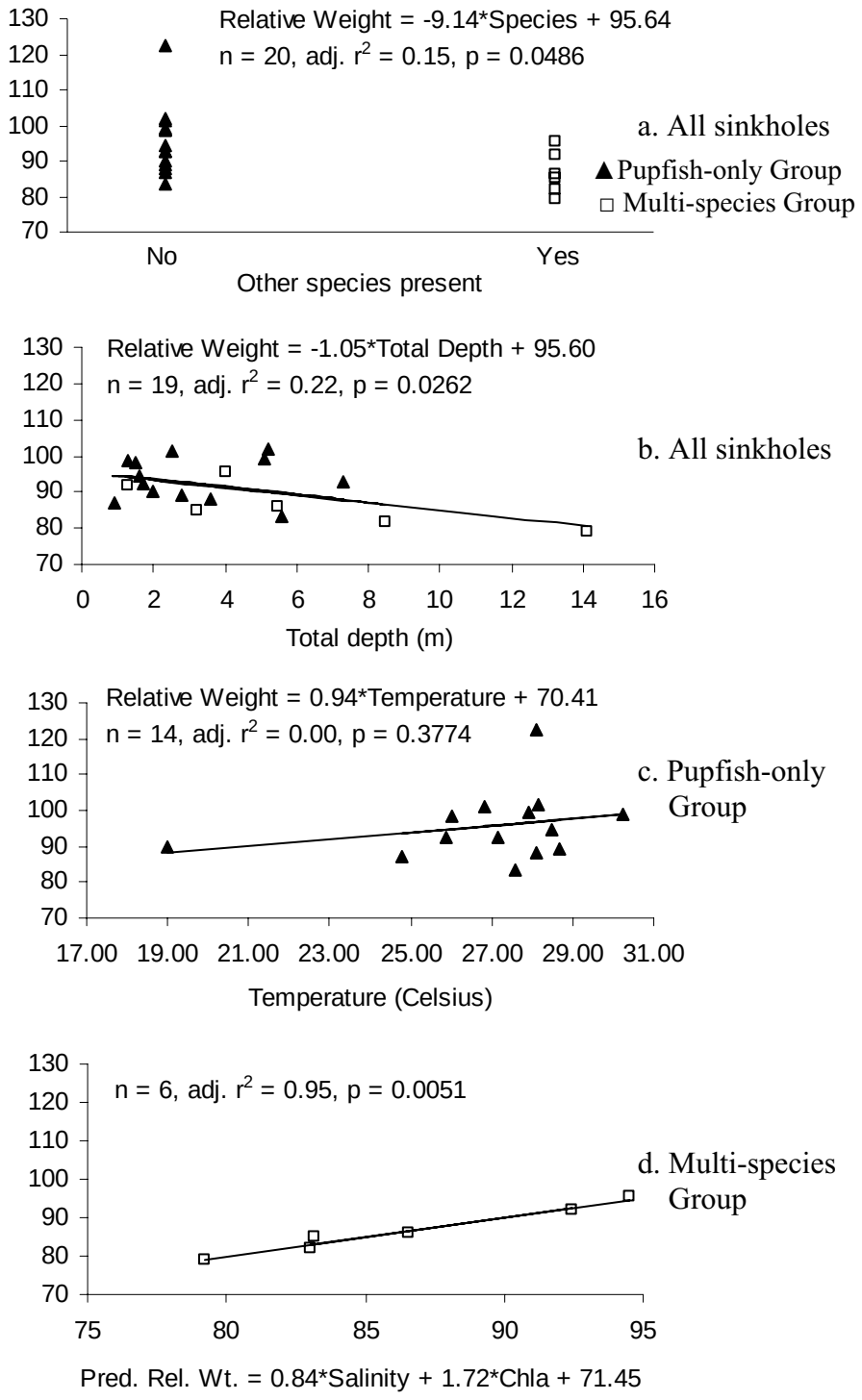


Figure 8. Predicted regression models for pupfish relative weight, 2006. Where there are two or more predictors, the x axis becomes a combination of the predictors so that results can be displayed graphically.

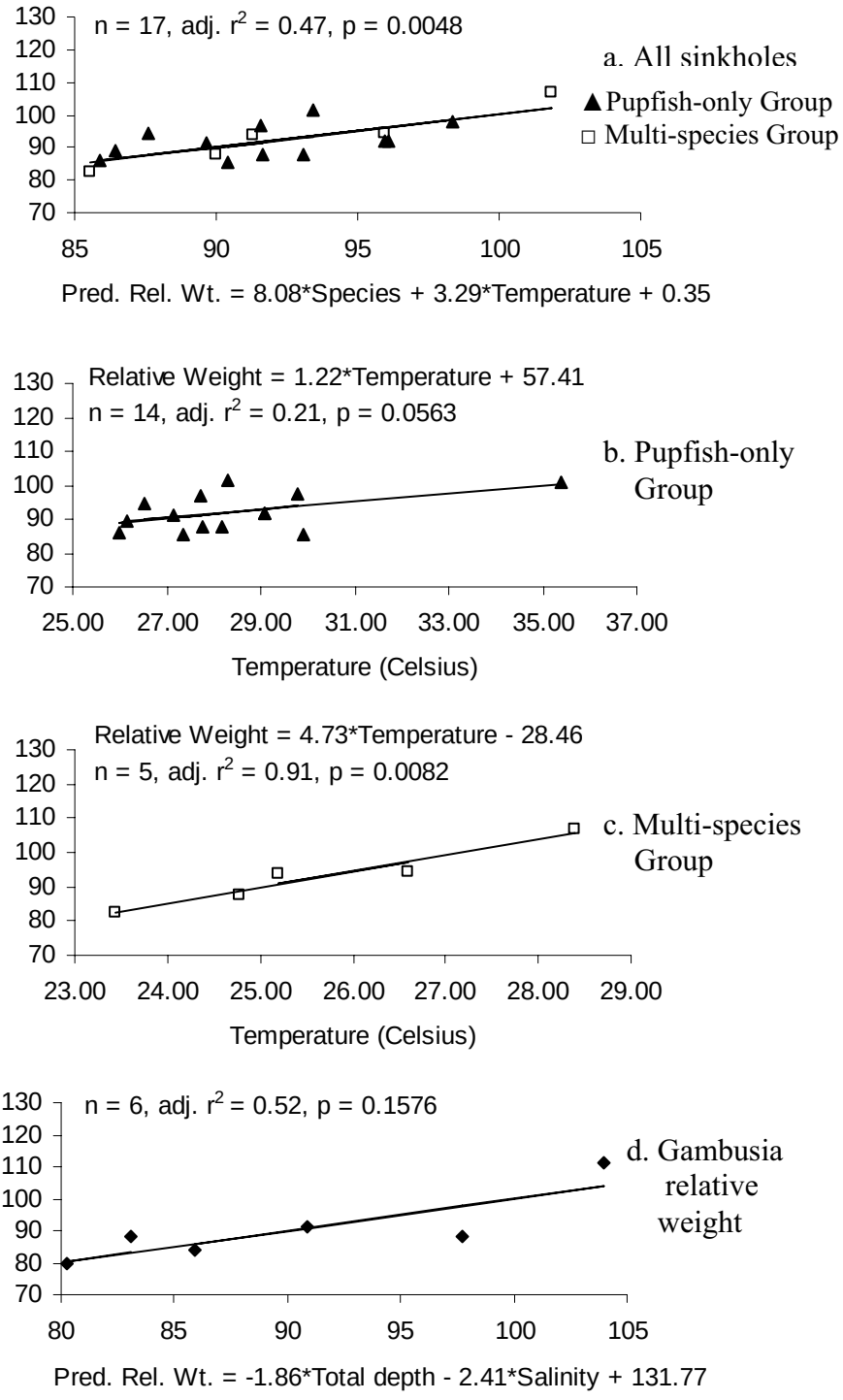


Figure 9. Predicted regression models for pupfish relative weight, 2007. Where there are two or more predictors, the x axis becomes a combination of the predictors so that results can be displayed graphically. Gambusia relative weight is also included.

Table 2. Summary of regression results.

	CPUE		**Relative Weight**	
	2006	2007	2006	2007
All sinkholes	Species (-) Oxygen (+) Chl a (+)	Species (-)	Species (-) and/or Total depth (-)	Species (+) Temperature (+)
Pupfish-only Group	Total depth (-) Oxygen (+) Chl a (+)	Temperature (+)	Temperature (+)	Temperature (+)
Multi-species Group	Temperature (+) Chl a (-)	Temperature (-)	Salinity (+) Chl a (+)	Temperature (+)
Gambusia	No data	Salinity (+) Oxygen (-) Chl a (-)	No data	Total depth (-) Salinity (-)

Diet

Table 3 provides the results from the cluster analysis. Pupfish from all sinkholes had large amounts of detritus and diatoms in their gut. Cluster 1, which contained sinkholes 16, 19, 22, 24, and 26, was comprised of pupfish that had larger amounts of detritus and algae in their gut. Cluster 2, which contained sinkholes 1, 2, 9, 10, 11, 20, 28, and 29, included pupfish that had larger amounts of diatoms and dinoflagellates in their gut. Lake St. Francis (LSF) stood out as a separate cluster because pupfish had larger amounts of gypsum and pollen in their gut. Significant

Table 3. Results from the cluster analysis on food items in the guts of Pecos pupfish. P-values are from tests comparing means of food items from Clusters 1 and 2.

	Cluster 1 Sinkholes 16, 19, 22, 24, 26		**Cluster 2** Sinkholes 1, 2, 9, 10, 11, 20, 28, 29		**Cluster 3** Sinkhole: Lake St. Francis		
Gut Item	**Mean Rank**	**Std. Dev**	**Mean Rank**	**Std. Dev**	**Mean Rank**	**Std. Dev**	**P-Value**
Detritus	1.0	0.00	2.0	0.53	1.0	x	0.0047
Diatoms	2.4	0.55	1.3	0.46	2.0	x	0.0124
Green algae	2.8	0.84	4.9	1.73	9.0	x	0.0202
Dinoflagellates	7.9	1.08	3.8	0.89	4.5	x	0.0008
Insects	6.4	2.68	7.7	1.25	6.0	x	0.5773
Copepods	4.8	0.84	4.3	1.75	9.0	x	0.7133
Gypsum	7.5	1.97	8.1	0.94	4.5	x	1.0000
Fish scales	5.9	1.52	7.1	1.27	7.0	x	0.1880
Pollen	8.4	0.22	8.4	1.13	3.0	x	0.7941
Woody plant material	7.9	1.08	7.6	2.50	9.0	x	0.6301

differences were present between clusters 1 and 2 for detritus, diatoms, algae, and dinoflagellates.

Additionally, fish from Sinkhole 20 and LSF had parasites. All five fish within each sinkhole were infected with numerous cysts embedded in the liver.

Discussion

Influence of Species Presence on Abundance

Pecos pupfish abundance was primarily influenced by biotic factors. That pupfish abundance was considerably affected by the presence of other species was surprising, as all species are native to the Pecos River and presumably sinkholes on BLNWR and have possibly coexisted for thousands of years. We would have expected abundance to be somewhat higher in sinkholes where no other species were present since pupfish could exploit all available habitats (Deacon and Minckley 1974). But where pupfish occurred with other species, abundance was one or more orders of magnitude lower. As an example, sinkholes 2 and 3 were of similar size, had comparable environmental conditions, and were set with the same number of traps. Sinkhole 2 had just pupfish and we captured over 2000 individuals. Sinkhole 3 also contained gambusia and we captured only three pupfish. Clearly, interspecific interactions must be playing a role in pupfish abundance. The lack of juvenile pupfish captured in sinkholes with multiple species was also troubling.

We suggest that Pecos gambusia was the principal species affecting pupfish abundance, as it most commonly occurred with pupfish and with the exception of two sinkholes was present in much higher numbers (plains killifish will be discussed subsequently). Both predation and competition should be considered as possibilities. While we have not found any information suggesting that Pecos gambusia exhibits piscivory, another species of gambusia, *Gambusia affinis*, is a known predator in systems in which it is introduced (Meffe 1985). Predation could also help to explain why almost no juvenile pupfish were captured in the Multi-species Group.

Although the specific mechanisms were not investigated, we will attempt to narrow down possible sources of competition. Species tend to separate along three dimensions: food, temporal, and habitat (Schoener 1974). Species that overlap in habitat tend to eat different foods or may eat at different times of the day. Both vertical and horizontal habitat segregation can occur. Overall, habitat is more important than food type, which is more important than temporal segregation (Schoener 1974), which has also been shown for fish (Werner et al. 1977).

Pupfish and gambusia do not appear to be competing for food. We found that Pecos pupfish diet consisted primarily of detritus and diatoms and the same result was found by Davis (1981) in Pecos pupfish collected from the Pecos River. The presence of items such as gypsum and sand indicate that pupfish are bottom foragers (Davis 1981 and Table 3). In contrast, Pecos gambusia is a carnivorous surface feeder, primarily ingesting dipterans and hemipterans; feeding occurs mostly at night (Bednarz 1979). Both species have dietary flexibility (Davis 1981, U.S. Fish and

Wildlife Service 1983) and therefore food should not be a source of competition. It is not known if there are ontogenetic shifts in diet.

The reproductive behaviors of Pecos pupfish and Pecos gambusia are substantially different. Pupfish have a territorial breeding system, in which males establish and defend territories that function as sites for courtship, mating, and oviposition (Kodric-Brown 1977, 1978). Females primarily oviposit on bare rock rather than algae or sand (Kodric-Brown 1977). By contrast, Pecos gambusia males use gonopodial thrusting, which does not entail courtship. Dominance hierarchies and territoriality are not present (Farr 1989). As livebearers, gambusia females do not need substrate on which to release eggs. The reproductive period apparently overlaps. Pecos pupfish reproduction peaks in late June/mid July (Kodric-Brown 1977). Bednarz (1979) collected gravid Pecos gambusia in late July from Blue Spring, Eddy County, NM. Although reproduction may coincide, it appears unlikely that pupfish and gambusia are competing for reproductive space.

Pupfish reproduction has been shown to be affected by plains killifish. In a study by Kodric-Brown and Mazzolini (1992), the pupfish breeding season coincided with the killifish's and they spawned on similar substrate. Where killifish were numerically dominant and physically larger, male pupfish spent a considerable amount of time chasing killifish and frequently abandoned their territories. This resulted in lower reproductive success and pupfish eggs could have been preyed upon. Low pupfish density also meant that more males were able to establish breeding territories, which reduced intraspecific competition and lowered

reproductive success. Similar results have been observed for desert pupfish (*Cyprinodon macularius*) defending territories from tilapia (see Schoenherr 1981). In the current study, killifish had abundances similar to pupfish (Table 1). This suggests that the role of killifish in disturbing pupfish reproduction is limited, since there were not large numbers of killifish to chase. Also, sinkholes 3 and 20 did not contain killifish but pupfish abundance was still low, so some other factor must be at work in these two sinkholes. (Gambusia was present in these sinkholes and red shiner was also in Sinkhole 20.) Furthermore, Echelle et al. (1972) suggested that Red River pupfish (*Cyprinodon rubrofluviatilis*) is a better competitor than plains killifish.

Pecos gambusia may perform a similar role though. Both Pecos pupfish and Pecos gambusia inhabit the nearshore (personal observation and Bednarz (1979) for gambusia). *Gambusia* species typically inhabit shallow areas (Meffe and Snelson 1989) and Pecos pupfish spawn in water less than two meters deep (Kodric-Brown 1978). Although their body shape and morphology suggest they primarily reside near the surface, we captured a large percentage (up to fifty percent) of gambusia in bottom traps. If gambusia are spending a large amount of time near the substrate and occur in such high densities then they may be interfering with pupfish reproduction if male pupfish are spending time chasing individuals from their territories. This could partly explain the low number of juvenile pupfish captured and low body condition observed for adult pupfish (see "Influence of Species Presence on Body Condition"). But what would cause gambusia to shift to greater depths? A response to oxygen is unlikely since it was most abundant at the surface. In the lab, Gehlbach et al. (1978)

found that when kept separate, both Pecos gambusia and Comanche Springs pupfish (*Cyprinodon elegans*) preferred temperatures of 26-30°C. When placed together, pupfish shifted to temperatures between 21 and 25°C and gambusia stayed in the 26-30°C zone. Therefore, it seems unlikely that gambusia would move deeper to find cooler temperatures, especially since surface temperatures ranged from 26.69-29.30°C. Gambusia could be reacting to intense solar radiation though. Deacon and Minckley (1974) documented fishes with sloughing tissue on dorsolateral surfaces and damaged caudal and dorsal fins, which they attributed to sunburn. This could be highly likely in clear water and all of the sinkholes in the Multi-species Group were clear (Appendix B). It is possible that even a temporary shift of gambusia to greater depths could be sufficient to disrupt pupfish reproduction.

The physical nature of the sinkholes may contribute to species interactions. Compared to lakes in general, sinkholes were small and shallow. The aquatic macrophyte community was simple and overhanging vegetation was minimal (the occasional tamarisk tree notwithstanding). As such, fish habitat could be considered homogeneous. Small, simple lakes increase the likelihood of contact between species because patterns of habitat use overlap (Tonn and Paszkowski 1987). While pupfish and gambusia seem to have different ecological requirements, it is something to keep in mind.

Obviously, pupfish-gambusia-killifish interactions and pupfish-gambusia-shiner interactions should be given further consideration. Without observational or experimental data, however, the contribution of each species is difficult to tease apart.

Red shiner could quite possibly influence abundance because both pupfish and gambusia abundances were low in the sinkhole in which shiner was present. While red shiner are omnivorous, they are not known to be piscivorous (Sublette et al. 1990).

Influence of Species Presence on Body Condition

Pupfish body condition was negatively associated with the presence of other species in 2006. This could be due to males chasing individuals from territories, which would use sizeable amounts of energy and could correspond to lower body condition. Alternatively, if gambusia does prey upon pupfish, then pupfish could also be spending energy attempting to hide from gambusia. Interestingly, pupfish body condition was positively associated with the presence of other species in 2007, even though there were no significant differences in condition between the two groups of sinkholes and pupfish condition did not differ from gambusia condition. Since pupfish relative weight was also positively associated with temperature (Fig. 9a), perhaps there was an interaction of species presence and temperature.

Additional Environmental Influences on Abundance and Body Condition

Temperature – Pupfish abundance was positively associated with temperature in the Pupfish-only Group in 2007 and the Multi-species Group in 2006. A preference for warmer temperatures has been observed for pupfish (Heath et al. 1993, Rogowski et al. 2006), although it has also been suggested that optimum temperatures

exist, particularly for reproduction (Gerking et al. 1979). In 2007, the range of average temperatures in the Pupfish-only Group was 25.99-29.92°C (Sinkhole 21, which had temperatures as high as 39.5°C was deemed an outlier and was not part of the regression analysis). This range can be expanded to 25.50-33.40°C when values are not averaged, as temperatures tended to be warmer at the surface and cooler with depth. In the Multi-species Group, the range of average temperatures in 2006 was 24.73-27.99°C and can be expanded to 21.22-29.19°C when values are not averaged. Within a sinkhole, pupfish could have inhabited cooler or warmer temperatures than the average temperature. In 2007, pupfish abundance in the Multi-species Group was negatively associated with temperature. This result was unexpected: since sinkholes within the Pupfish-only Group had higher temperatures and more fish, one would expect abundance to increase with temperature. Again, the average temperatures given for each sinkhole do not take into account changes in temperature that occur with depth. Neither of the models in which temperature was positively associated with temperature were statistically significant. Ultimately, temperature may not influence abundance.

Temperature was positively associated with pupfish relative weight in the Pupfish-only Group in both 2006 and 2007 and the Multi-species Group in 2007. Growth increases with increasing temperature (Moyle and Cech 2004) and higher relative weight may indicate more growth. However, in the Pupfish-only Group both models were poor. This suggests that relative weight was not related to any environmental variables for this group.

Chlorophyll a — In the Pupfish-only Group in 2006, pupfish abundance was positively associated with chlorophyll a. In this group, quantities ranged from 0-15.13 mg/m^3. Since chlorophyll a is an indicator of phytoplankton biomass, increases in chlorophyll a indicate greater productivity and suggest that more food (e.g., diatoms and detritus) is available. In the Multi-species Group, pupfish abundance was negatively associated with chlorophyll a in 2006. Quantities ranged from 0-5.34 mg/m^3. The amount of chlorophyll a in this group implies that they are oligotrophic (Wetzel 2001) so it was surprising that abundance would increase; this also contradicts the results from the analysis of all sinkholes combined and from the Pupfish-only Group in which abundance increased with greater amounts of chlorophyll a (Figs. 6a and 6b). However, phytoplankton communities do exhibit seasonal patterns and successions (Wetzel 2001) and perhaps some sinkholes in the Multi-species Group were more productive earlier in the spring or summer prior to or during reproduction. It is also important to keep in mind that this model was not significant. Pecos gambusia abundance was also connected negatively to chlorophyll a, but again, the model was not significant.

Pupfish relative weight was positively associated with chlorophyll a in the Multi-species Group in 2006. Even though sinkholes within this group were considered to be oligotrophic and thus of low productivity, any increase in chlorophyll a could indicate greater productivity and more food production. A link between greater food availability and higher body condition is reasonable.

Salinity – For the Multi-species Group, pupfish relative weight was positively associated with salinity in 2006. Optimal growth and reproduction can occur in salinities as high as 35 ppt (Kinne 1960) and some amount of salinity may be necessary for pupfish survival (Gerking and Lee 1980). Since pupfish relative weight was higher in sinkholes with greater salinity in 2006 it is plausible that some amount of salinity is needed for greater growth and reproduction that is higher than the salinities in the Multi-species Group (range: 7.26 to 18.71 ppt) and this could explain why condition increases with salinity.

Salinity was positively associated with Pecos gambusia abundance and negatively with gambusia relative weight. Pecos gambusia does not tolerate the high salinities that Pecos pupfish does (Bednarz 1979) so an increase in abundance with salinity was not anticipated. It has been suggested that Pecos gambusia cannot tolerate salinities above 30 ppt (Echelle and Echelle 1980). The range of salinities in the Multi-species Group (6.95 to 16.42 ppt) was fairly narrow, so this effect may not be biologically meaningful. How salinity affects body condition and growth is not well understood: some poeciliid species grow more in higher salinities while for others the reverse is true (see Snelson 1989). Neither model regarding gambusia abundance and body condition was significant.

Total depth and Oxygen – In the Pupfish-only Group in 2006, pupfish abundance was positively associated with dissolved oxygen and negatively associated with total depth. Oxygen was also positively related to pupfish abundance when all sinkholes were analyzed together. Oxygen is essential to bodily functions like

metabolism (Moyle and Cech 2004) and increases in oxygen have been shown to increase the rate of embryo development in pupfish (Kinne and Kinne 1962), so this result is not unexpected. In general, deeper (>4 m) sinkholes were less turbid and had lower amounts of chlorophyll a, suggesting they were nutrient- or light-limited (Wetzel 2001). A potentially confounding factor is that deeper sinkholes also tended to be steeper-sided, meaning that the shoreline was not very shallow. Since pupfish spawn in fairly shallow water, this implies that pupfish have less area in which to spawn. Indeed, vertical substrate has been shown to be less-optimal for spawning (Kodric-Brown 1977). This seemed to be a plausible explanation for low pupfish abundance except that in 2007 the deeper sinkholes caught considerably more fish.

Pecos gambusia abundance was connected negatively to oxygen. A negative association with oxygen is unusual. However, this model was not significant and could not account for changes in oxygen levels with depth. Gambusia relative weight was negatively associated with total depth. Once more, deeper sinkholes tended to have less productivity, and this may have been reflected in lower body condition, but again, the model was not significant.

The effect of species presence on pupfish abundance was quite striking and it compelled me to divide sinkholes into two groups based on species presence. This resulted in a narrowing of the variation in environmental factors within the two groups. Sinkholes within the Pupfish-only Group had significantly higher temperatures and amounts of chlorophyll a in 2007 and higher salinities in both years than the Multi-species Group. Sinkholes within the Multi-species Group had

significantly more oxygen in 2006. This could cause one to conclude that pupfish have a preference for higher salinity, temperature, and chlorophyll a and lower amounts of oxygen but this would be misleading since it is not known how pupfish got into these sinkholes or how long they have been in them. Unfortunately, these factors are confounded with the presence of other species. If species presence had not been such an obvious factor then I could have analyzed all sinkholes together and environmental variation would have been much greater. I suggest that temperature, chlorophyll a, salinity, oxygen, and total depth may have ultimately not been useful indicators of abundance and body condition, especially since the influence of these factors differed between years and because the relationships (positive or negative) also varied. The non-significance of both models of gambusia abundance and relative weight provides supporting evidence.

Relative weight may have not been an appropriate condition index to use. Indeed, Blackwell et al. (2000) noted that published studies regarding relative weight and small fishes are few. Perhaps calculating an average relative weight per sinkhole was too simplistic and did not allow for length-related trends to be detected, but we did not notice any meaningful patterns (Appendix A). Obviously, this study occurred over a small period of time and condition may vary between seasons and years.

Effect of Parasites

Parasites found on the liver of fish from Sinkhole 20 and LSF were likely trematode metacercaria. Fish serve as intermediate hosts for the parasite, whose life

cycle also involves fish-eating birds and snails as hosts (Hoffmann 1999). Rogowski and Stockwell (2006) found that trematode prevalence in White Sands pupfish increased with the presence of an endemic springsnail, which they presumed served as a host for the parasite. White Sands pupfish collected from sites that lacked snails also lacked trematodes. The presence of trematodes resulted in lower condition and lipid levels in pupfish and fewer older fish were collected, indicating a higher mortality rate (Rogowski and Stockwell 2006). Both Sinkhole 20 and LSF contained snails. Pupfish dissected from these two sinkholes had the lowest amounts of fat compared to other sinkholes in which fish were dissected. I think it is likely that the relationship observed between White Sands pupfish, springsnails, and trematodes is similar for Pecos pupfish where snails are also present. Parasites may have contributed to the low body condition seen in Sinkhole 20 and LSF (although relative weight was much higher for Sinkhole 20 in 2007). It is not known if parasites also infect Pecos gambusia, but this appears likely.

Contributions to Multi-Lake Studies

This research brought a new perspective for multi-lake studies by providing information about desert systems. Although this study would be considered to have a small taxonomic scale it had a large environmental scale and studies such as this one have not been common (Hinch 1991). Biotic interactions were so strong that sinkholes had to be grouped to account for multiple species. Even though abiotic variation was lessened by grouping sinkholes, it does not diminish the fact that

sinkholes had wide-ranging amounts of oxygen, salinity, etc. It was surprising that in a system with low species diversity, biotic interactions were strong. Our results agree with Quist et al.'s (2003) hypothesis that biotic processes dominate abiotic factors when competitor densities are high. However, due to the fact that different factors were significant between years we also emphasize that the importance of variables may be habitat-specific.

Management Implications

The results presented here potentially have serious consequences for Pecos pupfish, a state-threatened species, and Pecos gambusia, a federally-endangered species. As is typical for many native fishes in the western United States, both species have declined due to habitat alteration and non-native species introductions. Pecos pupfish formerly occurred in the mainstem Pecos River from Roswell, NM to the mouth of Independence Creek, TX and in small tributaries, springs, and sinkholes (Echelle and Echelle 1978). The construction of several dams along the river has altered both the flow and thermal regimes. Spring snowmelt and rain events are attenuated, flooding is essentially non-existent, and river reaches are seasonally-desiccated (Propst 1999). Non-native sheepshead minnow (*Cyprinodon variegatus*), likely introduced in the early 1980s in Texas (Echelle and Connor 1989), hybridizes with Pecos pupfish (Echelle et al. 1987). Hybrids have rapidly moved upstream (Echelle and Connor 1989, Wilde and Echelle 1992, Echelle et al. 1997). The largest populations of Pecos pupfish are on BLNWR (Brooks and Wood 1988). Pecos

gambusia populations have primarily declined because of groundwater pumping that reduced or eliminated habitat and restricted gambusia to springs (U.S. Fish and Wildlife Service 1983). The species is now limited to four areas: BLNWR; Blue Spring, in southern NM; a series of springs near Toyahvale, TX; and Diamond Y Spring and Leon Creek near Fort Stockton, TX (Johnson and Hubbs 1989). Gambusia had been introduced into several sinkholes on BLNWR but most populations were extirpated; failure was attributed to high salinity (Bednarz 1979).

Undoubtedly, BLNWR serves as an important refuge for both Pecos pupfish and Pecos gambusia. Pecos pupfish numbers are fairly high when they are the only species present and they do occur in a number of sinkholes as well as nearby Bottomless Lakes State Park. While Pecos gambusia abundance is quite high they are limited to fewer sinkholes. Augmenting both species' populations would need to be done in a very careful manner. Until more observational or experimental data is available, we think it would be unwise to stock these species together. Fishless sinkholes that could be stocked with gambusia include sinkholes 4, 40, 42N, 42S, and 59. Pupfish could be introduced into sinkholes 5, 15, 17, and 25. However, I say this with great hesitation, since environmental conditions can vary greatly from year to year and because fish have previously been stocked into some of these sinkholes but have since been extirpated. The invertebrate communities within fishless sinkholes are of importance too, and the effects on them should be given consideration.

Limitations of This Study

This study was conducted in the summer over two years. As such, seasonal variation could not be addressed and two years is not sufficient to encompass yearly differences. The fact that different factors influenced abundance and body condition between years suggests that either it is necessary to collect data for several years and over the course of a year or it may be that in desert systems conditions are so variable that finding predictable patterns is nearly impossible.

The results of some of these analyses may be limited by small sample sizes. We suggest that these results should be interpreted for general patterns but placing significance on them should be done with caution.

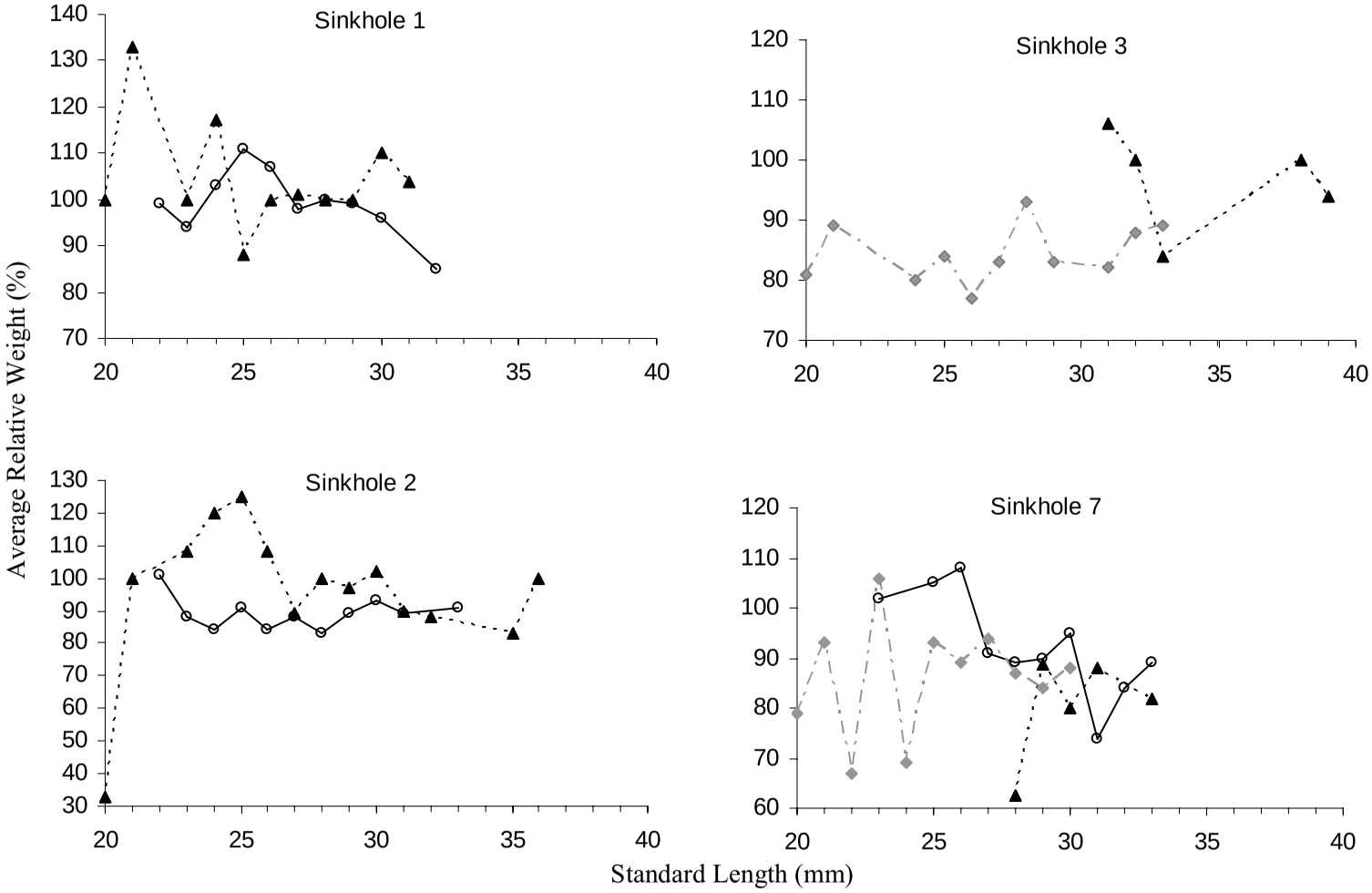
Future Research

This study could benefit from future research in a couple of ways. First, direct observation (via snorkel surveys) could further illuminate interactions between pupfish and gambusia, as well as any role plains killifish and red shiner may play. Second, laboratory experiments could specifically evaluate where resources overlap or are limiting, allowing for the determination of the particular mechanisms of competition. Finally, examination of both juvenile and adult Pecos gambusia gut contents would provide a simple answer as to whether gambusia prey upon pupfish.

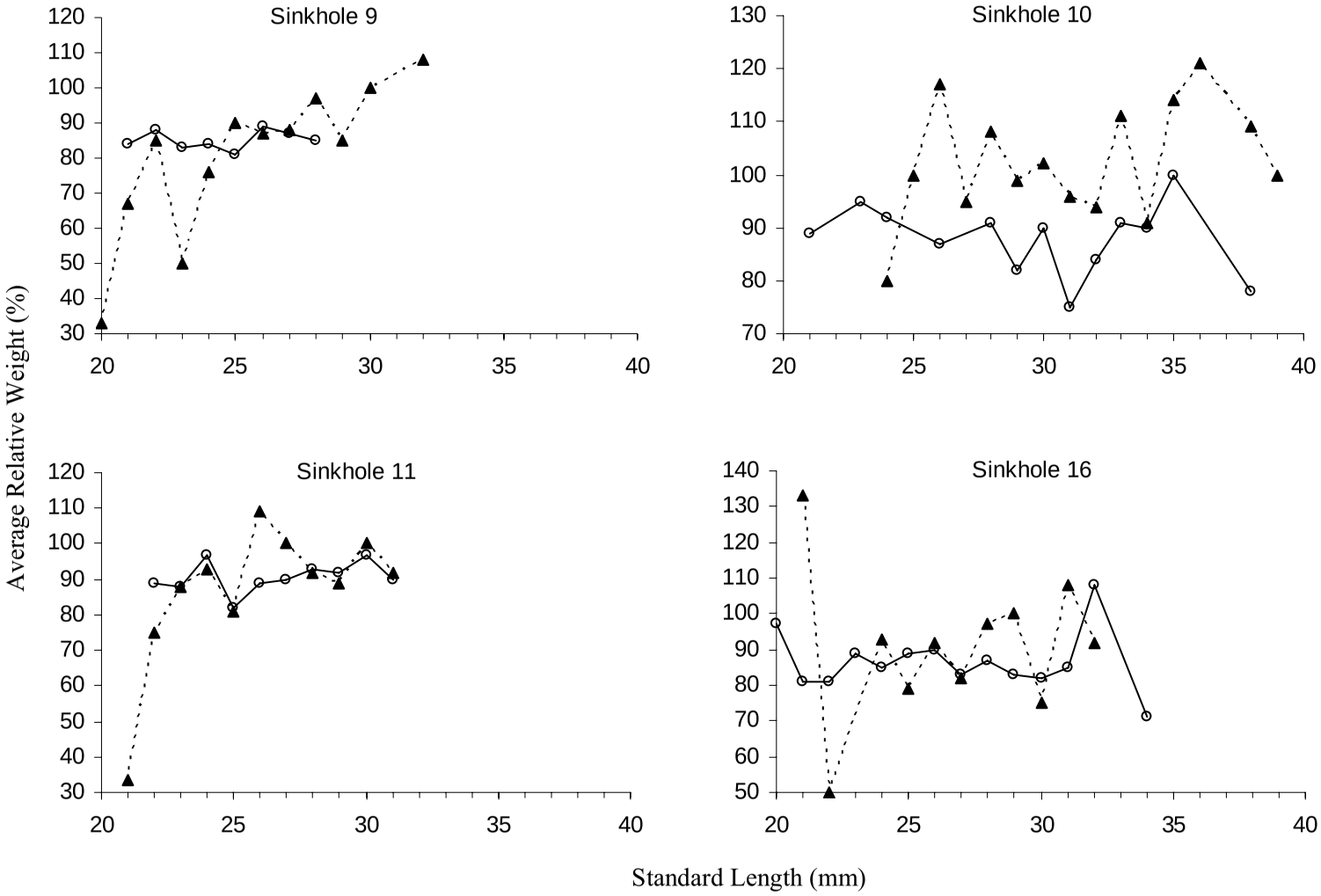
Conclusion

It has been shown that biotic factors have an effect on pupfish abundance in a desert system, more so than abiotic factors. Biotic interactions were prominent enough that the survival of Pecos pupfish may seem uncertain where it coexists with other species. In small lakes, there can be great temporal variation in environmental factors like temperature and oxygen, such that periodic reductions in species abundance may occur (Jackson et al. 1992). Even though desert species can tolerate environmental extremes, conditions may occasionally go beyond what even they can withstand. Indeed, it has been suggested that poeciliid populations never reach carrying capacity because they are reduced by "seasonal or unpredictable abiotic events" (Meffe and Snelson 1989). The occasional reduction in gambusia populations could ultimately benefit pupfish where they co-occur, assuming pupfish are not similarly affected. That pupfish were seemingly on the verge of extirpation in a sinkhole where salinity was 122 ppt but then recovered the following year is a testament to how desert species can survive extremely harsh conditions and then thrive once conditions improve. It would be worthwhile to maintain monitoring programs for these species to see if indeed their populations fluctuate over time relative to one another. This could indicate that both biotic and abiotic factors affect abundance but that their importance varies on a periodic basis.

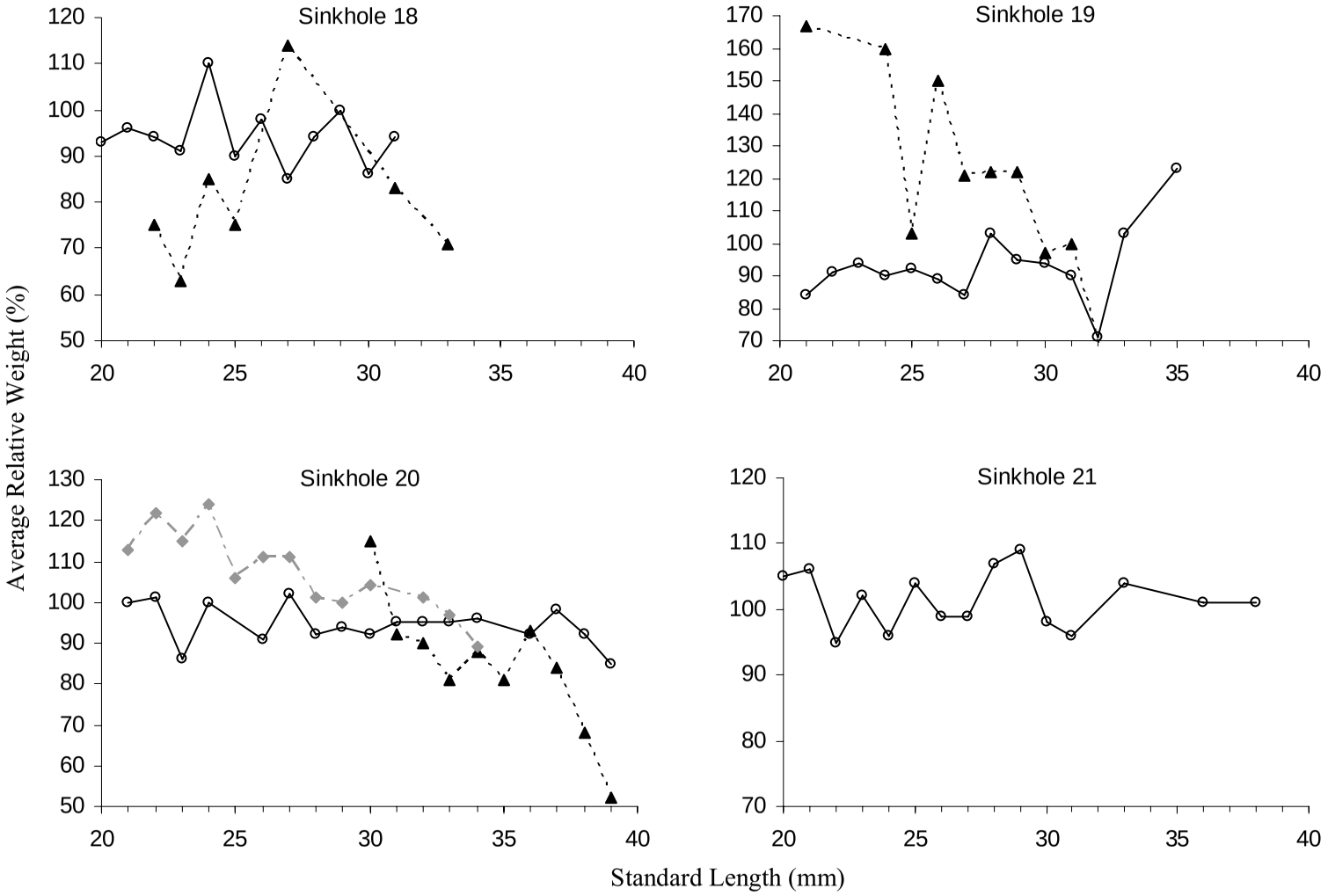
Appendix A. Trends in relative weight with respect to length for each sinkhole. ▲ = Pupfish 2006 ○ = Pupfish 2007 ♦ = Gambusia 2007



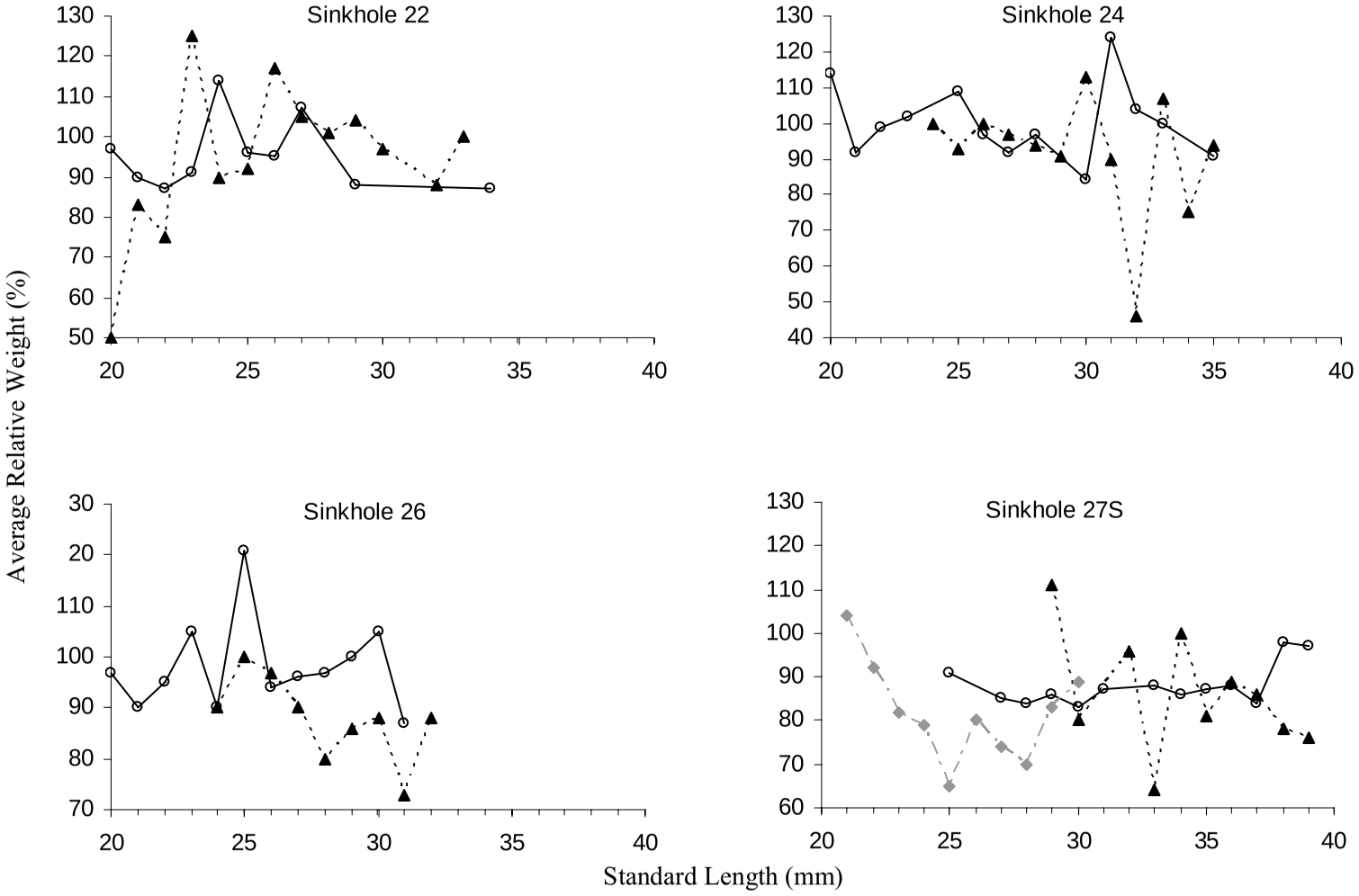
Appendix A (continued)



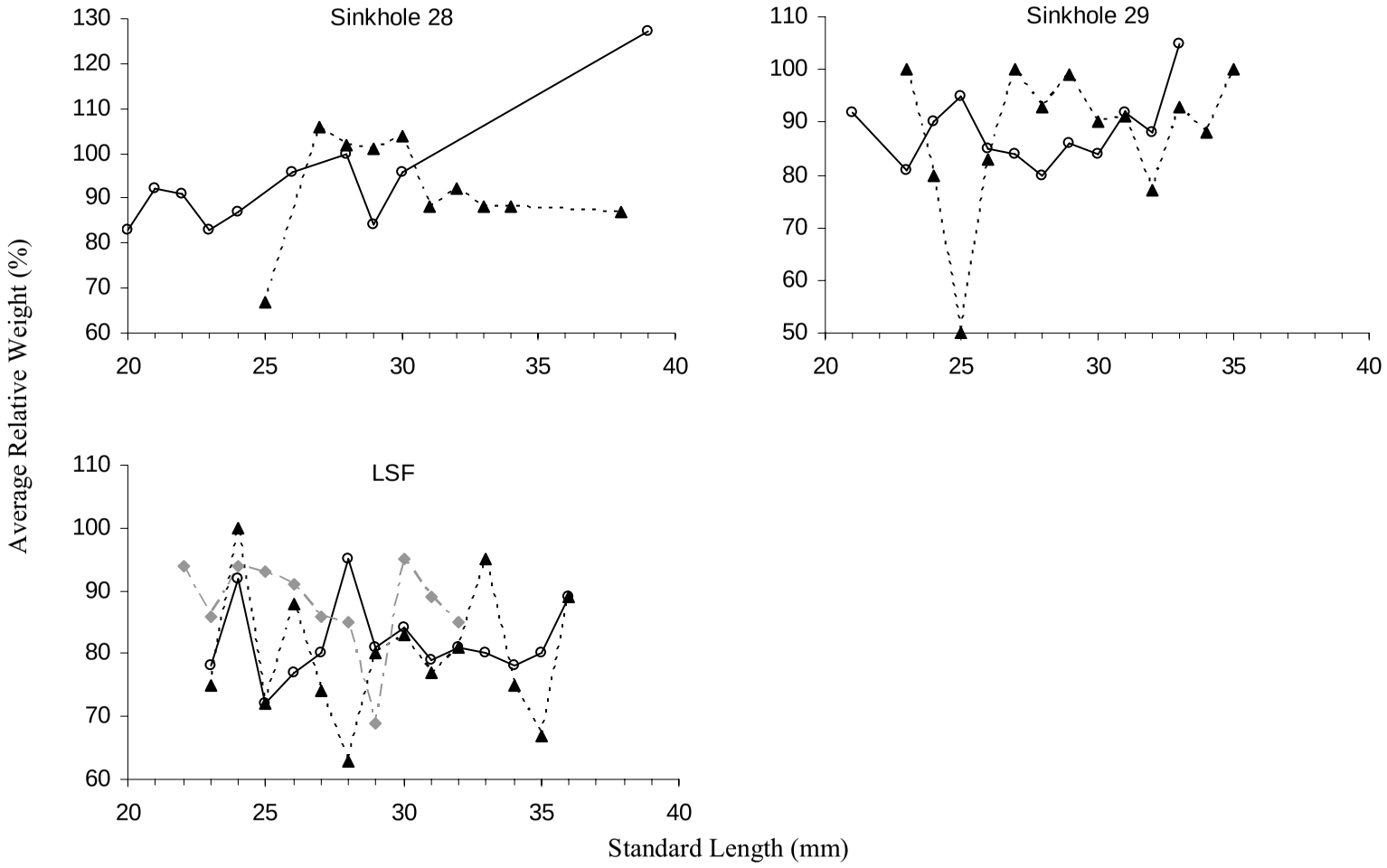
Appendix A (continued)



Appendix A (continued)



Appendix A (continued)



Appendix B. Environmental variables measured on sinkholes of Bitter Lake NWR, 2006 and 2007. Values are averaged from 1-meter depth interval measurements. An 'x' indicates the variable was not measured. An asterisk indicates a sinkhole that contains fish. Diameter was not measured in 2007.

Sinkhole	Total Depth (m)		Diameter (m)		Secchi Depth (m)		Temperature (°C)		Salinity (ppt)		Turbidity (NTU)	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
1*	5.2	5.5	32.0	32.0	2.3	1.7	28.14	28.30	22.97	20.47	0.0	0.6
2*	5.1	5.6	28.5	28.5	3.0	2.3	27.91	28.18	16.80	15.05	0.0	0.2
3*	4.0	4.0	30.0	30.0	2.8	2.95	27.99	28.40	18.71	15.98	0.0	0.6
4	1.7	2	14.5	14.5	1.7	1.25	28.17	28.95	27.61	19.35	0.0	126.8
5	2.3	3	23.0	23.0	0.7	0.75	29.63	32.44	51.16	35.57	1.8	172.9
6	2.1	2.8	21.5	21.5	1.4	1.05	30.47	28.93	48.38	34.48	0.4	119.4
7*	8.5	9.3	41.0	41.0	3.8	2.25	25.95	25.19	7.26	6.95	0.2	0.8
8	0.8	1	10.0	10.0	0.4	0.8	28.20	28.35	67.23	27.78	12.6	10.4
9*	5.6	6.2	39.0	39.0	3.2	2.25	27.58	27.37	25.29	22.83	0.0	0.0
10*	2.5	2.9	17.0	17.0	1.3	1.1	26.81	27.75	17.41	14.60	0.0	0.6
11*	7.3	6.6	36.0	36.0	3.1	1.5	27.16	27.15	31.55	28.64	0.0	0.4
14	0.7	1.4	14.5	14.5	0.1	0.5	30.93	29.85	94.18	27.60	130.9	6.0
15	2.9	3.3	15.5	15.5	0.9	0.85	28.30	28.03	30.84	25.69	0.3	9.4
16*	2.8	3.4	17.0	17.0	1.1	1.3	28.68	29.92	49.44	36.49	0.6	45.0
17	2.0	3.2	15.0	15.0	0.7	0.3	27.91	28.26	90.28	53.38	8.7	19.6
18*	0.9	1.8	9.0	9.0	0.6	0.7	24.79	26.52	33.52	13.23	0.0	25.8
19*	2.5	3.3	32.5	32.5	1.8	1.85	28.12	29.07	36.00	25.41	0.0	6.4
20*	3.2	4.2	23.5	23.5	1.3	2.5	27.76	26.60	9.54	8.28	0.0	1.5
21*	3.6	4.2	41.0	41.0	0.3	0.6	26.93	35.37	121.60	86.62	29.2	44.9
22*	1.3	2	7.0	7.0	0.4	0.4	30.26	29.10	90.74	33.74	16.6	19.3
23	2.1	2.9	x	x	0.8	0.8	32.08	34.28	64.64	40.52	3.4	11.9
24*	1.6	2.6	11.0	11.0	0.5	0.75	28.50	29.78	42.88	25.91	15.1	4.9
25	1.4	2.3	20.0	20.0	1.4	1.7	29.31	26.42	24.61	16.75	0.0	2.7
26*	3.6	4	31.0	31.0	0.9	2.35	28.11	27.73	41.38	32.16	0.0	10.8
27N*	0.6	1.2	11.0	11.0	0.6	0.8	26.41	24.97	31.18	16.03	3.8	14.3

Appendix B (continued)

Sinkhole	Total Depth (m)		Diameter (m)		Secchi Depth (m)		Temperature (°C)		Salinity (ppt)		Turbidity (NTU)	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
27S*	5.5	6.4	26.0	26.0	2.4	2.3	25.90	24.79	17.95	16.42	0.0	1.4
28*	1.5	2.2	10.5	10.5	1.1	0.9	26.03	26.17	33.13	25.07	0.0	5.9
29*	1.7	2.4	15.5	15.5	0.8	0.9	25.86	25.99	30.26	22.70	0.2	4.0
31*	0.9	1	19.0	19.0	0.9	0.95	24.31	20.45	5.92	6.34	0.0	12.2
32*	1.3	1.8	19.0	19.0	1.3	1.4	25.93	27.25	14.09	10.10	0.0	2.6
LSF*	14.1	14.5	59.0	59.0	4.7	4.25	24.73	23.44	9.25	9.00	0.0	0.0
38*	2.0	2.1	7.5	7.5	2.0	1.5	19.00	20.03	4.92	6.26	0.0	10.5
40	1.4	2.6	7.0	7.0	1.0	1.2	24.98	30.94	28.90	14.89	0.0	46.9
42N	0.4	0.5	x	x	0.4	0.5	27.15	30.52	12.47	7.27	3.4	4.5
42S	0.3	0.7	x	x	0.3	0.7	27.65	31.25	17.31	7.31	2.1	115.3
44	1.1	2.2	15.0	15.0	0.1	0.85	24.70	32.37	85.32	85.32	103.4	55.0
48	0.6	1.2	16.0	16.0	0.2	0.2	31.32	27.97	102.22	41.77	50.3	90.6
50	1.7	2.8	x	x	0.1	0.5	25.11	30.80	74.10	38.87	302.6	49.3
51	1.0	1.7	9.0	9.0	0.1	0.8	26.37	32.33	96.98	26.03	106.9	75.4
52	0.6	1.1	14.0	14.0	0.2	0.55	30.63	25.90	91.14	38.40	75.8	7.1
59	2.8	4.3	12.0	12.0	2.8	4.3	25.42	26.20	3.85	4.08	0.0	0.0

Appendix B (continued)

Sinkhole	Dissolved Oxygen (mg/L)		pH		$CaCO_3$ (mg/L)		Total Phosphorus (mg/L)		Chlorophyll a (mg/m^3)	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
1*	4.30	5.63	7.81	8.165	3545	x	<0.05	x	0.534	2.670
2*	6.11	6.86	8.07	8.40	6570	x	<0.05	x	1.068	2.670
3*	5.32	6.85	7.80	8.39	6430	x	<0.05	x	4.272	1.068
4	0.32	1.50	7.29	7.38	7285	x	0.07	x	9.612	118.370
5	0.84	4.65	7.64	7.79	11835	x	<0.05	x	16.020	142.400
6	2.23	1.43	7.94	7.44	8290	x	<0.05	x	6.230	205.590
7*	5.30	4.33	7.69	7.99	3485	x	<0.05	x	3.204	0.890
8	0.54	3.25	7.49	8.12	16230	x	<0.05	x	37.380	4.272
9*	4.45	3.89	7.99	7.93	8570	x	<0.05	x	3.738	1.602
10*	2.97	7.13	7.63	8.13	5940	x	<0.05	x	5.340	3.738
11*	3.89	6.45	7.81	8.25	5250	x	<0.05	x	2.670	1.068
14	2.64	2.66	7.60	7.88	16340	x	0.16	x	x	4.272
15	3.15	4.42	7.98	7.99	7710	x	<0.05	x	4.005	81.880
16*	5.86	6.57	8.03	8.26	13800	x	0.09	x	3.204	46.725
17	5.99	2.38	8.00	7.87	16275	x	<0.05	x	1.526	18.690
18*	1.61	2.29	7.83	7.61	10030	x	<0.05	x	3.738	5.340
19*	4.55	3.89	8.08	8.04	9440	x	<0.05	x	0.000	12.816
20*	6.31	3.91	8.02	7.90	3800	x	<0.05	x	2.136	4.272
21*	0.09	3.28	7.69	7.90	17100	x	0.1	x	6.408	2.670
22*	3.97	2.12	7.85	7.90	17920	x	0.09	x	7.120	23.140
23	0.91	2.10	7.93	7.79	11790	x	<0.05	x	10.680	10.680
24*	5.50	1.06	8.10	7.75	9715	x	<0.05	x	10.680	1.335
25	9.90	4.65	9.07	8.77	6250	x	<0.05	x	1.602	3.738
26*	5.54	3.88	8.02	8.03	9270	x	<0.05	x	1.335	16.554
27N*	4.01	2.07	8.06	8.23	8525	x	<0.05	x	0.534	7.476

Appendix B (continued)

Sinkhole	Dissolved Oxygen (mg/L)		pH		$CaCO_3$ (mg/L)		Total Phosphorus (mg/L)		Chlorophyll a (mg/m^3)	
	2006	2007	2006	2007	2006	2007	2006	2007	2006	2007
27S*	6.12	4.98	7.92	8.01	5050	x	<0.05	x	-0.534	2.136
28*	3.67	3.80	8.23	8.37	8000	x	<0.05	x	2.465	6.230
29*	2.04	1.20	8.02	7.80	10005	x	<0.05	x	15.130	5.874
31*	6.16	4.58	6.89	7.24	3120	x	<0.05	x	1.335	20.292
32*	6.83	6.77	8.66	8.75	5265	x	<0.05	x	5.340	1.068
LSF*	4.22	4.26	7.69	7.90	3295	x	<0.05	x	0.000	0.534
38*	2.68	1.61	6.87	7.15	2920	x	<0.05	x	2.136	2.136
40	0.17	4.27	7.18	7.75	6605	x	<0.05	x	16.554	x
42N	21.21	14.89	8.71	8.12	4440	x	<0.05	x	5.340	3.204
42S	15.93	15.47	8.83	9.46	5580	x	<0.05	x	1.526	3.204
44	1.15	1.97	7.59	7.61	15730	x	0.23	x	x	32.040
48	6.38	5.53	7.86	8.62	x	x	x	x	x	19.580
50	1.49	2.04	7.45	7.38	14840	x	0.59	x	x	82.770
51	2.14	2.15	7.59	7.67	17530	x	<0.05	x	x	13.350
52	3.76	3.45	7.65	8.51	17535	x	<0.05	x	x	1.602
59	11.70	7.10	8.18	8.02	2410	x	1.57	x	0.534	0.534

Appendix E

Morphology and Genetics of the New Mexico Meadow Jumping Mouse (*Zapus hudsonius luteus*):

Jennifer K. Frey

2008

Morphology and Genetics of the New Mexico Meadow Jumping Mouse (*Zapus hudsonius luteus*)

USNM 3322/36046. The original specimen of *Zapus luteus* collected by Dr. W. W. Anderson from "Camp Burgwyn", Taos County, in 1858. Photograph by J.K. Frey.

Final Report

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Note: Some portions of this report regarding use of dental characters have been temporarily blocked out, pending confirmation of methods via ongoing genetic analyses.

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BACKGROUND

The New Mexico meadow jumping mouse (*Zapus hudsonius luteus*) is endemic to the American Southwest where it is known as disjunct Pleistocene relict populations in several major mountain ranges and along the Rio Grande. Currently, it is listed as a candidate for federal Endangered Species Act protection by the US Fish and Wildlife Service, endangered under the New Mexico Wildlife Conservation Act, sensitive by the US Forest Service and Bureau of Land Management, a species of special concern in Arizona, and it has a Natural Heritage conservation status of imperiled (S2) in Arizona and critically imperiled (S1) in Colorado and New Mexico. Status surveys of montane populations conducted in 2005 and 2006 documented dramatic declines in distribution and abundance of the species in comparison with its status just 15 years ago (Frey 2005, 2006). Frey (2005, 2006) found that the mouse is a habitat specialist occurring in herbaceous wetland habitats, especially those dominated by sedges. Further, the primary proximate cause of the species' decline was determined to be the loss of wetland habitats due to livestock grazing, although drought, development, recreations, forest fire, and loss of beaver also were contributing factors (Frey 2005, 2006).

A series of recent controversial papers have focused on the taxonomic validity of Preble's meadow jumping mouse (*Z. h. preblei*), which is a federally threatened subspecies found along the Front Range in southern Wyoming and northern Colorado (Ramey et al. 2005, Vignieri et al. 2006, Ramey et al. 2006, Martin 2006, Crandall 2006, King et al. 2006). Although focused on the taxonomic status of *Z. h. preblei*, data indicated that *Z. h. luteus* was the most taxonomically distinctive of the western subspecies (Ramey et al. 2005, Vignieri et al 2006, King et al. 2006). However, no study has adequately addressed geographic variation within *Z. h. luteus*. Because *Z. h. luteus* is distributed as a series of disjunct Pleistocene relicts, it is possible that each isolated population has evolved unique characteristics, and some may represent taxonomically distinctive units. It is important to identify populations that are distinctive, especially if taxonomic recognition is warranted, because it would facilitate directing appropriate conservation measures at each distinctive unit.

Traditionally, the range of *Z. h. luteus* has been considered to include the Jemez, White, and Sacramento mountains, as well as the Rio Grande drainage (Miller 1911, Hafner et al. 1981, Hoffmeister 1986, Morrison 1992, Frey 2004). In this traditional view, records from along El Rito in the southern San Juan Mountains and from Taos Ski Valley in the Sangre de Cristo Range have been considered peripheral locations associated with the northern Rio Grande population (Hafner et al. 1981, Hafner and Yensen 1998, D. Hafner, personal communication). However, Frey (2006) reported 9 specimen records of *Z. h. luteus* from both the Rio Grande and Canadian River drainages in the Sangre de Cristo Mountains, which suggested that the Sangre de Cristos represented a fourth montane population. The morphologically similar western jumping mouse (*Z. princeps*) is a relatively common inhabitant of this mountain range and there is considerable uncertainty about the identification of some specimens. All jumping mice in the Southwest were assigned to *Z. princeps* prior to the systematic study of Hafner et al. (1981), which relegated some populations as *Z. hudsonicus*. The morphological similarity between *Z. hudsonius* and *Z. princeps* has been a major problem in the conservation of *Z. h. preblei*, which also occurs in an area of potential overlap between the species. Records must be reliably identified in order for appropriate conservation plans to be enacted.

The identification problem between *Z. h. luteus* and *Z. princeps* may be even more problematic than between *Z. h. preblei* and *Z. princeps*. For example, Hafner et al. (1981)

identified a specimen from Taos Ski Valley as *Z. hudsonius* that was captured along with a large series of *Z. princeps*. These records suggest not only broad sympatry (i.e., distributional overlap) between the species but also syntopy (i.e., local co-occurrence). Indeed, cursory examination of both historical specimens and those collected during field surveys for *Z. hudsonius* in the Sangre de Cristo Mountains revealed some individuals captured with characteristics intermediate to the two species and could not be confidently identified.

PURPOSE

The purpose of this study was two-fold. The first objective was to use quantitative morphological and genetic data to provide verified identifications of jumping mouse specimens in the zone of sympatry in northern New Mexico and adjacent areas of Colorado. Accurate identifications are necessary for understanding a species' historical and potential distribution, biogeography, and ecology, as well as providing fundamental information required for enacting conservation measures. Further, these results will elucidate the range of variation within both *Z. h. luteus* and *Z. princeps*, which will allow for more accurate species' identifications in future studies. The second objective was to assess variation among populations of *Z. h. luteus.* This will allow for a determination of the degree of evolutionary differentiation among the populations and if any of the relict populations warrant taxonomic recognition. Knowledge of patterns of variation may be essential for establishing different management for different populations.

METHODS

Genetics

Total genomic DNA was extracted from frozen tissues (muscle, heart or liver) or from skin samples taken from voucher specimens. Protocols followed Lessa and Cook (1998) and Halanych et al. (1999) for DNA extraction, polymerase chain reaction (PCR) amplification, and cycle sequencing. Amplification of the cyt *b* gene was conducted with primers, L14724 and cyt *b* reverse (Irwin et al. 1991). PCR products were sequenced using BigDye Terminator Cycle Sequencing Ready Reaction mix. v. 3.1 (Applied Biosystems) with the additional internal primer MVZ 16 (Smith and Patton, 1993). PCR products were assessed in both directions using an Applied Biosystems 3100 automated DNA sequencer in the Molecular Biology Facility, Biology Department, University of New Mexico, Albuquerque, USA. Sequences were navigated using SEQUENCHER 4.5 (Gene Codes) with the reference sequence from GenBank (*Z. trinotatus*, AF119262). Alignments were completed using default parameters and algorithms of CLUSTAL X (Thompson et al. 1994). Species identifications were made by comparing sequences with reference sequences from a concurrent study by Joe Cook and Jason Malaney at the University of New Mexico, and from those archived in GenBank.

Morphology

Specimens.—Museums were queried for specimens of *Z. hudsonius* and *Z. princeps* from southern Colorado, New Mexico and Arizona. Museums were visited or loans of specimens were obtained in order to examine the following: 1) putative specimens of *Z. h. luteus* from the zone of sympatry in southern Colorado and northern New Mexico, 2) comparative material for *Z. p. princeps* in the zone of sympatry, 3) representative samples of *Z. h. luteus* populations from central and southern New Mexico and Arizona, and 4) representative samples of other subspecies of *Z. hudsonius* (*Z. h. preblei*, *Z. h. campestris*, *Z. h. pallidus*).

I collected quantitative data on 326 specimens of jumping mice, although I also qualitatively examined an additional ca 429 specimens, for a total of 755 specimens examined. In addition, I reviewed hundreds of other museum records for specimen localities that may represent additional unknown populations of *Z. h. luteus*. Museums and sample sizes of specimens examined are as follows: American Museum of Natural History (AMNH; N=9), Academy of Natural Science of Philadelphia (ANSP; N = 10), Frey Tissue (ET or FT; N=71), University of Kansas (KU; N=8 with quantitative data; also qualitatively examined all ca 179 additional specimens in collection), Museum of Southwestern Biology (MSB; N=138 with quantitative data; also qualitatively examined all ca 250 additional specimens from New Mexico and Colorado), New Mexico Museum of Natural History and Science (NMMNHS; N=9), New Mexico State University Vertebrate Collection (NMSU; N=8); Texas Tech University (TTU; N=18), University of Illinois Museum of Natural History (UIMNH [collection transferred to MSB]; N=9), Utah Museum of Natural History (UMNH; N=21), United States National Museum (USNM; N=24).

Sex and age.—Each specimen was assigned to sex according to information on the specimen tag. Two methods were used to assess age. Specimens were assigned to 1 of 6 age classes according to wear on the cheekteeth as described by Krutzsch (1954). Specimens also were assigned to 1 of 8 age classes based on eruption and wear on the third upper molar (M3) and closure of the basioccipital-basisphenoid suture according to Jones (1981). The Krutzsch and Jones age classes for a specimen were transformed into fractions of the total age class possible (e.g., a Krutzsch age class 4 = 4/6 = 0.66). The average age class was the mean of the two fractions for an individual.

Pelage color.—Pelage color was assessed on the dorsum (center of mid-dorsal stripe) and the side (center of side below the mid-dorsal stripe) by comparison with Munsell soil color charts following Spellman et al. (1987). Each color chip is represented by a standard Munsell color name, and a unique combination of hue, value, and chroma. Hue is the color's relation to the rainbow (i.e., red, yellow, green, blue, and purple). Jumping mice are hues of yellow-red (YR) and yellow (Y). A number from 0 to 10 precedes the hue and represents its gradation from red to yellow as numbers increase (i.e., 10YR = 0Y). Value is the color's lightness, and varies from 0, which is absolute black, to 10, which is absolute white. Chroma is the color's strength or departure from neutral of the same lightness. Chroma varies from 0, which is neutral gray up to 20 for the most intense colors. Thus, higher chroma corresponds to richer color. Thus, for both Dorsum and Side there were 4 variables (color name, hue, value, chroma). In addition, I recorded whether the venter was pure white, or had a wash of ochraceous color. I also recorded

whether there appeared to be a prominent pale fringe of hairs lining the edge of the ears when the specimen was viewed head-on from ca 45 cm distance.

Dentition.—I recorded a total of 4 dental characteristics on each side of the jaw (8 characters total) that were considered important for species identification as described by Jones (1981). Molar notation followed convention wherein a lower case "m" referred to a lower molar, an upper case "M" referred to a upper molar, and the following number referred to its position in the molar toothrow (i.e., M2 = the second upper molar). Molar cusp terminology followed Wood and Wilson (1936), Klingener (1963), and Jones (1981).

External and cranial measurements.—A total of 18 morphometric characters were assessed. These included 5 standard external body measurements recorded from specimen tags including, total length, tail length, hindfoot length, ear length, and mass. Cranial measurements were taken to 0.01 mm with digital calipers with automated data input. Cranial characters included: Condylo-incisive length (CBL), taken from the anterior junction of the incisors with the premaxillae to the occipital condyles; rostral length (RL) taken from the zygomatic arch to the anterior end of nasal; zygomatic breadth (ZB), taken at the widest point; depth of skull (DS), taken at deepest point; interorbital constriction (IOC) taken at the narrowest point; maxillary toothrow length (MTR) taken from the anterior edge of P4 to the posterior edge of M3 (not taken if M3 not fully erupted); palatal length (PL), taken from the posterior edge of the incisors to the posterior edge of the palate; palatal breadth (PB), taken between the lingual edge of the P4s; incisive foramen length (IFL), taken at longest point; incisive foramen breadth (IFB), taken at the widest point; interbullar width (IBW), taken at the narrowest point between the auditory bullae; and mastoid breadth (MB), taken perpendicular to the long axis of the skull and at the widest part of the braincase. Five ratios between different pairs of variables were calculated for use in analyses of geographic variation within *Z. h. luteus*, including: tail length/body length; hindfoot length/body length; RL/CBL; IFW/IFL; and IFW/IBW.

Statistics.—Statistical analyses of morphological data were calculated using SPSS version 10.0. Box and whisker plots factored by species (all ages combined) were used to assess

normality for each morphological character. Extreme statistical outliers for cranial measurements revealed by box and whisker plots were removed from the data set. Where possible, nonparametric statistics were used for dental and pelage characters, which were non-normal.

Analyses of non-geographic variation were performed on *Z. hudsonius* and *Z. princeps* separately. Correlations were used to assess relationships of average age class with external and cranial measurements, as well as with value and chroma of the dorsum and side. Kruskal-Wallis tests were used to test if average age class differed with different dental and pelage conditions. Analysis of variance (ANOVA) was used to test for univariate differences in external and cranial characters between the sexes. Discriminant function analysis (DFA) was used to test for multivariate differences between the sexes. Mann-Whitney tests were use to test for differences in pelage and dental characters between the sexes.

Pearson Chi-square tests were used to test for pelage differences between the species including presence of the pale ear fringe, venter color, dorsum and side color and hue. Kolmogorov-Smirnov tests were used to test for differences between the species in value and chroma of the dorsum and side. DFA was used to test for multivariate differences between the species in pelage characters.

Kolmogorov-Smirnov tests were used to test for differences between the species in dental characters. Correlations were used to test for relationships between average age class and dental conditions within each species. DFA was used to test for multivariate differences between the species in pelage characters.

For analyses of external and cranial differences between *Z. h. luteus* and *Z. p. princeps* in the region of sympatry (i.e., southern Colorado and northern New Mexico), I used individuals of all ages, but deleted those missing a large majority of cranial measurements. For *Z. h. luteus* (N = 63) this included individuals from the Canadian River drainage (N = 12), upper Rio Grande basin including El Rito (N = 16), Sambrito Creek (N = 7), and Jemez Mountains (N = 28). For *Z. princeps* (N = 121) the sample included individuals from both the Sangre de Cristo (N = 95) and San Juan (N = 26) Mountains. Seven specimens with uncertain identification were not assigned to species. These included USNM 3322 from “Camp Burgwyn” (Taos County, NM; hereafter, Fort Burgwin); TTU 2388 from “2 1/2 M. N of Williams lake, Grid Station A-3” (Taos County, NM; hereafter, Taos Ski Valley); MSB 4943 from “2 mi NE Tres Ritos” (Taos County, NM; hereafter Tres Ritos); USNM 59732 from “Santa Fe” (probably Santa Fe County, NM); NMMNHS 1228 and 1229 from “T20N, R15E along Mora R. next to sewage ponds 1.5 mi down river from town“ (Mora County, NM; hereafter, Mora], and KU 16038 from “Florida, 6800 ft.” (La Plata County, CO; hereafter, Florida).

For univariate ANOVAs of external and cranial characters, I subdivided both species into young (average age class < 0.5) and old (average age class $\geq$ 0.5) age groups. Further, because *Z. p. princeps* exhibited significant sexual dimorphism, I also subdivided the old *Z. p. princeps* subgroup into male and female subgroups. Post-hoc Student-Newman-Kuels tests were used to identify non-significant subgroupings. DFAs were used to test for multivariate differences among these 5 subgroups and between the species. Principal components analysis (PCA) was used to examine the multivariate variation in external and cranial morphology among the specimens. Additional PCAs were done that combined the external and cranial measurement data with either the pelage or dentition data.

For analyses of geographic variation, *Z. h. luteus* was subdivided into 7 populations (Canadian River drainage, upper Rio Grande drainage, Bosque del Apache [i.e., southern Rio Grande], San Juan Mountains, Jemez Mountains, Sacramento Mountains, White Mountains), while *Z. p. princeps* was subdivided into 2 populations (Sangre de Cristo Mountains, San Juan Mountains). Likelihood ratio tests were used to examine geographic variation in pelage and dentition. ANOVAs and Student-Newman-Keuls range tests were used to examine geographic variation of each external and cranial measurement. DFAs were used to test for multivariate differences among the populations.

All DFAs used a chi-square transformation of the overall Wilks' lambda to test for multivariate differences between or among group centroids. In some cases step-wise selection DFA was used to determine which variables accounted for the variation. Wilks' Lambda was used to rank the variables in ability to discriminate by passing the tolerance tests (0.05 to enter; 0.10 to remove) and a chi-square transformation of the overall Wilks' lambda to test for differences in the group centroids. DFA models were applied to a classification routine in order to predict taxon of specimens with uncertain identification. Because the original classification results can provide overly optimistic estimates, a cross-validation procedure was used whereby each case in the analysis was classified by the functions derived from all cases other than that case (SPSS 1999). The percentage of correct classifications was compared between the original and cross-validated cases in order to assess whether there were too many predictors in the model. An excess of predictors was indicated by a substantially lower percentage of correct classification for the cross-validated cases.

In all PCAs missing values were replaced with the mean of that variable so that all specimens could be included in analyses. There was no rotation of the variables and only components that had eigenvalues greater than or equal to 1.0 were extracted because these usually are sufficient to describe the variance within the variables (Chatfield and Collins 1980; McGarigal et al. 2000). Components retained for interpretation were based on the scree plot criterion (McGarigal et al. 2000, McCune and Grace 2002). Loadings with a minimum absolute value of ca 0.50 were considered significant (McGarigal et al. 2000).

RESULTS

Nongeographic Variation

Sexual dimorphism.—Within *Z. hudsonius*, females were significantly larger in total length, tail length, ear length, mass, and ZB; no other external or cranial characters exhibited significant differences between the sexes. A discriminant function analysis of all 19 external and cranial characters revealed no significant difference between the group centroids (Eigenvalue = 24.988, canonical correlation = 0.981, Wilks' lambda = 0.38, chi-square = 24.432, P = 0.058). Within *Z. princeps*, females were significantly larger in total length, tail length, body length, hindfoot length, mass, ZB, DS, IOC, PL, PB, IFL, and MB. A discriminant function analysis of all 19 external and cranial characters revealed a significant difference between the group centroids (Eigenvalue = 1.592, canonical correlation = 0.784, Wilks' lambda = 0.386, chi-square = 45.248, P = 0.001). There were no significant differences in dental or pelage characters between the sexes in either species. Given the virtual lack of sexual dimorphism in *Z. hudsonius*, sexes were pooled in further analyses.

Age.—Within *Z. hudsonius*, average age class exhibited highly significant ($P \leq 0.005$) positive correlations with all external and cranial measurements except hindfoot length, ear length, and MTR, which were nonsignificant. Further, there was a highly significant relationship between average age class with condition of the anteromedian fold on the first lower molar (Chi-square = 20.142, df = 2, $P < 0.001$; Figure 1). The pattern between age and fold suggests that "dents" are not remnants of the fold, but rather are age related wear or damage to the molar. A marginally significant (P = 0.042) positive correlation with pelage side chroma (i.e., older animals had richer colors) had very low R-square values ($R^2 = 0.063$).

Within *Z. princeps*, average age class exhibited highly significant ($P \leq 0.002$) positive correlations with body length, mass, CBL, CBL2, RL, ZB, PL, PB, IBW, and MB, a significant ($P < 0.05$) positive correlation with total length, and a significant negative correlation with MTR (note that all individuals without M3 erupted were excluded). [redacted] Average age class exhibited a significant positive ($P < 0.05$) correlation with pelage side value (i.e., older animals were paler) and chroma (i.e., older animals were less gray and richer), although R-square values were low ($R^2 = 0.066$ and 0.050, respectively).

For both species, fusion of the basioccipital-basisphenoid suture began around average age class 0.5, with complete fusion in most individuals by average age class 0.6 (Figure 3). Based on external and cranial characters that had the highest correlation coefficients with age in *Z. hudsonius*, growth rate based on cubic regression declined at ca. age class 0.4 to 0.6, depending on the character (Figure 4). Consequently, only individuals with an average age class ≥ 0.5 were included in general analyses of geographic variation.

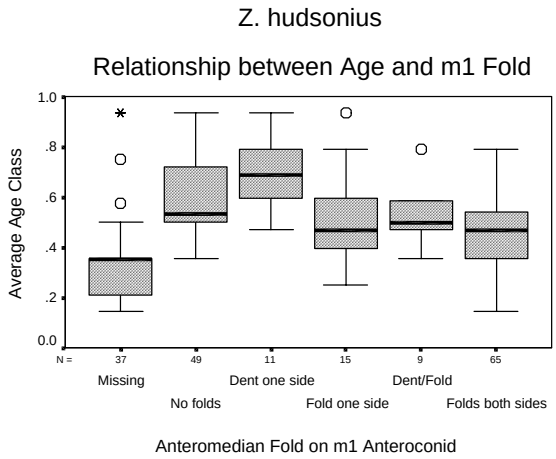


Figure 1. Relationship between age and condition of the anteromedian fold on the anteroconid of the first lower molar in *Z. hudsonius* from the American Southwest.

[redacted]

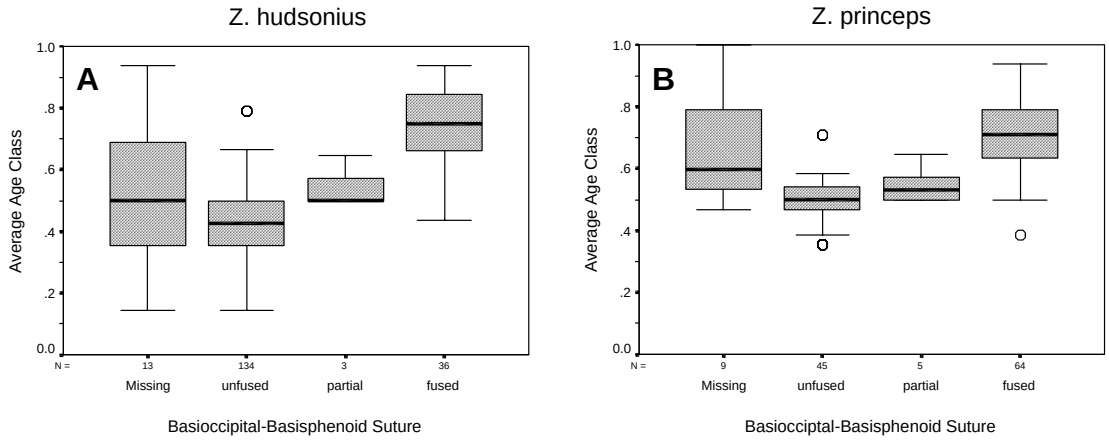


Figure 3. Relationship between age and fusion of the basioccipital-basisphenoid suture in A) *Z. hudsonius*, and B) *Z. princeps*.

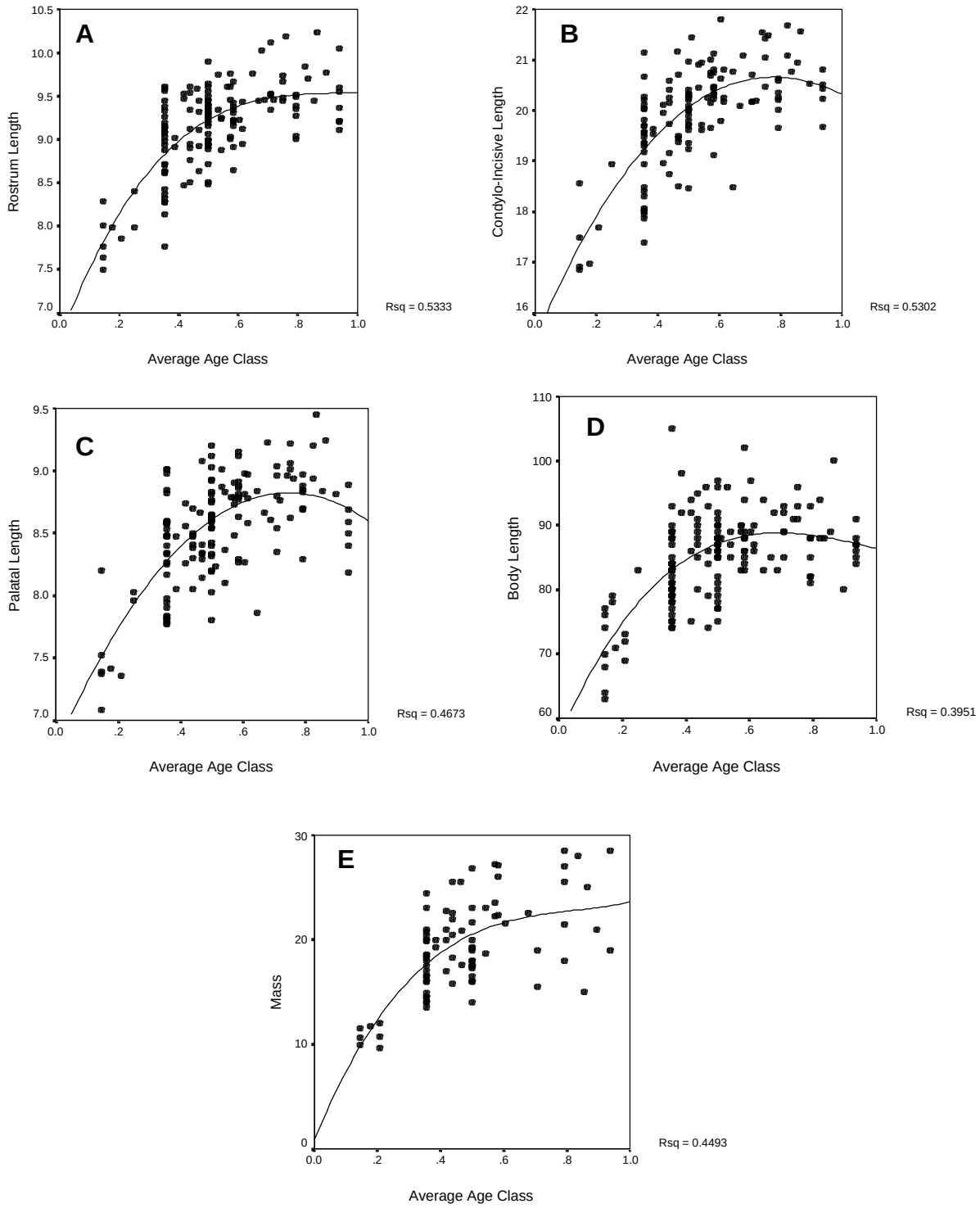


Figure 4. Relationship between average age class and selected external and cranial characters in *Z. hudsonius*, including: A) rostrum length; B) condylo-incisive length; C) palatal length; D) body length; and E) mass.

Species Differences

Genetics

Genetic data confirmed that only *Z. h. luteus* occurred along the mainstem of the Rio Grande, and in the Jemez, Sacramento, and White mountains, while both species occurred in association with the Sangre de Cristo and San Juan mountains (Appendix 1).

Pelage

There was a highly significant relationship between species (excluding *Z. h. preblei*) and presence of a prominent pale ear fringe (Pearson Chi-square = 166.048; df = 1; $P < 0.001$). A prominent pale ear fringe was scored as present in only 1 of 64 (1.6%) *Z. h. luteus*, but 116 of 119 (97.5%) *Z. p. princeps*. Of 4 *Z. h. preblei*, 2 (50%) were scored as having the prominent pale ear fringe. Of the 7 specimens of uncertain identification, only the individual from Taos Ski Valley (TTU 2388) was scored as having a prominent pale ear fringe.

There was no significant difference between the species (excluding *Z. h. preblei*) in white versus ochraceous-washed venter: 50% of 28 *Z. h. luteus* and 59% of 32 *Z. p. princeps* had the washed condition. Thus, this character had no value for discriminating between these taxa. Of 4 specimens of *Z. h. preblei*, 3 had the washed venter.

There was a highly significant difference between the species (including *Z. h. preblei*) in color of the dorsum (Pearson Chi-square = 53.452; df = 6; $P < 0.001$) and side (Pearson Chi-square = 68.198; df = 8; $P < 0.001$). The dorsum of all *Z. h. luteus* was dark yellowish brown, dark brown, or dark grayish brown, while 95.6% of *Z. p. princeps* had a dorsum of other colors (Table 1). For the side pelage, 91.1% of *Z. h. luteus* were shades of yellowish brown, while 82.5% of *Z. p. princeps* were shades of olive brown (Table 2).

Based on a comparison between *Z. h. luteus* (N = 34) and *Z. p. princeps* (N = 69) there was a highly significant difference in hue of the dorsum (Pearson Chi-square = 83.288; df = 1; $P < 0.001$) and side (Pearson Chi-square = 63.534; df = 2; $P < 0.001$). All *Z. h. luteus* had 10yr dorsum hue and 94.1% had 10yr side hue, while for *Z. p. princeps*, 92.8% had 2.5Y dorsum hue and 82.6% had 2.5Y side hue (Tables 1 and 2). There was a significant difference between the species in dorsum value (Kolmogorov-Smirnov $Z = 2.144$, $P < 0.001$) and dorsum chroma (Kolmogorov-Smirnov $Z = 2.958$, $P < 0.001$), with the dorsum in *Z. h. luteus* being both paler and richer than *Z. princeps* (Figure 5). However for the side, there was a significant difference between the species only for chroma (Kolmogorov-Smirnov $Z = 3.660$, $P < 0.001$); side value did not differ between the species ($P = 0.173$). In other words, the side in *Z. h. luteus* was richer than *Z. p. princeps*, but was not appreciably different in darkness (Figure 5). For dorsal stripe distinctiveness (i.e., distinctiveness = dorsum - side), I found a significant difference between the species in chroma (Kolmogorov-Smirnov $Z = 2.183$, $P < 0.001$); but not for value ($P = 0.313$). In other words, the dorsal stripe in *Z. h. luteus* was relatively less rich and more gray in comparison to the side, than in *Z. p. princeps* (Figure 6). This was due largely to the relatively richer sides in *Z. h. luteus* (Figure 5).

A DFA based on 9 pelage characters resulted in a significant difference between the group centroids of the species (Eigenvalue = 12.028, canonical correlation = 0.961, Wilks' lambda = 0.077, chi-square = 250.289, df = 7, $P < 0.001$). The classification procedure resulted in 98.1% of original groups and cross-validated groups correctly classified. The questionable

specimens from Tres Ritos, Fort Burgwin, and Florida were predicted to be *Z. h. luteus* with high probability (> 0.7). However, the specimen from Taos Ski Valley (TTU 2388) was predicted to be *Z. p. princeps*, although this classification had a low probability (0 = 0.089) and was considered an outlier based on a high squared Mahalanobis distance to the centroids (2.895). A stepwise DFA revealed that the most important discriminating pelage characters were presence/absence of the distinct pale ear fringe and dorsum hue. When ear fringe or both ear fringe and dorsum hue were deleted from the dataset, TTU 2388 was predicted to be *Z. h. luteus*, and when only ear fringe was eliminated, the probability that TTU 2388 is *Z. h. luteus* was high (p = 0.775). Thus, the fact that TTU 2388 was coded as having the prominent pale ear fringe was primarily responsible for classification of TTU 2388 as *Z. p. princeps* in the original analysis.

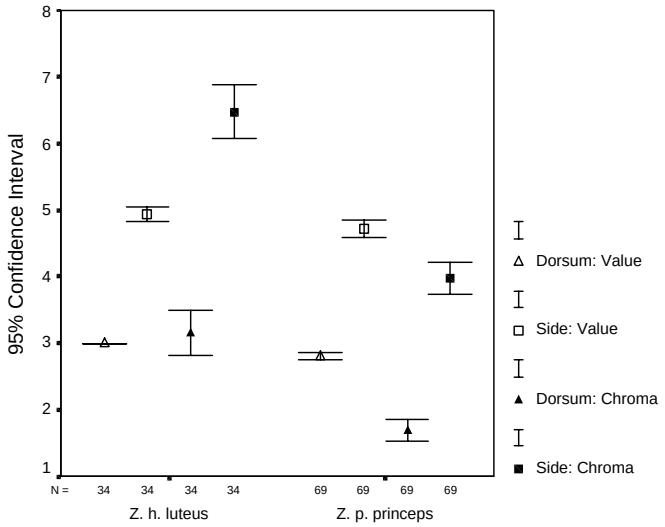


Figure 5. Comparison of dorsum and side value and chroma between *Z. h. luteus* and *Z. p. princeps* in the American Southwest.

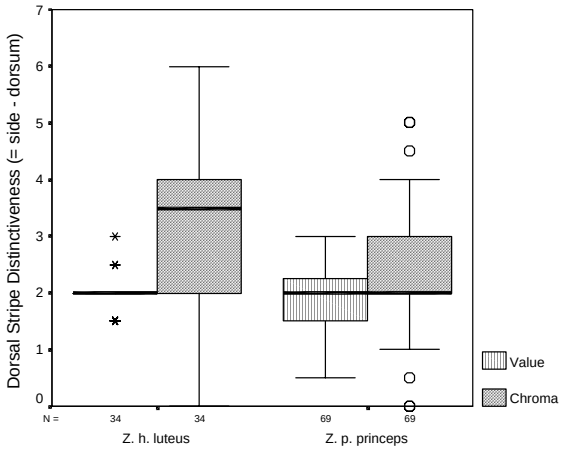


Figure 6. Comparison of the distinctiveness (distinctiveness = side – dorsum) of value and chroma of the dorsal stripe in *Z. h. luteus* and *Z. p. princeps* in the American Southwest.

Table 1. Percentage of jumping mice (*Zapus*) in the American Southwest with different hues of the dorsum pelage.

	Hue 10YR		Hue 10YR and 2.5Y				Hue 2.5Y
Species	Dark yellowish brown	dark brown	Dark grayish brown	very dark grayish brown	very dark gray	black	dark olive brown
Z. h. luteus (N = 34)	35.3	29.4	35.3				
Z. h. preblei (N=4)			50.0				50.0
Z. p. princeps (N = 68)		4.4		30.9	23.5	30.9	10.3

Table 2. Percentage of jumping mice (*Zapus*) in the American Southwest with different hues of the side pelage.

	Hue 7.5YR	Hue 10YR				Hue 2.5Y			
Species	strong brown	brownish yellow	yellowish brown	Dark yellowish brown	brown	light olive brown	olive brown	dark olive brown	dark grayish brown
Z. h. luteus (N = 34)	5.9	2.9	67.6	23.5					
Z. h. preblei (N=4)			50.0				50.0		
Z. princeps (N = 69)		2.9	10.1	1.4	1.4	42.0	39.1	1.4	1.4

Dentition

Data on dentition were collected from a total of 270 individuals of all ages representing 142 *Z. hudsonius* (included 139 *Z. h. luteus* and 3 *Z. h. preblei*), 121 *Z. princeps*, and the 7 specimens with uncertain identification. Below, results are presented for each dental character separately. That is then followed by an analysis of combined dental characters including the specimens with uncertain identification.

Anteromedian fold m1.—There was a highly significant relationship (Kolmogorov-Smirnov $Z = 4.031$, $P < 0.001$) between species and presence of the anteromedian fold on the anteroconid of the first lower molar (Figure 7). The fold was present on at least one side of the jaw in 59% of *Z. hudsonius*, but absent from both sides of the jaw in 91% of the *Z. princeps* (Table 3). Within *Z. hudsonius* there was a highly significant relationship between average age class and presence of the fold ($r = 0.361$, $F = 21.016$, $P < 0.001$); no significant relationship between age and presence of the fold existed in *Z. princeps* (Figure 8). Although specimens that have the anteromedian fold on at least one molar are likely to be *Z. hudsonius*, absence of this character in *Z. hudsonius* was considered too frequent to use this variable alone as a diagnostic character for species identification.

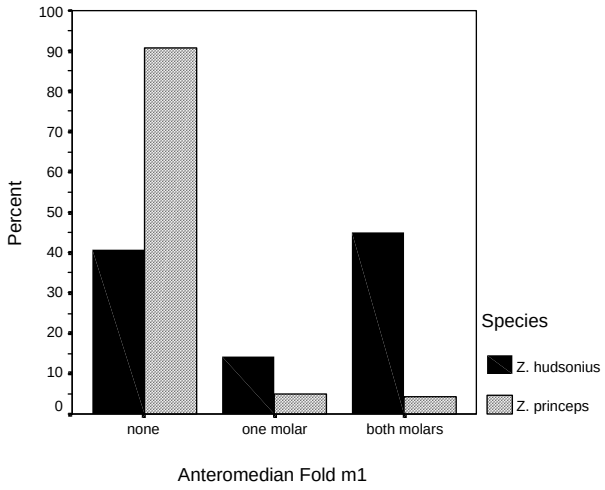


Figure 7. Percent of *Z. hudsonius* and *Z. princeps* in the American Southwest with the anteromedian fold on the anteroconid of the first lower molar.

Table 3. Frequency of the anteromedian fold on the anteroconid of the first lower molar in *Zapus hudsonius* and *Zapus princeps* in the American Southwest.

	Z. hudsonius (N = 142)		*Z. princeps* (N = 120)	
	count	%	count	%
No folds	58	40.8	109	90.8
Fold on one side jaw	20	14.1	6	5.0
Fold on both sides jaw	64	45.1	5	4.2

External and Cranial Measurements

Results of ANOVAs performed on each external and cranial measurement for 5 subgroups (i.e., young *Z. h. luteus*, old *Z. h. luteus*, young *Z. princeps*, old male *Z. princeps*, old female *Z. princeps*) are presented in Appendix 1. Based on post-hoc Student-Newman-Keuls range tests, 13 variables formed significantly different (P = 0.01) groupings between *Z. h. luteus* and *Z. p. princeps* including: total length, tail length, body length, hindfoot length, CBL, ZB, MTR, PL, PB, IFL, IFB, IBW, and MB. Each of these variables, except hindfoot length, and CBL, also formed significantly different groupings at P = 0.001.

A DFA based on the same 5 subgroups resulted in a highly significant difference among the group centroids (Eigenvalue = 8.123, canonical correlation = 0.944, Wilks' lambda = 0.029, chi-square = 268.538, df = 68, P < 0.001). The classification procedure resulted in 59.8% of original groups and 40.2% of cross-validated groups correctly classified. The percentage of original groups correctly classified was highest for young of both species. All specimens of uncertain identification were predicted to be *Z. h. luteus*, with exception of that from Fort Burgwin, which was predicted to be a young *Z. princeps*. However, this specimen had 12 missing variables and a low prediction probability (0.155).

A PCA based on 18 external and cranial characters (replaced missing variable with means) resulted in the extraction of 3 components, which together accounted for 67.3% of the variation. The scree plot indicated that a single component was needed for interpretation. A scatter plot of components 1 and 2 revealed considerable overlap between the two species (Figure 14). Further, the 7 specimens of uncertain identification plotted at or near the region of overlap (Figure 14). Poor separation in this analysis likely was primarily due to replacement of missing variables with means. This would more heavily skew specimens with missing values towards *Z. princeps*, which had a larger sample size. Because of the large number of missing variables the PCA would not run without replacing missing values.

A DFA of 18 external and cranial characters resulted in a highly significant difference between the group centroids for *Z. p. princeps* and *Z. h. luteus* (Eigenvalue = 6.750, canonical correlation = 0.933, Wilks' lambda = 0.129, chi-square = 158.692, df = 17, P < 0.001). The classification procedure resulted in 95.1% of original groups and 86.4% of cross-validated groups correctly classified. The percentage of original groups misclassified was approximately equal for both species, while the percentage of cross-validated groups misclassified was about twice as high (i.e., 22%) for individuals originally identified as *Z. h. luteus*. Specimens with uncertain identification from Taos Ski Valley, Tres Ritos, Mora, and Florida were predicted to be *Z. h. luteus*, each of which had < 50% of predictor variables missing. However, the specimens from Santa Fe and Fort Burgwin were predicted to be *Z. p. princeps*. This likely was due to a large number (> 50%) of variables missing in these specimens. Thus, both were extreme outliers based on squared Mahalanobis distance to the centroids and corresponding very low probability (< 0.04) of belonging to the predicted group. Thus, results for these 2 specimens are not reliable.

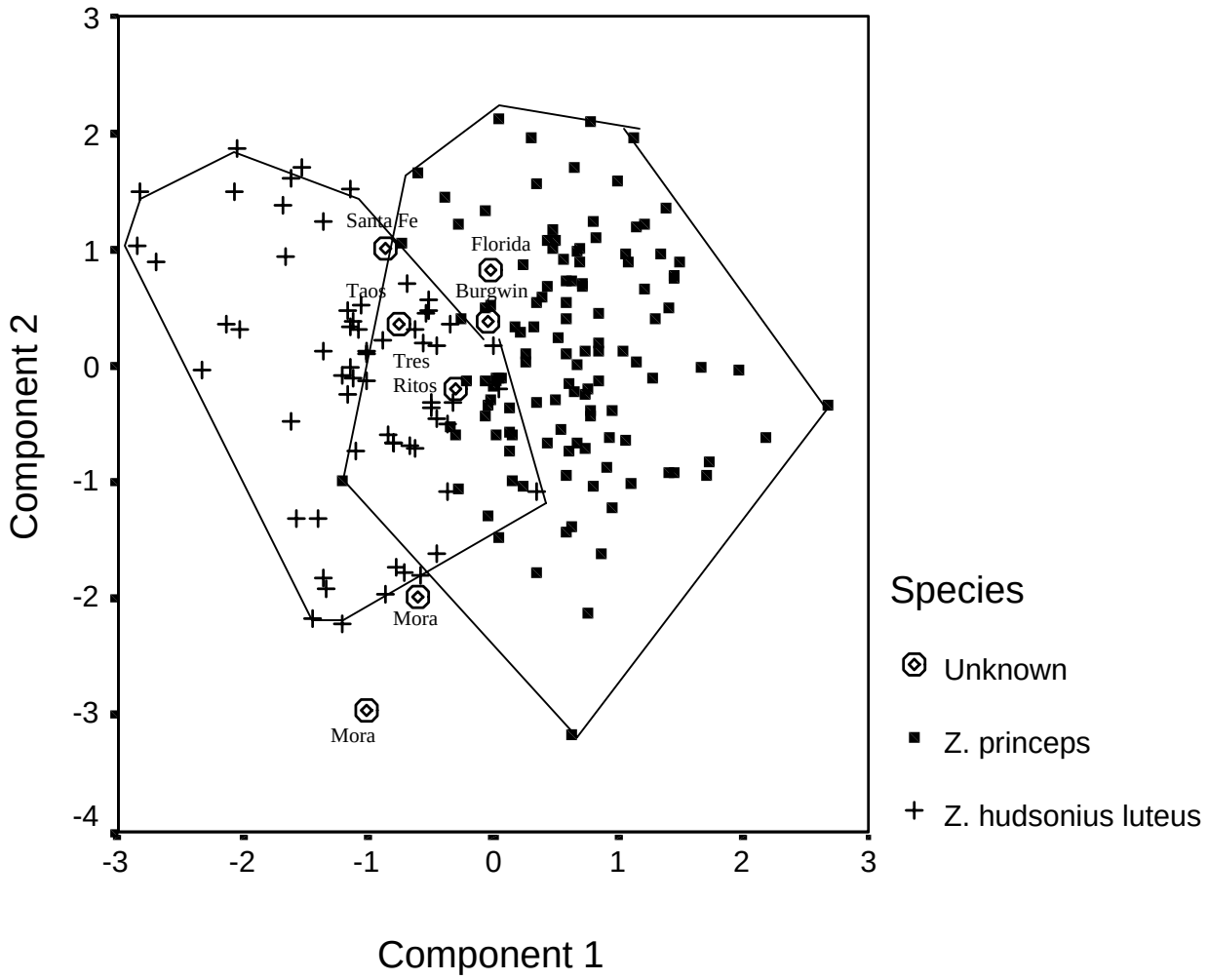


Figure 14. Multivariate variation in external and cranial measurements in jumping mice from southern Colorado and northern New Mexico. Specimens with uncertain identification are from Mora, Taos Ski Valley, Fort Burgwin, Tres Ritos, Santa Fe, and Florida.

Combined Data

A PCA based on the dataset of 191 specimens (i.e., used in analyses of external and cranial measurements) using 8 external and cranial and 4 dental characters (missing variables replaced by mean) extracted 3 components, which accounted for 63.79% of the variation. The scree plot indicated that a single component in needed for interpretation. A scatter plot of components 1 and 2 revealed complete separation between *Z. p. princeps* and *Z. h. luteus* (Figure 15). Further, each of the 7 specimens with uncertain identification grouped with *Z. h. luteus* (Figure 15).

I conducted a PCA based on a database of 107 individuals of all ages (*Z. h. preblei* excluded) using the 18 external and cranial and 9 pelage characters (missing variables replaced by mean). The PCA extracted 6 components, which accounted for 76.1% of the variation. The scree plot indicated that two components were needed for interpretation. A scatter plot of components 1 and 2 revealed complete separation between *Z. p. princeps* and *Z. h. luteus* (Figure 16). Further, all 4 specimens with uncertain identification and pelage data (Taos Ski Valley, Fort Burgwin, Tres Ritos, and Florida) grouped with *Z. h. luteus* (Figure 16).

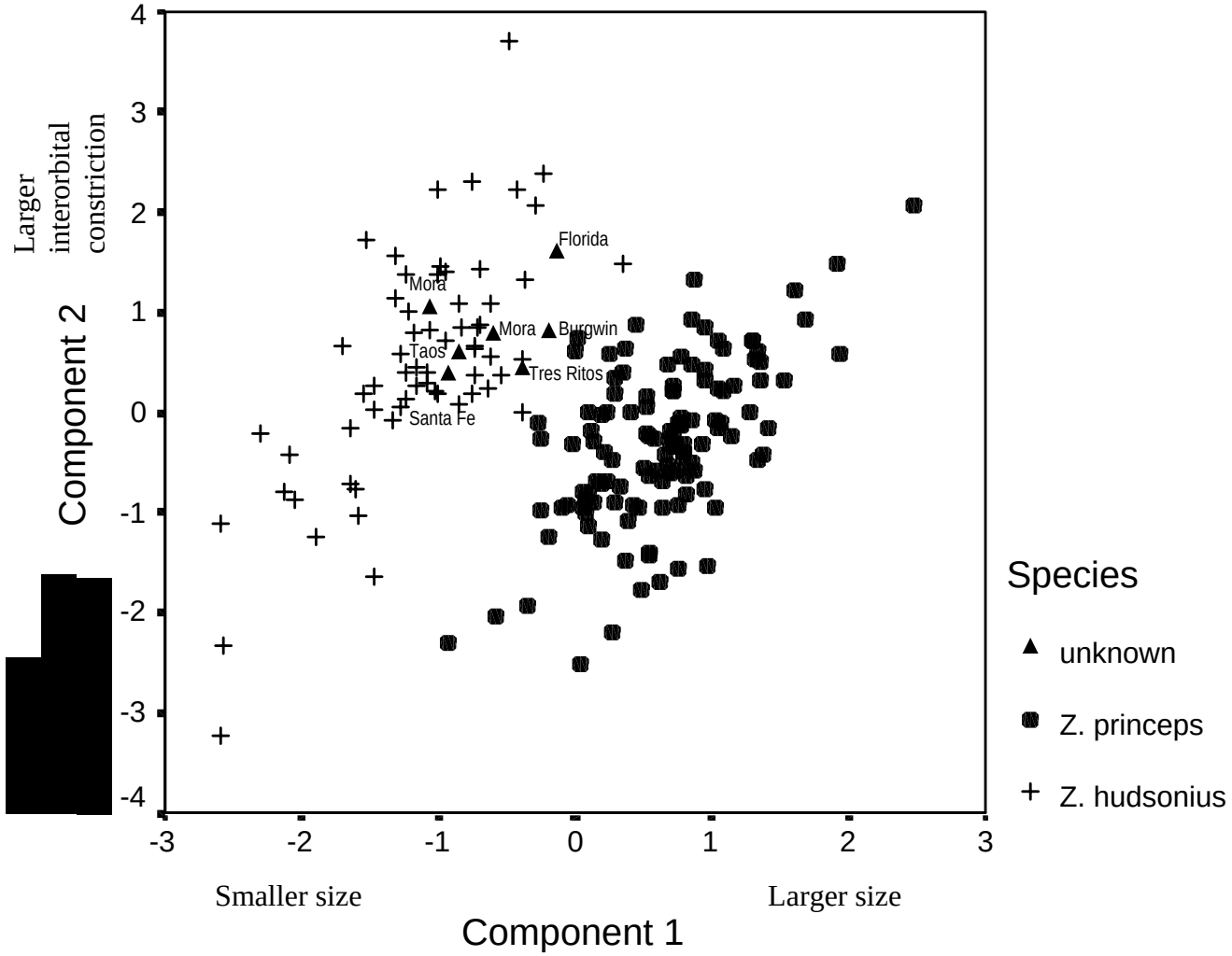


Figure 15. Multivariate variation in external, cranial, and dental characters in jumping mice from southern Colorado and northern New Mexico. Specimens with uncertain identification are from Mora, Taos Ski Valley, Fort Burgwin, Tres Ritos, Santa Fe, and Florida.

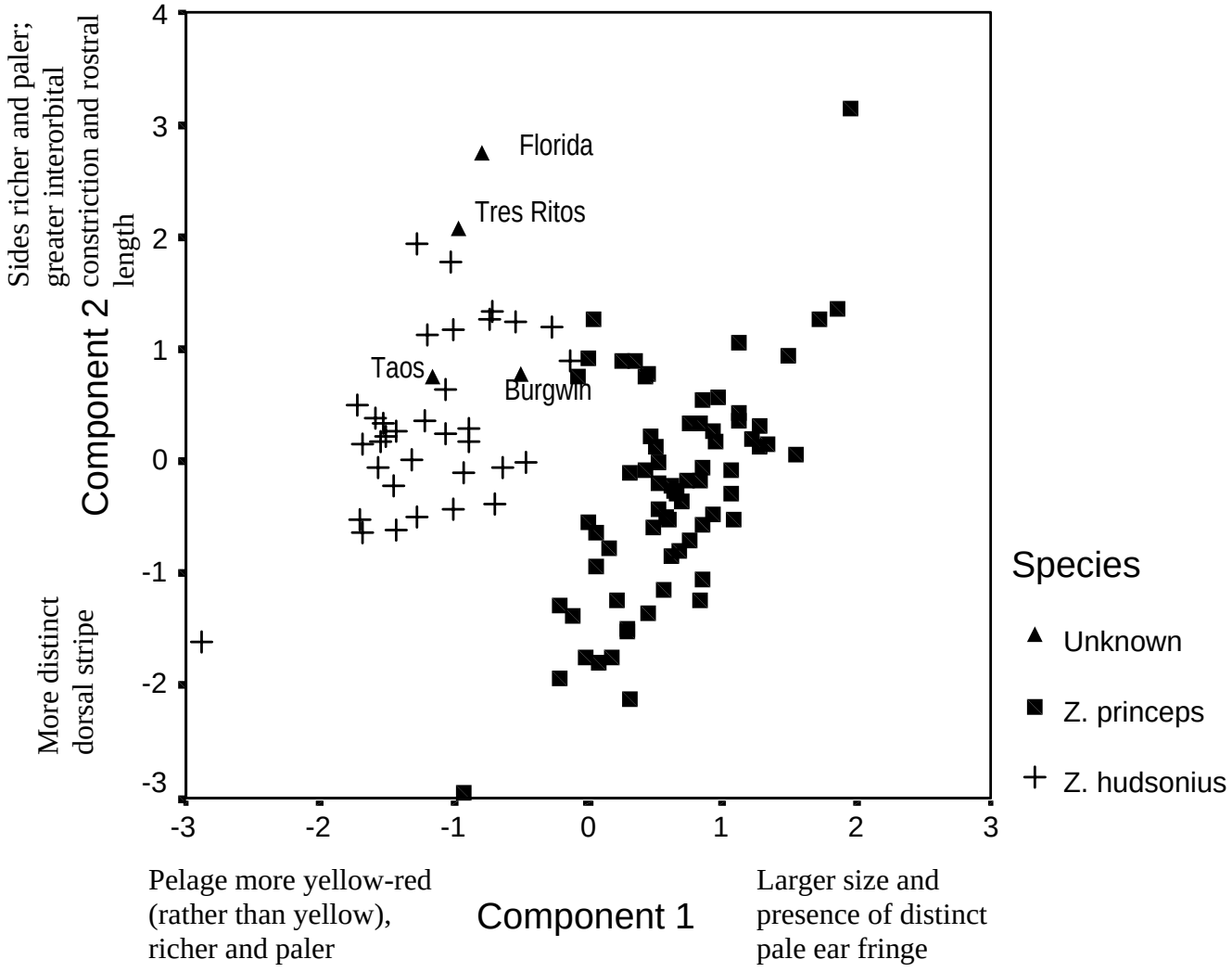


Figure 16. Multivariate variation in external, cranial, and pelage characters in jumping mice from southern Colorado and northern New Mexico. Specimens with uncertain identification are from Taos Ski Valley, Fort Burgwin, Tres Ritos, and Florida.

Geographic Variation

Zapus hudsonius

Pelage.—Using Likelihood ratio tests, the only pelage characteristic exhibiting significant variation among populations of *Z. hudsonius* was dorsum color (chi-square = 31.805, df = 18, P = 0.023). The only discernable patterns were the high frequency of specimens from the Canadian and White populations that were dark brown, and the high frequency of *Z. h. preblei* specimens that were dark olive brown, which is similar to *Z. princeps* (Table 9). Failure to find additional significance may be due to small sample sizes because graphs suggested other differences. For example, pelage color was fairly uniform within the San Juan population, and the two specimens included in the pelage analysis were distinct in having pale sides (i.e., yellow and brownish-yellow; Figure 17A), which accentuated the distinctiveness of the dorsal stripe. Additionally, *Z. h. preblei* was distinct in having dull, grayish sides—typically olive brown as in *Z. princeps* (Figure 17B).

Table 9. Variation in color of dorsum among in 6 populations of *Z. h. luteus* and *Z. h. preblei*.

	N	dark brown	dark olive brown	Dark yellowish brown	very dark grayish brown
Canadian	12	50.0		8.3	41.7
Jemez	9	11.1		44.4	44.4
Rio Grande	8	25.0		62.5	12.5
Sacramento	4			50.0	50.0
San Juan	2			50.0	50.0
White	3	66.7		33.3	
Z. h. preblei	4		50.0		50.0

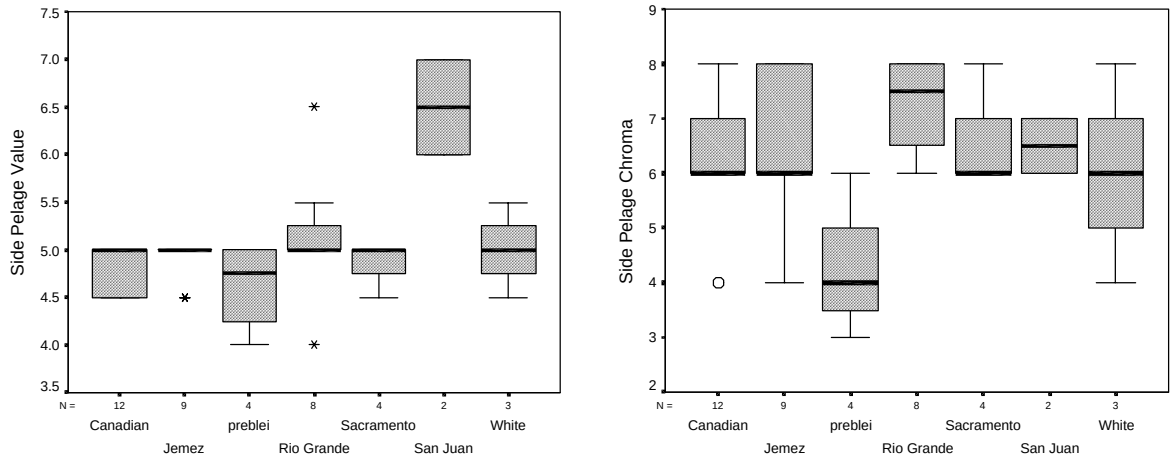
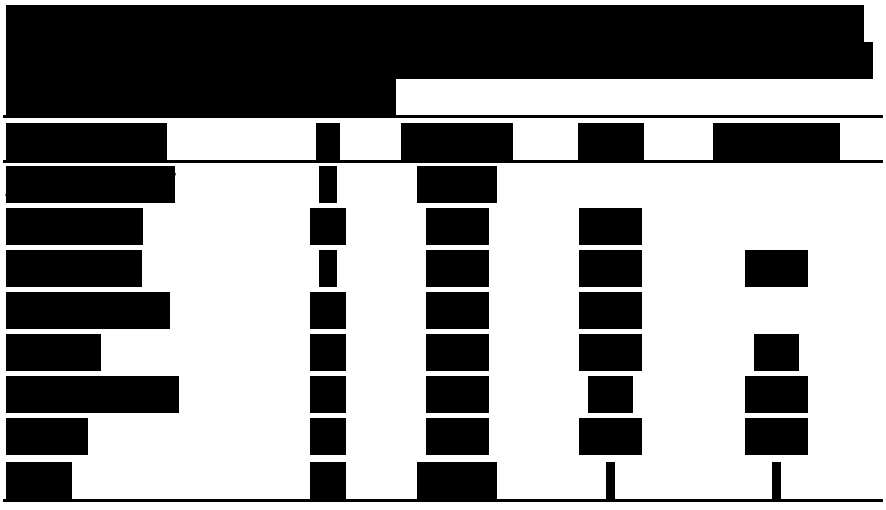


Figure 17. Side pelage A) value, and B) chroma, in 6 populations of *Z. h. luteus* and *Z. h. preblei*.

Dentition.—Using Likelihood ratio tests, the only dental characteristics exhibiting significant variation among populations of *Z. hudsonius* were conditions of the m1 anteromedian fold (chi-square = 42.672, df = 16, P < 0.001) and the [redacted] The anteromedian fold on the anteroconid of the first lower molar was most consistently present in *Z. h. preblei*, as well as in populations of *Z. h. luteus* from the Rio Grande basin (i.e., BDA, Rio Grande, and Jemez Mountains) and White Mountains (Table 10). The populations with the highest frequency of absence of the fold were the populations from the Sacramento and San Juan mountains. [redacted]

Table 10. Percentage of specimens in 6 populations of *Z. h. luteus* and *Z. h. preblei* with the anteromedian fold on the anteroconid of the first lower molar.

Population	N	Absent	One molar	Both molars
Z. h. preblei	3		33.3	66.7
Canadian	14	42.9	14.3	42.9
San Juan	8	62.5	12.5	25.0
Rio Grande	18	27.8	11.1	61.1
Jemez	28	17.9	17.9	64.3
Sacramento	41	73.2	7.3	19.5
White	20	30.0	5.0	65.0
BDA	14	28.6	35.7	35.7



External and cranial measurements.—Descriptive statistics for 95 adult (i.e., average age class $\geq$ 5.0) *Z. h. luteus* in 7 populations are in Appendix 2. ANOVAs revealed significant differences among the 7 populations for all external and cranial variables except body length, ear length, mass, RL, MTR, PB, RL/CBL, HF/Body. Based on Student-Newman-Keuls range tests, significant non-overlapping groups occurred only for three variables (PL, MB, IFB/IFL). The San Juan population had a significantly greater MB and IFB/IFL than all other populations of *Z. h. luteus* (Figure 18).

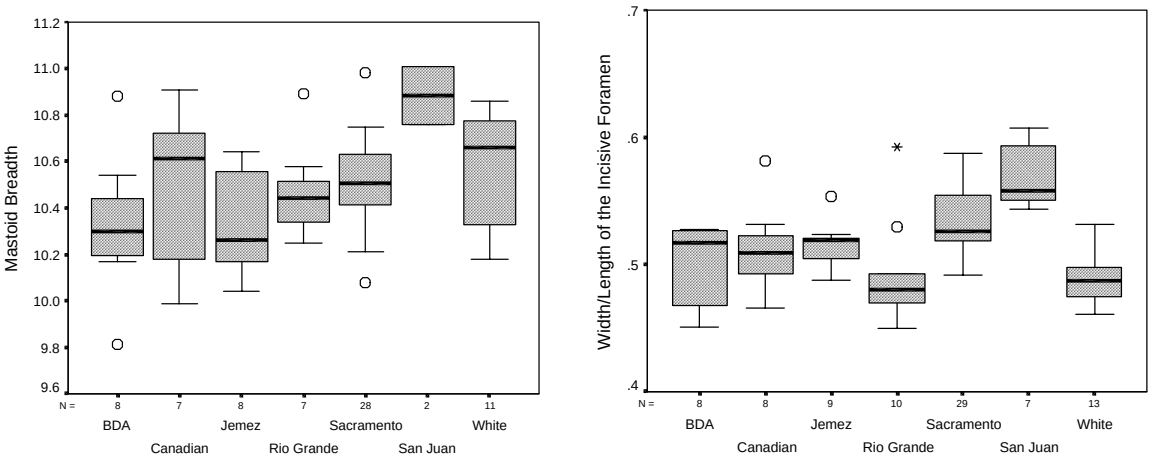


Figure 18. Variation among 7 populations of *Z. h. luteus* in A) mastoid breadth (MB), and B) the ration between the width and length of the incisive foramen (IFW/IFL).

As a group, the 3 populations from the Rio Grande basin (i.e., Bosque del Apache [BDA], upper Rio Grande, and Jemez Mountains) had significantly shorter PL than the remaining populations of *Z. h. luteus* (Figure 19). Together, these 3 populations were among the 4 populations with the smallest measurements for most variables (except body length, IOC, MTR, and PB), and appeared to share more similarities in comparison with the remainder of the populations. The overall uniformity of these 3 populations in external and cranial morphology also was demonstrated by ANOVAs among the 3 populations, which resulted in significant differences in only two variables (IOC, IFW/IBW). The Jemez population had a significantly ($P = 0.047$) smaller interorbital constriction than BDA, while the upper Rio Grande population did not exhibit significant differences with either (Figure 20A). For the ratio between the incisive foramen width and interbullar breadth, the upper Rio Grande was significantly ($P = 0.013$) smaller than the other 2 populations. Finally, a DFA of external and cranial characters among the 3 Rio Grande Basin populations did not result in a significant difference among the centroids ($P = 0.511$), which supported the similarity among these populations in external and cranial measurements.

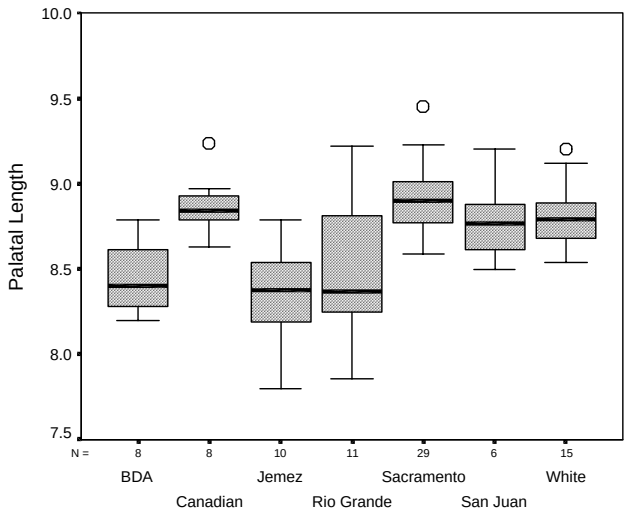


Figure 19. Variation among 7 populations of *Z. h. luteus* in palatal length.

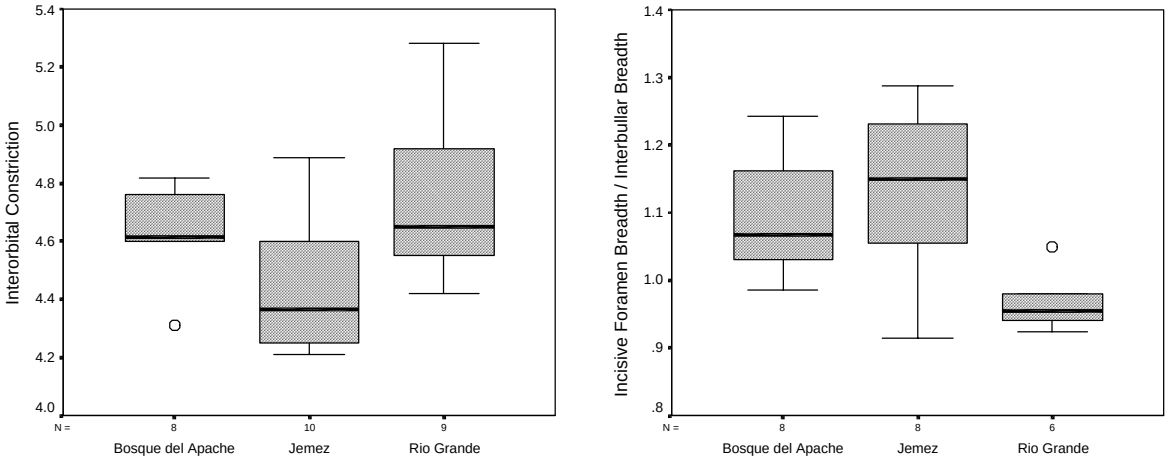


Figure 20. Variation among populations of *Z. h. luteus* from the Rio Grande basin in A) interorbital constriction (IOC), and B) the ratio between the width of the incisive foramen and interbullar breadth (IFW/IBW).

To further examine geographic variation in external and cranial characters within *Z. h. luteus*, I used only adult individuals and combined all populations from the Rio Grande basin into a single population. ANOVAs revealed significant differences among the populations in most characters, except body length, ear length, mass, CBL, RL, MTR, PB, and HF/Body. Post-hoc Student-Newman-Keuls range tests revealed non-overlapping groups for 7 measurements (i.e., tail length, hindfoot length, IFL, IFW/IFL, MB, IFW/IBW). Together, the Rio Grande Basin and Canadian populations had significantly shorter tail lengths than other populations. The White Mountains population had a significantly greater hindfoot length than all other populations. In comparison with the remainder of the populations, the San Juan Mountains population had a significantly shorter IFL, greater IFW/IFL, and greater MB. The Sacramento Mountains population had a significantly greater IFW/IBW than all other populations, and a greater IFW/IFL than all other populations except the San Juan Mountains. When the Rio Grande Basin population was removed, ANOVAs resulted in significant differences among the 4 remaining populations for hindfoot length, DS, IOC, IFL, IFB, IBW, t/b, IFW/IFL, IFB/IBW. Differences were essentially the same as compared with the analyses that included the Rio Grande Basin population, except that IFW/IFL exhibited non-overlapping groups among all 4 populations (Figure 21).

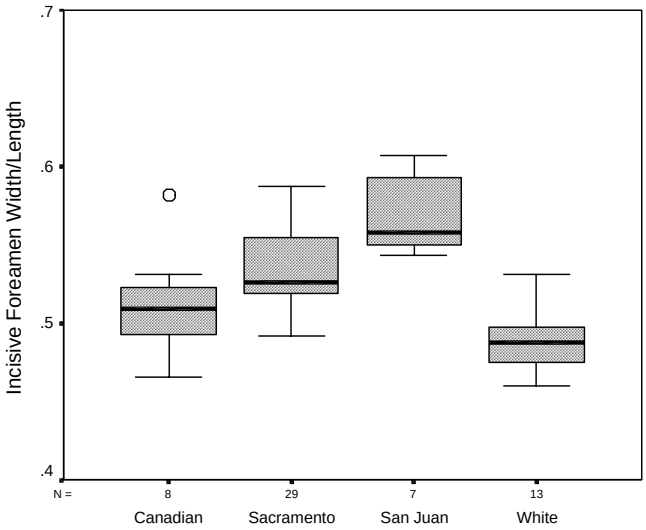


Figure 21. Variation in the ratio of the width and length of the incisive foramen among populations of *Z. h. luteus* excluding he Rio Grande Basin.

A DFA among the 5 populations (Canadian, Sacramento, San Juan, White, Rio Grande Basin) and among the 4 populations exclusive of the Rio Grande Basin (Canadian, Sacramento, San Juan, White) were marginally non-significant (P = 0.055 and P = 0.051, respectively). However, over 80% of the specimens from the Sacramento Mountains were correctly classified in original and cross-validated analyses in both DFAs.

Zapus princeps

Based on ANOVAs of external and cranial characters, *Z. princeps* from the Sangre de Cristo Mountains were significantly larger than those from the San Juan Mountains in body length, CBL, PB, IFB, and IBW. Based on Mann-Whitney tests, there were no significant differences in dental characters or presence of the distinct pale ear fringe (other pelage characters were not collected on the San Juan population). Direct DFA resulted in a significant difference between the group centroids based on 18 external and cranial characters (Eigenvalue = 1.458, canonical correlation = 0.770, Wilks' lambda = 0.407, chi-square = 32.824, df = 17, P = 0.012). However, a PCA revealed complete overlap of the San Juan population by the Sangre de Cristo population (Figure 22). The PCA extracted 6 components accounting for 72.0% of the variation. The scree plot indicated that the first 2 components were required to interpret results, which together accounted for 46.8% of the variation.

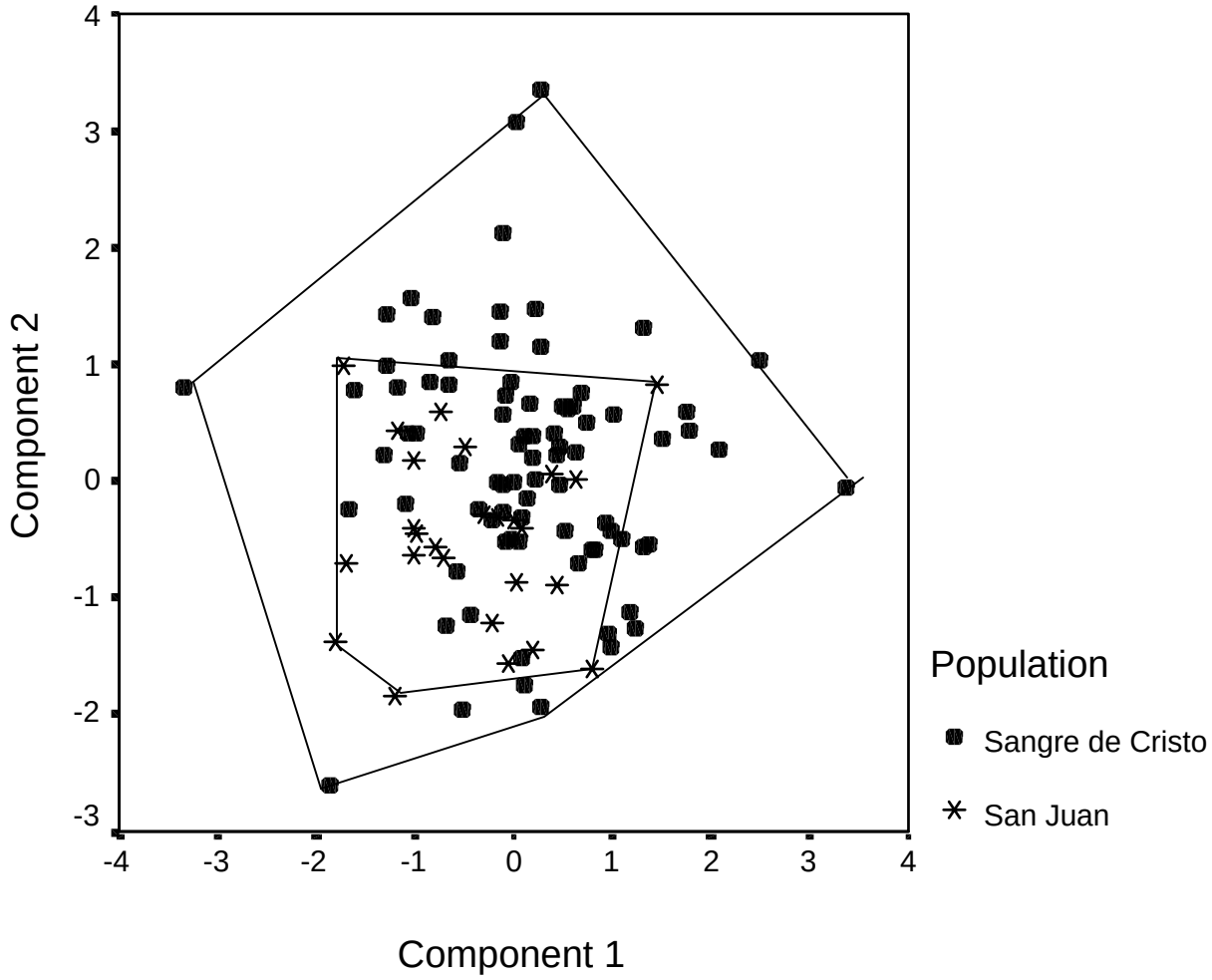


Figure 22. Geographic variation in 18 external and cranial characters in *Z. princeps* as summarized on principal component axes 1 and 2.

DISCUSSION

Species Identification

Accurate taxonomic identification is critical to managing endangered species because identifications have biological, legal, and economic implications (Conner and Shenk 2003). Previously, Conner and Shenk (2003) reported difficulty in distinguishing the federally endangered *Z. h. preblei* from *Z. p. princeps* in the field. Further, they found that the single dental character evaluated (presence of anteromedian fold on m1) was unreliable for species identification, and that human errors in collecting cranial measurements could lead to erroneous identifications (Conner and Shenk 2003). Similarly, I also found that presence/absence of the anteromedian fold on m1 was not a diagnosable character alone, and that while most external and cranial characters exhibited significant differences between the species, there was overlap that could render identifications difficult based on these characters alone. However, my analyses included characteristics of the pelage and dentition that could be used to unequivocally differentiate between *Z. h. luteus* and *Z. p. princeps* based on careful analysis of appropriately collected data (Appendix 4). Further, unlike cranial measurements, which are generally restricted to use with adult animals, the pelage and dental characters were applicable to specimens of all ages. Thus, specimens collected in the zone of sympatry between *Z. h. luteus* and *Z. p. princeps* can be reliably identified on basis of morphology, which is less expensive and less prone to laboratory difficulties in comparison with DNA data. It also seems likely that the upper molar characters used in this study can provide a reliable means for identifying specimens of *Z. h. preblei*, although this must be corroborated with larger samples. Finally, although pelage differences were evident between *Z. h. luteus* and *Z. p. princeps*, studies of jumping mice in the zone of sympatry should confirm species' identifications based on evaluation of properly prepared specimens by a taxon expert (or based on DNA). This is particularly important given that this study documented not only broad sympatry, but also local co-occurrence of the species.

Taxonomic Conclusions

Geographic variation among isolated populations *Z. h. luteus* was found in terms of prevalence of certain characteristics of pelage or dentition, and in significant differences of some measurements within certain populations. However, on the whole, differences among populations were slight or involved few characters. Hence, no taxonomic revisions are recommended and all populations (including *Z. h. australis*) should be regarded as *Z. h. luteus*. However, it should be noted that sample sizes generally were small and additional data could reveal more differentiation that would indicate some populations require unique taxonomic status.

Z. h. luteus Distribution in Zone of Allopatry

Results based on morphological and genetic data confirmed that *Z. h. luteus*, to the exclusion of *Z. p. princeps*, occurred in the Jemez and Sacramento mountains in New Mexico, the White Mountains in Arizona, and along the mainstem of the Rio Grande in New Mexico. Through the course of this research several new locality records were discovered. In the

Sacramento Mountains, these included a specimen (ANSP 14779) from Weed, which is located along the lower Agua Chiquita. During surveys in 2005, I found no water or suitable riparian habitat at this location (Frey 2005). I also confirmed a series of 9 *Z. h. luteus* captured in June 1932 on Tularosa Creek, 1 and 2 miles above Mescalero, Otero County (Appendix 1). These specimens were from the Tularosa Basin, and represent the first records of the species from outside the Rio Peñasco drainage. This indicates that the species had a larger distribution in the Sacramento Mountains than previously thought. During summer 2006 I observed the riparian zone along Tularosa Creek from public roads and considered areas to have potentially suitable habitat for the species.

Verde River Basin.— I found a record in the American Museum of Natural History of an alcohol preserved specimen cataloged as a *Zapus* sp. collected by Edgar A. Mearns from Fort Verde, Yavapai Co., Arizona (AMNH 23014). Unfortunately, although a concerted search was made of the entire *Zapus* skin collection and Dipodidae fluid collection, the specimen was not found, and apparently it has been missing from the AMNH at least since the 1950's or 1960's (D. Lunde, Pers. Com.). Currently, *Zapus* only is known in Arizona from the higher elevations of the White Mountains in the east-central portion of the state, including the Colorado and Gila river drainages. Fort Verde is located at 3,155 ft elevation on the Verde River, which is a major river that drains much of the high elevation on the western edge of the Mogollon Plateau into the Gila River. Based on the species' association with other major river systems in the American Southwest, this record should be considered potentially accurate. Further, Prince (1944) also reported *Zapus* in Yavapai County, which lends additional credibility to the Mearns specimen. To my knowledge there have been no surveys for *Zapus* in the Verde River Basin. However, at least one other riparian species, the Camp Verde Arizona cotton rat (*Sigmodon arizonae arizonae*), also presumably is extirpated from this area (Hoffmeister 1981). Arizona Game and Fish Department has had difficulty determining collection localities for other specimens collected by Mearns because he used the name of the place from which he mailed the specimen as the locality (J. Underwood, Pers. Com.), which was not uncommon during early survey work (see Frey and Malaney 2006). Regardless, since Fort Verde is not near the White Mountains, any collection of *Zapus* in vicinity of Fort Verde represents an important record.

Z. h. luteus Distribution in Zone of Sympatry

I identified specimens of *Z. h. luteus* from 10 localities in the zone of sympatry with *Z. princeps* that were associated with the Sangre de Cristo and San Juan mountains of southern Colorado and northern New Mexico (Appendix 1, Figure 23). These included records from the three major river basins in the region: Canadian River, Rio Grande, and San Juan River. This broad distribution suggests that the species also historically occupied the Pecos River Basin.

Arkansas River Basin

Purgatorie River.—A specimen (USNM14925) from "Purgatorie R." collected by W.L. Carpenter on 12 August 1875 could not be assigned to species. The specimen likely was captured during the Hayden Survey along the Purgatorie River near Trinidad in Las Animas Co., Colorado (Frey 2006c; Figure 23). The specimen is a poorly prepared skin, lacking a tail, and with the skull inside the skin. Strangely, Preble (1899) did not include this specimen in his

monograph of the genus. However, according to Armstrong (1972), Preble identified this specimen as *Z. hudsonius* in 1900. Apparently, this identification was made in the museum because the back of the skin tag is printed with "Determined by E. A. Preble, 1900." Armstrong (1972) concluded that the specimen was an immature *Z. princeps* based on white ear margins, but thought the specimen resembled *Z. hudsonius* (presumably *Z. h. preblei*) in color and dorsal pattern. I agree that the specimen has distinctive white ear margins. The color of the dorsum was very dark grayish brown (10YR3/2) and the color of the side was yellowish brown (10yr5/6). In DFAs based on all pelage variables USNM 14925 was classified as *Z. p. princeps*, but when ear fringe was excluded it was classified *Z. h. luteus*. It also remains a possibility that the specimen could be *Z. h. preblei.*

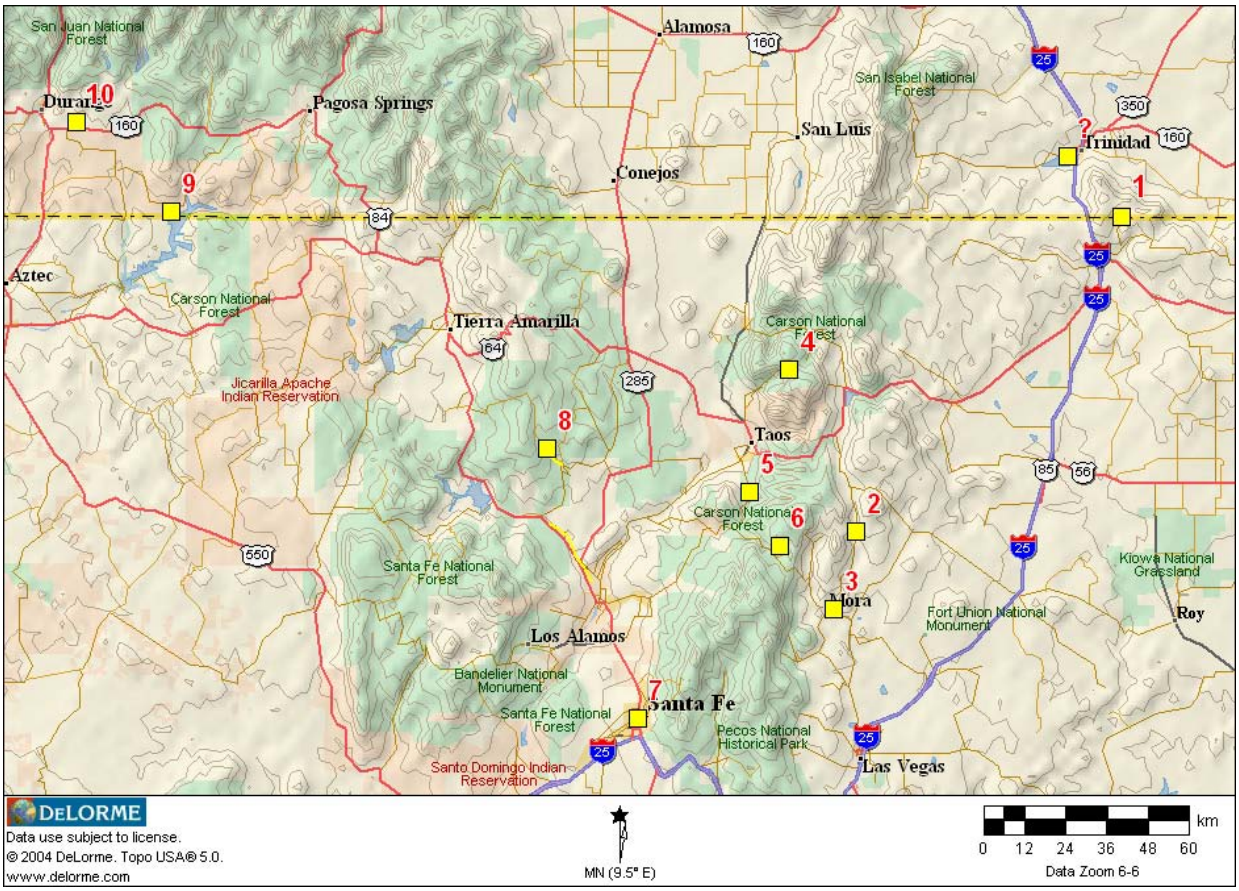


Figure 23. Locations of specimens of *Zapus hudsonius luteus* in the zone of sympatry with *Z. princeps* in southern Colorado and northern New Mexico. Localities are: 1) Sugarite Canyon, Colfax Co., 2) Coyote Creek, Mora Co., 3) Mora Valley, Mora Co., 4) Taos Ski Valley, Taos Co., 5) Fort Burgwin, Taos Co., 6) Tres Ritos, Taos Co., 7) Santa Fe, Santa Fe Co., 8) El Rito, Rio Arriba Co., 9) Sambrito Creek, Archuleta Co., 10) Florida River, La Plata Co. The question mark represents a specimen from the Purgatoire River that has an uncertain identification.

Canadian River Basin

I confirmed *Z. h. luteus* from three locations in the Canadian River Basin along the eastern flank of the Sangre de Cristo Mountains. These locations included Sugarite Canyon in Sugarite Canyon State Park, Colfax County (location 1), Coyote Creek in Coyote Creek State Park, Mora County (location 2), and the Mora River near the town of Mora, Mora County (location 3; Figure 23).

Sugarite Canyon.—The 10 specimens of *Z. h. luteus* from Sugarite Canyon were captured in 2006 during survey work at Sugarite Canyon State Park, as described by Frey and Schwenke (2006, 2007). The specimens were unequivocally identified as *Z. h. luteus* on basis of pelage, dentition, measurements, and cytochrome-B sequences. Previously, Jones (1999, 2002) reported captures of *Z. h. luteus* from areas adjacent to Sugarite Canyon State Park on the Raton Mesa Complex in Las Animas County Colorado. Jones' identifications were based on pelage, cranial measurements, and DNA, and represented the first published records of the taxon from Colorado. Due to relatively low elevations, biogeographic isolation, limited availability of riparian habitats typical of *Z. princeps*, and occupation of suitable riparian jumping mouse habitat by *Z. h. luteus*, it seems unlikely that *Z. princeps* occurs on the Raton Mesa complex (Frey 2006c, Frey and Schwenke 2007).

Mora Valley.—I discovered two specimens of *Z. h. luteus* from the Mora Valley in the New Mexico Museum of Natural History (NMMNH), that were unequivocally identified based on dentition, external/cranial measurements, and a combination of the dentition and measurement data. Pelage characters also were typical of *Z. h. luteus* (see Appendix 5: photograph 2). Tags on both specimens had the date 22 August 1990 and bore the name Joan Morrison (with field numbers "10" and "11" on NMMNH 1228 and 1229, respectively). However, the specimens were actually captured by Dale Stahlecker during an Environmental Assessment for the Mora National Fish Hatchery (D. Stahlecker, in litt. 8 Jan. 2008). The specimens were captured in a wetland at the sewage ponds 1.5 miles east of Mora, which was an alternative site for the hatchery (D. Stahlecker, in litt. 8 Jan. 2008). Stahlecker took the specimens to Morrison in Los Alamos (D. Stahlecker, in litt. 8 Jan. 2008); presumably Morrison prepared the specimens and deposited them at the NMMNH. The Mora Valley seems ideally suited to *Z. h. luteus*. The valley is large and level, ranging in elevation from ca. 7,100 to 7,600 feet. It is well watered by perennial streams and springs, and is used for agriculture with water delivered through a network of irrigation canals and drains. No recent surveys for *Z. h. luteus* have occurred in the Mora Valley and it is unknown if the species persists in this region.

Coyote Creek.—Two jumping mice were captured at 7,675 ft elevation on Coyote Creek in Coyote Creek State Park in 2006 (Frey 2006b, 2006c), which were unequivocally identified as *Z. h. luteus* on basis of pelage, dentition, measurements, and cytochrome-B sequences. Coyote Creek is a major tributary to the Mora River that junctions downstream of the Mora Valley, between Buena Vista and Watrous. The Mora and Coyote Creek populations likely were connected via gene flow through riparian corridors of suitable habitat prior to European settlement. However, given widespread habitat changes and observed riparian habitat conditions along riparian corridors between these populations during 2006 (Frey 2006b, 2006c), it seems

likely that the two populations are currently isolated, presuming the Mora population has persisted.

Coyote Creek drains some of the highest elevations along the eastern crest of the Sangre de Cristo Mountains, and hence heads within the primary distribution of *Z. princeps*. I unequivocally identified two specimens (NMMNH 4040, 4042) of *Z. princeps* on Coyote Creek on basis of both genetic and morphological data. Pelage characters also were typical of *Z. p. princeps* (see Appendix 5: photograph 2). D. W. Stahlecker collected the specimens 9-10 July 2000 from "Coyote Creek, 7 mi. N Guadalupita" at an elevation of ca 2,495 m (= 8,184 ft). Thus, these *Z. princeps* were collected ca 7.5 km upstream and 155 m (= 509 ft) above the records of *Z. h. luteus* from Coyote Creek State Park. This documents both species in close proximity along the same watercourse (Figure 24).

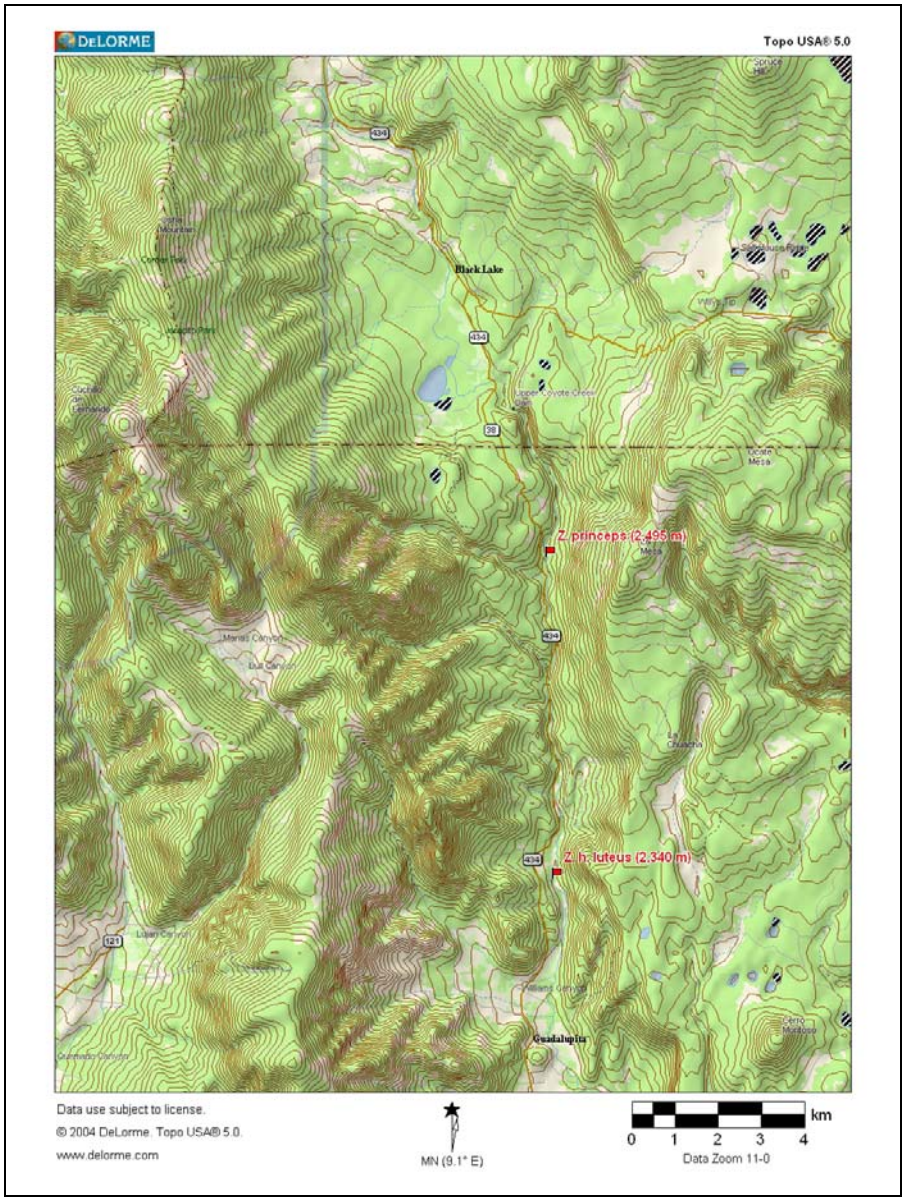


Figure 24. Locations where specimens of *Zapus princeps* and *Zapus hudsonius luteus* have been collected on Coyote Creek, Mora County, New Mexico.

Rio Grande Basin

Sangre de Cristo Mountains

Individual specimens from 4 localities in the Rio Grande Basin in the Sangre de Cristo Mountains were identified as *Z. h. luteus*. These included Taos Ski Valley (location 4), Tres Ritos (location 5), and Fort Burgwin (location 6) in Taos County, and Santa Fe in Santa Fe County (locality 7; Figure 23).

Taos Ski Valley.—Hafner et al. (1981) examined 7 jumping mice collected during July 1966 from 2.5 miles N Williams Lake, Taos Co., New Mexico, which is in vicinity of Taos Ski Valley (Frey 2006c). They identified 1 of the series (TTU 2388), which was collected by Kay Verkerk from "2 ½ M, N of Williams Lake, Taos Co. New Mexico, Grid Station A-3", as *Z. h. luteus* on basis of 1) relatively pale, ochraceous mid-dorsal pelage color as determined with aid of a spectrophotometer; 2) lack of white ear fringes; and 3) a principal components analysis based on 8 cranial characters that resulted in the specimen falling within the cluster of *Z. h. luteus* specimens. The remaining 6 specimens were identified as *Z. p. princeps* (Hafner et al. 1981).

I obtained a loan of the complete series of 17 jumping mice collected by TTU from Taos Ski Valley during 13 to 21 July 1966, and collected complete data on pelage, dentition, and external and cranial measurements. TTU 2388 was a young male (average age class 0.47), and was confidently identified as *Z. h. luteus*. Although lacking the anteromedian fold on m1, the upper cusp pattern of M1 and M2 quintessentially represented *Z. hudsonius* (Table 8), and all DFAs based on dentition classified it as *Z. h. luteus*. Likewise, all DFAs based on external and cranial measurements (or DFAs based on measurements combined with dentition or pelage data) classified the specimen as *Z. h. luteus*. However, I coded the specimen as having a prominent pale ear fringe, which caused it to be classified as *Z. p. princeps* in DFAs based on pelage. However, when this variable was excluded, it was classified as *Z. h. luteus*. Coding of the ear fringe as prominent or not prominent was subjective, and, while I coded the pale ear fringe as present, Hafner et al. (1981) stated that it lacked the white ear fringe. Thus, the weight of evidence clearly verifies TTU 2388 as *Z. h. luteus*. The remaining 16 specimens were unambiguously referred to *Z. p. princeps*.

Nine of the 17 TTU jumping mouse specimens had localities designating "2.5 mi N Williams Lake" along with specific grid stations (the remainder were taken at various sites in proximity to the Saint Bernard Hotel in Twining). Frey (2006) thought that the trapping grid was located on Lake Fork Rio Hondo in the village of Taos Ski Valley about 770 m SE of the junction with the Rio Hondo. Confirmation that both species were captured on the same trapping grid is important because it not only establishes local syntopy between *Z. h. luteus* and *Z. p. princeps*, but also establishes occurrence and syntopy at high elevations within the Sangre de Cristo Mountains. Thus, the historical distribution of *Z. h. luteus* was not restricted to lower elevations as suggested by Frey (2006c).

Tres Ritos.—I unambiguously referred a second specimen, MSB 4943, to *Z. h. luteus* that also was collected at high elevations in the Sangre de Cristo Mountains and in syntopy with *Z. princeps*. MSB 4943 was collected on 24 July 1958 from "Taos Co.; 2 mi NE Tres Ritos, Rio la Junta". Previously, Frey (2003) tentatively identified this specimen as *Z. h. luteus* on basis of

overall pelage color, absence of white ear fringe, and a PCA of *Z. h. luteus* and *Z. p. princeps* based on 5 external measurements, 11 cranial characters, and 1 pelage character. It is unknown if MSB 4943 was included in the study of Hafner et al. (1981; David Hafner personal communication). In the current study, the specimen was classified as *Z. h. luteus* in all DFAs based on pelage, dentition, external and cranial measurements, or combinations of characters.

I examined field notes to determine more about the circumstances of this capture. MSB 4943 was captured by a field crew consisting of Dr. James Findley, his son Stuart Findley, and his students Clyde Jones and Eugene Fleharty. The group camped 21-24 July 1958 at the mouth of Duran Canyon (= Duran Creek) along the "Rio la Junta" (= Rito la Presa, which flows through La Junta Canyon), which is at the modern location of Duran Canyon Campground. Rito la Presa is a tributary to the Rio Pueblo, which is a major tributary to Embudo Creek, which is a major tributary to the Rio Grande. They set traps along both streams in shrubby riparian areas and in a grassy meadow. Ponds created by beaver (*Castor canadensis*) were present. Besides the specimen of *Z. h. luteus*, they captured 3 additional jumping mice. I examined two of these (MSB unambiguously referred them to *Z. princeps* (see Appendix 5: photograph 3). Thus, this record confirms a second instance of syntopy (the other being Taos Ski Valley). In addition to the 4 jumping mouse specimens collected during the 1958 trip, I also examined 16 additional specimens collected from the same area during 1969, 1976, 1977, and 1994, all of which were *Z. princeps*. (see Appendix 5: photograph 4 for a comparison of MSB 4943 with typical *Z. princeps* collected in same vicinity). Further, all specimens collected by me along the Rio Pueblo near the junction of La Junta Canyon in 2006 (Frey 2006c) were referred to *Z. p. princeps.*

Fort Burgwin.—I refer a specimen (USNM 3322/36046) to *Z. h. luteus* that was collected by Dr. W. W. Anderson from "Camp Burgwyn" in 1858 (see photograph on cover page). Preble (1899) referred two specimens from this location to *Z. princeps*, although the second specimen could not be located in the USNM. The specimen was included in the original species description of *Z. luteus* by Miller (1911). In fact, Miller opened his paper with a detailed discussion of this specimen and noted that it differed widely in color and cranial characters from *Z. princeps*. Miller regarded it as a "long overlooked form" and consequently named it a distinct species. However, because the specimen was in poor condition (broken skull, imperfect skin), he used another more recently collected specimen from Espanola as the type. All subsequent published treatments of New Mexico Zapus have overlooked this specimen record. In the current study, the specimen was classified as *Z. h. luteus* in DFAs based on pelage and dentition. The specimen was classified as *Z. p. princeps* in DFAs based on external and cranial characters. However, this was likely due to the lack of external measurements and large number of missing cranial measurements due to the broken skull. Thus, the preponderance of evidence verifies the specimen as *Z. h. luteus*.

As discussed in Frey (2006c) Camp Burgwyn (= Cantonment Burgwyn, Cantonment Burgwin, and Fort Burgwin) was located 14.6 km south of Taos at the junction of the Rito de la Olla with the Rio Grande del Rancho, although the specimen may have been collected in suitable habitat anywhere in vicinity of the fort. Two specimens captured by me at Fort Burgwin during 2006, were unequivocally referable to *Z. p. princeps*.

Santa Fe.—I refer a specimen, USNM 59732, from "Santa Fe" to *Z. h. luteus*. No other data accompany the specimen, which is a carcass in alcohol with a cleaned skull. Based on records in the USNM, the specimen was cataloged 11 April 1894 (R. Fisher, pers. comm.). In

addition, Preble (1899) apparently examined this specimen, and referred it to *Z. princeps*. *Z. h. luteus* had not yet been described, and Preble referred both the Santa Fe and Fort Burgwin specimens to *Z. princeps*. The specimen has not been included in any subsequent published taxonomic treatments. The specimen was classified as *Z. h. luteus* on basis of dentition. It had anteromedian folds on the both m1s, and [redacted]. Because the skin was in fluid, I did not collect quantitative pelage measurements, although the specimen had the unique coloration similar to other *Z. h. luteus*. DFAs based on external and cranial measurements classified the specimen as *Z. h. luteus* when the species were subdivided by age and sex, but classified the specimen as *Z. p. princeps* when based only on species. Those results were considered unreliable because the specimen was missing all external and many cranial characters. Thus, the preponderance of evidence verifies the specimen as *Z. h. luteus*.

This represents the first verified record of *Z. h. luteus* from the southern end of the Sangre de Cristo Mountains. However, the specific capture location is unknown and could be from anywhere near the city of Santa Fe since locations on specimen tags of older specimens are often do not refer to the exact place where a specimen was collected (Frey and Malaney, in press).

Misidentifications.—Three of 9 putative *Z. h. luteus* records from the Sangre de Cristo Mountains listed by Frey (2006a, 2006c) were unambiguously referred to *Z. p. princeps* based on all analyses of pelage, dentition, and external and cranial measurement. These included 1) KU 58984 from Santa Fe County "13 mi. NE Santa Fe, Pacheco Canyon" which was collected by H. C. Owen on 28 August 1953; Hafner et al. (1981) also regarded this specimen as *Z. p. princeps*; 2) KU 120040 from Santa Fe County "11 mi NE Santa Fe, Hwy 475, 2,894 m", likely on Tesuque Creek, which was collected by P.B. Robertson on 9 June 1969; and 3) USNM 133430 from "Hondo Canyon, altitude 8200 ft.", which was collected by Jas. H. Gaut 10 August 1904. See Appendix 5: photograph 4 for skins of KU 58984 and KU 120040.

San Juan Mountains

I verified identification of 4 *Z. h. luteus* (KU 5832-5835) based on pelage, dentition, and measurements, that were collected by T.E. White on various dates in July 1928 from Rio Arriba County, 4 mi. N El Rito, alt. 7,000 ft. (location 8; Figure 23). Krutzsch (1954) originally assigned the series to *luteus*, but thought they exhibited intergradation with a specimen (USNM 134355) of *Z. princeps* from "Tierra Amarillo" (= Tierra Amarilla, Rio Arriba County) in braincase breadth and shapes of certain parts of the skull. I found that each of the series was unambiguously referable to *Z. h. luteus* on basis of dentition and pelage (see Appendix 5: photograph 5). All specimens were classified as *Z. h. luteus* in a DFA based on external and cranial measurements. I ran ANOVAs and Student-Newman-Keuls range tests on 14 external and cranial variables with complete data for El Rito (N=4), northern populations of *Z. h. luteus* (N = 64), and *Z. p. princes* (N = 121). Ten of the variables, including mastoid breadth (=breadth of braincase) exhibited non-significant differences between El Rito and *Z. h. luteus*, but a significant difference between those groups with *Z. princeps*. Post hoc tests revealed that the El Rito series was unique in having a significantly larger interorbital constriction than either other *Z. h. luteus* or *Z. p. princeps*.

Although Krutzsch (1954) ultimately referred the specimen from Tierra Amarilla to *Z. princeps*, he considered it to resemble *Z. h. luteus* in some cranial characters. However, I examined this specimen and it was predicted to be *Z. p. princeps* in both the original and cross-

validated classification procedure of a DFA based on external and cranial measurements. Further, although it was scored as having the anteromedian fold on the right m1, it had the [redacted] of *Z. p. princeps* and never found in specimens of *Z. h. luteus*. Thus, the specimen was referred to *Z. princeps*.

El Rito is a major tributary to the lower Chama River, and they confluence ca 22 km above the junction of the Chama River with the Rio Grande. Thus, this locality suggests that the historical distribution of *Z. h. luteus* may have occupied suitable habitat throughout the Chama River Basin, including within the San Juan and Jemez mountains. During 2006 I observed many areas of potentially suitable habitat for *Z. h. luteus* along many areas of both the upper and lower reaches of the Chama River. There has been little recent small mammal work in this region and it is a distinct possibility that populations of *Z. h. luteus* could exist in the Chama River Basin. The only known specimen of jumping mouse from vicinity of the upper Chama River is the specimen of *Z. princeps* from Tierra Amarilla. This record does not negate the possibility for *Z. h. luteus* to occur in vicinity of Tierra Amarilla because old specimens tended to use the most prominent nearby place name for localities, rather than the actual locality (Frey and Malaney 2006), and because the ecological setting and habitats near Tierra Amarilla appeared most suitable for *Z. h. luteus*.

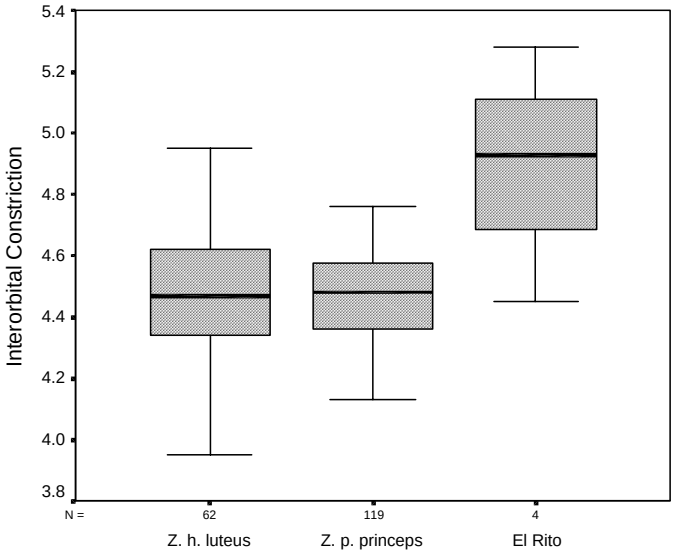


Figure 25. Width of the interorbital constriction in *Z. h. luteus*, *Z. p. princeps*, and a series of jumping mice from El Rito, Rio Arriba County.

San Juan River Basin

I identified specimens of *Z. h. luteus* from two locations in the San Juan River Basin along the southwestern edge of the San Juan Mountains in Colorado. These included Sambrito Creek, in the Piedra River drainage near the New Mexico border in Archuleta County (location 9), and near Florida on the Florida River, La Plata County (location 10; Figure 23). Together with the series of *Z. h. luteus* from El Rito, these records indicate that *Z. h. luteus* historically

occupied a broad area along the southwestern edge of the San Juan Mountains including the Chama and San Juan river basins. Surveys for *Z. h. luteus* have not yet occurred in this area. However, I have observed many areas of potentially suitable habitat in both Colorado and New Mexico. These findings point to the need for intensive *Z. h. luteus* surveys in the Chama and San Juan watersheds in order that any extant populations are found and protected.

Sambrito Creek.—Initially, I examined and tentatively identified as *Z. h. luteus*, a specimen (MSB 10238) that was collected 25 July 1960 by A. H. Harris at a locality (i.e., NW1/4 Sec. 23, T32N-R6W) near Arboles in the drainage of the Piedra River, Archuleta County, Colorado (see Appendix 5: photograph 4). Harris (1963) reported the circumstances of this capture, and identified the specimen as *Z. princeps*. The specimen is a young juvenile (average age class = 0.18), which posed some difficulty because I had no comparative samples of similar aged *Z. princeps*. However, I referred the specimen to *Z. h. luteus* on basis of pelage most similar to *Z. h. luteus*, especially in side chroma, prominent anteromedian folds on both m1s, [redacted] Harris (1963) mentioned that additional jumping mouse specimens had been collected "in similar habitat in the same general area" by researchers from Utah. I located the series of specimens in the Utah Museum of Natural History (UMNH) and acquired them on loan.

The UMNH series consisted of 7 specimens that were collected 17 to 20 July 1960 from Sambrito Creek, 0.5 miles north of the New Mexico border at an elevation of 6,100 feet, Archuleta County. Durrant and Dean (1961) reported the circumstances of these captures and identified the series as *Z. p. princeps*, although remarked that the capture site was an unusual ecological setting for that species. Armstrong (1972) subsequently reported the record as *Z. p. princeps*, but apparently did not examine the specimens. Indeed, the series is unambiguously referable to *Z. h. luteus* on basis of dentition as well as external and cranial measurements. Quantitative pelage measurements were not collected on the series, but the series was unremarkable in comparison with other specimens of *Z. h. luteus*. I ran ANOVAs and Student-Newman-Keuls range tests on 17 external and cranial variables with complete data for Sambrito Creek (N=7, including MSB 10238), northern populations of *Z. h. luteus* (N = 61), and *Z. p. princes* (N = 121). For 14 of the 17 variables, the Sambrito Creek series was not different from *Z. h. luteus*, but was significantly different from *Z. princeps*. No variables were significantly unique in the Sambrito Creek series. In addition, all specimens were classified as *Z. h. luteus* in a DFA based on external and cranial measurements.

Florida River.—I examined a specimen (KU 16038) from Florida, 6800 ft., La Plata County, Colorado, which was collected by H. W. Setzer on 4 September 1945 (see Appendix 5: photograph 5). Previously, Armstrong (1972) referred this specimen to *Z. princeps*, but noted its resemblance to *Z. h. luteus* in pelage color. I unambiguously refer the specimen to *Z. h. luteus* on basis of results of all analyses of pelage, dentition, and external and cranial measurements. However, I note that the specimen was large in many external and cranial characters.

Armstrong may have been influenced by the fact that "Florida" is the type location from which *Z. princeps* was described, and that there were no other known specimens of *Z. hudsonius* from southwestern Colorado. The type series of *Z. princeps* consists of 12 specimens collected by Charles P. Rowley 22 June to 3 July 1892 (Allen 1893). I examined 9 of the topotypes, which are now in the AMNH (AMNH 4134-4136, 4138-4139, 4141, 4143-4145), and unambiguously referred them *Z. p. princeps*. None of the specimens had the anteromedian fold

on m1, and all had [redacted]. I ran ANOVAs and Student-Newman-Keuls range tests on 16 external and cranial variables with complete data for Rowley's Florida specimens (N=9), northern populations of *Z. h. luteus* (N = 67), and *Z. p. princes* (N = 112). For 12 of the variables, there were non-significant differences between Rowley's series and *Z. princeps*, but a significant difference between Rowley's series with *Z. h. luteus*. A DFA based on dentition and external and cranial measurements classified all 9 of Rowley's specimens as *Z. p. princeps*. Quantitative pelage measurements were not collected on the series, but the series was unremarkable in comparison with other specimens of *Z. princeps*.

On 5 and 7 July 2007, Jason Malaney and Andrew Hope from the Museum of Southwestern Biology captured two jumping mice near Florida as part of a field study by Malaney to secure genetic samples from type localities of all *Z. princeps* subspecies (J. Malaney pers. comm.). The specimens (MSB 154917, 155117) were collected from "Higgens Residence; Florida River; 2.5 km. N. Florida; 37.2388; -107.7586; 2077 m". I confidently referred both specimens to *Z. h. luteus* on basis of the pelage and external measurements (the skeletons were not available for examination; see Appendix 5: photograph 6). I ran ANOVAs and Student-Newman-Keuls range tests on five external measurements for the two MSB Florida samples, northern populations of *Z. h. luteus* (N = 68), and *Z. p. princes* (N = 121). For total length, tail length, body length, and hindfoot length, the MSB Florida specimens were not significantly different from *Z. h. luteus*, but were significantly smaller than *Z. princeps.* Thus, these specimens confirm the persistence *Z. h. luteus* in southwestern Colorado and the San Juan River basin.

Results indicate that both *Z. h. luteus* and *Z. p. princeps* occur in vicinity of Florida. This has particular importance because this is the type locality for *Z. princeps*. Allen's (1893) descriptions of the type and topotypes do not suggest that any *Z. h. luteus* specimens were included in his sample, and I verified 9 of the topotypes as *Z. princeps*. Thus, there does not appear to be an issue with taxonomic nomenclature. However, discovery of *Z. h. luteus* from near Florida does require that the type locality of *Z. princeps* be further investigate. In his taxon description of *Z. princeps*, Allen (1893) reported the type as from "Florida, La Plata Co., Colorado" and collected by Rowley on 27 June 1892. However, the introduction of Allen's (1893:69) paper states that Rowley's "field of operations" was "at an altitude of 7200 feet". Indeed, 3 of the 9 specimens I examined (AMNH 4134-4136) bore original hand-written field tags that included "Florida" and "7200 elev", which confirm the location at 7,200 feet elevation (= 2,195 m). These specimens also bore a second expedition tag, which was also found on the remaining 4 specimens, that was printed with the locality "Florida" with no indication of elevation. Apparently, it was a custom of the times to not augment expedition tags or type localities with additional details of locality. Typically, locations were given the nearest place name, and did not necessarily reflect the actual collection site (Frey and Malaney 2006). In contrast, Setzer's specimen of *Z. h. luteus* was collected at 6,800 feet (2,073 m) and the Malaney/Hope specimens were collected at 2,077 m (= 6,814 feet). Thus, the specimens of *Z. princeps* were collected ca 400 feet (120 m) higher in elevation than the specimens of *Z. h. luteus*, which is a distance of ca 11 km. The *Z. h. luteus* specimens came from a broad irrigated valley at the base of the mountains, while the specimens of *Z. p. princeps* came from a narrow canyon within the mountains. These differences in elevations and ecological situation are typical of the habitat separation found for both species in the Sangre de Cristo Mountains (Frey 2006). Further, Setzer's field notes indicated that his *Z. h. luteus* specimen was captured in traps set "along an irrigation ditch whose banks were covered with willows and grasses as well as in the

marshy areas on a hillside where grasses, cattails, and rushes were growing". These habitats are more typical of *Z. h. luteus* than of *Z. princeps* (Frey 2006). Thus, the type locality for *Z. princeps* should be restricted to "Florida, 7200 feet elevation".

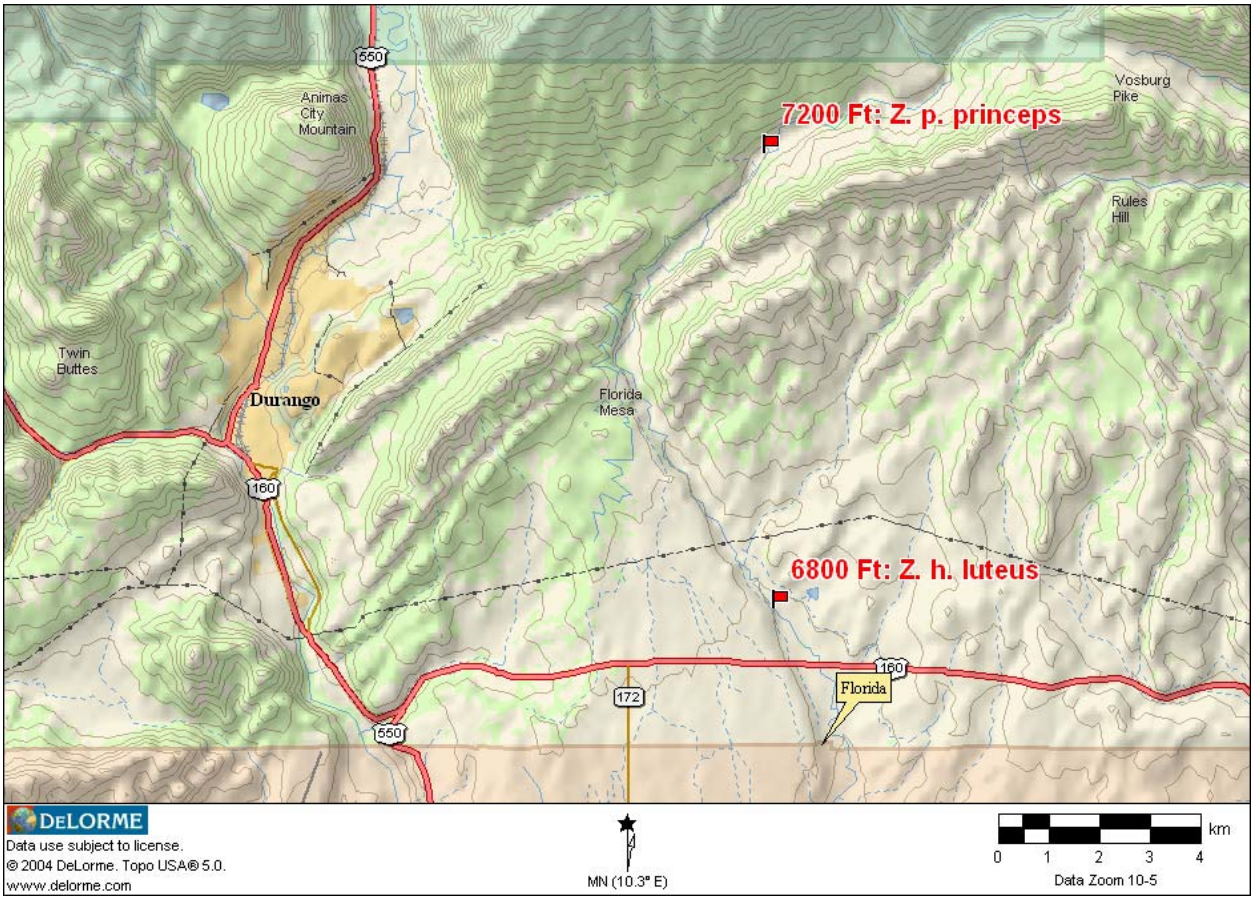


Figure 26. Locations where specimens of *Zapus p. princeps* and *Zapus hudsonius luteus* have been collected on the Florida River, La Plata County, Colorado.

MANAGEMENT IMPLICATIONS AND RECOMMENDATIONS

1) Geographic distribution of *Z. h. luteus*. Results alter current understanding of the geographic distribution of *Z. h. luteus*. Previously, published records for *Z. h. luteus* in southern Colorado and northern New Mexico were from Fort Burgwin, El Rito, Taos Ski Valley, and Sugarite Canyon (Miller 1911, Krutsch 1954, Hafner et al. 1981, Jones 1999, 2002), although the record from Fort Burgwin was overlooked in published literature for nearly 100 years (e.g., Krutzsch 1954, Hafner et al. 1981, Hall 1981, Morrison 1992, but see Jones 1981). Results of this study confirm that *Z. h. luteus* has a broad distribution associated with the Sangre de Cristo and southern San Juan mountains in southern Colorado and New Mexico (see Figure 23 for map). Results also suggest that the distribution of *Z. h. luteus* might have included the Verde River watershed in central Arizona. Thus, intensive surveys for *Z. h. luteus* should occur in southern Colorado, northern New Mexico, and the Verde River basin in Arizona to confirm presence of any relict populations. Further, southern Colorado and northern New Mexico should be included in conservation planning for this species.

2) Elevational distribution of *Z. h. luteus*. Previously, Frey (2006) suggested that *Z. h. luteus* might be restricted to foothills < 8,000 ft. elevation in the Sangre de Cristo and San Juan mountains. However, results of this study documented *Z. h. luteus* at two high elevation locations in the Sangre de Cristo Mountains: 8,750 ft at Tres Ritos and 9,600 ft at Taos Ski Valley. Frey (2006) found that relative abundance of *Z. p. princeps* increased with elevation. In contrast, based on absolute and proportionate numbers of specimens of *Z. h. luteus* and *Z. p. princeps* at localities within the zone of sympatry, it appears that *Z. h. luteus* is relatively more abundant in the lower elevation foothills. Thus, while the two species may prefer different elevations, there is substantial overlap in elevations occupied, and elevation alone cannot be used as a basis for species identification. This conclusion also is supported by specimens collected by Frey in 2006 from Fort Burgwin at 7,408 ft (=2,258 m) elevation that were confirmed to be *Z. p. princeps* based on DNA and morphology in this study. In Colorado, elevation has been used to designate populations of *Z. h. preblei*. However, because results indicate that *Z. hudsonius* is capable of occurring at high elevations, *Z. h. preblei* also might occur at high elevations, which would require redefining means for classifying potentially occupied habitat of *Z. h. preblei*.

3) Syntopy with *Z. princeps*. Results of this study confirm that *Z. h. luteus* and *Z. p. princeps* are not only broadly sympatric but also occur together, including at high elevations. Consequently extreme care must be taken in identifying jumping mice in the region of sympatry. It is recommended that all inventory and monitoring studies of jumping mice in the zone of sympatry collect and properly prepare representative series of specimens that are submitted to a taxon expert for conclusive identification using DNA or the morphological characters described in this study.

4) Status of northern populations of *Z. h. luteus*. In the Sangre de Cristo Mountains, there are six confirmed historical locations of *Z. h. luteus* (i.e., Sugarite Canyon, Taos Ski Valley, Fort Burgwin, Tres Ritos, Mora, Santa Fe). In 2006, Frey surveyed for *Z. h. luteus* in the Sangre de Cristo Mountains, which included vicinity of each of these historical locations except Mora (the Mora specimens were discovered after the 2006 study concluded). However, *Z. h.*

luteus only was found at Sugarite Canyon and one new location, Coyote Creek (Frey 2006). Thus, *Z. h. luteus* had disappeared from 80 % (i.e., 4 of 5) of historical locations surveyed in the Sangre de Cristo Mountains. This rate of loss is similar to what has been observed in the Jemez (73%) and Sacramento mountains (94%; Frey and Malaney in press). However, because of the larger area of the Sangre de Cristo Mountains, a smaller fraction of potential habitat was surveyed and it remains a distinct possibility that other populations may have persisted but have remained undetected. Thus, it is imperative that additional surveys for *Z. h. luteus* be conducted in the Sangre de Cristo Mountains, including in Colorado where no recent surveys have occurred.

Prior to this study, the only report of *Z. h. luteus* from the San Juan Mountains region was the series of specimens from El Rito, Rio Arriba County, NM (Krutsch 1954). Results of this study not only confirmed identification of that series, but also documented the species at two locations in Archuleta (i.e., Sambrito Creek) and La Plata (i.e., Florida) counties, in southwestern Colorado. Together, these three locations suggest a broad distribution for *Z. h. luteus* in the upper elevations of the San Juan and Chama river watersheds. In 2006 Frey was unable to find suitable habitat for *Z. h. luteus* at or near the El Rito location. No survey has occurred for *Z. h. luteus* at other locations in the southern San Juan Mountains and adjacent areas. However, results of this study confirmed two specimens as *Z. h. luteus* that were captured in 2007 from near Florida, La Plata County. Thus, the species is known to persist at 33% (i.e., 1 of 3) of historical locations in the San Juan Mountains region. These results are critically important because they not only document this species in southwestern Colorado for the first time, but also confirm the species persistence in that region. Given the alarming rate of recent decline documented for this species, Colorado should consider immediate management strategies to conserve this species in that state. Further, it is critically important that comprehensive surveys for *Z. h. luteus* be conducted in the San Juan, Rio Grande, and Chama river watersheds in southwestern Colorado and northwestern New Mexico. Further, this region must be included in conservation planning for *Z. h. luteus*.

5) Value of morphological characters. Results demonstrate that morphology can be used to confirm identifications of *Z. h. luteus* and *Z. p. princeps*. In comparison with genetic techniques, morphology has the advantage of providing faster and less expensive means of identification, and easily can be applied to historical samples. However, genetic techniques may be more suitable for identifying relationships among populations and potential hybrids. Further, preliminary data indicate that upper molar characters may provide an independent and reliable means for identifying specimens of *Z. h. preblei*.

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APPENDIX 1

Appendix 1. Jumping mouse specimens included in morphologic and/or genetic analyses. Museums include: American Museum of Natural History (AMNH), Academy of Natural Science of Philadelphia (ANSP), Frey Tissue (ET or FT), University of Kansas (KU), Museum of Southwestern Biology (MSB), New Mexico Museum of Natural History and Science (NMMNHS), New Mexico State University Vertebrate Collection (NMSU); Texas Tech University (TTU), University of Illinois Museum of Natural History (UIMNH), Utah Museum of Natural History (UMNH), United States National Museum (USNM).

Museum	Catalog No.	Morphology	Genetics	Identification	state	county	Descriptive	Date
AMNH	4134/5254	y		princeps	CO		Florida, 7200 elev	6/22/1892
AMNH	4135/5155	y		princeps	CO		Florida, 7200 elev	6/23/1892
AMNH	4136/5256	y		princeps	CO		Florida, 7200 elev	6/24/1892
AMNH	4138/5258	y		princeps	CO		Florida	6/26/1892
AMNH	4139/5259	y		princeps	CO		Florida	6/26/1892
AMNH	4141/5260	y		princeps	CO		Florida	6/30/1892
AMNH	4143/5263	y		princeps	CO		Florida	7/1/1892
AMNH	4144/5264	y		princeps	CO		Florida	7/2/1892
AMNH	4145/5265	y		princeps	CO		Florida	7/3/1892
ANSP	14779	y		luteus	NM		Weed, east of Cloudcroft, Sacramento Mts.	Jul-31
ANSP	15771	y		luteus	NM		Bank of Tularosa Creek, 1 mi. above Mescalero	18-Jun-32
ANSP	15772	y		luteus	NM		Bank of Tularosa Creek, 1 mi. above Mescalero	18-Jun-32
ANSP	15773	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	27-Jun-32
ANSP	15774	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	27-Jun-32
ANSP	15775	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	27-Jun-32
ANSP	15776	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	1-Jul-32
ANSP	15777	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	1-Jul-32
ANSP	15778	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero Agency	1-Jul-32
ANSP	15779	y		luteus	NM		Bank of Tularosa Creek, 2 mi. above Mescalero	2-Aug-32
ET	814		y	princeps	NM		Cimarron Range	
FT	73	y		princeps	NM	Taos	Camino Real Ranger District, Rito de la Olla, 10.0 mi. S, 2.75 mi. E Taos; T24N, R13E, NE ¼ Sec. 2; N 36° 15.732', W 105° 31.604', 2,435 m (= 7,987 ft.)	20-Jul-03
FT	98	y		princeps	NM	Taos	Camino Real Ranger District, Rito de la Olla, 10.0 mi. S, 2.75 mi. E Taos; T24N, R13E, NE ¼ Sec. 2; N 36° 15.732', W 105° 31.604', 2,435 m (= 7,987 ft.)	21-Jul-03
FT	107	y		princeps	NM	Taos	Camino Real Ranger District, Rito de la Olla, 10.0 mi. S, 2.75 mi. E Taos; T24N, R13E, NE ¼ Sec. 2; N 36° 15.732', W 105° 31.604', 2,435 m (= 7,987 ft.)	21-Jul-03

FT	156	y		princeps	NM	Taos	Camino Real Ranger District, Maestas Ridge, 12.0 mi. S., 2.75 mi. E Taos; T23N, R13E, NE ¼ Sec. 14; N 36° 14.030, W 105° 31.564', 3,029 m (9,935 ft.).	23-Jul-03
FT	163	y		princeps	NM	Taos	Camino Real Ranger District, Maestas Ridge, 12.0 mi. S, 2.5 mi. E Taos; N 36° 13.958', W 105° 31.518', 3,020 m (= 9,906 ft.)	23-Jul-03
FT	191	y		princeps	NM	Taos	Camino Real Ranger District, upper Rio Grande del Rancho, 11.5 mi. S, 6.25 mi. E Taos; T23N, R14E, SW ¼ Sec. 9; N 36° 14.395', W 105° 27.988, 2,956 m (= 9,696 ft.)	26-Jul-03
FT	217	y		princeps	NM	Taos	Camino Real Ranger District, upper Rio Grande del Rancho, 11.5 mi. S, 6.25 mi. E Taos; T23N, R14E, SW ¼ Sec. 9; N 36° 14.395', W 105° 27.988, 2,956 m (= 9,696 ft.)	26-Jul-03
FT	218	y		princeps	NM	Taos	Camino Real Ranger District, upper Rio Grande del Rancho, 11.5 mi. S, 6.25 mi. E Taos; T23N, R14E, SW ¼ Sec. 9; N 36° 14.395', W 105° 27.988, 2,956 m (= 9,696 ft.)	26-Jul-03
FT	340	y		luteus	NM	Sandoval	Jemez Mountains, Fenton Lake State Park, Lake Fork Day Use Area, mouth of small tributary that flows W along NM Hwy 126 and entering S side Fenton Lake	29-Jun-05
FT	348	y		luteus	NM	Sandoval	Jemez Mountains, Fenton Lake State Park, marsh at upper end of lake along Rio Cebolla above NM Hwy 126	29-Jun-05
FT	353	y	y	luteus	NM	Sandoval	Jemez Mountains, Seven Springs State Fish Hatchery	1-Jul-05
FT	354	y		luteus	NM	Sandoval	Jemez Mountains, Seven Springs State Fish Hatchery	1-Jul-05
FT	355	y		luteus	NM	Sandoval	Jemez Mountains, Rio Cebolla, 1.7 N, 0.4 mi W jct Rio Cebolla and Rio de las Vacas	4-Jul-05
FT	356	y		luteus	NM	Sandoval	Jemez Mountains, Rio Cebolla at junction with Lake Fork Canyon, above FS Rd 376 bridge	5-Jul-05
FT	357	y		luteus	NM	Sandoval	Jemez Mountains, Rio Cebolla at junction with Lake Fork Canyon, above FS Rd 376 bridge	5-Jul-05
FT	358	y	y	luteus	NM	Otero	Sacramento Mountains, Agua Chiquita Creek, 5.75 mi S, 6.5 mi W Sacramento	19-Jul-05
FT	359	y	y	luteus	NM	Otero	Sacramento Mountains, Silver Springs Creek at jct Turkey Pen Canyon and FS Rd 405 (= County Rd C7), 2.9 mi N, 4.6 mi E Cloudcroft	22-Jul-05
FT	360	y	y	luteus	NM	Sandoval	Jemez Mountains, San Antonio Creek, south end San Antonio Campground, 1.2 mi N, 0.5 mi W junction NM Hwy 4 and NM Hwy 126	28-Jun-05
FT	361	y		princeps	NM	Mora	3.15 mi (by road) S, Jct FS Rd 76 and FSRd 153 on FSRd 76, T23N, R15E, E 1/2 Sec. 3, N36 15.599, W 105 19.992 Elev. 3253 m	10-Aug-02
FT	431	y	y	princeps	NM	Taos	Rito de la Olla (=Pot Creek), Fort Burgwin, Southern Methodist University-Taos campus, 7.4 mi S, 2.0 mi E Talpa	28-Jun-06
FT	432	y	y	princeps	NM	Taos	Rito de la Olla (=Pot Creek), Fort Burgwin, Southern Methodist University-Taos campus, 7.4 mi S, 2.0 mi E Talpa	28-Jun-06

FT	434	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	435	y	y	princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	436	y	y	princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	437	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	438	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	439	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	440	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	29-Jun-06
FT	442	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	443	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	444	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	445	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	446	y	y	princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	448	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	30-Jun-06
FT	450	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	1-Jul-06
FT	451	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	1-Jul-06
FT	453	y		princeps	NM	Taos	Rio Hondo, Taos Ski Valley (= Twining), 4.5 mi N, 2.4 mi W Williams Lake	1-Jul-06
FT	456	y		princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	457	y	y	princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	458	y		princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	459	y		princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	460	y		princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06

FT	461	y		princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	463	y	y	princeps	NM	Santa Fe	Big Tesuque Campground, along North Fork Tesuque Creek and small tributary to southeast, 0.6 km N, 11.1 km E Tesuque	6-Jul-06
FT	466	y	y	princeps	NM	Santa Fe	small tributary to Rio en Medio in Aspen Basin Campground at bottom of Santa Fe Ski Area, 3.6 km N, 11.7 km E Tesuque	6-Jul-06
FT	467	y	y	princeps	NM	Santa Fe	small tributary to Rio en Medio in Aspen Basin Campground at bottom of Santa Fe Ski Area, 3.6 km N, 11.7 km E Tesuque	6-Jul-06
FT	468	y	y	princeps	NM	Santa Fe	small tributary to Rio en Medio in Aspen Basin Campground at bottom of Santa Fe Ski Area, 3.6 km N, 11.7 km E Tesuque	6-Jul-06
FT	475	y	y	princeps	NM	Taos	Rio Santa Barbara, west end Hodges Camp Area	9-Jul-06
FT	476	y	y	princeps	NM	Taos	Rio Santa Barbara, west end Hodges Camp Area	9-Jul-06
FT	487	y	y	princeps	NM	Taos	Vega del Estillero, Rio Pueblo at mouth Raton Canyon in New Mexico Highway 518 right-of-way, 5.5 km S, 4.5 km E Tres Ritos	10-Jul-06
FT	488	y	y	princeps	NM	Taos	Vega del Estillero, Rio Pueblo at mouth Raton Canyon in New Mexico Highway 518 right-of-way, 5.5 km S, 4.5 km E Tres Ritos	10-Jul-06
FT	489	y	y	princeps	NM	Taos	Vega del Estillero, Rio Pueblo at mouth Raton Canyon in New Mexico Highway 518 right-of-way, 5.5 km S, 4.5 km E Tres Ritos	10-Jul-06
FT	493	y	y	princeps	NM	Taos	Rio Pueblo, beaver ponds just below junction Agua Sarca Canyon, 1.1 mi (by road) above La Junta Canyon, 1.6 km S, 1.4 km E Tres Ritos	10-Jul-06
FT	494	y	y	princeps	NM	Taos	Rio Pueblo, beaver ponds just below junction Agua Sarca Canyon, 1.1 mi (by road) above La Junta Canyon, 1.6 km S, 1.4 km E Tres Ritos	10-Jul-06
FT	495	y	y	princeps	NM	Taos	Rio Pueblo, beaver ponds just below junction Agua Sarca Canyon, 1.1 mi (by road) above La Junta Canyon, 1.6 km S, 1.4 km E Tres Ritos	10-Jul-06
FT	500	y		princeps	NM	Taos	Rio Pueblo, beaver ponds just below junction Agua Sarca Canyon, 1.1 mi (by road) above La Junta Canyon, 1.6 km S, 1.4 km E Tres Ritos	10-Jul-06
FT	501	y		princeps	NM	Taos	Rio Pueblo, beaver ponds just below junction Agua Sarca Canyon, 1.1 mi (by road) above La Junta Canyon, 1.6 km S, 1.4 km E Tres Ritos	10-Jul-06
FT	502	y		luteus	NM	Colfax	Sugarite Canyon State Park, small tributary to Soda Pocket Creek, 7.9 km N, 3.8 km E Raton	12-Jul-06
FT	506	y	y	luteus	NM	Colfax	Sugarite Canyon State Park, small tributary to Soda Pocket Creek, 7.9 km N, 3.8 km E Raton	12-Jul-06
FT	507	y	y	luteus	NM	Colfax	Sugarite Canyon State Park, Chicorica Creek, picnic area 0.4 mi S (by NM Hwy 526) Lake Maloya spillway, 8.4 km N, 5.6 km E Raton	12-Jul-06

FT	520	y	y	luteus	NM	Colfax	Sugarite Canyon State Park, Chicorica Creek, upper end of Lake Alice, 6.0 km N, 4.7 km E Raton	12-Jul-06
FT	521	y		luteus	NM	Colfax	Sugarite Canyon State Park, Chicorica Creek, upper end of Lake Alice, 6.0 km N, 4.7 km E Raton	12-Jul-06
FT	528	y		luteus	NM	Colfax	Sugarite Canyon State Park, Soda Pocket Campground, southern tributary to Soda Pocket Creek, 7.4 km N, 3.9 km E Raton	13-Jul-06
FT	529	y		luteus	NM	Colfax	Sugarite Canyon State Park, Soda Pocket Campground, southern tributary to Soda Pocket Creek, 7.4 km N, 3.9 km E Raton	13-Jul-06
FT	541	y	y	luteus	NM	Colfax	Sugarite Canyon State Park, Segerstrom Creek, above junction with Lake Maloya, 9.6 km N, 5.1 km E Raton	14-Jul-06
FT	542	y		luteus	NM	Colfax	Sugarite Canyon State Park, Segerstrom Creek, above junction with Lake Maloya, 9.6 km N, 5.1 km E Raton	14-Jul-06
FT	543	y		luteus	NM	Colfax	Sugarite Canyon State Park, Segerstrom Creek, above junction with Lake Maloya, 9.6 km N, 5.1 km E Raton	14-Jul-06
FT	601	y	y	princeps	NM	Taos	La Cueva Creek at La Cueva Camp along forest road 1900, 175 m above confluence with East Fork Costilla Creek, 11.3 km S, 12.9 km E Amalia	26-Jul-06
FT	604	y	y	luteus	NM	Mora	Coyote Creek, Coyote Creek State Park, 10.3 mi. W Ocate	27-Jul-06
FT	605	y	y	luteus	NM	Mora	Coyote Creek, Coyote Creek State Park, 10.3 mi. W Ocate	27-Jul-06
FT	613	y	y	luteus	NM	Sandoval	Rio Cebolla, 0.6 miles (by Forest Road 376) southwest of Forest Road 376 bridge over Rio Cebolla, which is located at the junction of Lake Fork Canyon, 9.5 km N, 6.5 km W Jemez Springs, T19N, R2E, W ½ of NE ¼ Sec. 30	15-Aug-06
KU	2045	y		preblei	CO	Boulder	Semper	31-Oct-09
KU	5832	y		luteus	NM	Rio Arriba	4 mi. N. of El Rito, Alt. 7000 Ft. Heavy timber along alfalfa field	6-Jul-28
KU	5833	y		luteus	NM	Rio Arriba	4 mi. N. of El Rito, Alt. 7000 Ft. Heavy oak timber along alfalfa field	14-Jul-28
KU	5834	y		luteus	NM	Rio Arriba	4 mi. N. of El Rito, Alt. 7000 Ft. In patch of scrub oak	18-Jul-28
KU	5835	y		luteus	NM	Rio Arriba	4 mi. N. of El Rito, Alt. 7000 Ft. Heavy timber along alfalfa field	3-Jul-28
KU	16038	y		luteus	CO	LaPlata	Florida, 6800 ft.	4-Sep-45
KU	58984	y		princeps	NM	Santa Fe	13 miles N.E. Santa Fe, Pacheco Canyon	28-Aug-53
KU	120040	y		princeps	NM	Santa Fe	11 mi. NE Santa Fe Hwy 475, 9500',	9-Jun-69
MSB	4943	y		luteus	NM	Taos	2 mi NE Tres Ritos	24-Jul-58
MSB	4944	y		princeps	NM	Taos	2 mi. NE Tres Ritos, Rio La Junta	24-Jul-58
MSB	4945	y		princeps	NM	Taos	2 mi. NE Tres Ritos	25-Jul-58
MSB	10238	y		luteus	CO	Archleta	NW1/4 Sec. 23, T32N-R6W	25-Jul-60
MSB	29292	y		princeps	NM	Taos	Duran Canyon Campground, 2 mi. N Tres Ritos, Carson Natl. Forest	17-Jun-69
MSB	29293	y		princeps	NM	Taos	Duran Canyon Campground, 2 mi. N Tres Ritos, Carson Natl. Forest	17-Jun-69
MSB	35034	y		luteus	NM	Otero	8 mi W Cloudcroft	

MSB	35648	y		princeps	NM	Taos	2.7 mi. NE Tres Ritos	8-Jun-77
MSB	35649	y		princeps	NM	Taos	4 mi. NE Tres Ritos	9-Jun-77
MSB	35650	y		princeps	NM	Taos	4 mi. NE Tres Ritos	9-Jun-77
MSB	35651	y		princeps	NM	Taos	2 mi. NE Tres Ritos	9-Jun-77
MSB	35652	y		princeps	NM	Taos	2 mi. NE Tres Ritos	9-Jun-77
MSB	35653	y		princeps	NM	Taos	2 mi. NE Tres Ritos	9-Jun-77
MSB	36119	y		luteus	NM	Socorro	Bosque del Apache Game Refuge, 11 mi. S San Antonio, 4500 ft.	28-Aug-76
MSB	36131	y		princeps	NM	Taos	Rio La Junta, 17 mi. S, 6 mi. E Taos, 9400 ft.	5-Sep-76
MSB	36133	y		princeps	NM	Taos	Rio La Junta, 17 mi. S, 6 mi. E Taos, 9400 ft.	4-Sep-76
MSB	36139	y		princeps	NM	Taos	Rio La Junta, 17 mi. S, 6 mi. E Taos, 9400 ft.	4-Sep-76
MSB	36142	y		luteus	NM	Otero	Silver Creek, 8 mi. NE. Cloudcroft	21-Jul-77
MSB	36143	y		luteus	NM	Socorro	Bosque del Apache Game Refuge, 11 mi. S San Antonio, 4500 ft.	22-Jul-77
MSB	36159	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	30-Jun-77
MSB	36160	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	22-Jun-77
MSB	36161	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	22-Jun-77
MSB	36162	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	22-Jun-77
MSB	36164	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	14-Jul-77
MSB	36165	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	14-Jul-77
MSB	36166	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	14-Jul-77
MSB	36167	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	14-Jul-77
MSB	36169	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	17-Aug-77
MSB	36170	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	17-Aug-77
MSB	36171	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	17-Aug-77
MSB	36172	y		luteus	NM	Socorro	Bosque del Apache Game Refuge	17-Aug-77
MSB	36174	y		luteus	NM	Socorro	GAME REFUGE, 11 MI S SAN ANTONIO, BOSQUE DEL APACH	16-Sep-77
MSB	36175	y		luteus	NM	Socorro	GAME REFUGE, 11 MI S SAN ANTONIO, BOSQUE DEL APACH	16-Sep-77
MSB	37154	y		luteus	NM	Otero	8 mi E of Coudcroft	21-Jul-77
MSB	37155	y		luteus	NM	Otero	8 mi E of Coudcroft	21-Jul-77
MSB	37323	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	3-Sep-78
MSB	37323	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	3-Sep-78
MSB	37324	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	3-Sep-78
MSB	37325	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	3-Sep-78
MSB	37326	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	3-Sep-78
MSB	37754	y		luteus	NM	Socorro	Bosque del Apache Wildlife Refuge	20-Aug-78
MSB	37756	y		luteus	NM	Socorro	Bosque del Apache Wildlife Refuge	20-Aug-78
MSB	37757	y		luteus	NM	Socorro	Bosque del Apache Wildlife Refuge	20-Aug-78
MSB	37758	y		luteus	NM	Socorro	Bosque del Apache Wildlife Refuge	20-Aug-78
MSB	40949	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40950	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40951	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40952	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40953	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40954	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40955	y		luteus	Az	Apache	4 mi S, 16 mi W Alpine	17-Aug-79

MSB	40956	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	17-Aug-79
MSB	40994	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	18-Aug-79
MSB	40995	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	18-Aug-79
MSB	40996	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	18-Aug-79
MSB	40997	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	18-Aug-79
MSB	40998	y		luteus	AZ	Apache	4 mi S, 16 mi W Alpine	18-Aug-79
MSB	41055	y		luteus	NM	Sandoval	Fenton Lake, Jemez Mts.	5-Aug-79
MSB	41058	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	18-Aug-79
MSB	41059	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	18-Aug-79
MSB	41060	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41061	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41062	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41063	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41064	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41065	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41066	y		luteus	NM	Otero	3.2 mi (by road) E Cloudcroft	17-Aug-79
MSB	41223	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache National Wildlife Refuge	23-Aug-79
MSB	41224	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache National Wildlife Refuge	24-Aug-79
MSB	41225	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	1-Sep-79
MSB	41226	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	1-Sep-79
MSB	41227	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	1-Sep-79
MSB	41228	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	2-Sep-79
MSB	41229	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	2-Sep-79
MSB	41230	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache NWR	2-Sep-79
MSB	41231	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	2-Sep-79
MSB	41232	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	2-Sep-79
MSB	41234	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	3-Sep-79
MSB	41235	y		luteus	NM	Socorro	8 mi S San Antonio, Bosque del Apache Natl. Wildlife Refuge	3-Sep-79
MSB	54801	y		campestris	SD	Lawrence	10.5 mi SSE Cheyenne Crossing	13-Jul-84
MSB	56979	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	27-Aug-85
MSB	56980	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	28-Aug-85
MSB	56981	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	28-Aug-85
MSB	56982	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	23-Aug-85

MSB	56983	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	27-Aug-85
MSB	56984	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	27-Aug-85
MSB	56985	y		luteus	NM	Sandoval	T19N, R2E, SW Sec 10, Fenton Lake, marsh e of Lake, w of Rte 126	30-Aug-85
MSB	56986	y		luteus	NM	Sandoval	T20N, R1E, west central Sec 25, Rio de Las Vacas x Turkey Creek	6-Sep-85
MSB	56987	y		luteus	NM	Sandoval	T20N, R2E NE Sec 3 Rito Penas Negras 8360 ft.	6-Sep-85
MSB	56988	y		luteus	NM	Sandoval	T20N, R2E NE Sec 3 Rito Penas Negras 8360 ft.	6-Sep-85
MSB	56989	y		luteus	NM	Sandoval	T20N, R2E NE Sec 3 Rito Penas Negras 8360 ft.	6-Sep-85
MSB	56990	y		luteus	NM	Sandoval	T20N, R2E NE Sec 3 Rito Penas Negras 8360 ft.	5-Sep-85
MSB	56991	y		luteus	NM	Sandoval	T20N, R3E, south central Sec 20 San Antonio Creek	5-Sep-85
MSB	56992	y		luteus	NM	Sandoval	T20N, R3E, south central Sec 20 San Antonio Creek	5-Sep-85
MSB	56993	y		luteus	NM	Sandoval	T20N, R2E, NW Sec 35 Seven Springs Fish Hatchery	23-Aug
MSB	56994	y		luteus	NM	Sandoval	T20N, R2E, NW Sec 35 Seven Springs Fish Hatchery	27-Aug-85
MSB	56995	y		luteus	NM	Sandoval	?	
MSB	56996	y		luteus	NM	Sandoval	?	
MSB	56997	y		luteus	NM	Sandoval	?	
MSB	58368	y		luteus	NM	Bernalillo	Isleta T8N, R2E, Sec 12	19-Aug-87
MSB	58369	y		luteus	NM	Rio Arriba	T22N R7E Sec 36	15-Sep-87
MSB	58370	y		luteus	NM	Rio Arriba	San Juan Pueblo, T21N, R8E, Sec 15	12-Sep-87
MSB	58371	y		luteus	NM	Rio Arriba	San Juan Pueblo, T21N, R8E, Sec 15	15-Sep-87
MSB	61678	y		luteus	NM	Otero	Rio Penasco, Int. Rt. 164, Rt. 64	7/13/1988
MSB	61679	y		luteus	NM	Otero	Rio Penasco, Int. Rt. 164, Rt. 64	13-Jul-88
MSB	61680	y		luteus	NM	Otero	Rio Penasco, Int. Rt. 164, Rt. 64	13-Jul-88
MSB	61684	y		luteus	NM	Otero	Int. Pumphouse Canyon, Rt. 82	15-Jul-88
MSB	61686	y		luteus	NM	Otero	Rio Penasco	16-Jul-88
MSB	61687	y		luteus	NM	Otero	Rio Penasco	16-Jul-88
MSB	61688	y		luteus	NM	Otero	Potato CanyonT18S, R13E Sec5	17-Jul-88
MSB	61690	y		luteus	NM	Otero	Water Canyon	17-Jul-88
MSB	61691	y		luteus	NM	Otero	Agua Chiquita	18-Jul-88
MSB	61692	y		luteus	NM	Otero	Agua Chiquita	18-Jul-88
MSB	61693	y		luteus	NM	Otero	Spring Canyon	19-Jul-88
MSB	61696	y		luteus	NM	Otero	Rio Penasco, T17S, R13E, Sec 3, Int with Rte 541	20-Jul-88
MSB	61700	y		luteus	NM	Otero	Silver Springs Canyon, T15S, R13E, Sec 29	22-Jul-88
MSB	61701	y		luteus	NM	Otero	Silver Springs Canyon, T15S, R13E, Sec 29	22-Jul-88
MSB	61702	y		luteus	NM	Otero	Silver Springs Canyon, T15S, R13E, Sec 29	22-Jul-88
MSB	61703	y		luteus	NM	Otero	Silver Springs Canyon, T15S, R13E, Sec 22	22-Jul-88
MSB	61704	y		luteus	NM	Otero	Silver Springs Canyon, T15S, R13E, Sec 22	22-Jul-88
MSB	61712	y		luteus	NM	Otero	Hay Canyon Int. 257, 541 T17S, R12E, sec 19	31-Jul-88
MSB	62096	y		luteus	NM	Sandoval	Virgin Canyon T18N, R2E, No Section	2-Aug-89
MSB	62097	y		luteus	NM	Sandoval	Rio Cebolla T19N, R1E, No Section 1 mi up from R de la V	24-Aug-89
MSB	62098	y		luteus	NM	Sandoval	Rio Cebolla T19N, R1E, No Section 1 mi up from Rio de la Vacas	24-Aug-89
MSB	62101	y		luteus	NM	Sandoval	Rio Cebolla T20N, R2E Sec 24 near Hay Canyon	4-Aug-89
MSB	62102	y		luteus	NM	Sandoval	Rito Penas Negras T20N R1E Sec 13 int. Rio de las	3-Aug-89

							Vacas	
MSB	62103	y		luteus	NM	Valencia	S of Belen near Turn, along farm ditch T5N R2E no section	1-Aug-87
MSB	66793	y		campestris	SD	Lawrence	10.5 mi SSE Cheyenne Crossing	12-Jul-84
MSB	67525	y		luteus	NM	Sandoval	17 km SE of Cuba, T20N R1E S12, elev 2600 m	12-Jul-85
MSB	86344	y		luteus	AZ		White Mtns., Centerfire Creek, Apache-sitgreavs National Forest T4N R28E Sec6 Off Rte 25	11-Aug-91
MSB	89194	y		luteus	AZ		Apache/Sitgreaves NF Boggy Creek	12-Aug-91
MSB	91627	y		luteus	AZ		Apache/Sitgreaves NF T6N R27E Sec 27	13-Aug-91
MSB	91675	y		luteus	AZ	Navajo	White Mtns., Centerfire Creek, Apache-Sitgreavs National Forest T4N R28E Sec 6 Off Rte 25	11-Aug-91
MSB	141305	y		pallidus	KS	Riley	Fort Riley	3-7 May 1998
MSB	146179	y		campestris	SD		Willow Creek, N 43 53.633' W 103 32.149', 5061 ft. elev. (accuracy 22 feet)	18-Jun-05
MSB	146188	y		campestris	SD	Lawrence	Black Hills National Forest, 6 mi w Timon Campground, N 44 22.502 W 103 57.962, 5341' elev.	15-Jun-05
NMMNH	1228	y		luteus	NM	Mora	T20N, R15E along Mora R. next to sewage ponds 1.5 mi down river from town	22-Aug-90
NMMNH	1229	y		luteus	NM	Mora	T20N, R15E along Mora R. next to sewage ponds 1.5 mi down river from town	22-Aug-90
NMMNH	2172	y		princeps	NM	Taos	3 mi. N, 4 mi. E Tres Ritos	19-Aug-94
NMMNH	2173	y		princeps	NM	Taos	3 mi. N, 4 mi. E Tres Ritos	19-Aug-94
NMMNH	2174	y		princeps	NM	Taos	3 mi. N, 4 mi. E Tres Ritos	19-Aug-94
NMMNH	2175	y		princeps	NM	Taos	3 mi. N, 4 mi. E Tres Ritos	19-Aug-94
NMMNH	2176	y		princeps	NM	Taos	3 mi. N, 4 mi. E Tres Ritos	19-Aug-94
NMMNH	4040	y	y	princeps	NM	Mora	Coyote Creek, 7 mi. N Guadalupita	9-Jul-00
NMMNH	4042	y	y	princeps	NM	Mora	Coyote Creek, 7 mi. N Guadalupita	10-Jul-00
NMSU	5001	y		princeps	NM	Rio Arriba	24.1 mi W, 3.8 mi N Res Piedras, 9800', T29W, R7E, Sec 31	8/22/1973
NMSU	5405	y		princeps	NM	Rio Arriba	15.5 mi W, 5.8 mi N Tres Piedras, 9800', T29N, R7E, Sec 19	13-Sep-75
NMSU	13825	y		luteus	NM	Bernalillo	0.7 mi E, 0.3 mi N Isleta, 4900', T8N, R2E, sec 13	28-Aug-82
NMSU	13826	y		luteus	NM	Bernalillo	0.9 mi. N, 0.6 mi E Isleta, 4900', T8N, R2E, sec 13	17-Jun-82
NMSU	13827	y		luteus	NM	Bernalillo	1.2 mi N, 0.3 mi E Isleta, 4900', T8N, R2E, sec 12	24-May-82
NMSU	13828	y		luteus	NM	Bernalillo	1.2 mi N, 0.3 mi E Isleta, 4900', T8N, R2E, sec 12	24-May-82
NMSU	13829	y		luteus	NM	Bernalillo	1.4 mi N, 0.7 m. E Isleta, 4880', T8N, R2E, sec 12	13-Jun-81
NMSU	13830	y		luteus	NM	Bernalillo	2.2 mi S, 1.3 mi Isleta, 4900', T8N, R2E, sec 27	24-May-82
TTU	1363	y		princeps	NM	Taos	Red River	10-Sep-63
TTU	2372	y		princeps	NM	Taos	200? Yds N W St Bernard's Hotel, Twining, bank of Rio Hondo River	15-Jul-66
TTU	2373	y		princeps	NM	Taos	940 yds N of Hotel St. Bernard, on rio Hondo	15-Jul-66
TTU	2374	y		princeps	NM	Taos	350 yds. N.W. Hotel St. Bernarde, twining	15-Jul-66
TTU	2375	y		princeps	NM	Taos	2 1/2 mi. N. Williams Lake, Grid Station J-4	17-Jul-66
TTU	2376	y		princeps	NM	Taos	2.5 mi N Lake Williams, (B-1)	13-Jul-66
TTU	2377	y		princeps	NM	Taos	2 1/2 M. N . Williams lake, Grid Stat. J-4	17-Jul-66
TTU	2378	y		princeps	NM	Taos	2 1/2 Mi. N. of Willimas lake, H-1	13-Jul-66
TTU	2379	y		princeps	NM	Taos	450 yds. N.W. Hotel St. Bernard, twining	14-Jul-66
TTU	2380	y		princeps	NM	Taos	380 yds. N.W. St. Benard [sic] Hotel, Twining	14-Jul-66

TTU	2381	y		princeps	NM	Taos	2 1/2 mi. N. Williams Lake, Grid Station H-1	19-Jul-66
TTU	2382	y		princeps	NM	Taos	2 1/2 Mi. N. Williams lake, grid sta. H-2	21-Jul-66
TTU	2383	y		princeps	NM	Taos	2 1/2 M. N. of William Lake grid station F-6	12-Jul-66
TTU	2384	y		princeps	NM	Taos	500 yds. N.W. St. Bernard Hotel Twining	14-Jul-66
TTU	2385	y		princeps	NM	Taos	Rio Hondo River bank 860 yds N.W. St Bernard's Hotel Twining	14-Jul-66
TTU	2386	y		princeps	NM	Taos	950 yds. N.W. of St. Bernard Hotel, Twinning [sic]	14-Jul-66
TTU	2387	y		princeps	NM	Taos	2 1/2 M. N. of Williams Lake, Grid Station G-3	16-Jul-66
TTU	2388	y		luteus	NM	Taos	2 1/2 M. N of Williams lake, Grid Station A-3	19-Jul-66
UIMNH	28305	y		luteus	AZ	Apache	North fork of White River White Mts, alt. 8200	4-Jul-33
UIMNH	28405	y		luteus	AZ		White Mts.	4-Jul-33
UIMNH	28406	y		luteus	AZ	Apache	North fork of White River White Mts, alt. 8200	2-Jul-33
UIMNH	29077	y		luteus	AZ	Apache	Sheep Crossing, on Little Colorado River, [in grass in meadow]	4-Sep-63
UIMNH	29078	y		luteus	AZ	Apache	Sheep Crossing, 9100 ft, on Little Colo. Riv.,	5-Sep-63
UIMNH	50967	y		princeps	NM	Taos	1 mi. NE Red River	20-Jul-74
UIMNH	50968	y		princeps	NM	Taos	1 mi. NE Red River	20-Jul-74
UIMNH	50974	y		luteus	AZ	Apache	13 mi WSW Alpine	30-Jun-74
UIMNH	55331	y		princeps	NM	San Miguel	3 mi N Cowles	25-Jul-77
UMNH	16896	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 mi N. N. Mex-Colo. Line, 6100'	17-Jul-60
UMNH	16910	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 Mi. N. State Line, 6100'	19-Jul-60
UMNH	16911	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 Mi. N State Line, 6100'	20-Jul-60
UMNH	16912	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 Mi. N State Line, 6100'	20-Jul-60
UMNH	16976	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 mi. N. New Mexico-Colorado state line, 6,100'	20-Jul-60
UMNH	16977	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 mi. N. Colorado-New Mexico State line, 6,100'	20-Jul-60
UMNH	16978	y		luteus	CO	Archuleta	Sambrito Creek, 1/2 mi. N Colorado-New Mexico state line, 6,080'	17-Jul-60
UMNH	17992	y		princeps	CO	Gunnison	Streamside 4 mi. up Soap Creek from Sapinero 7520 ft.	13-Jul-61
UMNH	18075	y		princeps	CO	Gunnison	Junction of Dry Gulch and Gunnison River, 7,400'	19-Jul-61
UMNH	18127	y		princeps	CO	Gunnison	Elymus condensata meadow at edge of Red Cr. 1/4 mi above jct. With Gunnison Riv. 7340 ft.	10-Jul-61
UMNH	18128	y		princeps	CO	Gunnison	Dry Gulch at jct. With gunnison River 7,350 14 mi above Blue mesa Dam	30-Jun-61
UMNH	18129	y		princeps	CO	Gunnison	Shot in daylight in meadow along Red Cr. In streamside grasses 7400 ft.	8-Jul-61
UMNH	18130	y		princeps	CO	Gunnison	Junction Dry Gulch & Gunnison River 7,400'	19-Jul-61
UMNH	18131	y		princeps	CO	Gunnison	Junction Dry Gulch & Gunnison River 7,400'	19-Jul-61
UMNH	18132	y		princeps	CO	Gunnison	Junction of Dry Gulch & Gunnison River 14 mi up from Blue Mesa Dam 7,350	30-Jun-61
UMNH	18133	y		princeps	CO	Gunnison	Junction of Dry Gulch & Gunnison River 14 mi up from Blue Mesa Dam 7,350	6/30/1961
UMNH	18134	y		princeps	CO	Gunnison	0.1 Mi N. of Gunnison River on W. Elk Creek, 7,400'	4-Jul-61
UMNH	18135	y		princeps	CO	Gunnison	1 Mi up Red Creek from Gunnison River 7,544'	10-Jul-61
UMNH	18136	y		princeps	CO	Gunnison	1 Mi up Red Creek from Gunnison River 7,544'	10-Jul-61
UMNH	18137	y		princeps	CO	Gunnison	2 River Miles up Lake Fork of the Gunnison River 7,295'	18-Jul-61

UMNH	18138	y		princeps	CO	Gunnison	1.4 mi up Stuben Creek from Gunnison River 7,440	6-Jul-61
USNM	14925	y		preblei	CO		Purgatorie R.	8/12/1875
USNM	59732	y		luteus	NM	Santa Fe	Santa Fe	
USNM	73084	y		preblei	CO		Loveland	7/22/1895
USNM	112062	y		preblei	CO		Boulder	1-Sep-00
USNM	118798	y		luteus	NM		Cloudcroft, 10 mi NE	10-Sep-02
USNM	119032	y		luteus	NM		Cloudcroft, 12 mi E at 7500 feet.	7-Sep-02
USNM	129250	y		princeps	NM		Taos Mts., East slope 8800 ft.	19-Sep-03
USNM	133430	y		princeps	NM		Hondo Canyon, altitude 8200 ft.	10-Aug-04
USNM	133602	y		luteus	NM		Espanola, 5,000 ft.	24-Jun-04
USNM	133703	y		princeps	CO		Antonito	30-Aug-04
USNM	134355	y		princeps	NM		Tierra Amarillo	13-Sep-04
USNM	205366	y		luteus	AZ		Alpine, 8000 ft.	19-Sep-14
USNM	205373	y		luteus	AZ			20-Sep-14
USNM	205585	y		luteus	AZ	Apache	Alpine, 8000'	20-Sep-14
USNM	208660	y		luteus	AZ		Alpine, 8000 ft.	2-Aug-15
USNM	3322/36046	y		luteus	NM		Camp Burgwyn	..1858..
USNM	47300/35035	y		princeps	CO		Fort Garland	7/26/1892
USNM	47301/35036	y		princeps	CO		Fort Garland	7/26/1892
USNM	47302/35037	y		princeps	CO		Fort Garland	7/26/1892
USNM	47303/35038	y		princeps	CO		Fort Garland	7/27/1892
USNM	47304/35039	y		princeps	CO		Fort Garland	7/28/1892
USNM	47305/35040	y		princeps	CO		Fort Garland	7/28/1892
USNM	47306/35041	y		princeps	CO		Fort Garland	7/28/1892
USNM	47307/035042	y		princeps	CO		Fort Garland	7/28/1892

APPENDIX 2

Appendix 2. Descriptive statistics for external and cranial measurements in *Zapus hudsonius luteus and Zapus princeps princeps* from the zone of sympatry in southern Colorado and northern New Mexico.

						95% Confidence Interval for Mean			
Variable	Taxon/Age/Sex	N	Mean	Std. Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
Total	luteus young	31	207.9	12.35	2.22	203.34	212.40	181	230
length	luteus old	31	212.4	8.82	1.58	209.12	215.59	197	233
	princeps young	14	231.1	9.88	2.64	225.37	236.78	213	243
	princeps old male	53	228.8	12.31	1.69	225.44	232.22	188	256
	princeps old female	42	239.1	8.55	1.32	236.41	241.74	219	262
Tail	luteus young	31	125.3	6.10	1.10	123.08	127.56	112	137
length	luteus old	31	125.1	6.18	1.11	122.86	127.40	114	139
	princeps young	14	137.3	6.40	1.71	133.59	140.98	125	146
	princeps old male	52	137.0	7.84	1.09	134.85	139.22	122	161
	princeps old female	42	141.0	6.81	1.05	138.93	143.17	124	156
Body	luteus young	31	82.5	8.71	1.56	79.36	85.74	63	98
length	luteus old	32	87.0	4.93	0.87	85.22	88.78	77	100
	princeps young	14	93.8	6.42	1.72	90.08	97.49	82	105
	princeps old male	52	92.6	5.69	0.79	90.99	94.16	72	102
	princeps old female	42	98.0	5.25	0.81	96.39	99.66	86	107
Hindfoot	luteus young	31	30.1	1.02	0.18	29.69	30.44	28	33
length	luteus old	31	29.9	1.21	0.22	29.43	30.32	27	32
	princeps young	13	31.9	0.98	0.27	31.33	32.51	30	33
	princeps old male	50	31.0	1.25	0.18	30.67	31.37	28	33
	princeps old female	41	32.1	1.29	0.20	31.71	32.53	28	34
Ear									
length	luteus young	31	13.9	1.65	0.30	13.33	14.54	10	16
	luteus old	31	13.8	1.50	0.27	13.22	14.32	10	15
	princeps young	14	14.1	1.29	0.35	13.40	14.89	12	17
	princeps old male	44	14.2	1.27	0.19	13.83	14.60	12	18

	princeps old female	34	14.5	1.41	0.24	14.05	15.03	12	17
Mass	luteus young	29	17.6	4.07	0.76	16.05	19.15	9.9	25.5
	luteus old	19	21.4	4.10	0.94	19.42	23.37	15.5	28.5
	princeps young	14	21.6	3.35	0.90	19.62	23.49	17	29.5
	princeps old male	36	24.0	2.79	0.46	23.03	24.92	17	30.4
	princeps old female	30	29.7	4.62	0.84	27.96	31.41	22	40
CBL	luteus young	29	19.24	0.91	0.17	18.90	19.59	16.97	20.58
	luteus old	24	20.25	0.84	0.17	19.90	20.60	18.47	21.8
	princeps young	14	20.85	0.75	0.20	20.41	21.28	19.66	21.89
	princeps old male	56	21.38	0.72	0.10	21.19	21.58	19.62	23.32
	princeps old female	40	21.75	0.62	0.10	21.55	21.94	20.49	22.74
RL	luteus young	30	8.84	0.51	0.09	8.65	9.03	7.77	9.61
	luteus old	28	9.37	0.42	0.08	9.21	9.53	8.48	10.23
	princeps young	14	9.32	0.37	0.10	9.11	9.53	8.68	9.9
	princeps old male	60	9.58	0.35	0.05	9.49	9.67	8.47	10.3
	princeps old female	42	9.73	0.31	0.05	9.63	9.83	8.96	10.39
ZB	luteus young	25	10.99	0.53	0.11	10.77	11.20	10.07	11.87
	luteus old	25	11.37	0.44	0.09	11.19	11.55	10.44	12.33
	princeps young	12	12.35	0.35	0.10	12.13	12.57	11.78	12.9
	princeps old male	48	12.35	0.39	0.06	12.23	12.46	11.3	13.51
	princeps old female	38	12.70	0.48	0.08	12.54	12.85	11.61	13.71
DS	luteus young	27	8.17	0.22	0.04	8.08	8.26	7.48	8.61
	luteus old	18	8.43	0.23	0.05	8.32	8.54	7.98	8.82
	princeps young	14	8.58	0.28	0.07	8.42	8.74	8.04	9.04
	princeps old male	53	8.64	0.27	0.04	8.56	8.71	8.18	9.43
	princeps old female	38	8.79	0.29	0.05	8.69	8.89	8.19	9.55
IOC	luteus young	31	4.42	0.16	0.03	4.36	4.48	3.95	4.69
	luteus old	31	4.57	0.25	0.04	4.48	4.66	4.21	5.28
	princeps young	14	4.46	0.15	0.04	4.37	4.54	4.18	4.72
	princeps old male	60	4.45	0.13	0.02	4.41	4.48	4.18	4.65
	princeps old female	45	4.50	0.15	0.02	4.45	4.54	4.13	4.76
MTR	luteus young	27	3.75	0.10	0.02	3.71	3.79	3.48	3.94
	luteus old	32	3.77	0.18	0.03	3.70	3.83	3.27	4.05
	princeps young	14	4.04	0.09	0.02	3.98	4.09	3.91	4.18

	princeps old male	61	4.02	0.14	0.02	3.99	4.06	3.65	4.29
	princeps old female	46	4.03	0.17	0.03	3.98	4.08	3.38	4.37
PL	luteus young	30	8.23	0.42	0.08	8.07	8.38	7.36	8.85
	luteus old	31	8.53	0.34	0.06	8.41	8.66	7.8	9.24
	princeps young	14	8.99	0.29	0.08	8.82	9.16	8.38	9.46
	princeps old male	61	9.14	0.30	0.04	9.06	9.21	8.39	9.59
	princeps old female	46	9.30	0.30	0.04	9.21	9.39	8.55	9.8
PB	luteus young	31	3.31	0.18	0.03	3.24	3.37	2.97	3.68
	luteus old	32	3.39	0.16	0.03	3.33	3.44	3.13	3.87
	princeps young	14	3.76	0.15	0.04	3.67	3.84	3.46	3.97
	princeps old male	61	3.77	0.18	0.02	3.73	3.82	3.3	4.15
	princeps old female	46	3.87	0.15	0.02	3.83	3.92	3.54	4.22
IFL	luteus young	31	3.88	0.23	0.04	3.80	3.96	3.36	4.3
	luteus old	32	4.01	0.27	0.05	3.91	4.10	3.16	4.47
	princeps young	14	4.67	0.18	0.05	4.57	4.78	4.39	4.97
	princeps old male	60	4.58	0.30	0.04	4.50	4.66	3.69	5.05
	princeps old female	46	4.73	0.30	0.04	4.64	4.82	3.89	5.25
IFB	luteus young	31	2.03	0.16	0.03	1.97	2.09	1.71	2.37
	luteus old	32	2.10	0.16	0.03	2.05	2.16	1.8	2.49
	princeps young	14	2.19	0.10	0.03	2.13	2.25	2.05	2.36
	princeps old male	60	2.23	0.15	0.02	2.19	2.27	1.89	2.63
	princeps old female	46	2.22	0.12	0.02	2.18	2.25	1.99	2.52
IBW	luteus young	24	1.88	0.25	0.05	1.77	1.98	1.47	2.26
	luteus old	21	1.96	0.17	0.04	1.88	2.03	1.6	2.24
	princeps young	14	2.21	0.17	0.04	2.12	2.31	1.92	2.46
	princeps old male	55	2.32	0.19	0.03	2.27	2.37	1.94	2.84
	princeps old female	39	2.40	0.19	0.03	2.34	2.46	2.06	2.93
MB	luteus young	22	10.17	0.30	0.06	10.04	10.31	9.45	10.79
	luteus old	21	10.43	0.29	0.06	10.29	10.56	9.99	11.01
	princeps young	13	10.78	0.24	0.07	10.63	10.92	10.39	11.25
	princeps old male	56	10.89	0.29	0.04	10.82	10.97	10.07	11.64
	princeps old female	39	11.12	0.31	0.05	11.02	11.23	10.4	12.13

APPENDIX 3

Appendix 3. Descriptive statistics for external and cranial measurements in 7 populations of *Zapus hudsonius luteus*.

						95% Confidence Interval			
Variable	Population	N	Mean	Std. Deviation	Std. Error	Lower Bound	Upper Bound	Minimum	Maximum
Total	Bosque del Apache	3	211.33	5.51	3.18	197.65	225.01	205	215
	Canadian	8	214.50	11.48	4.06	204.91	224.09	196	233
	Jemez	10	208.00	5.66	1.79	203.95	212.05	199	218
	Rio Grande	9	211.89	9.08	3.03	204.91	218.86	197	231
	Sacramento	28	219.18	8.52	1.61	215.87	222.48	203	239
	San Juan	7	218.00	10.15	3.84	208.61	227.39	204	233
	White	11	220.45	7.97	2.40	215.10	225.81	208	235
	Total	76	216.12	9.34	1.07	213.98	218.25	196	239
Tail	Bosque del Apache	3	123.33	2.52	1.45	117.08	129.58	121	126
	Canadian	8	125.13	7.24	2.56	119.07	131.18	114	133
	Jemez	10	122.30	4.99	1.58	118.73	125.87	115	133
	Rio Grande	9	124.22	5.24	1.75	120.20	128.25	114	134
	Sacramento	28	131.07	5.18	0.98	129.06	133.08	120	147
	San Juan	7	131.71	7.36	2.78	124.90	138.53	121	140
	White	12	132.33	6.51	1.88	128.19	136.47	123	145
	Total	77	128.47	6.78	0.77	126.93	130.01	114	147
Body	Bosque del Apache	3	88.00	4.00	2.31	78.06	97.94	84	92
	Canadian	8	89.38	5.40	1.91	84.86	93.89	82	100
	Jemez	10	85.70	4.03	1.27	82.82	88.58	77	90
	Rio Grande	10	86.90	5.59	1.77	82.90	90.90	78	97
	Sacramento	30	88.03	6.09	1.11	85.76	90.31	75	102
	San Juan	7	86.29	4.03	1.52	82.56	90.01	82	94
	White	13	87.38	3.52	0.98	85.25	89.51	82	94
	Total	81	87.48	5.09	0.57	86.36	88.61	75	102
Hindfoot	Bosque del Apache	3	28.67	0.58	0.33	27.23	30.10	28	29
	Canadian	8	30.06	1.02	0.36	29.21	30.91	28	31.5
	Jemez	10	30.05	0.96	0.30	29.37	30.73	28	31
	Rio Grande	10	29.70	1.49	0.47	28.63	30.77	28	32
	Sacramento	30	30.20	0.89	0.16	29.87	30.53	28	32
	San Juan	6	29.83	2.04	0.83	27.69	31.98	27	33
	White	15	31.27	1.22	0.32	30.59	31.94	30	34
	Total	82	30.22	1.26	0.14	29.94	30.50	27	34
Ear	Bosque del Apache	3	13.33	0.58	0.33	11.90	14.77	13	14
	Canadian	8	13.63	2.26	0.80	11.73	15.52	10	15
	Jemez	10	13.00	1.94	0.61	11.61	14.39	10	15
	Rio Grande	9	13.44	1.24	0.41	12.49	14.39	11	15
	Sacramento	29	12.72	2.27	0.42	11.86	13.59	9	16
	San Juan	7	14.57	0.79	0.30	13.84	15.30	13	15
	White	13	14.00	2.58	0.72	12.44	15.56	10	19
	Total	79	13.33	2.09	0.23	12.86	13.80	9	19

Mass	Bosque del Apache	1	14.00	.	.	.	.	14	14
	Canadian	8	21.81	4.43	1.57	18.11	25.52	17.5	28.5
	Jemez	10	21.52	4.39	1.39	18.38	24.66	15.5	28.5
	Rio Grande	3	22.27	4.34	2.51	11.48	33.05	18.7	27.1
	Sacramento	12	19.56	3.95	1.14	17.05	22.07	15	28
	San Juan	0	.	.	.	.	.	.	.
	White	3	24.97	2.89	1.67	17.78	32.15	21.7	27.2
	Total	37	21.08	4.32	0.71	19.64	22.52	14	28.5
CBL	Bosque del Apache	8	19.66	0.44	0.15	19.30	20.03	19.11	20.28
	Canadian	7	20.40	0.65	0.25	19.79	21.00	19.72	21.56
	Jemez	7	20.30	0.20	0.07	20.12	20.48	20.04	20.59
	Rio Grande	8	20.35	1.17	0.41	19.38	21.33	18.49	21.80
	Sacramento	29	20.55	0.42	0.08	20.39	20.71	19.90	21.48
	San Juan	4	20.59	0.87	0.43	19.21	21.96	19.65	21.69
	White	14	20.48	0.39	0.11	20.25	20.70	19.99	21.13
	Total	77	20.39	0.61	0.07	20.25	20.53	18.49	21.80
RL	Bosque del Apache	8	9.16	0.33	0.12	8.88	9.44	8.51	9.61
	Canadian	8	9.50	0.33	0.12	9.22	9.77	9.15	10.23
	Jemez	10	9.32	0.44	0.14	9.00	9.64	8.48	10.12
	Rio Grande	7	9.16	0.38	0.15	8.80	9.51	8.64	9.77
	Sacramento	29	9.42	0.31	0.06	9.31	9.54	8.92	10.19
	San Juan	6	9.58	0.33	0.14	9.23	9.93	9.04	10.05
	White	16	9.32	0.30	0.07	9.16	9.48	8.71	9.84
	Total	84	9.36	0.35	0.04	9.29	9.44	8.48	10.23
ZB	Bosque del Apache	8	11.03	0.31	0.11	10.77	11.29	10.61	11.56
	Canadian	5	11.57	0.19	0.09	11.33	11.81	11.33	11.85
	Jemez	9	11.31	0.49	0.16	10.93	11.69	10.68	11.95
	Rio Grande	6	11.28	0.65	0.27	10.59	11.96	10.44	12.33
	Sacramento	26	11.61	0.35	0.07	11.46	11.75	10.85	12.34
	San Juan	6	11.45	0.25	0.10	11.19	11.72	11.04	11.78
	White	10	11.53	0.38	0.12	11.25	11.80	10.84	12.03
	Total	70	11.45	0.42	0.05	11.35	11.55	10.44	12.34
DS	Bosque del Apache	8	8.53	0.13	0.04	8.42	8.63	8.30	8.70
	Canadian	7	8.48	0.19	0.07	8.31	8.65	8.23	8.71
	Jemez	8	8.35	0.28	0.10	8.11	8.58	7.98	8.82
	Rio Grande	4	8.46	0.09	0.04	8.33	8.60	8.35	8.55
	Sacramento	29	8.73	0.19	0.04	8.66	8.80	8.11	9.06
	San Juan	1	8.75	.	.	.	.	8.75	8.75
	White	11	8.68	0.14	0.04	8.59	8.77	8.45	8.92
	Total	68	8.61	0.23	0.03	8.56	8.67	7.98	9.06
IOC	Bosque del Apache	8	4.64	0.16	0.06	4.50	4.77	4.31	4.82
	Canadian	8	4.48	0.14	0.05	4.36	4.60	4.30	4.74
	Jemez	10	4.45	0.24	0.08	4.28	4.63	4.21	4.89
	Rio Grande	9	4.73	0.27	0.09	4.52	4.94	4.42	5.28
	Sacramento	29	4.41	0.13	0.02	4.36	4.46	4.20	4.66
	San Juan	7	4.61	0.19	0.07	4.44	4.79	4.39	4.95
	White	15	4.62	0.15	0.04	4.54	4.70	4.42	4.87
	Total	86	4.53	0.21	0.02	4.48	4.57	4.20	5.28

MTR	Bosque del Apache	8	3.77	0.14	0.05	3.66	3.89	3.53	3.96
	Canadian	8	3.78	0.23	0.08	3.59	3.97	3.38	4.04
	Jemez	10	3.75	0.12	0.04	3.66	3.84	3.58	3.94
	Rio Grande	11	3.80	0.22	0.07	3.65	3.95	3.27	4.05
	Sacramento	29	3.70	0.11	0.02	3.66	3.74	3.41	3.88
	San Juan	7	3.72	0.18	0.07	3.55	3.88	3.39	3.91
	White	15	3.81	0.10	0.02	3.75	3.86	3.64	3.98
	Total	88	3.75	0.15	0.02	3.72	3.78	3.27	4.05
PL	Bosque del Apache	8	8.45	0.21	0.07	8.27	8.62	8.20	8.79
	Canadian	8	8.87	0.18	0.06	8.72	9.02	8.63	9.24
	Jemez	10	8.35	0.30	0.09	8.14	8.56	7.80	8.79
	Rio Grande	11	8.50	0.41	0.12	8.23	8.77	7.86	9.22
	Sacramento	29	8.90	0.20	0.04	8.82	8.97	8.59	9.45
	San Juan	6	8.79	0.25	0.10	8.53	9.05	8.50	9.20
	White	15	8.80	0.19	0.05	8.70	8.91	8.54	9.20
	Total	87	8.72	0.32	0.03	8.65	8.78	7.80	9.45
PB	Bosque del Apache	8	3.40	0.13	0.05	3.29	3.51	3.15	3.56
	Canadian	8	3.43	0.20	0.07	3.26	3.59	3.28	3.87
	Jemez	10	3.35	0.14	0.04	3.25	3.45	3.14	3.55
	Rio Grande	10	3.32	0.16	0.05	3.21	3.43	3.13	3.60
	Sacramento	29	3.39	0.14	0.03	3.34	3.44	3.13	3.64
	San Juan	7	3.48	0.08	0.03	3.40	3.55	3.39	3.65
	White	14	3.32	0.13	0.03	3.25	3.40	3.15	3.57
	Total	86	3.38	0.15	0.02	3.35	3.41	3.13	3.87
IFL	Bosque del Apache	8	3.99	0.28	0.10	3.76	4.22	3.46	4.33
	Canadian	8	4.19	0.26	0.09	3.98	4.40	3.73	4.47
	Jemez	10	4.03	0.12	0.04	3.94	4.11	3.83	4.21
	Rio Grande	11	4.00	0.25	0.07	3.84	4.17	3.37	4.27
	Sacramento	29	4.14	0.20	0.04	4.07	4.22	3.66	4.43
	San Juan	7	3.81	0.39	0.15	3.45	4.16	3.16	4.17
	White	15	4.23	0.11	0.03	4.17	4.29	3.97	4.36
	Total	88	4.09	0.24	0.03	4.04	4.14	3.16	4.47
IFB	Bosque del Apache	8	1.99	0.10	0.04	1.91	2.07	1.82	2.13
	Canadian	8	2.14	0.09	0.03	2.07	2.21	2.05	2.29
	Jemez	10	2.12	0.17	0.05	2.00	2.25	1.93	2.49
	Rio Grande	11	2.02	0.18	0.05	1.90	2.14	1.80	2.41
	Sacramento	29	2.21	0.07	0.01	2.19	2.24	2.10	2.38
	San Juan	7	2.16	0.13	0.05	2.04	2.29	1.92	2.32
	White	13	2.08	0.09	0.03	2.03	2.14	1.92	2.28
	Total	86	2.13	0.14	0.01	2.10	2.16	1.80	2.49
IBW	Bosque del Apache	8	1.83	0.13	0.04	1.72	1.93	1.61	1.99
	Canadian	7	1.99	0.21	0.08	1.79	2.19	1.72	2.24
	Jemez	8	1.89	0.16	0.06	1.76	2.02	1.60	2.11
	Rio Grande	7	1.96	0.14	0.05	1.83	2.09	1.70	2.11
	Sacramento	27	1.82	0.17	0.03	1.75	1.88	1.49	2.26
	San Juan	2	2.09	0.11	0.08	1.13	3.04	2.01	2.16
	White	12	2.04	0.14	0.04	1.95	2.13	1.83	2.29
	Total	71	1.90	0.18	0.02	1.86	1.95	1.49	2.29

MB	Bosque del Apache	8	10.32	0.31	0.11	10.06	10.58	9.81	10.88
	Canadian	7	10.47	0.36	0.14	10.14	10.81	9.99	10.91
	Jemez	8	10.33	0.22	0.08	10.15	10.52	10.04	10.64
	Rio Grande	7	10.47	0.21	0.08	10.27	10.67	10.25	10.89
	Sacramento	28	10.51	0.19	0.04	10.43	10.58	10.08	10.98
	San Juan	2	10.89	0.18	0.13	9.30	12.47	10.76	11.01
	White	11	10.56	0.25	0.07	10.40	10.73	10.18	10.86
	Total	71	10.48	0.25	0.03	10.42	10.54	9.81	11.01
Tail/Body	Bosque del Apache	3	1.40	0.06	0.03	1.26	1.55	1.34	1.44
	Canadian	8	1.40	0.07	0.02	1.34	1.46	1.33	1.51
	Jemez	10	1.43	0.10	0.03	1.36	1.50	1.34	1.58
	Rio Grande	9	1.42	0.09	0.03	1.35	1.49	1.37	1.64
	Sacramento	28	1.49	0.12	0.02	1.45	1.54	1.25	1.73
	San Juan	7	1.53	0.08	0.03	1.46	1.60	1.46	1.64
	White	11	1.52	0.07	0.02	1.47	1.57	1.39	1.62
	Total	76	1.47	0.10	0.01	1.45	1.50	1.25	1.73
IFW/IFL	Bosque del Apache	8	0.50	0.03	0.01	0.47	0.53	0.45	0.53
	Canadian	8	0.51	0.03	0.01	0.48	0.54	0.47	0.58
	Jemez	10	0.52	0.02	0.01	0.50	0.53	0.49	0.55
	Rio Grande	11	0.49	0.04	0.01	0.46	0.52	0.45	0.59
	Sacramento	29	0.53	0.02	0.00	0.53	0.54	0.49	0.59
	San Juan	7	0.57	0.03	0.01	0.55	0.60	0.54	0.61
	White	13	0.49	0.02	0.01	0.48	0.50	0.46	0.53
	Total	86	0.52	0.04	0.00	0.51	0.53	0.45	0.61
RL/CBL	Bosque del Apache	8	0.47	0.01	0.00	0.45	0.48	0.44	0.48
	Canadian	7	0.46	0.01	0.00	0.45	0.48	0.45	0.48
	Jemez	8	0.47	0.02	0.01	0.45	0.48	0.45	0.50
	Rio Grande	4	0.47	0.01	0.01	0.45	0.48	0.45	0.48
	Sacramento	29	0.46	0.01	0.00	0.45	0.46	0.44	0.49
	San Juan	3	0.47	0.01	0.00	0.45	0.49	0.46	0.47
	White	14	0.45	0.01	0.00	0.45	0.46	0.42	0.47
	Total	73	0.46	0.01	0.00	0.46	0.46	0.42	0.50
Hindfoot/Body	Bosque del Apache	3	0.33	0.02	0.01	0.29	0.37	0.32	0.35
	Canadian	8	0.34	0.02	0.01	0.32	0.35	0.30	0.35
	Jemez	10	0.35	0.01	0.00	0.34	0.36	0.34	0.37
	Rio Grande	10	0.34	0.03	0.01	0.32	0.36	0.32	0.41
	Sacramento	30	0.34	0.02	0.00	0.34	0.35	0.31	0.39
	San Juan	6	0.34	0.02	0.01	0.32	0.37	0.31	0.38
	White	13	0.36	0.02	0.00	0.35	0.37	0.34	0.39
	Total	80	0.35	0.02	0.00	0.34	0.35	0.30	0.41
IFB/IBW	Bosque del Apache	8	1.09	0.09	0.03	1.02	1.17	0.98	1.24
	Canadian	7	1.09	0.12	0.05	0.98	1.20	0.96	1.31
	Jemez	8	1.13	0.12	0.04	1.03	1.24	0.91	1.29
	Rio Grande	7	1.03	0.18	0.07	0.87	1.19	0.92	1.42
	Sacramento	27	1.22	0.10	0.02	1.18	1.27	1.02	1.51
	San Juan	2	1.03	0.04	0.03	0.68	1.38	1.00	1.05
	White	10	1.03	0.07	0.02	0.98	1.09	0.95	1.14
	Total	69	1.13	0.13	0.02	1.10	1.16	0.91	1.51

APPENDIX 4

Appendix 4. Typical conditions of external and cranial measurements, incisive foramen, pelage, and dentition in *Zapus hudsonius luteus* and *Z. princeps princeps*.

	Z. h. luteus	***Z. p. princeps***
External and cranial measurements	small[1]	large[1]
Incisive foramen[2]	relatively narrow and less truncate posteriorly; more evenly wide along length	deer-hoof shaped; broad and truncate posteriorly; narrow anteriorly
Pelage[2]		
Prominent pale ear fringe	absent	present
Color of dorsum	rich dark brownish	very dark grayish or black
Color of side	rich yellowish brown	olive brown
[redacted]		

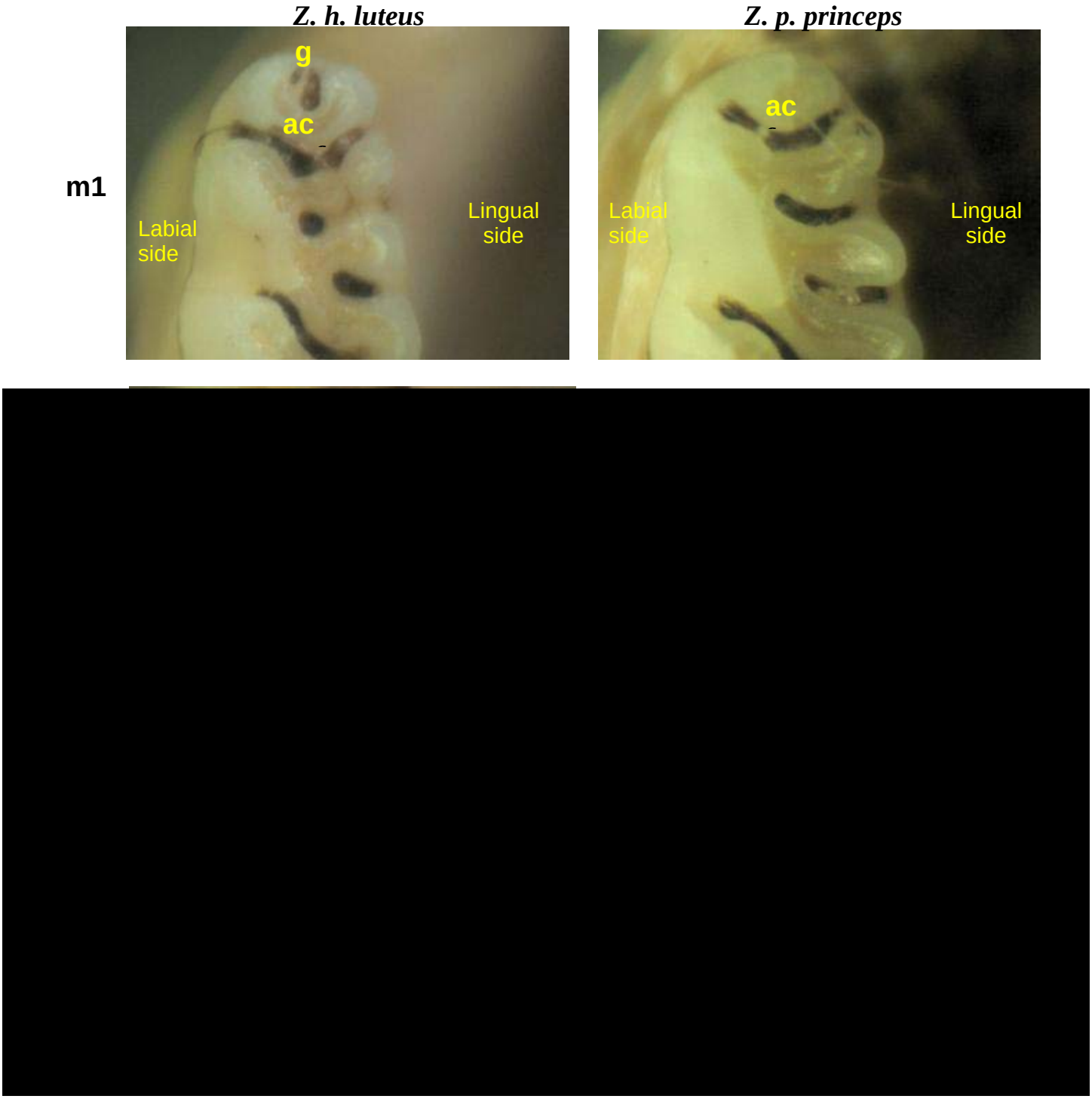
[1]See Appendix 2 for details.

[2]See Appendix 5 for photographs.

[3]The fold is more likely to be present in young animals

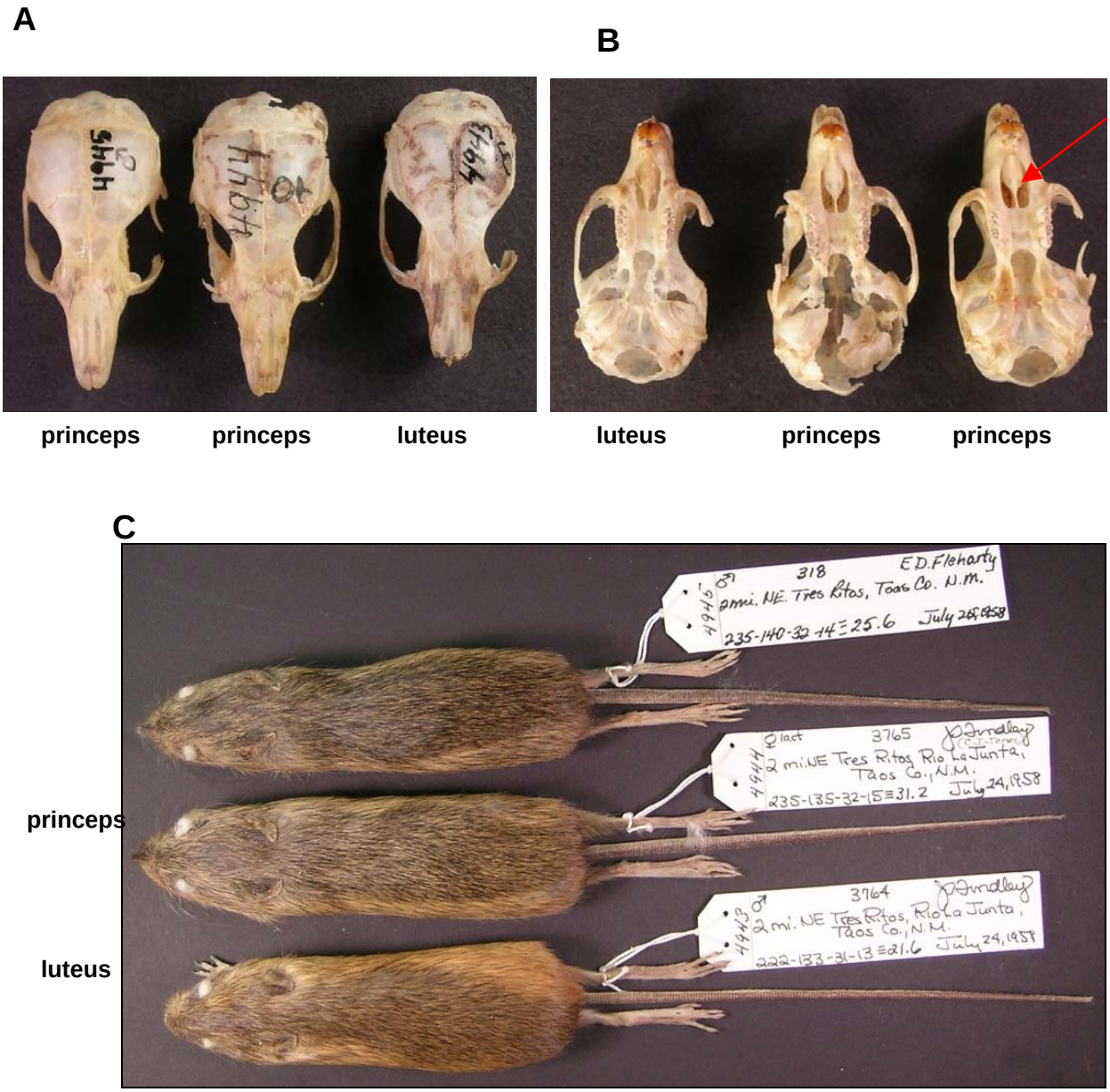
[redacted]

APPENDIX 5: PHOTOGRAPHS



Photograph 1. Typical conformations of the left first lower molar, m1 (top row); right first upper molar, M1 (middle row), and right second upper molar, M2 (lower row), for *Zapus hudsonius luteus* (left column; FT 604 from Coyote Creek, Mora Co.) and *Zapus princeps princeps* (right column; FT 435 from Taos Ski Valley, Taos Co.). Orientation of the tooth in each photo: anterior end of tooth is at the top; lingual side is to right; labial side is to left. Relevant features include: ac-anteroconid of m1; g-anteromedian groove of the anteroconid of m1, [redacted]

Photograph 2. Skins of two *Z. h. luteus* (bottom) from near Mora, Mora County (NMMNH 1228, 1229), and two *Z. p. princeps* (top) from Coyote Creek, Mora County (NMMNH 4040, 4042). Note the prominent white ear fringe, distinct blackish dorsal strip, and olive-yellow sides in *Z. p. princeps*, and lack of an ear fringe, overall orange coloration and indistinct dorsal strip in *Z. h. luteus*.



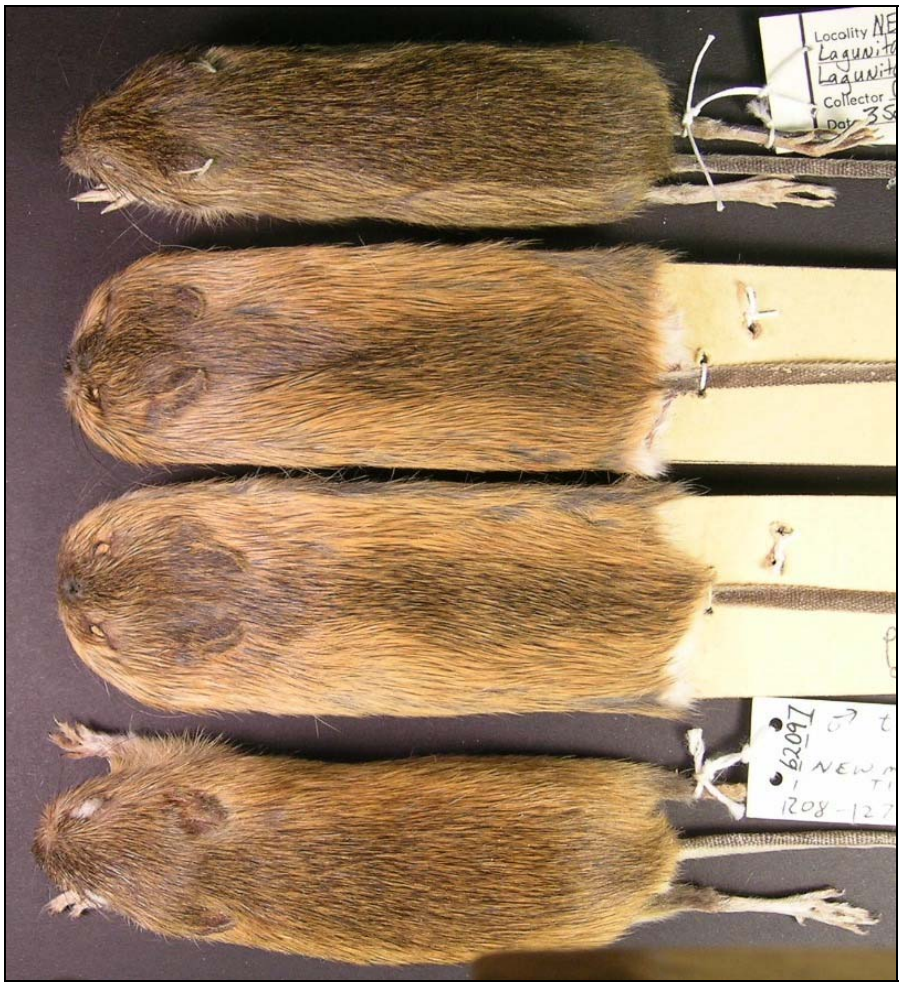
Photograph 3. Dorsal (A) and ventral (B) views skulls and skins (C) of one *Zapus hudsonius luteus* (MSB 4943) and two *Zapus princeps princeps* (MSB 4944, 4945) captured near Tres Ritos, Taos County, 24-25 July 1958. All three specimens are adults (average age class: 0.6 for MSB 4943; 0.5 for MSB 4944 and MSB 4945). In *Z. princeps* the skull is relatively larger (note that the nasals on the *Z. h. luteus* skull are broken) and "deer-hoof" shaped incisive foramen (red arrow). Although the pelage patterns are similar, note the more orangish and richly colored pelage of *Z. h. luteus*, and the slight whitish ear fringe and more blackish dorsal stripe on *Z. p. princeps*.

Photograph 4. Specimens of jumping mice (*Zapus*) from Colorado and New Mexico, including (from top to bottom):

Z. h. luteus (MSB 37323 Otero Co., NM; Sacramento Mountains)
Z. h. luteus (MSB 56982 Sandoval Co., NM; Jemez Mountains)
Z. h. luteus (MSB 10238 Archuleta Co., CO; near Arboles)
Z. h. luteus (MSB 4943 Taos Co., NM: Tres Ritos)
Z. p. princeps (MSB 36133 Taos Co.: near Tres Ritos)
Z. p. princeps (MSB 35653 Taos Co.: near Tres Ritos)

Photograph 5. Specimens of jumping mice (*Zapus*) from Colorado and northern New Mexico, including (from left to right):

Z. h. preblei (KU2045 Boulder Co.; Semper)
Z. p. princeps (KU 58984 Santa Fe Co.; Pacheco Canyon)
Z. p. princeps (KU 120040 Santa Fe Co.; 11 mi NE Santa Fe)
Z. h. luteus (KU 16038 Colorado: La Plata Co., Florida)
Z. h. luteus (KU 5835 Rio Arriba Co.; 4 mi N El Rito)
Z. h. luteus (KU 5834 Rio Arriba Co.; 4 mi N El Rito)
Z. h. luteus (KU 5833 Rio Arriba Co.; 4 mi N El Rito)
Z. h. luteus (KU 5832 Rio Arriba Co.; 4 mi N El Rito)



Photograph 6. Skins of two *Z. h. luteus* (flat skins in center) captured by Jason Malaney and Andrew Hope in 2007 from Florida, La Plata County, Colorado (MSB 154917, 155117). Comparative specimens are *Z. p. princeps* (MSB 60177) from San Juan Mountains, Taos County, NM (top), and *Z. h. luteus* (MSB 62097) from the Jemez Mountains, Sandoval County, NM (bottom).

Appendix F

Distribution of New Mexico's Reptiles and Amphibians:

Howard L. Snell and J. Tom Giermakowski

2008

Final report to the New Mexico Department of Game and Fish Share with Wildlife Program

[includes DVD with electronic data]

Distribution of New Mexico's Amphibians and Reptiles

Howard L Snell and J Tom Giermakowski

Summary

In our previous effort we used an algorithm based on information theory (MaxEnt) to calculate likelihoods of occurrence for all 124 species of amphibians and reptiles in New Mexico. Several recent studies supported the use of MaxEnt as an algorithm that ranks as the most accurate given presence data only. During preliminary field work in 2007, we have accumulated enough observations and specimens for several species of lizards to start the examination of MaxEnt-derived maps. Analyses of these maps revealed several issues that severely limited the utility of these potential distribution maps. First, the algorithm uses an approach which is understood easily only by people trained in information theory. Furthermore, variables in this algorithm undergo different kinds of transformations, rendering any ecological links to the original modeling variables unclear. Finally, many of our new field observations fell within areas of different likelihoods given by the MaxEnt algorithm. We have therefore chosen to pick a new approach that would take advantage of the spatial information for New Mexico that we already compiled, including known specimens of amphibians and reptiles, environmental data, and new observations. Using principal component analyses, we produced maps of potential habitat and likely distributions of New Mexican amphibians and reptiles. We purposefully used understandable statistical analyses so that the results could be easily explained in an ecological context. We further investigated the validity of these maps by using nearly 1400 new observations of 73 species throughout New Mexico, made during field work supported by this project. Using these field observations, we estimate the likelihood that suitable habitat is actually occupied by the species. We hope that the resulting maps will be accepted and used by a wide range of natural resource management stakeholders.

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Project objectives and goals

The objective of this project was to conduct a rigorous, sampling-based evaluation of the accuracy of a subset of previously developed maps of distribution of New Mexico's amphibians and reptiles. The maps were originally created using an algorithm that outputs a likelihood of occurrence. However, for several species the resulting maps contained substantial outliers from their known distribution. Furthermore, the maps were only representing probabilities which were difficult to interpret without a validation step. Thus, subsequent to evaluation, our goal became to develop a new set of maps that would portray species distribution more accurately and that could be explained in clear and concise ecological terms. We focused on species that are of interest to the state, that is, those treated by NMGDF as species of greatest conservation need. We chose to pick a new approach that would take advantage of the spatial information for New Mexico that we already compiled, including known specimens of amphibians and reptiles, environmental data, and new observations gathered during field surveys.

Description of field surveys

At the beginning of the project (spring and summer 2007), we concentrated on identifying areas where conspicuous species had a high likelihood of being observed, but in areas that were not already known for specimens. In other words, we avoided areas where museum specimens were collected. Museum specimens provide the only major source of information on New Mexico's herpetofauna, since no comprehensive atlas or survey exists for the state.
To fine tune our selection of sampling areas, we also examined published maps and localities of other known specimens. We also took into consideration land ownership and access factors such as travel time. As summer progressed, we adjusted our selections to sample areas that were previously lacking specimens or areas that lacked confirmed presence of conspicuous species. We formed our selections on a square kilometer grid for New Mexico, which matched our map data (see section on Environmental Data Sets).

Between April 2007 and May 2008, we were able to sample in 7051 square kilometers throughout the state. This is in contrast with 4924 square kilometers where specimens of amphibians and reptiles have been documented in the state until 2007. During the course of field work, we observed 1357 individual animals that belong to 73 species of amphibians and reptiles (geographic coordinates listed in Appendix 5). In the majority of cases, most observations were made in square kilometers where a particular species was not observed previously. Across all species, there were a total of 670 square kilometers where a species was not observed before (Appendix 1).

Our field surveys consisted of travelling to several localities in a general area and visually searching for amphibians and reptiles. In this manner, we were able to cover different areas within New Mexico in relatively short amounts of time. Several multi-day trips were required for areas that were further from Albuquerque. Visual encounter surveys are a common surveying technique that works well with open habitats and conspicuous animals (such as lizards or large snakes). Upon observation, we usually relied on hand capture or noosing for capture and examination. Since often snakes are found on roads, either dead or alive, we have

also recorded observations of any amphibians or reptiles on roads while driving. In areas where water presence suggested occupancy by amphibians, we used dip nets and waders to thoroughly sample near shore and around banks or canyon bases. For each observed animal we recorded its position with a GPS unit as well as noted species, and sex (if known). In addition, we recorded our own movements with the track feature of the GPS unit. This allowed us to quantify our effort and map areas visited where no observations were made.

Map redevelopment

Our previous efforts at estimating the distribution of potential habitat for the reptiles and amphibians of New Mexico were based upon MaxEnt (Phillips et al 2006), a well regarded computational method with its roots in "machine learning." As we progressed with validating the results of that analysis we were struck with the difficulty of actually understanding what the results were based upon. We also became aware of some fairly significant results that couldn't be reconciled with what we and others knew about the distributions of some of the species. We decided to attempt a completely new analysis from the ground up with two major goals:

1) the production of comprehensive maps of potential suitable habitat and likely distributions of New Mexican amphibians and reptiles, and
2) Basing those maps on understandable and "tweakable" statistical analyses so that the results would be easily explained and hopefully accepted by a wide range of natural resource management stakeholders.

To facilitate evaluation and comparison with the previous analysis, we decided to use the same suite of environmentally relevant variables averaged within each square kilometer of the state of New Mexico.

Description of variables

The environmental variables that we used in this study can be divided into four major categories: measures related to climate, topography, soils and vegetation (Table 1). Using geographic information system software, we transformed all data into a common spatial resolution of 0.0083333333 degrees, equivalent to approximately $1km^2$ on the ground. We maintained all data in a geographic projection (unprojected) for ease of data manipulation and consistency with GPS data. Descriptions of all variables, which covered the extent of the entire state of New Mexico, are shown in Appendix 2.

Climate

To represent climate, we used the WorldClim data sets (Hijmans et al 2005). This data archive includes 19 climatic variables: mean annual temperature, mean diurnal temperature range, isothermality (mean diurnal temperature range divided by annual temperature range), temperature seasonality, maximum temperature of the warmest month, minimum temperature of the coldest month, temperature annual range, annual mean precipitation, precipitation of the wettest month, precipitation of the driest month and precipitation seasonality (coefficient of variation), as well as mean temperature and precipitation of the wettest, driest, warmest and coldest quarters. Although these data form a large number of

variables, species of amphibians and reptiles are likely to respond strongly to at least some key variables relating to temperature and/or precipitation. Moreover, simple means are often not the best measures to represent climate variability. We therefore used all 19 climatic variables in the analysis (Appendix 2).

Table 1. Summary of data used in species distributions.

Data category	Data type	Data source	Brief description
Climate	Climatic variables	Worldclim http://www.worldclim.org/	Climatic variables describing variation in temperature and precipitation at a resolution of 30 arc-seconds (~1km)
Topography	Elevation	RGIS http://rgis.unm.edu/intro.cfm	Average elevation derived from 30m resolution digital elevation model (DEM)
	Aspect	derived	Aspect derived using above DEM
	Slope	derived	Slope derived using above DEM
Soils	Soil map units	Pennsylvania State University http://www.soilinfo.psu.edu/index.cgi?soil_data&conus	Soil map units from national and regional data sources at 1km resolution
	Geology	RGIS http://rgis.unm.edu/intro.cfm	183 different geological classes from the Geologic Map of New Mexico at a scale of 1:500000. Although each class represents a distinct formation, the variable is ordinal. Smaller numbers represent a younger formation.
Vegetation	Land cover	SWREGAP http://ftp.nr.usu.edu/swgap/	125 categories of modeled natural and semi-natural vegetation types based on 90m resolution data.
	Structure of habitat	University of Maryland http://glcf.umiacs.umd.edu/data/vcf/	Percent of ground that is bare, herbaceous, or tree-covered. Derived from MODIS VCF (vegetation continuous field) product at a 500m resolution.
	Distance from permanent water source	derived	Distance to nearest permanent water source calculated at 1km resolution.

Topography

Elevation and its derivatives are major factors that determine climate for an area. Variables summarizing topography were developed from a statewide digital elevation model distributed by New Mexico Resource Geographic Information System Program (RGIS). Since the original resolution of the elevation data is 30m, elevation for each $1km^2$ cell was calculated as the average elevation within that $1km^2$. Slope and aspect, as two additional variables, were calculated from this re-sampled grid of elevation.

Soils

Soils are likely to affect many ecological processes and variables such as types of vegetation and likelihood of water accumulation. They are also likely to influence many life history parameters of animals, such as their ability to burrow. To more accurately portray these factors we included two data sets. We used a soil map unit layer developed Miller and White (1998), which is based on a nationwide database created by generalizing soil-survey maps, including published and unpublished detailed soil surveys, county general soil maps, state general soil maps, state major land resource area maps, and, where no soil survey information was available, Landsat imagery. Since major soil characteristics, such as percentage of clay, permeability, texture, or rock content, are mapped as constant within each map unit, we used map units as a categorical variable in analyses. In addition, we included a map of 183 different geological classes for New Mexico, developed by NM Bureau of Geology and Mineral Resources. This data set complements the data on soils well, since it represents the distribution of different types of rock and surficial deposits, as well as locations of geologic structures such as faults and folds. These, in turn, are likely to relate to different types of environments available to different species, such as areas of volcanic rock. In addition, these data also represent relative ages of formations (Appendix 3).

Vegetation

Although traditionally land cover classes are not used in species distribution modeling, different types of vegetation often relate particularly well to vertebrates and are an excellent integrator of more fundamental physical variables such as soils, topography, and climate. To incorporate data on types of vegetation and structural properties of habitat we used three major data sources. We used a land cover map of New Mexico developed by the Southwest ReGAP project (USGS National Gap Analysis Program 2004). This data source relied on satellite imagery and topography to model natural and semi-natural vegetation types into 125 categories (Appendix 4). We treated this variable as categorical and did not arrange categories on an ordinal scale for analysis since the original algorithm (MaxEnt) we used did not require it. In addition to vegetation type, we used data from a satellite sensor that quantifies each square kilometer into percentage that is bare ground, herbaceous cover, and tree-covered. This provides an additional measure of habitat structure rather than composition. Finally, to address the dependence on water of many riparian species, we used a measure of distance from permanent water sources. Using the National Hydrological Database (USGS CITE), we created a grid where each cell is assigned a value that represents distance to nearest permanent water in meters.

Statistical Analyses

Our basic approach followed five steps (detailed descriptions of how the steps were carried out follow the list):

1) Characterize environmental variation across the state based on the mean values of the aforementioned variables for each km^2.
2) For each species, determine characteristics from step #1 that occur in the km^2, as well as the nature of variation in those characteristics, where the presence of the species is documented by a specimen in the Museum of Southwestern Biology's collection of amphibians and reptiles.
3) Using the species-specific summaries from step #2, estimate the likelihood that each km^2 of New Mexico consists of habitat suitable for each of the species. We call the results of this step "Estimates of Habitat Suitability."
4) Test the success of #3 with a large set of new observations and specimens collected during the field work supported by this project.
5) Use the results of step #4 to estimate potential distributions of the species, in other words, estimate the likelihood that suitable habitat is actually occupied by the species.

Characterization of Environmental Variation (Step 1) – We used principal components analysis to reduce the 29 environmental variables (Appendix 2) to five significant (eigenvalues greater than 1) principal components or factors. This method of analysis reduces data dimensionality by performing a covariance analysis between factors. As such, it strives to retain those characteristics of the data set that contribute most to its variance but reduces the number of variables. Each factor is then informative when compared with original data. By examining the "correlations" or "loadings" of the environmental variables with the five principal components (Table 2) we characterized the factors as follows:

Factor 1: Generally a temperature component negatively correlated with altitude. Thus km^2 with high values of Factor 1 (Factor 1 scores) have high temperatures, low elevation, and severe dry seasons as shown by negative correlations with driest month precipitation. Negative scores for Factor 1 would be cooler, higher, with less severe dry seasons.

Factor 2: This is clearly a precipitation factor with high positive loadings of a number of measures of rainfall, a negative loading for the amount of bare ground and a corresponding high loading for the amount of herbaceous cover, and, to a lesser degree, lower temperatures.

Factor 3: The strong negative correlations with thermal seasonality and temperature range coupled with a positive correlation with "Isothermality" demonstrate that Factor 3 measure thermal stability across the year. Areas with high scores for Factor 3 have little annual variation in temperature, and to a lesser degree might be slightly characterized as having a sloping topography.

Factor 4: Primarily appears to indicate strong variation in temperature within a day and perhaps less within a year.

Factor 5: is strongly influenced by geology and areas with high Factor 5 scores are composed of older major formations and southern exposures.

We then assigned each km^2 its score for each factor – providing five different estimates of environmental variation.

Table 2. Rotated Factor Loading Matrix

Environmental Variable*	Factor 1	Environmental Variable	Factor 2	Environmental Variable	Factor 3	Environmental Variable	Factor 4	Environmental Variable	Factor 5
bio08	0.9197	bio18	0.9033	bio04	-0.9037	bio02	0.9251	geology	0.6352
bio01	0.8957	bio16	0.8255	bio07	-0.8798	bio03	0.6850	dem_aspect	-0.6082
dem	-0.8941	bio13	0.8037	bio03	0.6589	bio15	0.3779	bio19	0.2570
bio10	0.8889	bio12	0.7432	bio15	0.4757	bio17	-0.3075	bio09	0.2341
bio11	0.8662	modis_b	-0.7247	bio16	0.4498	bio07	0.3044	dem_slope	-0.1966
bio05	0.8406	modis_h	0.7208	dem_slope	0.4351	bio14	-0.2939	permhydro	0.1844
bio06	0.8379	bio09	-0.6985	bio13	0.4311	soilmu	-0.2830	dem	-0.1835
bio17	-0.8363	bio05	-0.4560	bio06	0.3805	bio09	0.2349	bio12	0.1580
bio19	-0.8337	bio10	-0.3753	bio11	0.3300	bio12	-0.1756	bio11	0.1568
bio14	-0.8102	bio01	-0.3359	bio18	0.3183	modis_t	-0.1741	bio01	0.1518
bio15	0.6890	bio14	0.3093	bio09	0.3144	permhydro	0.1703	modis_t	0.1513
dem_slope	-0.5827	bio17	0.3077	bio19	0.2878	bio04	-0.1643	bio03	0.1469
bio12	-0.5116	bio06	-0.3039	permhydro	0.2713	bio06	-0.1304	bio17	0.1405
landcover	0.5113	bio08	-0.2830	modis_t	0.2552	geology	0.1188	bio06	0.1299
modis_t	-0.4980	bio11	-0.2827	bio12	0.2228	bio10	-0.0922	bio02	0.1282
modis_b	0.3937	bio04	-0.2734	landcover	-0.1975	dem	0.0845	bio15	-0.1257
dem_aspect	-0.3823	dem	0.2482	geology	0.1719	bio18	-0.0719	bio05	0.1256
soilmu	0.3559	permhydro	-0.2461	bio01	0.1514	bio08	-0.0710	bio10	0.1226
permhydro	0.3231	modis_t	0.2244	dem_aspect	0.1510	bio01	-0.0706	bio14	0.1179
bio13	-0.3214	bio07	-0.2182	soilmu	0.1412	dem_slope	-0.0698	bio08	0.1099
bio16	-0.2534	landcover	0.2114	bio05	-0.1178	bio13	0.0583	landcover	-0.0942
modis_h	-0.1598	dem_slope	0.1536	modis_b	-0.0893	bio16	0.0488	soilmu	0.0861
bio18	-0.1558	bio15	0.1490	modis_h	-0.0792	bio05	0.0420	modis_h	0.0811
geology	-0.1140	bio02	-0.1477	bio02	-0.0629	modis_h	0.0419	bio04	-0.0765
bio09	0.1055	soilmu	-0.1168	dem	0.0628	bio11	-0.0267	modis_b	-0.0570
bio03	0.0994	bio19	0.0924	bio14	-0.0554	dem_aspect	0.0175	bio16	0.0570
bio07	-0.0960	dem_aspect	-0.0710	bio17	0.0226	landcover	-0.0095	bio13	0.0321
bio04	0.0935	geology	0.0516	bio10	-0.0126	modis_b	0.0077	bio07	-0.0228
bio02	0.0361	bio03	0.0186	bio08	-0.0093	bio19	0.0066	bio18	0.0027

* Note that the variables are ranked by the absolute value of the loading for each Factor. Negative loadings equate negative correlations.

Species Specific Environmental Characteristics (Step 2) – Once each km^2 was characterized by the five factor scores, we summarized the factor scores for the km^2 occupied by each species. This provides an estimate of the habitat requirements for each species (Table 3).

Factor scores are computed such that their mean value is 0. Thus looking at Table 3, one can quickly see which factors help distinguish the habitat of particular species by identifying the factor with the values furthest from 0. In addition, the shape of the distribution of factor scores could also be helpful in identifying species requirements and we hope to develop that technique further. In this report we use the means. For example, square kilometers where *Plethodon neomexicanus* occur have a mean value of nearly -3 for Factor 1. This indicates cooler, higher areas with less severe dry seasons. The mean value for Factor 4 is nearly -2, indicating great diurnal variation in temperature. The combination of cooler, high altitude areas with great diurnal variation in temperature is hardly surprising for a mountain salamander.

Table 3. Mean and standard deviations for the environmental factor scores where species occur.

Species	Mean Factor 1	Mean Factor 2	Mean Factor 3	Mean Factor 4	Mean Factor 5	s.d. Factor 1	s.d. Factor 2	s.d. Factor 3	s.d. Factor 4	s.d. Factor 5
Acris crepitans	1.1061	0.1758	-0.4047	-0.5056	0.7199	0.1833	0.5484	0.6712	0.5432	0.5086
Ambystoma tigrinum	-0.8737	0.4758	-0.0264	-0.2132	0.3398	1.3827	0.7025	1.1400	1.4022	1.1149
Aneides hardi	-1.1969	1.8950	3.5407	-2.4845	-0.6461	0.3424	0.4321	0.3792	0.4308	0.4862
Apalone mutica	1.0024	1.0424	-1.0006	-0.7766	-0.5341	0.2792	0.2560	0.2180	0.5558	1.2188
Apalone spinifera	0.7420	0.1357	-0.8004	0.0619	0.5020	0.4142	0.6038	0.8970	0.9155	0.8200
Arizona elegans	0.5019	-0.0468	-0.8439	0.0523	0.2426	0.4710	0.7283	0.7370	0.9415	0.7435
Aspidoscelis burti	0.4946	-0.0757	1.8441	0.9667	0.3059	0.1286	0.1742	0.0970	0.1389	0.2680
Aspidoscelis dixoni	0.4272	-0.7288	1.0919	0.9831	0.6295	0.0196	0.0980	0.0771	0.0026	0.4726
Aspidoscelis exsanguis	0.1835	0.1848	0.5281	0.3773	0.1461	0.6281	0.5296	1.1926	1.0631	0.9228
Aspidoscelis flagellicauda	-0.1820	0.0192	1.0336	1.3353	0.9108	0.3793	0.4818	0.6549	0.4824	0.4142
Aspidoscelis gularis	1.0553	0.0154	0.0875	-0.9328	0.9439	0.1247	0.2779	0.4455	0.3904	0.3706
Aspidoscelis inornata	0.4843	-0.1713	-0.2657	-0.1984	0.1696	0.6066	0.6494	0.8343	0.9947	0.8156
Aspidoscelis neomexicana	0.2439	-0.4607	-1.0271	-0.0085	-0.0942	0.3767	0.5083	0.6653	1.0205	0.7566
Aspidoscelis sexlineata	0.8470	0.7172	-0.3340	-0.2509	0.4432	0.2538	0.4996	0.4448	0.4425	0.7710
Aspidoscelis sonorae	0.3347	0.0619	1.9595	0.7805	0.4481	0.3004	0.2328	0.3756	0.2355	0.4541
Aspidoscelis tesselata	0.5295	-0.1636	-0.1941	-0.2911	-0.2390	0.5380	0.7377	0.7926	0.9584	1.0907
Aspidoscelis tigris	0.5262	-0.3421	-0.2142	0.0885	0.4464	0.5340	0.7299	0.7568	1.0415	0.7612
Aspidoscelis uniparens	0.3062	-0.2104	0.4288	0.8797	0.4540	0.4108	0.5047	1.0999	0.7115	0.8641
Aspidoscelis velox	-0.6535	-0.3512	-1.0494	-0.2390	0.0699	0.7180	0.9672	0.8812	1.0847	1.6678
Bogertophis subocularis	0.7080	-0.7062	0.8321	-1.2196	-1.2405	0.1375	0.5282	0.6357	0.7913	0.7200
Bufo alvarius	0.4588	-0.0523	1.5629	0.8949	0.4139	0.1262	0.5918	0.5131	0.2220	0.4201
Bufo boreas	-3.8198	0.7543	0.4438	-2.1266	2.6576	0.2426	0.3863	0.4838	0.5051	0.6959
Bufo cognatus	0.5708	-0.1135	-0.5567	0.4214	0.6034	0.3135	0.6247	1.0917	0.8484	0.7954
Bufo debilis	0.7561	-0.1621	0.2049	-0.0115	0.3921	0.3383	0.8832	0.6915	0.9211	0.9159
Bufo microscaphus	-0.8187	0.5082	1.0109	2.1300	0.5203	0.4774	0.3867	0.5727	0.5538	0.4614
Bufo punctatus	0.2274	-0.1474	0.5708	-0.1413	-0.2101	0.6323	0.6386	1.1634	1.0687	1.0232
Bufo speciosus	0.9564	0.0758	0.1073	-0.7364	0.5453	0.2391	0.4385	0.6676	0.5656	0.6999
Bufo woodhousii	0.1689	0.1312	-0.9380	0.2058	0.3371	0.7585	0.7565	1.0211	1.0806	0.9389
Callisaurus draconoides	0.4419	-0.9123	0.9384	0.9950	0.5725	0.1161	0.3546	0.1473	0.1150	0.6774
Chelydra serpentina	0.7603	0.7991	-0.8053	-0.3059	-0.4489	0.4137	0.5394	0.6183	0.6740	1.0086
Chrysemys picta	0.5179	-0.0290	-1.2802	0.2453	0.4486	0.4248	0.5905	0.7287	0.9252	0.7477
Coleonyx brevis	0.8602	-0.2459	0.6694	-1.2424	-0.1291	0.3039	0.4003	0.7170	0.5952	1.0579
Coleonyx variegatus	0.0694	-0.3141	0.6142	1.5908	1.4136	0.3902	0.3217	0.7075	0.2488	0.8530
Coluber constrictor	0.3777	0.7606	-1.0510	0.3690	-0.2275	0.4919	0.8516	0.8775	0.8760	1.0975
Cophosaurus texanus	0.3897	-0.3253	0.2822	0.2735	0.0751	0.4021	0.5928	0.7899	1.0959	1.1049
Crotalus atrox	0.3989	-0.1571	0.0251	0.1997	0.0386	0.5866	0.6533	1.0385	1.0317	0.8917
Crotalus lepidus	-0.1011	0.1515	1.6457	0.1107	-0.3185	0.6073	0.6727	0.9335	0.9911	0.9092
Crotalus molossus	-0.0168	-0.0557	1.0761	0.1126	-0.3903	0.6820	0.5727	1.0082	1.3632	0.9694
Crotalus scutulatus	0.6615	-0.4875	0.7277	1.0843	1.0448	0.1700	0.2778	0.2014	0.0918	0.5856
Crotalus viridis	0.0895	-0.2199	-0.4346	0.2666	0.1248	0.7401	0.7847	0.8943	1.0158	0.8978
Crotalus willardi	-0.4788	0.9981	3.1102	-0.1269	0.4876	0.1775	0.4856	0.2820	0.3112	0.4434
Crotaphytus collaris	0.0602	-0.1230	-0.1929	-0.1562	-0.1145	0.8107	0.8943	1.0591	1.1045	1.2608
Diadophis punctatus	0.2822	0.2000	0.3455	0.0461	-0.5559	0.4375	0.8020	1.0887	1.0638	0.9211

Species	Mean Factor 1	Mean Factor 2	Mean Factor 3	Mean Factor 4	Mean Factor 5	s.d. Factor 1	s.d. Factor 2	s.d. Factor 3	s.d. Factor 4	s.d. Factor 5
Elaphe emoryi	0.5430	0.2140	-0.3041	-0.7276	-0.1099	0.8177	0.7089	0.8682	0.7409	0.7985
Eleutherodactylus augusti	0.7609	0.0832	-0.3498	-0.0677	0.3034	0.1939	0.3335	0.9018	0.5760	0.7293
Elgaria kingii	-0.3711	0.3544	1.8018	0.8642	0.3072	0.7788	0.5528	0.9858	0.6886	0.7163
Eumeces callicephalus	0.5174	-0.1240	1.8344	0.9943	0.3201	0.0948	0.1166	0.0900	0.1279	0.3491
Eumeces multivirgatus	-0.4935	0.4036	0.2225	-0.9424	0.2179	1.2614	0.6342	1.0490	1.1569	0.8989
Eumeces obsoletus	0.3174	0.2670	-0.3297	-0.4217	-0.0880	0.8003	0.7586	1.1928	0.9752	1.0906
Ficimia cana	0.2292	0.3116	1.1965	1.2851	1.0315	0.3279	0.1853	0.8012	0.8030	0.1938
Gambelia wislizenii	0.3435	-0.6467	-0.6384	0.0399	-0.0800	0.3452	0.4442	0.7483	1.0607	0.6219
Gastrophryne olivacea	0.9843	-0.1810	0.5728	-0.6042	-0.1270	0.1590	0.0912	0.8748	1.7396	0.8585
Gyalopion canum	0.4677	-0.3135	0.3292	0.0702	0.0407	0.4423	0.4857	1.1779	1.1471	0.8997
Heloderma suspectum	0.4351	-0.3810	0.3107	1.6910	1.0871	0.4490	0.3825	0.4386	0.3642	0.2246
Hemidactylus turcicus	0.9738	-0.1417	0.2456	-0.4791	-0.8713	0.3026	0.0109	0.4036	0.0653	0.4099
Heterodon nasicus	0.4869	-0.0218	-0.4071	0.2992	0.4473	0.3877	0.7396	1.0133	0.9331	0.7538
Holbrookia maculata	0.3828	0.0452	-0.2208	-0.0024	0.1909	0.5194	0.8277	1.0570	0.8559	0.8691
Hyla arenicolor	-0.5087	0.3659	1.0704	0.6688	0.2501	0.7180	0.5108	1.0829	1.1629	0.8301
Hyla wrightorum	-1.4369	1.2650	1.6458	1.3482	0.6173	0.5397	0.1686	0.8552	0.8359	0.6396
Hypsiglena torquata	0.4607	-0.0817	-0.2244	-0.1850	0.0733	0.6026	0.8343	0.8884	1.0691	1.0028
Kinosternon flavescens	0.8797	0.4296	-0.3129	-0.3748	0.4084	0.4586	0.7697	0.6646	0.8479	0.8957
Kinosternon sonoriense	-0.0828	0.2185	1.9217	0.8671	0.5573	0.4023	0.3531	0.7373	0.7572	0.3868
Lampropeltis alterna	0.9296	0.0228	1.5358	-2.2506	-1.2114	.	.	.	.	.
Lampropeltis getula	0.6061	-0.1115	-0.4041	0.6391	0.7411	0.3884	0.7143	1.0059	0.9347	0.7347
Lampropeltis pyromelana	-0.6358	0.6156	2.0621	0.9431	0.3021	0.4168	0.6110	0.7541	0.7421	0.6111
Lampropeltis triangulum	-0.0324	0.1687	-0.1691	-0.3553	0.3962	0.9312	0.5312	0.7056	0.8392	0.7703
Leptotyphlops dulcis	0.6530	0.2286	-0.0617	0.0197	-0.1814	0.4606	0.6659	1.1364	0.9694	0.9959
Leptotyphlops humilis	0.5653	-0.5091	0.3027	0.3093	0.3163	0.4898	0.4719	0.5563	0.9051	0.9540
Masticophis bilineatus	0.2002	0.1421	1.9240	0.6239	0.7596	0.3790	0.4801	0.6953	0.3983	0.6291
Masticophis flagellum	0.4757	-0.0348	-0.6218	-0.0563	0.2074	0.4710	0.6674	0.7968	0.9469	0.8431
Masticophis taeniatus	-0.0415	-0.1364	0.3657	0.2184	-0.0892	0.6443	0.6360	0.9588	1.3072	0.9145
Micruroides euryxanthus	-0.0845	-0.3306	0.9167	1.4983	0.7176	0.4089	0.2836	0.3639	0.3682	0.5038
Nerodia erythrogaster	1.2545	0.1542	-0.2168	-0.7322	0.7122	0.1964	0.4254	0.2799	0.1285	0.4596
Opheodrys vernalis	-1.3555	1.0472	0.1919	-0.4834	-0.3055	0.6203	0.6085	0.6864	0.8749	1.1117
Phrynosoma cornutum	0.6765	0.0396	-0.0429	0.1128	0.2531	0.3905	0.8189	0.8668	0.9570	0.9463
Phrynosoma hernandesi	-0.6506	0.2300	0.2788	-0.2300	0.0822	0.9649	0.8890	1.5642	1.4103	1.1151
Phrynosoma modestum	0.4030	-0.2508	-0.3475	0.0078	-0.0108	0.5785	0.6970	0.9190	1.0567	0.9242
Phrynosoma solare	0.6665	0.0005	1.7743	1.0874	0.2907	.	.	.	.	.
Pituophis catenifer	-0.0446	-0.1189	-0.4267	0.2180	0.1650	0.7696	0.7866	1.0776	1.1819	1.1410
Plethodon neomexicanus	-2.8735	0.4666	1.1894	-1.9273	1.3135	0.5315	0.3703	0.4403	0.4539	0.6896
Pseudacris triseriata	-1.0441	0.6013	-0.5692	-0.2345	0.5876	1.5099	0.7321	1.2027	1.2182	1.0800
Pseudemys gorzugi	1.1546	0.0060	0.0334	-0.8189	0.5168	0.3206	0.5167	0.4922	0.7256	0.4497
Rana berlandieri	0.8554	-0.2250	0.8974	-1.2593	-0.4272	0.3178	0.3583	0.9179	0.5208	0.9793
Rana blairi	0.5586	0.7897	-0.4811	0.0282	-0.3113	0.6372	0.5617	0.9585	0.8477	1.0324
Rana catesbeiana	0.1918	0.1070	-0.4290	0.7477	0.4071	0.5765	0.5057	1.3074	1.1660	0.7012
Rana chiricahuensis	-0.5304	0.3961	1.1623	1.7123	0.5501	0.6841	0.3995	0.5894	0.7831	0.8325
Rana pipiens	-0.3058	0.2487	-0.5650	0.3150	0.2338	1.0196	0.7506	1.2023	1.2094	0.8701
Rana yavapaiensis	-0.1849	0.2071	1.4960	1.0670	0.7866	0.2893	0.3618	0.6590	0.5829	0.0903
Rhinocheilus lecontei	0.5728	-0.1068	-0.3959	-0.1121	0.2629	0.4126	0.6407	0.7686	1.0046	0.8781

Species	Mean Factor 1	Mean Factor 2	Mean Factor 3	Mean Factor 4	Mean Factor 5	s.d. Factor 1	s.d. Factor 2	s.d. Factor 3	s.d. Factor 4	s.d. Factor 5
Salvadora deserticola	0.5026	-0.4646	0.4856	0.7542	0.3075	0.3533	0.3823	0.7070	0.8349	0.9945
Salvadora grahamiae	-0.0347	-0.0795	0.5757	0.0344	-0.3116	0.6844	0.5520	1.0802	1.2628	1.0292
Scaphiopus couchii	0.6442	-0.1218	-0.3613	0.2076	0.3197	0.4352	0.7712	0.9035	0.9347	0.8454
Sceloporus arenicolus	0.8113	0.5264	-0.1268	-0.2807	0.5904	0.1150	0.3110	0.2646	0.4561	0.4338
Sceloporus clarkii	-0.1094	0.1170	1.2968	1.2569	0.7460	0.5623	0.4360	0.7163	0.5690	0.5099
Sceloporus graciosus	-0.6104	-1.1700	-1.1864	-0.3390	-0.3792	0.7179	1.0284	0.6325	0.5513	0.8884
Sceloporus jarrovii	-0.0646	0.3696	2.3545	0.4638	0.6468	0.2962	0.4952	0.4950	0.4144	0.6142
Sceloporus magister	0.2611	-0.5436	-0.5961	0.7656	0.0807	0.5265	0.5601	0.8093	0.8056	0.8751
Sceloporus poinsettii	-0.2500	0.4078	1.3117	0.6194	-0.2893	0.7191	0.5837	0.7673	1.2569	0.9221
Sceloporus scalaris	0.4678	0.4427	1.6309	0.7179	1.3198	0.1847	0.2961	0.2948	0.1983	0.6264
Sceloporus undulatus	-0.1693	0.1308	-0.1769	-0.1857	-0.0189	0.9293	0.9099	1.0637	1.0616	1.1055
Sceloporus virgatus	-0.1739	0.5997	2.6174	0.2225	0.5184	0.4241	0.6627	0.7780	0.5246	0.4986
Senticolis triaspis	0.5997	-0.0870	1.7821	1.0567	0.3445	0.0681	0.0763	0.1001	0.0461	0.3929
Sistrurus catenatus	0.4459	-0.2944	-0.5475	-0.0160	0.2341	0.4345	0.7807	0.5521	0.7779	0.6064
Sonora semiannulata	0.7904	0.1324	-0.1727	-0.4883	-0.3166	0.3745	0.8411	0.9581	0.8813	1.1384
Spea bombifrons	0.3649	0.0891	-0.9284	-0.1079	0.1401	0.6191	1.0831	0.7246	0.8168	0.8652
Spea multiplicata	0.0361	-0.2185	-0.2195	0.3333	0.0174	0.6719	0.8126	1.0486	0.9797	1.0238
Tantilla hobartsmithi	0.8237	-0.1556	0.9904	-0.5491	-0.2197	0.3211	0.2425	0.8231	1.1274	0.7197
Tantilla nigriceps	0.5280	0.0310	-0.7340	-0.1267	0.2850	0.4884	0.7916	0.7598	1.0596	0.9280
Tantilla yaquia	0.5269	-0.2311	1.6351	0.9872	0.2708	0.0629	0.3211	0.3789	0.1515	0.3693
Terrapene ornata	0.6978	0.4024	-0.4663	-0.0518	0.3042	0.4372	0.8635	0.8455	0.8379	0.9331
Thamnophis cyrtopsis	-0.0972	0.0412	0.5236	0.6468	0.1528	0.6034	0.5747	1.1957	1.1665	1.2527
Thamnophis elegans	-1.1529	0.4961	0.4149	-0.3117	0.1522	1.1038	0.7720	1.3385	1.6082	1.0921
Thamnophis marcianus	0.8071	0.2159	-0.1896	-0.0568	0.3251	0.3154	0.6875	0.9741	1.0426	0.9714
Thamnophis proximus	0.8815	0.7743	-0.6565	-0.3664	0.7120	0.5955	0.5884	0.7520	0.9429	1.2671
Thamnophis radix	0.5294	1.7628	-1.1480	0.4877	-0.2268	0.3194	0.3761	0.3263	0.7673	0.6616
Thamnophis rufipunctatus	-0.7361	0.3490	1.0553	2.0668	0.5789	0.5046	0.3623	0.4976	0.6008	0.3041
Thamnophis sirtalis	0.4725	-0.0243	-1.6933	0.0922	0.7219	0.3452	0.4906	0.5357	0.8972	0.6224
Trachemys gaigeae	0.6857	-0.4774	-0.2479	0.2556	0.3943	0.2741	0.4529	0.4939	0.8562	1.0411
Trimorphodon biscutatus	0.3444	-0.0501	1.0743	0.7212	0.2031	0.3743	0.5487	0.7257	0.4834	1.2614
Tropidoclonion lineatum	0.1217	0.7649	-0.4503	-0.4612	-0.2742	0.7078	0.6707	0.7605	0.8305	1.1718
Urosaurus ornatus	-0.1998	-0.0118	0.9359	0.7154	0.2178	0.6440	0.5822	1.0411	1.1386	0.9589
Uta stansburiana	0.4000	-0.3481	-0.5711	-0.1155	0.0823	0.5879	0.7959	0.7324	0.8917	0.8309

Habitat Suitability (Step 3) - To establish the characteristics that a species might require (step 2 above) we looked for mean factor scores that were farther from 0. To establish whether or not a particular km^2 might be suitable for a particular species, we measured how similar the mean factor score for the km^2 was to the mean of that species. In order to measure the "distance" a km mean was from the species habitat requirement we used Z scores so that the resulting measures might be conceptually related to probabilities that the habitat was suitable and could be compared across species. To express probabilities from these Z scores, we looked up a value of each Z score in a normal distribution. We established five levels of habitat suitability from these analyses: Completely Suitable, Likely Suitable, Potentially Suitable, Rarely Suitable, and Completely Unsuitable.

Testing the Habitat Suitability (Step 4): Our field work produced over 1,300 observations and specimens from 802 km^2. Six hundred and seventy of those km^2 represent areas where a particular species had not been previously recorded and thus could provide tests for the habitat analysis. Our initial investigations with previously developed maps based on MaxEnt algorithm (see Interim report for this project) suggested great variability of predicted habitat suitability for different species. In other words, probabilities calculated with MaxEnt for square kilometers where a species was observed during field work were ranging from nearly 0% to more than 90%. We compared the probabilities developed with the two methodologies (our new PCA-based method and MaxEnt algorithm) for species where observations during field work occurred in more than 10 new 1-km^2 cells (n=21). We used paired t-tests to compare means of calculated probabilities for each species between the two methods (Table 4).

Table 4. Results of paired t-test comparisons between means of PCA-based and MaxEnt-based calculated probabilities of habitat suitability, calculated for each species from 1-km^2 cells with new observations.

Species	**Number of km^2 cells**	**Mean of PCA-based probability (%)**	**Mean of MaxEnt-based probability (%)**	**P-value of paired t-test**
Arizona elegans	17	41.06	34.44	0.408
Aspidoscelis exsanguis	11	52.13	32.44	0.021
Cophosaurus texanus	47	57.77	46.98	0.018
Crotalus atrox	45	56.29	38.81	0.001
Crotalus scutulatus	12	54.85	78.73	0.001
Crotalus viridis	48	54.85	47.85	0.131
Crotaphytus collaris	57	61.16	29.74	<0.0001
Gambelia wislizenii	14	50.36	20.94	<0.0001
Masticophis flagellum	21	49.2	42.38	0.218
Masticophis taeniatus	10	60.78	24.56	0.013
Phrynosoma cornutum	28	49.64	28.33	<0.0001
Phrynosoma modestum	16	59.33	38.61	0.008
Pituophis catenifer	47	59.9	31.55	<0.0001
Rhinocheilus lecontei	19	40.33	32.27	0.245
Sceloporus magister	22	68.82	20.07	<0.0001
Sceloporus poinsetti	47	63.1	25.61	<0.0001
Sceloporus undulatus	68	54.86	35.05	<0.0001
Sistrurus catenatus	13	43.08	38.7	0.504
Terrapene ornata	17	40.95	49.48	0.307
Urosaurus ornatus	42	54.93	23.03	<0.0001
Uta stansburiana	40	49.76	33.07	<0.0001

For a majority of species (66%), the means of PCA-based probabilities were significantly higher than the means of MaxEnt-based probabilities. Only in one instance (*Crotalus scutulatus*), the mean of MaxEnt-based probabilities was higher for square kilometer cells with new observations. For 28.6% of species analyzed (6 of 21), there were no statistically significant differences between the means of probabilities calculated with the two methodologies. Nevertheless, for new observations of 19 out of 21 species (90.5%) means of PCA-based probabilities were higher than those for based on MaxEnt. These results suggest that the PCA-based methodology is better than MaxEnt at calculating habitat suitability for a species. Put differently, new observations are expected to be found in highly suitable habitats. We found that for a majority of species mean values of habitat suitability were consistently higher when using the PCA-based methodology.

Estimation of Potential Distributions (Step 5) – One criticism of our previous analysis was that some of the identified habitat was very distant from reasonable expectations of occurrence (specifically the situation with *Callisaurus draconoides*). Here we combine the identification of suitable habitat with empirically determined distances from known specimen localities to estimate what areas of suitable habitat are likely to be occupied – thus providing statistically valid estimates of potential distributions. For each 1 km^2 in New Mexico we measured the distance to the nearest 1 km^2 occupied by a species. Thus each 1 km^2 has a different measure for each of the 120+ species. In order to establish what distances are appropriate we analyzed distances among known localities for the species along with our new observations from Step 4. For instances where new observations of species were available, we calculated the distance as 100% or 150% of a maximum distance between a specimen and a new observation. In instances where new observations did not exist for species, we calculated the distance as 100% or 150% of a maximum distance between specimens. We used either 100% or 150% based on species biology (its potential for dispersal) and its known distribution.

Revised maps of distribution

Revised maps of distribution for all 47 reptile and amphibian Species of Greatest Conservation Need, as identified within the Comprehensive Wildlife Conservation Strategy for New Mexico, are included electronically on the enclosed DVD. They are formatted as LZW-compressed TIFF files, a common image file format, easily printed from many image handling applications. In addition, data used to produce these maps, most importantly, calculated habitat suitability for each species, is included as ESRI shapefiles. These data can be easily imported into most Geographic Information Systems for further analyses and manipulation.

For all species, each square kilometer within the state of New Mexico is assigned a habitat suitability value that ranges between 0 and 100. These measures of habitat suitability should not be confused with probabilities of species occurrence. High values of habitat suitability indicate that a particular 1km^2 has environmental characteristics that are very close to that 1km^2 where the species is known to occur. In order to move toward probability of species occurrence, we needed to combine this habitat suitability with potential range. To do this, we

looked at outliers of specimens or observations, as explained above, to derive lines beyond which the species is unlikely to be found. We suggest that within those lines, habitat suitability can approach likelihood of occurrence. On the other hand, while areas outside the lines might be highly suitable, they are unlikely to relate to likelihood of occurrence.

In Appendix 6 we include several examples of revised maps of distribution. These can be printed on standard letter paper in portrait format.

Potential uses of maps for conservation planning and monitoring

Maps of species distributions have one of their greatest utilities in planning for conservation and monitoring; however, the maps produced in this project are probabilistic and therefore should be treated as such. Although the maps were developed by using best available data to date, several issues limit their utility. First, the scale of one square kilometer is a compromise between effective use of data and its use in land management. Finer scales require processing of air photographs and detailed knowledge of species populations and movement patterns, whereas coarser scales would not be useful for more practical reasons. For example, land ownership changes too frequently at scales much coarser than 100 km^2. In other words, maps of habitat suitability for a 10km x 10km piece of land would not be useful since it is likely that many land owners share those 100 km^2.

We anticipate that these maps will be useful and that they will be accepted and used by a wide range of people that are involved in natural resource management. The most effective use of maps produced in this project is for comparison of habitat suitability for different species between different areas. Those areas could vary in land ownership and/or status. This can help identify conservation opportunities for certain areas within the state. They are also useful in planning monitoring effort because some areas will have highly suitable habitats for many different species of interest. We do not recommend the use of these maps as a substitute for thorough surveys of species presence. While the maps can guide monitoring efforts, they should be treated as probabilistic expressions of habitat suitability, and within certain limits, as approaching likelihood of occurrence.

Appendices

Appendix 1. Field observations during 2007-2008 summarized by square kilometers

Species observed	Number of sq.km cells	Number of new sq.km cells
Ambystoma tigrinum	7	6
Apalone spinifera	1	1
Arizona elegans	17	17
Aspidoscelis exsanguis	11	11
Aspidoscelis inornata	4	4
Aspidoscelis neomexicana	6	4
Aspidoscelis tesselata	8	7
Aspidoscelis tigris	27	27
Aspidoscelis uniparens	1	1
Aspidoscelis velox	1	1
Bogertophis subocularis	2	2
Bufo alvarius	4	4
Bufo cognatus	7	6
Bufo debilis	1	1
Bufo microscaphus	1	1
Bufo punctatus	2	2
Bufo woodhousii	5	4
Chelydra serpentina	4	4
Coleonyx brevis	1	1
Coleonyx variegatus	1	1
Coluber constrictor	2	2
Cophosaurus texanus	48	47
Crotalus atrox	46	45
Crotalus lepidus	5	5
Crotalus molossus	6	6
Crotalus scutulatus	12	12
Crotalus viridis	48	48
Crotaphytus collaris	57	57
Diadophis punctatus	2	2
Elgaria kingii	5	5
Eumeces multivirgatus	2	2
Eumeces obsoletus	3	3
Gambelia wislizenii	14	14
Gyalopion canum	1	1
Heterodon nasicus	3	2
Holbrookia maculata	8	8
Hyla arenicolor	2	2
Hypsiglena torquata	5	5
Kinosternon flavescens	1	1
Lampropeltis getula	4	3
Leptotyphlops dulcis	1	1
Masticophis flagellum	22	21
Masticophis taeniatus	11	10
Phrynosoma cornutum	28	28
Phrynosoma hernandesi	8	7
Phrynosoma modestum	16	16
Pituophis catenifer	47	47

Plethodon neomexicanus	1	1
Pseudacris triseriata	2	2
Rana blairi	2	2
Rana pipiens	1	1
Rhinocheilus lecontei	19	19
Salvadora deserticola	1	1
Salvadora grahamiae	3	3
Scaphiopus couchi	2	2
Sceloporus clarkii	2	2
Sceloporus magister	22	22
Sceloporus poinsetti	47	47
Sceloporus undulatus	68	58
Sistrurus catenatus	13	13
Spea bombifrons	1	1
Spea multiplicata	2	2
Tantilla nigriceps	4	4
Terrapene ornata	18	17
Thamnophis cyrtopsis	3	2
Thamnophis elegans	10	8
Thamnophis marcianus	2	2
Thamnophis sirtalis	1	1
Trimorphodon biscutatus	1	1
Tropidoclonion lineatum	3	3
Urosaurus ornatus	44	42
Uta stansburiana	61	40

Appendix 2. Detailed listing of variables used in modeling.

Data type	Variable name	Units	Description
Climatic variables	bio01	Degrees Celsius * 100	Annual Mean Temperature
	bio02	Degrees Celsius * 100	Mean Diurnal Range (Mean of monthly (max temp - min temp))
	bio03	Dimensionless	Isothermality (bio02/bio07) (* 100)
	bio04	Dimensionless	Temperature Seasonality (standard deviation *100)
	bio05	Degrees Celsius * 100	Max Temperature of Warmest Month
	bio06	Degrees Celsius * 100	Min Temperature of Coldest Month
	bio07	Degrees Celsius * 100	Temperature Annual Range (bio05-bio06)
	bio08	Degrees Celsius * 100	Mean Temperature of Wettest Quarter
	bio09	Degrees Celsius * 100	Mean Temperature of Driest Quarter
	bio10	Degrees Celsius * 100	Mean Temperature of Warmest Quarter
	bio11	Degrees Celsius * 100	Mean Temperature of Coldest Quarter
	bio12	Millimeters	Annual Precipitation
	bio13	Millimeters	Precipitation of Wettest Month
	bio14	Millimeters	Precipitation of Driest Month
	bio15	Dimensionless	Precipitation Seasonality (Coefficient of Variation)
	bio16	Millimeters	Precipitation of Wettest Quarter
	bio17	Millimeters	Precipitation of Driest Quarter
	bio18	Millimeters	Precipitation of Warmest Quarter
	bio19	Millimeters	Precipitation of Coldest Quarter
Elevation	dem	Meters	average of 30m DEM from RGIS
Aspect	dem_aspect	Degrees (range 0-359, where 90 is East)	aspect derived using elevation DEM
Slope	dem_slope	Degress (range 0-90, where 90 is vertical)	slope derived using elevation DEM
Soil map units	soilmu	Categorical	USGS map unit numbers, which relate to constant soil characteristics, such as soil texture, permeability, water capacity or clay content
Geology	geology	Categorical	183 classes, ordinal when related to formation age (smaller number represents younger formation, see Table 3)

Landcover	landcover	Categorical	90 classes of land cover, including vegetation types related to ecological zones (see Table 4)
Structure of habitat	modis_b	Percentage	Percentage of bare ground
	modis_h	Percentage	Percentage of herbaceous cover
	modis_t	Percentage	Percentage of tree cover
Distance from permanent water source	permhydro	Meters	Distance to permanent water source

Appendix 3. Classes used in the geological map of New Mexico. Note that order of classes represents a chronological order from youngest to oldest for major formations.

Class	Name	Definition
1	&	Pennsylvanian rocks, undivided; in Sangre de Cristo Mountains may include
2	&lc	Lead Camp Formation; San Andres and Organ Mountains
3	&m	Madera Formation (Limestone
4	&me	Madera Limestone, exotic blocks; present only in the Chloride area of Sierra County
5	&ps	Panther Seep Formation; Organ, Franklin, and San Andres Mountains
6	&s	Sandia Formation; predominately clastic unit (commonly arkosic) with minor black shales
7	@	Triassic rocks, undivided; continental red beds
8	@b	Bull Canyon Formation; Norian
9	@c	Chinle Group; Upper Triassic; includes Moenkopi Formation (Middle Triassic) at base in many areas;
10	@cu	Upper Chinle Group, Garita Creek through Redonda Formations, undivided
11	@g	Garita Creek Formation; Carnian
12	@m	Moenkopi Formation; Middle Triassic
13	@r	Redonda Formation
14	@rp	Rock Point Formation of Chinle Group; Upper Triassic.
15	@s	Santa Rosa Formation; Carnian; includes Moenkopi Formation (Middle Triassic) at base in most areas
16	@t	Trujillo Formation; Norian
17	D	Percha Shale; southern Caballo Mountains; includes the Onate and Sly Gap Formations
18	ds	disturbed ground
19	J	Jurassic rocks, Middle and Upper, undivided
20	Je	Entrada Sandstone, Middle Jurassic; Callovian
21	Jm	Morrison Formation; Upper Jurassic nonmarine rocks present only in northern one-third of state
22	Jmsu	Morrison Formation and upper San Rafael Group
23	Jsr	San Rafael Group; consists of Entrada Sandstone, Todilto and Summerville Formations,
24	Jz	Zuni Sandstone; consists of undivided equivalents of the Summerville Formation and Bluff Sandstone;
25	Jze	Zuni and Entrada Sandstones, undivided
26	K	Cretaceous rocks, undivided
27	Ka	Uppermost Cretaceous andesite flows; restricted to southwestern area
28	Kbm	Mancos Formation and Beartooth Quartzite (and Sarten Sandstone); Mancos
29	Kc	Carlile Shale; limited to northeastern area; Turonian-Coniacian
30	Kcc	Crevasse Canyon Formation; coal-bearing units are Dilco and Gibson Coal Members;
31	Kch	Cliff House Sandstone; transgressive marine sandstone; Campanian
32	Kd	Dakota Sandstone; includes Oak Canyon, Cubero, and Paguate Tongues plus Clay Mesa Tongue of Mancos Shale;
33	Kdg	Dakota Group of east-central and northeast New Mexico;
34	Kdm	Intertongued Dakota-Mancos sequence of west-central New Mexico;
35	Kdr	Dakota Sandstone and Rio Salado Tongue of the Mancos Shale.
36	Kg	Gallup Sandstone; generally regressive marine sandstone; Turonian
37	Kgc	Greenhorn Formation and Carlile Shale, undivided; locally includes Graneros Shale
38	Kgg	Graneros Shale and Greenhorn Formation; limited to northeastern area;
39	Kgh	Greenhorn Formation; limited to northeastern area.
40	Kgr	Graneros Shale; limited to northeastern area; Cenomanian
41	Ki	Uppermost Cretaceous intrusive rocks; restricted to Copper Flats area in Sierra County
42	Kkf	Kirtland and Fruitland Formations; coal-bearing, coal primarily in the Fruitland; Campanian to Maastrichtian

43	Kl	Lower Cretaceous, undivided; in northern Lea and Roosevelt Counties includes equivalents of Tucumcari Shale.
44	Kls	Lewis Shale; marine shale and mudstone
45	Klv	La Ventana Tongue of the Cliff House Sandstone
46	Km	Mancos Shale; divided into Upper and Lower parts by Gallup Sandstone
47	Kma	Moreno Hill Formation and Atarque Sandstone; in Salt Lake coal field and extreme southern Zuni basin;
48	Kmc	McRae Formation; Engle basin - Cutter sag area; Maastrichtian
49	Kmf	Menefee Formation; mudstone, shale, and sandstone; coal-bearing
50	Kmg	Gallup Sandstone and underlying D-Cross Tongue of the Mancos Shale; Turonian
51	Kml	Mancos Shale, Lower part
52	Kmm	Mulatto Tongue of Mancos Shale
53	Kmr	Rio Salado Tongue of the Mancos Shale. Overlies Twowells Tongue of Dakota Sandstone;
54	Kms	Satan Tongue of Mancos Shale
55	Kmu	Mancos Shale, Upper part
56	Kmv	Mesaverde Group includes the Gallup Sandstone, Crevasse Canyon Formation,
57	Knf	Fort Hays Limestone Member of Niobrara Formation
58	Kpc	Pictured Cliffs Sandstone; prominent cliff-forming marine sandstone
59	Kpg	Pescado Tongue of the Mancos Shale and Gallup Sandstone; in Zuni Basin only.
60	Kph	Hosta Tongue of Point Lookout Sandstone; transgressive marine sandstone
61	Kpl	Point Lookout Sandstone; regressive marine sandstone in McKinley and Sandoval Counties.
62	Kpn	Pierre Shale and Niobrara Formation
63	Kth	Tres Hermanos Formation; formerly designated as Lower Gallup Sandstone in the Zuni Basin; Turonian
64	Ku	Upper Cretaceous, undivided. Includes Virden Formation in northern Hidalgo County,
65	Kvt	Vermejo Formation and Trinidad Sandstone; Maastrichtian
66	M	Mississippian rocks, undivided; Arroyo Penasco Group in Sangre de Cristo
67	M_	Mississippian through Cambrian rocks, undivided; includes Lake Valley Limestone;
68	MD	Mississippian and Devonian rocks, undivided; includes the Lake Valley Limestone,
69	O_	Ordovician and Cambrian rocks, undivided; includes Bliss Sandstone, El Paso Formation,
70	O_p	Ordovician-Cambrian plutonic rocks of Florida Mountains
71	P	Permian rocks, undivided
72	P&	Permian and Pennsylvanian rocks
73	P&sc	Sangre de Cristo Formation, in Sangre de Cristo Mountains
74	Pa	Abo Formation; red beds, arkosic at base, finer and more mature above;
75	Pat	Artesia Group; shelf facies forming broad south-southeast trending outcrop
76	Pau	Upper part of Abo Formation; Wolfcampian
77	Pay	Abo and Yeso Formations, undivided
78	Pb	Bursum Formation; shale, arkose, and limestone; earliest Permian
79	Pbc	Bell Canyon Formation; basin facies-sandstone, limestone, and shale; Guadalupian
80	Pc	Castile Formation; dominantly anhydrite sequence; Upper Permian
81	Pcc	Cherry Canyon Formation; basin facies-sandstone, limestone, and shale
82	Pco	Cutoff Shale; in Brokeoff Mountains only
83	Pcp	Capitan Formation; Upper Guadalupian age limestone (reef facies)
84	Pct	Cutler Formation; used in northern areas and Chama embayment only
85	Pg	Glorieta Sandstone; texturally and mineralogically mature, high-silica quartz sandstone
86	Pgq	Grayburg and Queen Formations; sandstone, gypsum, anhydrite, dolomite, and red mudstone; Guadalupian
87	Ph	Hueco Formation; limestone unit restricted to south-central area; Pendejo
88	Playa	
89	Pqm	Quartermaster Formation; red sandstone and siltstone; Upper Permian
90	Pqr	Quartermaster and Rustler Formations; Upper Permian
91	Pr	Rustler Formation; siltstone, gypsum, sandstone, and dolomite; Upper Permian

92	Psa	San Andres Formation; limestone and dolomite with minor shale; Guadalupian in south, in part Leonardian to north
93	Psg	San Andres Limestone and Glorieta Sandstone; Guadalupian and Leonardian
94	Psl	Salado Formation; evaporite sequence; Upper Permian
95	Psr	Seven Rivers Formation; gypsum, anhydrite, salt, dolomite, and siltstone; Guadalupian
96	Pty	Yates and Tansill Formations; sandstone, siltstone, limestone, dolomite, and anhydrite; Guadalupian
97	Pvp	Victorio Peak Limestone; in Brokeoff Mountains only
98	Py	Yeso Formation; sandstones, siltstones, anhydrite, gypsum, halite, and dolomite; Leonardian
99	Pys	Yeso, Glorieta and San Andres Formations, undivided
100	Pz	Paleozoic rocks, undivided
101	Qa	Alluvium; upper and middle Quaternary
102	Qa/QTs	Mix
103	Qa/QTsf	Mix
104	Qb	Basalt and andesite flows and locally vent deposits
105	Qbo	Basalt or basaltic andesite; middle and lower Pleistocene
106	Qbt	Bandelier Tuff; Jemez Mountains area only
107	Qd	Glacial deposits; till and outwash: upper and middle Pleistocene
108	Qe	Eolian deposits
109	Qe/Qa	Mix
110	Qe/Qp	Mix
111	Qe/Qpl	Mix
112	Qe/QTs	Mix
113	Qe/QTsf	Mix
114	Qe/Tnb	Mix
115	Qeg	Gypsiferous eolian deposits
116	Ql	Landslide deposits and colluvium
117	Ql/QTs	Mix
118	Qoa	Older alluvial deposits of upland plains and piedmont areas, and calcic soils and eolian cover sediments of High Plains region;
119	Qoa/To	Mix
120	Qp	Piedmont alluvial deposits: upper and middle Quaternary;
121	Qp/QTs	Mix
122	Qp/QTsf	Mix
123	Qp/Tsf	Mix
124	Qpl	Lacustrine and playa-lake deposits;
125	Qr	Silicic volcanic rocks
126	QTb	Basaltic and andesitic volcanics interbedded with Pleistocene and Pliocene sedimentary units
127	QTg	Gila Group
128	QTp	Older piedmont alluvial deposits and shallow basin fill;
129	QTs	Upper Santa Fe Group
130	QTsf	Santa Fe Group, undivided. Basin fill of Rio Grande rift region;
131	QTt	Travertine
132	Qv	Basaltic volcanics; tuff rings, cinders, and proximal lavas
133	Qvr	Valles Rhyolite; Jemez Mountains area only
134	SO	Silurian and Ordovician rocks, undivided
135	SO_	Silurian through Cambrian rocks, undivided
136	Tc	Chuska Sandstone; restricted to Chuska Mountains
137	Tfl	Fence Lake Formation;
138	Thb	Hinsdale Basalt; northern Taos and eastern Rio Arriba Counties; basalt flows interbedded with Los Pinos Formation
139	Ti	Tertiary intrusive rocks; undifferentiated

140	Tif	Middle Tertiary felsic shallow-intrusive rocks; phonolites and trachytes of northeastern N.M.;
141	TKa	Animas Formation; in northeast San Juan Basin
142	TKav	Andesitic volcanics
143	TKi	Paleogene and Upper Cretaceous intrusive rocks;
144	TKpr	Poison Canyon and Raton Formations; undivided
145	TKr	Raton Formation; in Raton Basin; unit contains conformable K/T boundary
146	Tla	Lower Tertiary, (Lower Oligocene and Eocene) andesite and basaltic andesite flows, and associated volcaniclastic units.
147	Tli	Quartz monzonites (Eocene) in the Silver City and Los Pinos Range, intermediate intrusives of the Cooke's Range (Oli gocene), and other
148	Tlp	Los Pinos Formation of Lower Santa Fe Group (Miocene and upper Oligocene);
149	Tlrf	Lower Oligocene silicic (or felsic) flows, domes, and associated pyroclastic rocks and intrusions;
150	Tlrp	Lower Oligocene silicic pyroclastic rocks (ash-flow tuffs) (31-36.5 Ma)
151	Tlv	Lower Oligocene and Eocene volcanic rocks, undifferentiated; dominantly intermediate composition, with interbedded volcaniclastic rocks;
152	Tmb	Basalt and andesite flows; Miocene
153	Tn	Nacimiento Formation; Paleocene, San Juan Basin
154	Tnb	Basalt and andesite flows; Neogene. Includes flows interbedded with Santa Fe and Gila Groups
155	Tnr	Silicic to intermediate volcanic rocks; mainly quartz latite and rhyolite Neogene;
156	Tnv	Neogene volcanic rocks; primarily in Jemez Mountains
157	To	Ogallala Formation, alluvial and eolian deposits, and petrocalcic soils of the southern High Plains;
158	Toa	Ojo Alamo Formation; Paleocene, San Juan Basin
159	Tos	Mostly Oligocene and upper Eocene sedimentary and volcaniclastic sedimentary rocks with local andesitic to intermediate volcanics;
160	Tpb	Basalt and andesite flows; Pliocene
161	Tpc	Poison Canyon Formation; Paleocene, Raton Basin
162	Tps	Paleogene sedimentary units; includes Baca, Galisteo, El Rito, Blanco Basin,
163	Tsf	Lower and Middle Santa Fe Group.
164	Tsj	San Jose Formation; Eocene, San Juan Basin
165	Tual	Upper Oligocene andesites and basaltic andesites (26-29 Ma);
166	Tuau	Lower Miocene and uppermost Oligocene basaltic andesites (22-26 Ma).
167	Tui	Miocene to Oligocene silicic to intermediate intrusive rocks; dikes, stocks, plugs, and diatremes
168	Tuim	Upper and Middle Tertiary mafic intrusive rocks
169	Turf	Upper Oligocene silicic (or felsic) flows and masses and associated pyroclastic rocks;
170	Turp	Upper Oligocene rhyolitic pyroclastic rocks (ash-flow tuffs) (24-29 Ma)
171	Tus	Upper Tertiary sedimentary units;
172	Tuv	Volcanic and some volcaniclastic rocks, undifferentiated; lower Miocene and Upper Oligocene (younger than 29 Ma)
173	Tv	Middle Tertiary volcanic rocks, undifferentiated
174	Water	
175	X	Lower Proterozoic rocks, undivided
176	Xm	Lower Proterozoic metamorphic rocks, dominantly felsic volcanic, volcaniclastic
177	Xmo	Lower Proterozoic metamorphic rocks, dominantly mafic (1720-1760 Ma)
178	Xms	Lower Proterozoic metasedimentary rocks (1650-1700 Ma). Essentially equivalent to Hondo Group;
179	Xmu	Lower Proterozoic metamorphic rocks, undivided
180	Xp	Lower Proterozoic plutonic rocks (older than 1600 Ma)
181	Yp	Middle Proterozoic plutonic rocks (younger than 1600 Ma)

182	Ys	Middle Proterozoic sedimentary rocks of the Sacramento Mountains
183	YXp	Middle and Lower Proterozoic plutonic rocks, undivided

Appendix 4. Description of vegetation types and other classes used in the land cover dataset. Note that only 90 classes out of the 125 in the dataset occur in New Mexico.

Cell value	Database code	Description
0	none	Unclassified
2	S002	Rocky Mountain Alpine Bedrock and Scree
4	S004	Rocky Mountain Alpine Fell-Field
5	S006	Rocky Mountain Cliff and Canyon
7	S008	Western Great Plains Cliff and Outcrop
9	S010	Colorado Plateau Mixed Bedrock Canyon and Tableland
10	S011	Inter-Mountain Basins Shale Badland
11	S012	Inter-Mountain Basins Active and Stabilized Dune
12	S013	Inter-Mountain Basins Volcanic Rock and Cinder Land
13	S014	Inter-Mountain Basins Wash
14	S015	Inter-Mountain Basins Playa
15	S016	North American Warm Desert Bedrock Cliff and Outcrop
17	S018	North American Warm Desert Active and Stabilized Dune
18	S019	North American Warm Desert Volcanic Rockland
19	S020	North American Warm Desert Wash
20	S021	North American Warm Desert Pavement
21	S022	North American Warm Desert Playa
22	S023	Rocky Mountain Aspen Forest and Woodland
23	S024	Rocky Mountain Bigtooth Maple Ravine Woodland
24	S025	Rocky Mountain Subalpine-Montane Limber-Bristlecone Pine Woodland
26	S028	Rocky Mountain Subalpine Dry-Mesic Spruce-Fir Forest and Woodland
28	S030	Rocky Mountain Subalpine Mesic Spruce-Fir Forest and Woodland
29	S031	Rocky Mountain Lodgepole Pine Forest
30	S032	Rocky Mountain Montane Dry-Mesic Mixed Conifer Forest and Woodland
32	S034	Rocky Mountain Montane Mesic Mixed Conifer Forest and Woodland
33	S035	Madrean Pine-Oak Forest and Woodland
34	S036	Rocky Mountain Ponderosa Pine Woodland
35	S038	Southern Rocky Mountain Pinyon-Juniper Woodland
36	S039	Colorado Plateau Pinyon-Juniper Woodland
38	S042	Inter-Mountain West Aspen-Mixed Conifer Forest and Woodland Complex
41	S046	Rocky Mountain Gambel Oak-Mixed Montane Shrubland
42	S047	Rocky Mountain Lower Montane-Foothill Shrubland
43	S048	Western Great Plains Sandhill Shrubland
45	S051	Madrean Encinal
48	S054	Inter-Mountain Basins Big Sagebrush Shrubland
50	S056	Colorado Plateau Mixed Low Sagebrush Shrubland
51	S057	Mogollon Chaparral
52	S058	Apacherian-Chihuahuan Mesquite Upland Scrub
53	S059	Colorado Plateau Blackbrush-Mormon-tea Shrubland
55	S061	Chihuahuan Succulent Desert Scrub
56	S062	Chihuahuan Creosotebush, Mixed Desert and Thorn Scrub
57	S063	Sonoran Paloverde-Mixed Cacti Desert Scrub
58	S065	Inter-Mountain Basins Mixed Salt Desert Scrub
59	S068	Chihuahuan Stabilized Coppice Dune and Sand Flat Scrub
60	S069	Sonora-Mojave Creosotebush-White Bursage Desert Scrub
62	S071	Inter-Mountain Basins Montane Sagebrush Steppe
63	S074	Southern Rocky Mountain Juniper Woodland and Savanna

64	S075	Inter-Mountain Basins Juniper Savanna
65	S077	Apacherian-Chihuahuan Piedmont Semi-Desert Grassland and Steppe
67	S079	Inter-Mountain Basins Semi-Desert Shrub Steppe
68	S080	Chihuahuan Gypsophilous Grassland and Steppe
69	S081	Rocky Mountain Dry Tundra
70	S083	Rocky Mountain Subalpine Mesic Meadow
71	S085	Southern Rocky Mountain Montane-Subalpine Grassland
72	S086	Western Great Plains Foothill and Piedmont Grassland
74	S088	Western Great Plains Shortgrass Prairie
76	S090	Inter-Mountain Basins Semi-Desert Grassland
77	S091	Rocky Mountain Subalpine-Montane Riparian Shrubland
78	S092	Rocky Mountain Subalpine-Montane Riparian Woodland
79	S093	Rocky Mountain Lower Montane Riparian Woodland and Shrubland
80	S094	North American Warm Desert Lower Montane Riparian Woodland and Shrubland
81	S095	Western Great Plains Riparian Woodland and Shrubland
82	S096	Inter-Mountain Basins Greasewood Flat
83	S097	North American Warm Desert Riparian Woodland and Shrubland
84	S098	North American Warm Desert Riparian Mesquite Bosque
85	S100	North American Arid West Emergent Marsh
86	S102	Rocky Mountain Alpine-Montane Wet Meadow
89	S108	Western Great Plains Saline Depression Wetland
90	S109	Chihuahuan-Sonoran Desert Bottomland and Swale Grassland
91	S111	Madrean Upper Montane Conifer-Oak Forest and Woodland
92	S112	Madrean Pinyon-Juniper Woodland
93	S113	Chihuahuan Sandy Plains Semi-Desert Grassland
95	S115	Madrean Juniper Savanna
96	S116	Chihuahuan Mixed Salt Desert Scrub
97	S117	Coahuilan Chaparral
105	S129	Sonoran Mid-Elevation Desert Scrub
108	S136	Southern Colorado Plateau Sand Shrubland
109	S138	Western Great Plains Mesquite Woodland and Shrubland
110	N11	Open Water
111	N21	Developed, Open Space - Low Intensity
112	N22	Developed, Medium - High Intensity
113	N31	Barren Lands, Non-specific
114	N80	Agriculture
116	D02	Recently Burned
117	D03	Recently Mined or Quarried
118	D04	Invasive Southwest Riparian Woodland and Shrubland
119	D06	Invasive Perennial Grassland
122	D09	Invasive Annual and Biennial Forbland
123	D10	Recently Logged Areas
124	D11	Recently Chained Pinyon-Juniper Areas

Appendix 5. List of new observations made during field surveys in 2007-2008 (some additional observations included from other efforts). Geographic coordinates were obtained with GPS units in the field.

Genus	Species	Latitude WGS84	Longitude WGS84	UTM Northing NAD 83	UTM Easting NAD83	UTM Zone
Ambystoma	tigrinum	36.3053631	-105.3828064	4017886	465631	13
Ambystoma	tigrinum	34.95459666	-104.5252602	3868110	543344	13
Ambystoma	tigrinum	36.91460422	-104.2052245	4085694	570795	13
Ambystoma	tigrinum	36.76616642	-103.3066723	4070269	651132	13
Ambystoma	tigrinum	33.94928687	-107.5028386	3759355	268703	13
Ambystoma	tigrinum	36.02685289	-104.3926002	3987097	554725	13
Ambystoma	tigrinum	36.55467398	-106.3293085	4046294	381034	13
Apalone	spinifera	36.02543157	-104.3611682	3986957	557558	13
Arizona	elegans	34.391091	-106.686752	3806810	344941	13
Arizona	elegans	34.325926	-106.705222	3799611	343121	13
Arizona	elegans	34.352641	-106.883296	3802863	326792	13
Arizona	elegans	34.407391	-106.881773	3808933	327044	13
Arizona	elegans	34.350974	-106.879569	3802672	327131	13
Arizona	elegans	34.399121	-106.928954	3808097	322690	13
Arizona	elegans	34.395568	-106.895802	3807646	325730	13
Arizona	elegans	34.406511	-106.883126	3808838	326918	13
Arizona	elegans	34.394617	-106.929945	3807600	322589	13
Arizona	elegans	34.392583	-106.899807	3807322	325356	13
Arizona	elegans	34.384491	-106.911861	3806445	324231	13
Arizona	elegans	34.388259	-106.906616	3806854	324721	13
Arizona	elegans	32.148669	-108.3131961	3560077	753413	12
Arizona	elegans	32.12059909	-108.3185434	3556952	752986	12
Arizona	elegans	31.93433393	-108.4024894	3536102	745560	12
Arizona	elegans	32.30713776	-107.8093192	3577948	235487	13
Arizona	elegans	32.33697382	-107.811286	3581261	235388	13
Arizona	elegans	35.43385545	-103.4530428	3922256	640418	13
Arizona	elegans	35.13257406	-106.8199565	3889261	334184	13
Arizona	elegans	33.88578356	-106.7001595	3750792	342775	13
Arizona	elegans	31.90827493	-109.1108828	3531825	678629	12
Arizona	elegans	31.91430738	-109.1377374	3532450	676077	12
Arizona	elegans	35.01847683	-104.6759806	3875140	529560	13
Aspidoscelis	exsanguis	35.18510621	-106.4773566	3894570	365488	13
Aspidoscelis	exsanguis	34.56597308	-106.4367919	3825850	368196	13
Aspidoscelis	exsanguis	35.26593248	-105.3395107	3902587	469119	13
Aspidoscelis	exsanguis	34.67685375	-106.4679183	3838188	365520	13
Aspidoscelis	exsanguis	34.48546548	-107.0046483	3817809	315921	13
Aspidoscelis	exsanguis	34.43922596	-107.0096844	3812690	315356	13
Aspidoscelis	exsanguis	34.43359039	-106.9180387	3811901	323766	13
Aspidoscelis	exsanguis	34.43261758	-106.9203854	3811797	323548	13
Aspidoscelis	exsanguis	34.75246456	-107.3309425	3848067	286638	13
Aspidoscelis	exsanguis	34.3200068	-107.2721005	3799976	290946	13
Aspidoscelis	exsanguis	33.83853368	-106.3057415	3745019	379185	13
Aspidoscelis	inornata	32.57583484	-104.3324049	3604462	562661	13
Aspidoscelis	inornata	33.1129591	-107.1770424	3665918	296869	13

Aspidoscelis	inornata	33.1129591	-107.1770424	3665918	296869	13
Aspidoscelis	inornata	35.24843811	-107.1574674	3902727	303708	13
Aspidoscelis	inornata	35.24870155	-107.1562603	3902754	303819	13
Aspidoscelis	inornata	35.19606588	-107.0887561	3896784	309839	13
Aspidoscelis	inornata	35.19481229	-107.0847595	3896638	310200	13
Aspidoscelis	inornata	35.19518302	-107.0861184	3896681	310077	13
Aspidoscelis	inornata	35.19650501	-107.0848947	3896826	310191	13
Aspidoscelis	neomexicana	35.54854469	-106.786333	3935345	338080	13
Aspidoscelis	neomexicana	33.95067751	-106.9719214	3758438	317778	13
Aspidoscelis	neomexicana	35.42343926	-106.320809	3920803	380094	13
Aspidoscelis	neomexicana	35.25495445	-107.1580085	3903451	303675	13
Aspidoscelis	neomexicana	34.14478471	-106.9646795	3779953	318861	13
Aspidoscelis	neomexicana	34.09646731	-106.8334476	3774369	330865	13
Aspidoscelis	tesselata	33.11297628	-107.1770278	3665920	296870	13
Aspidoscelis	tesselata	33.11297628	-107.1770278	3665920	296870	13
Aspidoscelis	tesselata	32.95823998	-107.2608013	3648926	288683	13
Aspidoscelis	tesselata	32.45496369	-104.3022426	3591081	565580	13
Aspidoscelis	tesselata	32.45413036	-104.300061	3590990	565785	13
Aspidoscelis	tesselata	35.50178306	-106.9238192	3930392	325515	13
Aspidoscelis	tesselata	32.32280815	-107.8671485	3579830	230087	13
Aspidoscelis	tesselata	33.91132976	-106.9642695	3754061	318402	13
Aspidoscelis	tesselata	33.93246196	-107.0129018	3756492	313951	13
Aspidoscelis	tesselata	33.94358005	-106.9988399	3757699	315275	13
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Aspidoscelis	tigris	34.1025607	-106.8219685	3775026	331937	13
Aspidoscelis	tigris	34.10348305	-106.822342	3775129	331904	13
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Aspidoscelis	tigris	32.32210927	-107.8607796	3579736	230684	13
Aspidoscelis	tigris	32.31659632	-107.8585205	3579119	230881	13
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Aspidoscelis	tigris	32.33126968	-107.8920125	3580831	227770	13
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Aspidoscelis	tigris	32.3296591	-107.8966455	3580664	227329	13
Aspidoscelis	tigris	32.32364869	-107.8851654	3579969	228392	13
Aspidoscelis	tigris	32.33169263	-107.866962	3580815	230130	13

Aspidoscelis	tigris	32.32944192	-107.8689333	3580570	229938	13
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Aspidoscelis	tigris	32.32646031	-107.8782586	3580263	229051	13
Aspidoscelis	tigris	32.32604692	-107.8809211	3580224	228799	13
Aspidoscelis	tigris	32.32611288	-107.883643	3580238	228543	13
Aspidoscelis	tigris	32.32640357	-107.8861017	3580277	228312	13
Aspidoscelis	tigris	32.32682467	-107.8891332	3580331	228028	13
Aspidoscelis	tigris	32.3221034	-107.8916177	3579814	227780	13
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Aspidoscelis	tigris	32.32287143	-107.8675145	3579838	230052	13
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Aspidoscelis	tigris	32.33252881	-107.8936565	3580975	227619	13
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Aspidoscelis	tigris	32.33336893	-107.8647089	3580995	230348	13
Aspidoscelis	tigris	32.31937031	-107.8622014	3579436	230542	13
Aspidoscelis	tigris	32.31919563	-107.8669013	3579429	230099	13
Aspidoscelis	tigris	32.31718959	-107.8662352	3579204	230156	13
Aspidoscelis	tigris	32.33462932	-107.8929053	3581206	227696	13
Aspidoscelis	tigris	32.33462932	-107.8929053	3581206	227696	13
Aspidoscelis	tigris	36.02480493	-104.3596361	3986889	557696	13
Aspidoscelis	tigris	34.14179589	-106.8246413	3779382	331768	13
Aspidoscelis	tigris	34.13971885	-106.8237166	3779150	331849	13
Aspidoscelis	tigris	34.14005966	-106.8215893	3779184	332046	13
Aspidoscelis	tigris	34.11822631	-106.8116693	3776746	332917	13
Aspidoscelis	tigris	34.11879569	-106.8110185	3776808	332979	13
Aspidoscelis	uniparens	33.93149788	-107.0127267	3756385	313965	13
Aspidoscelis	uniparens	33.93166116	-107.0132441	3756404	313917	13
Aspidoscelis	uniparens	33.93197305	-107.0134397	3756439	313900	13
Aspidoscelis	uniparens	33.93222819	-107.013266	3756467	313917	13
Aspidoscelis	velox	36.00334165	-104.3625563	3984507	557449	13
Bogertophis	subocularis	32.4567456	-104.3195457	3591268	563952	13
Bogertophis	subocularis	32.46161733	-104.3208157	3591807	563829	13
Bufo	alvarius	31.90525124	-109.0358382	3531616	685732	12
Bufo	alvarius	31.90324436	-109.1018577	3531282	679492	12
Bufo	alvarius	32.00638846	-109.035933	3542829	685519	12
Bufo	alvarius	31.99150186	-109.0357892	3541179	685563	12
Bufo	cognatus	34.95469666	-104.5311647	3868119	542805	13
Bufo	cognatus	32.32147601	-107.8800911	3579715	228864	13
Bufo	cognatus	36.05477015	-104.3785568	3990202	555970	13
Bufo	cognatus	33.56904536	-107.1981338	3716539	295968	13
Bufo	cognatus	33.57451304	-107.1917569	3717132	296573	13
Bufo	cognatus	33.39936915	-107.2643408	3697853	289411	13
Bufo	cognatus	33.83704975	-106.7014764	3745390	342564	13
Bufo	cognatus	31.89124768	-109.0829225	3529984	681306	12
Bufo	debilis	32.44690005	-104.3046278	3590185	565361	13
Bufo	debilis	32.44690005	-104.3046278	3590185	565361	13

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Bufo	microscaphus	33.73408	-107.4670576	3735405	271437	13
Bufo	punctatus	33.11570082	-107.1924697	3666252	295436	13
Bufo	punctatus	34.03305285	-106.7695861	3767233	336636	13
Bufo	woodhousii	36.85256707	-103.8998795	4079082	598074	13
Bufo	woodhousii	34.58926169	-106.7394598	3828870	340473	13
Bufo	woodhousii	36.00288332	-104.3461944	3984465	558924	13
Bufo	woodhousii	35.48809114	-103.4906297	3928219	636914	13
Bufo	woodhousii	35.51158167	-103.5123763	3930795	634902	13
Chelydra	serpentina	35.00453889	-105.7311607	3873790	433283	13
Chelydra	serpentina	36.03085323	-104.3618739	3987558	557490	13
Chelydra	serpentina	35.01253883	-104.4296632	3874582	552036	13
Chelydra	serpentina	36.05481592	-104.3790732	3990206	555924	13
Chelydra	serpentina	36.05481592	-104.3790732	3990206	555924	13
Coleonyx	brevis	32.57099186	-104.3463364	3603917	561356	13
Coleonyx	variegatus	31.87991819	-109.0643672	3528759	683084	12
Coluber	constrictor	36.79392384	-103.9690187	4072507	591981	13
Coluber	constrictor	36.8827255	-103.8779515	4082450	599990	13
Cophosaurus	texanus	34.14482737	-106.9770642	3779980	317719	13
Cophosaurus	texanus	34.14551561	-106.9815638	3780064	317305	13
Cophosaurus	texanus	34.14384191	-106.9706256	3779859	318310	13
Cophosaurus	texanus	34.14430182	-106.984261	3779934	317054	13
Cophosaurus	texanus	34.14514337	-106.9685932	3779999	318501	13
Cophosaurus	texanus	34.14443895	-106.9887931	3779957	316636	13
Cophosaurus	texanus	34.14573077	-106.9808884	3780087	317368	13
Cophosaurus	texanus	34.14740682	-106.972591	3780258	318137	13
Cophosaurus	texanus	34.1474789	-106.9732793	3780267	318074	13
Cophosaurus	texanus	34.14637593	-106.9721453	3780142	318176	13

Cophosaurus	texanus	34.14519852	-106.9690269	3780006	318461	13
Cophosaurus	texanus	34.1442336	-106.9886034	3779934	316654	13
Cophosaurus	texanus	34.14729089	-106.9731661	3780246	318084	13
Cophosaurus	texanus	34.1444185	-106.9846866	3779948	317015	13
Cophosaurus	texanus	34.23921506	-107.0051964	3790498	315331	13
Cophosaurus	texanus	34.23675749	-107.0054962	3790226	315298	13
Cophosaurus	texanus	34.23745897	-107.0070345	3790307	315158	13
Cophosaurus	texanus	34.23693585	-107.0055409	3790246	315294	13
Cophosaurus	texanus	34.23316785	-107.0096326	3789836	314909	13
Cophosaurus	texanus	34.24036103	-107.005136	3790625	315339	13
Cophosaurus	texanus	34.2347351	-107.012679	3790015	314632	13
Cophosaurus	texanus	34.23580681	-107.011871	3790133	314708	13
Cophosaurus	texanus	34.23616572	-107.0115975	3790172	314734	13
Cophosaurus	texanus	34.23667409	-107.0097612	3790225	314905	13
Cophosaurus	texanus	34.23748042	-107.0083108	3790312	315040	13
Cophosaurus	texanus	34.2394863	-107.0062025	3790530	315239	13
Cophosaurus	texanus	34.23969333	-107.0065672	3790554	315205	13
Cophosaurus	texanus	34.2440484	-106.9912992	3791009	316621	13
Cophosaurus	texanus	33.13187957	-107.1884804	3668039	295845	13
Cophosaurus	texanus	33.09254061	-107.1675561	3663635	297707	13
Cophosaurus	texanus	33.0893865	-107.1647922	3663280	297958	13
Cophosaurus	texanus	33.08128875	-107.1686762	3662390	297577	13
Cophosaurus	texanus	33.08195746	-107.173477	3662473	297130	13
Cophosaurus	texanus	33.09281789	-107.1831218	3663696	296255	13
Cophosaurus	texanus	33.10376893	-107.1843959	3664913	296161	13
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Cophosaurus	texanus	33.11304275	-107.1952734	3665963	295168	13
Cophosaurus	texanus	33.11435938	-107.1936515	3666106	295322	13
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Cophosaurus	texanus	33.1065622	-107.1882751	3665231	295806	13
Cophosaurus	texanus	32.98636076	-107.2617379	3652046	288662	13
Cophosaurus	texanus	32.98046661	-107.2584197	3651386	288958	13
Cophosaurus	texanus	32.97798632	-107.2688594	3651132	287977	13
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Cophosaurus	texanus	33.57551375	-107.1905979	3717241	296682	13
Cophosaurus	texanus	33.91380703	-106.9423515	3754297	320433	13
Cophosaurus	texanus	33.91350126	-106.9424549	3754264	320423	13
Cophosaurus	texanus	33.93373534	-106.9444013	3756511	320286	13
Cophosaurus	texanus	33.9353129	-106.9479046	3756692	319965	13
Cophosaurus	texanus	33.95158569	-106.9701033	3758536	317948	13
Cophosaurus	texanus	33.93531382	-106.9478691	3756692	319969	13
Cophosaurus	texanus	33.93483974	-106.9394371	3756625	320747	13
Cophosaurus	texanus	33.93396023	-106.9432001	3756534	320397	13
Cophosaurus	texanus	33.9293687	-106.935811	3756012	321071	13
Cophosaurus	texanus	33.92838769	-106.934636	3755901	321177	13
Cophosaurus	texanus	33.92404737	-106.8987148	3755357	324489	13
Cophosaurus	texanus	33.91423878	-106.9421941	3754345	320449	13
Cophosaurus	texanus	33.9136575	-106.9438576	3754283	320294	13
Cophosaurus	texanus	33.91363604	-106.9442793	3754282	320255	13

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Cophosaurus	texanus	33.91134552	-106.9641829	3754063	318410	13
Cophosaurus	texanus	33.9112332	-106.9639308	3754050	318433	13
Cophosaurus	texanus	33.90574532	-106.968142	3753449	318032	13
Cophosaurus	texanus	33.90521474	-106.9687284	3753391	317976	13
Cophosaurus	texanus	33.90420933	-106.9690349	3753280	317946	13
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Cophosaurus	texanus	33.90636683	-107.019542	3753610	313280	13
Cophosaurus	texanus	33.90636683	-107.019542	3753610	313280	13
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Cophosaurus	texanus	34.14405875	-106.9888674	3779915	316629	13
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Cophosaurus	texanus	34.15232364	-106.9849555	3780825	317007	13
Cophosaurus	texanus	34.15249228	-106.9851234	3780844	316992	13
Cophosaurus	texanus	34.14667223	-106.9813763	3780192	317325	13
Cophosaurus	texanus	34.14456694	-106.9756036	3779948	317853	13
Cophosaurus	texanus	34.14280398	-106.9696306	3779742	318400	13
Cophosaurus	texanus	34.14269409	-106.9694759	3779729	318414	13
Cophosaurus	texanus	34.13933756	-106.9647745	3779349	318840	13
Cophosaurus	texanus	34.13933756	-106.9647745	3779349	318840	13
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Cophosaurus	texanus	34.13227404	-106.9556817	3778549	319664	13
Cophosaurus	texanus	34.12746057	-106.949453	3778004	320228	13
Cophosaurus	texanus	34.12554631	-106.9466768	3777787	320480	13
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Cophosaurus	texanus	34.14284706	-106.9676504	3779743	318583	13
Cophosaurus	texanus	34.14566204	-106.9671161	3780054	318638	13
Cophosaurus	texanus	34.14442454	-106.9665984	3779916	318683	13
Cophosaurus	texanus	34.14653292	-106.9596431	3780138	319329	13
Cophosaurus	texanus	34.14676652	-106.9574281	3780160	319534	13
Cophosaurus	texanus	34.1473556	-106.9544406	3780220	319810	13
Cophosaurus	texanus	34.14760103	-106.9525252	3780244	319987	13
Cophosaurus	texanus	34.15288791	-106.9372573	3780803	321406	13
Cophosaurus	texanus	34.24023271	-107.0057794	3790612	315279	13
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Cophosaurus	texanus	34.23974035	-107.0063739	3790559	315223	13
Cophosaurus	texanus	34.23978687	-107.0062098	3790564	315239	13
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Cophosaurus	texanus	34.22326078	-106.9872429	3788697	316950	13
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Crotalus	atrox	34.397008	-107.034991	3808054	312937	13
Crotalus	atrox	34.415875	-106.844254	3809811	330510	13
Crotalus	atrox	34.420848	-106.517892	3809864	360515	13
Crotalus	atrox	34.35659	-106.894889	3803321	325734	13
Crotalus	atrox	34.406567	-106.990659	3809033	317033	13
Crotalus	atrox	34.39863	-107.0099441	3808188	315243	13
Crotalus	atrox	34.398611	-107.02215	3808208	314121	13
Crotalus	atrox	34.368977	-106.533828	3804134	358963	13
Crotalus	atrox	33.22218661	-106.8689292	3677475	325838	13
Crotalus	atrox	32.57109018	-104.3679102	3603915	559331	13
Crotalus	atrox	32.53713844	-104.3692036	3600151	559232	13
Crotalus	atrox	34.23421307	-106.9759606	3789891	318013	13
Crotalus	atrox	31.95190893	-108.7913872	3537235	708747	12
Crotalus	atrox	35.80147575	-104.2100749	3962217	571372	13
Crotalus	atrox	35.65819709	-104.3790933	3946216	556201	13
Crotalus	atrox	34.67693171	-106.4679908	3838197	365513	13
Crotalus	atrox	34.00424693	-106.9904663	3764413	316179	13
Crotalus	atrox	36.07073332	-104.3347869	3991998	559900	13
Crotalus	atrox	35.7904553	-103.8079964	3961362	607718	13
Crotalus	atrox	33.59344013	-107.1699679	3719189	298639	13
Crotalus	atrox	34.01348479	-106.9351302	3765339	321310	13
Crotalus	atrox	34.02461613	-107.0417777	3766765	311485	13
Crotalus	atrox	33.9004472	-106.7726453	3752532	336099	13
Crotalus	atrox	32.21575079	-108.9517913	3566190	693027	12
Crotalus	atrox	32.21669384	-108.9517803	3566294	693026	12
Crotalus	atrox	31.87290145	-109.052664	3528001	684205	12
Crotalus	atrox	31.9140726	-109.1296957	3532437	676838	12
Crotalus	atrox	31.88354488	-109.0703432	3529151	682511	12
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Crotalus	atrox	31.90843376	-109.1112022	3531842	678598	12
Crotalus	atrox	31.98970528	-109.0357932	3540980	685566	12
Crotalus	atrox	32.07573219	-108.989594	3550598	689754	12
Crotalus	atrox	32.04998843	-109.0142514	3547701	687479	12
Crotalus	atrox	33.9514489	-106.9701744	3758521	317941	13

Crotalus	atrox	32.01209787	-109.0358105	3543462	685519	12
Crotalus	atrox	32.92242168	-107.5508351	3645573	261470	13
Crotalus	atrox	32.95391307	-107.316767	3648560	283440	13
Crotalus	atrox	33.91779824	-106.9011303	3754669	324253	13
Crotalus	atrox	33.97355567	-107.0014863	3761029	315095	13
Crotalus	atrox	34.14528519	-106.9883022	3780050	316684	13
Crotalus	atrox	34.1230216	-107.1478692	3777879	301917	13
Crotalus	atrox	34.41915348	-106.8401837	3810167	330891	13
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Crotalus	atrox	35.61961	-106.135826	3942352	397139	13
Crotalus	atrox	35.60924442	-106.1748797	3941244	393588	13
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Crotalus	atrox	35.65261625	-106.151991	3946030	395718	13
Crotalus	atrox	35.61380787	-106.1765132	3941752	393446	13
Crotalus	atrox	35.61385296	-106.1765322	3941757	393444	13
Crotalus	atrox	35.61381717	-106.1766038	3941753	393438	13
Crotalus	atrox	35.61381516	-106.1766307	3941753	393436	13
Crotalus	atrox	33.83883359	-106.30623	3745053	379141	13
Crotalus	lepidus	33.13830866	-107.1821971	3668739	296446	13
Crotalus	lepidus	34.14382833	-106.9861718	3779885	316877	13
Crotalus	lepidus	33.71434892	-107.5236954	3733344	266135	13
Crotalus	lepidus	33.71521167	-107.5215767	3733435	266334	13
Crotalus	lepidus	33.71401875	-107.5244324	3733309	266066	13
Crotalus	lepidus	33.92878465	-107.3389744	3756723	283797	13
Crotalus	lepidus	33.92947851	-107.3384167	3756799	283851	13
Crotalus	lepidus	33.92947851	-107.3384167	3756799	283851	13
Crotalus	lepidus	33.92947851	-107.3384167	3756799	283851	13
Crotalus	lepidus	31.85492227	-109.1914466	3525780	671108	12
Crotalus	lepidus	34.14553212	-106.9882225	3780078	316691	13
Crotalus	lepidus	32.54479908	-107.2099238	3602978	292482	13
Crotalus	molossus	34.14343648	-106.9858	3779841	316910	13
Crotalus	molossus	33.14936975	-107.2041864	3670009	294421	13
Crotalus	molossus	33.46705302	-107.2471123	3705325	291175	13
Crotalus	molossus	34.34154041	-107.2789959	3802379	290365	13
Crotalus	molossus	31.89606861	-109.1645583	3530385	673575	12
Crotalus	molossus	31.52071718	-109.0140287	3489021	688572	12
Crotalus	molossus	34.0764696	-107.154879	3772730	301162	13
Crotalus	molossus	34.07643129	-107.1548426	3772726	301165	13
Crotalus	scutulatus	31.9794512	-109.0358302	3539843	685583	12
Crotalus	scutulatus	31.95776956	-109.0358769	3537439	685623	12
Crotalus	scutulatus	31.88586406	-109.0741249	3529402	682149	12
Crotalus	scutulatus	31.68971814	-109.1330693	3507558	676946	12
Crotalus	scutulatus	31.570344	-109.2607787	3494125	665051	12
Crotalus	scutulatus	31.91400781	-109.0358083	3532587	685717	12
Crotalus	scutulatus	31.93431566	-109.0357976	3534839	685677	12
Crotalus	scutulatus	31.93581912	-109.0359204	3535005	685663	12
Crotalus	scutulatus	31.870666	-109.0420442	3527771	685214	12
Crotalus	scutulatus	31.99413068	-109.0359128	3541470	685546	12
Crotalus	scutulatus	31.97098003	-109.0359164	3538903	685592	12
Crotalus	scutulatus	31.94966166	-109.0359169	3536540	685635	12

Crotalus	scutulatus	31.93404777	-109.0358382	3534809	685674	12
Crotalus	scutulatus	32.04819261	-109.0158851	3547499	687328	12
Crotalus	scutulatus	31.96575047	-109.0359404	3538324	685600	12
Crotalus	scutulatus	32.00962747	-109.0358127	3543188	685524	12
Crotalus	viridis	34.3494652	-106.6287933	3802106	350195	13
Crotalus	viridis	34.3494652	-106.6287933	3802106	350195	13
Crotalus	viridis	34.4077531	-106.6784595	3808645	345734	13
Crotalus	viridis	34.4077531	-106.6784595	3808645	345734	13
Crotalus	viridis	34.3358153	-106.7001049	3800700	343611	13
Crotalus	viridis	34.3358153	-106.7001049	3800700	343611	13
Crotalus	viridis	34.4183454	-106.7841862	3809986	336036	13
Crotalus	viridis	34.4183454	-106.7841862	3809986	336036	13
Crotalus	viridis	34.397004	-106.893667	3807801	325930	13
Crotalus	viridis	34.406934	-106.877296	3808875	327455	13
Crotalus	viridis	34.406739	-106.857799	3808820	329247	13
Crotalus	viridis	34.389918	-106.903759	3807033	324987	13
Crotalus	viridis	34.334483	-106.630219	3800447	350038	13
Crotalus	viridis	34.338409	-106.629461	3800881	350114	13
Crotalus	viridis	34.336656	-106.723613	3800830	341449	13
Crotalus	viridis	34.334764	-106.730649	3800631	340799	13
Crotalus	viridis	34.403927	-106.678381	3808221	345734	13
Crotalus	viridis	34.334808	-106.631298	3800484	349939	13
Crotalus	viridis	34.334011	-106.742291	3800566	339726	13
Crotalus	viridis	34.336565	-106.629188	3800676	350136	13
Crotalus	viridis	34.33903	-106.6294	3800950	350121	13
Crotalus	viridis	34.336301	-106.630875	3800649	349980	13
Crotalus	viridis	34.348609	-106.621594	3802001	350856	13
Crotalus	viridis	34.337531	-106.629567	3800784	350103	13
Crotalus	viridis	34.339942	-106.625053	3801045	350522	13
Crotalus	viridis	34.407082	-106.678194	3808570	345757	13
Crotalus	viridis	34.332764	-106.725075	3800400	341308	13
Crotalus	viridis	34.355528	-106.688732	3802869	344693	13
Crotalus	viridis	34.344452	-106.725579	3801697	341283	13
Crotalus	viridis	34.402464	-106.92834	3808467	322754	13
Crotalus	viridis	34.404367	-106.861332	3808563	328917	13
Crotalus	viridis	34.38142	-106.923122	3806124	323189	13
Crotalus	viridis	34.40707	-106.877933	3808891	327397	13
Crotalus	viridis	35.38007163	-106.6368652	3916422	351320	13
Crotalus	viridis	31.96864424	-108.4444659	3539812	741501	12
Crotalus	viridis	31.96295712	-108.6763404	3538687	719596	12
Crotalus	viridis	31.96952082	-108.6309977	3539508	723867	12
Crotalus	viridis	35.70243258	-104.2167486	3951227	570857	13
Crotalus	viridis	35.70243258	-104.2167486	3951227	570857	13
Crotalus	viridis	32.33293877	-107.8070754	3580803	235773	13
Crotalus	viridis	33.97271236	-107.3330323	3761583	284458	13
Crotalus	viridis	35.39029629	-103.42281	3917468	643240	13
Crotalus	viridis	35.12783627	-106.7856897	3888679	337297	13
Crotalus	viridis	34.44736512	-106.989304	3813555	317247	13
Crotalus	viridis	31.95209669	-108.7899335	3537258	708884	12
Crotalus	viridis	34.63042765	-107.3811454	3834638	281721	13

Crotalus	viridis	34.15916847	-107.2297548	3782050	294452	13
Crotalus	viridis	34.23571536	-107.4784125	3791070	271731	13
Crotalus	viridis	34.00606949	-107.621145	3765927	257928	13
Crotalus	viridis	33.97478395	-107.6278646	3762472	257218	13
Crotalus	viridis	33.80241875	-107.3730283	3742780	280325	13
Crotalus	viridis	34.01712782	-107.0325951	3765918	312317	13
Crotalus	viridis	32.44436184	-108.6453543	3592132	721356	12
Crotalus	viridis	32.42122737	-108.7252477	3589404	713898	12
Crotalus	viridis	32.17562176	-108.9474049	3561748	693526	12
Crotalus	viridis	32.00299211	-109.0358978	3542453	685529	12
Crotalus	viridis	34.14424407	-106.9679235	3779899	318560	13
Crotalus	viridis	34.07708148	-107.0863953	3772667	307484	13
Crotalus	viridis	35.57945514	-106.1585354	3937923	395030	13
Crotalus	viridis	35.61384131	-106.176569	3941756	393441	13
Crotalus	viridis	33.86684926	-106.5732523	3748506	354480	13
Crotalus	viridis	33.87632919	-106.5778214	3749563	354073	13
Crotalus	viridis	33.84701961	-106.2998696	3745953	379741	13
Crotaphytus	collaris	32.57842527	-104.3349966	3604747	562416	13
Crotaphytus	collaris	32.61585172	-104.2963899	3608920	566012	13
Crotaphytus	collaris	32.78512669	-104.251086	3627714	570130	13
Crotaphytus	collaris	32.77187708	-104.290202	3626220	566477	13
Crotaphytus	collaris	34.1623199	-106.7539289	3781543	338327	13
Crotaphytus	collaris	34.17230484	-106.7317224	3782616	340393	13
Crotaphytus	collaris	33.96659533	-106.7384891	3759813	339382	13
Crotaphytus	collaris	34.07467503	-106.779989	3771865	335755	13
Crotaphytus	collaris	34.07843901	-106.7801102	3772283	335752	13
Crotaphytus	collaris	35.26509052	-105.3372745	3902493	469322	13
Crotaphytus	collaris	35.2658811	-105.339746	3902581	469098	13
Crotaphytus	collaris	35.26565772	-105.3390196	3902556	469164	13
Crotaphytus	collaris	34.11820292	-106.8123976	3776745	332850	13
Crotaphytus	collaris	34.11531561	-106.7999378	3776404	333994	13
Crotaphytus	collaris	34.11183746	-106.7905358	3776003	334854	13
Crotaphytus	collaris	34.086721	-106.7804137	3773202	335740	13
Crotaphytus	collaris	34.07621588	-106.7814129	3772038	335627	13
Crotaphytus	collaris	34.07251309	-106.776499	3771620	336073	13
Crotaphytus	collaris	34.0692822	-106.7767353	3771262	336045	13
Crotaphytus	collaris	34.0590261	-106.774867	3770121	336198	13
Crotaphytus	collaris	34.05556857	-106.7744772	3769737	336227	13
Crotaphytus	collaris	34.0520822	-106.7754367	3769352	336132	13
Crotaphytus	collaris	34.04449775	-106.7753049	3768511	336130	13
Crotaphytus	collaris	34.03449881	-106.7771053	3767405	335944	13
Crotaphytus	collaris	34.03447081	-106.7793804	3767406	335734	13
Crotaphytus	collaris	33.26053902	-106.7789638	3681582	334296	13
Crotaphytus	collaris	33.2632063	-106.7753528	3681872	334637	13
Crotaphytus	collaris	33.17058695	-106.7905172	3671626	333048	13
Crotaphytus	collaris	33.17534678	-106.7595316	3672104	335947	13
Crotaphytus	collaris	33.83560396	-106.682968	3745202	344274	13
Crotaphytus	collaris	35.44706	-105.760952	3922888	430940	13
Crotaphytus	collaris	36.06323445	-104.370772	3991145	556665	13
Crotaphytus	collaris	33.68366528	-105.9256587	3727466	414200	13

Crotaphytus	collaris	33.12559725	-107.1846253	3667334	296190	13
Crotaphytus	collaris	33.10722562	-107.1896781	3665307	295676	13
Crotaphytus	collaris	35.65645684	-104.3762773	3946024	556457	13
Crotaphytus	collaris	35.65465498	-104.3741335	3945826	556653	13
Crotaphytus	collaris	35.60558799	-107.0557602	3942149	313788	13
Crotaphytus	collaris	34.63715496	-106.5834771	3833946	354863	13
Crotaphytus	collaris	34.07149267	-107.1339338	3772137	303083	13
Crotaphytus	collaris	34.07915222	-107.1458269	3773010	302004	13
Crotaphytus	collaris	36.94819973	-103.4685039	4090221	636363	13
Crotaphytus	collaris	34.07117927	-107.1352304	3772105	302963	13
Crotaphytus	collaris	34.07486119	-107.1409836	3772525	302441	13
Crotaphytus	collaris	34.07967065	-107.14259	3773061	302304	13
Crotaphytus	collaris	34.07033371	-107.1317768	3772005	303280	13
Crotaphytus	collaris	36.0712939	-104.3344373	3992061	559931	13
Crotaphytus	collaris	36.01177753	-104.3785087	3985433	556005	13
Crotaphytus	collaris	36.02613347	-104.4633002	3986980	548355	13
Crotaphytus	collaris	34.0791622	-107.1458198	3773011	302004	13
Crotaphytus	collaris	34.08054689	-107.139515	3773152	302589	13
Crotaphytus	collaris	34.75102002	-107.3294917	3847904	286767	13
Crotaphytus	collaris	34.13957804	-106.8224606	3779132	331964	13
Crotaphytus	collaris	34.11827476	-106.8106407	3776750	333012	13
Crotaphytus	collaris	34.05716758	-106.7743507	3769914	336242	13
Crotaphytus	collaris	35.38929448	-106.3100125	3917003	381024	13
Crotaphytus	collaris	35.39072553	-106.3133313	3917166	380725	13
Crotaphytus	collaris	33.94520639	-106.99817	3757879	315340	13
Crotaphytus	collaris	35.2568258	-107.1542419	3903652	304022	13
Crotaphytus	collaris	33.89189104	-107.047939	3752057	310622	13
Crotaphytus	collaris	33.89782442	-107.0665015	3752749	308919	13
Crotaphytus	collaris	33.89782442	-107.0665015	3752749	308919	13
Crotaphytus	collaris	33.91759682	-107.081305	3754969	307594	13
Crotaphytus	collaris	33.90960569	-107.0798056	3754080	307715	13
Crotaphytus	collaris	33.90965573	-107.079799	3754086	307715	13
Crotaphytus	collaris	35.49517737	-106.921612	3929656	325701	13
Crotaphytus	collaris	33.98276855	-106.7724669	3761661	336273	13
Crotaphytus	collaris	35.58008295	-106.1771704	3938012	393342	13
Crotaphytus	collaris	35.57717501	-106.1803359	3937693	393051	13
Crotaphytus	collaris	35.57586199	-106.181361	3937549	392957	13
Crotaphytus	collaris	35.55833928	-106.1771559	3935601	393314	13
Crotaphytus	collaris	35.57679238	-106.1806892	3937651	393019	13
Crotaphytus	collaris	35.57118723	-106.1820303	3937031	392890	13
Crotaphytus	collaris	35.57706621	-106.1797293	3937680	393106	13
Crotaphytus	collaris	35.61329314	-106.1764053	3941695	393455	13
Crotaphytus	collaris	33.85242065	-106.3365686	3746596	376353	13
Crotaphytus	collaris	33.83992692	-106.3383505	3745213	376170	13
Crotaphytus	collaris	33.83541872	-106.3411355	3744716	375906	13
Crotaphytus	collaris	33.83495989	-106.3408424	3744665	375932	13
Diadophis	punctatus	34.345352	-106.620392	3801638	350961	13
Diadophis	punctatus	36.06720119	-104.3719084	3991584	556560	13
Elgaria	kingii	33.88317335	-107.5161665	3752052	267291	13
Elgaria	kingii	33.71486885	-107.5250306	3733404	266013	13

Elgaria	kingii	33.8116406	-107.5852535	3744276	260700	13
Elgaria	kingii	33.81161244	-107.5847278	3744272	260749	13
Elgaria	kingii	33.81216916	-107.5841914	3744333	260800	13
Elgaria	kingii	33.71768533	-107.5174016	3733700	266728	13
Elgaria	kingii	32.88106226	-108.2247024	3641517	759646	12
Eumeces	multivirgatus	33.71993177	-107.5223268	3733960	266277	13
Eumeces	multivirgatus	34.89606299	-106.0695015	3862038	402281	13
Eumeces	obsoletus	35.77914007	-106.2716145	3960198	385070	13
Eumeces	obsoletus	36.93737961	-103.4698945	4089019	636258	13
Eumeces	obsoletus	34.00359666	-106.9898544	3764339	316235	13
Gambelia	wislizenii	34.39737746	-106.6784521	3807494	345716	13
Gambelia	wislizenii	34.10339596	-106.8224042	3775119	331898	13
Gambelia	wislizenii	33.84078699	-106.6804233	3745773	344519	13
Gambelia	wislizenii	34.14501169	-106.9683715	3779984	318521	13
Gambelia	wislizenii	34.14645161	-106.9722163	3780151	318169	13
Gambelia	wislizenii	34.14595239	-106.9707556	3780093	318303	13
Gambelia	wislizenii	34.22563294	-106.9438584	3788882	320952	13
Gambelia	wislizenii	32.31607622	-107.8798775	3579115	228868	13
Gambelia	wislizenii	32.31923914	-107.8662984	3579432	230156	13
Gambelia	wislizenii	32.31723863	-107.8702458	3579220	229778	13
Gambelia	wislizenii	34.63715949	-106.6380323	3834026	349862	13
Gambelia	wislizenii	34.63713896	-106.6145912	3833989	352011	13
Gambelia	wislizenii	34.59139539	-106.6578726	3828980	347960	13
Gambelia	wislizenii	34.59128005	-106.659258	3828970	347833	13
Gambelia	wislizenii	34.24177833	-107.0009606	3790775	315726	13
Gambelia	wislizenii	33.91123228	-106.929592	3753990	321608	13
Gyalopion	canum	33.92437921	-106.9114595	3755416	323312	13
Heterodon	nasicus	36.04792264	-104.3781017	3989442	556016	13
Heterodon	nasicus	32.44758879	-104.305324	3590261	565295	13
Heterodon	nasicus	35.55936984	-106.7713592	3936521	339459	13
Holbrookia	maculata	34.4002881	-106.6626832	3807793	347170	13
Holbrookia	maculata	34.39011002	-106.6614901	3806663	347262	13
Holbrookia	maculata	33.93149494	-107.0128447	3756385	313954	13
Holbrookia	maculata	35.57571748	-106.1744558	3937525	393582	13
Holbrookia	maculata	35.575159	-106.17411	3937463	393613	13
Holbrookia	maculata	35.57537944	-106.1767982	3937490	393369	13
Holbrookia	maculata	35.57191981	-106.173368	3937103	393676	13
Holbrookia	maculata	35.56970045	-106.1731468	3936856	393693	13
Holbrookia	maculata	35.56959081	-106.1739524	3936845	393620	13
Holbrookia	maculata	35.56965091	-106.1740464	3936852	393611	13
Holbrookia	maculata	35.57078364	-106.1799622	3936984	393077	13
Holbrookia	maculata	35.56656084	-106.1769409	3936512	393345	13
Holbrookia	maculata	35.56711413	-106.1766318	3936573	393374	13
Holbrookia	maculata	35.5758205	-106.176239	3937539	393421	13
Hyla	arenicolor	33.71534376	-107.5223648	3733451	266261	13
Hyla	arenicolor	33.71489181	-107.5249613	3733407	266019	13
Hyla	arenicolor	33.71429284	-107.5230386	3733336	266196	13
Hyla	arenicolor	33.82655033	-107.5720332	3745899	261965	13
Hyla	arenicolor	33.71464991	-107.5227566	3733375	266223	13
Hypsiglena	torquata	34.350163	-106.877005	3802578	327365	13

Hypsiglena	torquata	34.00621793	-106.9877151	3764626	316438	13
Hypsiglena	torquata	31.89444554	-109.087864	3530330	680833	12
Hypsiglena	torquata	32.04890926	-109.0151387	3547579	687397	12
Hypsiglena	torquata	32.02355543	-109.0359535	3544732	685483	12
Kinosternon	flavescens	35.15935843	-103.7711463	3891406	611920	13
Lampropeltis	getula	34.4213986	-106.7325211	3810242	340790	13
Lampropeltis	getula	34.4213986	-106.7325211	3810242	340790	13
Lampropeltis	getula	34.391656	-106.901007	3807221	325244	13
Lampropeltis	getula	33.04839606	-107.2764941	3658955	287432	13
Lampropeltis	getula	31.94919286	-109.0358089	3536488	685646	12
Lampropeltis	getula	36.24979332	-102.2125947	4015258	750457	13
Leptotyphlops	dulcis	34.96441313	-104.6595619	3869149	531079	13
Masticophis	flagellum	34.400554	-106.673405	3807839	346185	13
Masticophis	flagellum	34.3469473	-106.6222754	3801817	350790	13
Masticophis	flagellum	34.306962	-106.676161	3797464	345761	13
Masticophis	flagellum	34.274659	-106.901697	3794246	324937	13
Masticophis	flagellum	34.339142	-106.628983	3800962	350160	13
Masticophis	flagellum	34.337667	-106.629783	3800799	350083	13
Masticophis	flagellum	34.362489	-106.622829	3803542	350767	13
Masticophis	flagellum	34.336801	-106.632337	3800707	349847	13
Masticophis	flagellum	34.336429	-106.633463	3800667	349743	13
Masticophis	flagellum	34.405563	-106.870509	3808711	328076	13
Masticophis	flagellum	34.98706807	-105.2001615	3871627	481732	13
Masticophis	flagellum	34.353893	-106.885851	3803007	326559	13
Masticophis	flagellum	34.336473	-106.723056	3800809	341500	13
Masticophis	flagellum	34.33756	-106.718216	3800922	341948	13
Masticophis	flagellum	34.331182	-106.723345	3800222	341464	13
Masticophis	flagellum	34.333521	-106.728227	3800489	341019	13
Masticophis	flagellum	33.01280483	-105.9956348	3653146	407003	13
Masticophis	flagellum	32.61646863	-107.2834827	3611072	285744	13
Masticophis	flagellum	31.95151012	-108.80427	3537166	707530	12
Masticophis	flagellum	35.59476729	-104.4268489	3939154	551920	13
Masticophis	flagellum	35.73707541	-104.1297646	3955136	578692	13
Masticophis	flagellum	34.97930526	-104.8096618	3870764	517373	13
Masticophis	flagellum	34.1219441	-107.2298825	3777922	294350	13
Masticophis	flagellum	35.55690707	-106.7819495	3936265	338495	13
Masticophis	flagellum	35.55690707	-106.7819495	3936265	338495	13
Masticophis	flagellum	31.91406967	-109.1270465	3532441	677089	12
Masticophis	flagellum	34.9492755	-104.6870258	3867462	528577	13
Masticophis	taeniatus	34.03325192	-106.7667418	3767250	336899	13
Masticophis	taeniatus	33.68507545	-105.9238896	3727621	414365	13
Masticophis	taeniatus	34.14351384	-106.9863263	3779850	316862	13
Masticophis	taeniatus	34.49739528	-107.0189967	3819158	314629	13
Masticophis	taeniatus	32.87658608	-107.8683956	3641253	231627	13
Masticophis	taeniatus	35.21715601	-106.4876582	3898139	364603	13
Masticophis	taeniatus	35.22216696	-106.490431	3898698	364359	13
Masticophis	taeniatus	34.15280074	-106.9843533	3780877	317064	13
Masticophis	taeniatus	34.12782828	-107.1572826	3778431	301060	13
Masticophis	taeniatus	33.90915533	-106.9405608	3753778	320589	13
Masticophis	taeniatus	35.60924225	-106.1748863	3941244	393587	13

Masticophis	taeniatus	33.83853469	-106.3057403	3745020	379186	13
Phrynosoma	cornutum	35.02701815	-104.6782673	3876086	529349	13
Phrynosoma	cornutum	32.60998079	-104.3013567	3608266	565550	13
Phrynosoma	cornutum	34.1573594	-106.8023515	3781071	333854	13
Phrynosoma	cornutum	33.99561114	-106.6775396	3762937	345066	13
Phrynosoma	cornutum	35.1699	-106.3841	3892761	373956	13
Phrynosoma	cornutum	34.16413517	-106.8018261	3781822	333915	13
Phrynosoma	cornutum	33.84986719	-106.6781402	3746776	344746	13
Phrynosoma	cornutum	33.23469182	-106.8006204	3678750	332229	13
Phrynosoma	cornutum	34.14426385	-106.9678713	3779901	318565	13
Phrynosoma	cornutum	34.14426385	-106.9678713	3779901	318565	13
Phrynosoma	cornutum	31.67690892	-108.8400214	3506651	704755	12
Phrynosoma	cornutum	31.69477763	-108.8359607	3508640	705101	12
Phrynosoma	cornutum	31.95150333	-108.3335753	3538165	752030	12
Phrynosoma	cornutum	31.98122707	-108.3416381	3541442	751187	12
Phrynosoma	cornutum	33.04460619	-107.2125787	3658408	293393	13
Phrynosoma	cornutum	32.95016661	-107.2581987	3648025	288907	13
Phrynosoma	cornutum	35.30887021	-104.4081389	3907457	553804	13
Phrynosoma	cornutum	35.46696967	-104.4150114	3924987	553076	13
Phrynosoma	cornutum	35.61848598	-104.4259795	3941786	551983	13
Phrynosoma	cornutum	35.65707349	-104.3771128	3946092	556381	13
Phrynosoma	cornutum	32.31161806	-107.8142685	3578457	235034	13
Phrynosoma	cornutum	32.31319327	-107.8159338	3578635	234882	13
Phrynosoma	cornutum	32.34165209	-107.8879318	3581972	228186	13
Phrynosoma	cornutum	35.44864783	-103.4631897	3923883	639472	13
Phrynosoma	cornutum	35.3759743	-103.4136215	3915893	644100	13
Phrynosoma	cornutum	34.43890854	-107.0098492	3812655	315341	13
Phrynosoma	cornutum	33.394597	-107.2665648	3697329	289192	13
Phrynosoma	cornutum	33.36785529	-107.2782246	3694387	288043	13
Phrynosoma	cornutum	33.9548346	-106.9252017	3758817	322105	13
Phrynosoma	cornutum	33.93371246	-106.9421079	3756504	320498	13
Phrynosoma	hernandesi	33.26308552	-106.7823957	3681869	333981	13
Phrynosoma	hernandesi	35.81770303	-106.6032319	3964915	355166	13
Phrynosoma	hernandesi	34.63714985	-106.6321127	3834016	350405	13
Phrynosoma	hernandesi	34.59141182	-106.6499902	3828970	348683	13
Phrynosoma	hernandesi	33.878625	-107.5237549	3751565	266576	13
Phrynosoma	hernandesi	34.08045578	-107.480287	3773853	271140	13
Phrynosoma	hernandesi	35.28336517	-107.5920296	3907549	264264	13
Phrynosoma	hernandesi	35.28336517	-107.5920296	3907549	264264	13
Phrynosoma	hernandesi	35.25282713	-107.1545345	3903209	303986	13
Phrynosoma	modestum	34.40334756	-106.6809004	3808160	345501	13
Phrynosoma	modestum	32.60016055	-104.3233	3607164	563498	13
Phrynosoma	modestum	34.11198808	-106.790659	3776020	334843	13
Phrynosoma	modestum	34.03490248	-106.7743194	3767445	336202	13
Phrynosoma	modestum	34.14481069	-106.9771176	3779978	317714	13
Phrynosoma	modestum	34.15445901	-106.9808807	3781055	317388	13
Phrynosoma	modestum	34.22367308	-106.9411376	3788660	321198	13
Phrynosoma	modestum	34.22442083	-106.944866	3788750	320856	13
Phrynosoma	modestum	32.32694043	-107.8783457	3580316	229044	13
Phrynosoma	modestum	34.14685755	-106.9569983	3780169	319573	13

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Phrynosoma	modestum	34.14685755	-106.9569983	3780169	319573	13
Phrynosoma	modestum	34.49365754	-107.1341141	3818961	304050	13
Phrynosoma	modestum	34.43653294	-106.9069639	3812208	324790	13
Phrynosoma	modestum	34.60522989	-107.3888875	3831860	280945	13
Phrynosoma	modestum	34.11853527	-106.8122052	3776781	332869	13
Phrynosoma	modestum	34.12123793	-106.809326	3777076	333140	13
Phrynosoma	modestum	34.14435404	-106.9735638	3779921	318041	13
Phrynosoma	modestum	34.14457331	-106.9760074	3779949	317816	13
Phrynosoma	modestum	34.14460089	-106.9760157	3779953	317815	13
Phrynosoma	modestum	34.13939841	-106.9648284	3779356	318836	13
Phrynosoma	modestum	34.13531777	-106.9601714	3778895	319256	13
Pituophis	catenifer	34.322614	-106.640425	3799146	349077	13
Pituophis	catenifer	34.331117	-106.632807	3800077	349793	13
Pituophis	catenifer	34.3470605	-106.6226349	3801831	350758	13
Pituophis	catenifer	34.3470605	-106.6226349	3801831	350758	13
Pituophis	catenifer	34.337433	-106.722029	3800913	341597	13
Pituophis	catenifer	34.337195	-106.699141	3800852	343702	13
Pituophis	catenifer	34.357584	-106.688476	3803096	344721	13
Pituophis	catenifer	35.52731878	-106.1567619	3932138	395122	13
Pituophis	catenifer	34.421333	-106.733747	3810237	340678	13
Pituophis	catenifer	33.01532057	-105.99665	3653426	406911	13
Pituophis	catenifer	34.364328	-106.634203	3803763	349724	13
Pituophis	catenifer	34.337155	-106.627472	3800739	350295	13
Pituophis	catenifer	34.357232	-106.688667	3803058	344702	13
Pituophis	catenifer	35.85048214	-106.6215615	3968578	353570	13
Pituophis	catenifer	34.9091758	-106.0522515	3863476	403872	13
Pituophis	catenifer	32.11099871	-104.4361351	3552878	553196	13
Pituophis	catenifer	32.84879001	-104.9087143	3634527	508542	13
Pituophis	catenifer	35.50146438	-106.8240162	3930185	334568	13
Pituophis	catenifer	34.05715032	-107.0623725	3770411	309656	13
Pituophis	catenifer	34.41673195	-106.8279056	3809878	332015	13
Pituophis	catenifer	32.54649541	-107.4794738	3603724	267169	13
Pituophis	catenifer	31.52661385	-108.9757003	3489742	692200	12
Pituophis	catenifer	31.54088538	-108.8856592	3491486	700720	12
Pituophis	catenifer	32.42918112	-104.2872032	3588232	567012	13
Pituophis	catenifer	35.78792632	-103.9673617	3960918	593319	13
Pituophis	catenifer	35.18868939	-105.4068339	3894044	462961	13
Pituophis	catenifer	34.00526231	-106.9846488	3764515	316719	13
Pituophis	catenifer	34.10435812	-107.283656	3776081	289346	13
Pituophis	catenifer	36.91425939	-103.8212824	4086009	604997	13
Pituophis	catenifer	35.11553985	-106.7947079	3887329	336451	13
Pituophis	catenifer	33.14796377	-107.0814137	3669619	305870	13
Pituophis	catenifer	34.75098272	-107.3284231	3847898	286865	13
Pituophis	catenifer	34.11369321	-107.2537082	3777055	292132	13
Pituophis	catenifer	33.8753895	-107.7053683	3751633	249765	13
Pituophis	catenifer	33.68694579	-107.5730932	3730417	261481	13
Pituophis	catenifer	34.0342492	-107.0473202	3767843	310995	13
Pituophis	catenifer	34.02324929	-107.0409874	3766612	311555	13

Pituophis	catenifer	36.26607693	-106.4227473	4014399	372199	13
Pituophis	catenifer	36.23957855	-106.4195564	4011456	372442	13
Pituophis	catenifer	31.91442196	-109.1433834	3532454	675543	12
Pituophis	catenifer	31.90849101	-109.1114356	3531848	678576	12
Pituophis	catenifer	31.88157546	-109.0669137	3528938	682840	12
Pituophis	catenifer	31.90213024	-109.1001513	3531162	679655	12
Pituophis	catenifer	31.90303992	-109.1015106	3531260	679525	12
Pituophis	catenifer	34.78881771	-107.9328198	3853544	231648	13
Pituophis	catenifer	33.9318552	-107.0124301	3756424	313993	13
Pituophis	catenifer	34.00742769	-106.9453899	3764685	320350	13
Pituophis	catenifer	34.10922951	-107.1211935	3776298	304346	13
Pituophis	catenifer	33.9110027	-106.9279331	3753961	321761	13
Pituophis	catenifer	34.46359945	-107.1582622	3815674	301761	13
Pituophis	catenifer	34.86334456	-106.0786635	3858419	401404	13
Pituophis	catenifer	35.61432721	-106.1291143	3941759	397740	13
Plethodon	neomexicanus	35.96426077	-106.4361873	3980937	370497	13
Plethodon	neomexicanus	35.96468414	-106.4362163	3980984	370495	13
Plethodon	neomexicanus	35.96493644	-106.4366682	3981013	370454	13
Plethodon	neomexicanus	35.96492437	-106.4373334	3981012	370394	13
Plethodon	neomexicanus	35.96455825	-106.4375445	3980972	370375	13
Plethodon	neomexicanus	35.96489168	-106.4375244	3981009	370377	13
Plethodon	neomexicanus	35.96529753	-106.4382046	3981055	370317	13
Plethodon	neomexicanus	35.96555779	-106.437989	3981084	370336	13
Plethodon	neomexicanus	35.96527456	-106.4375564	3981052	370375	13
Plethodon	neomexicanus	35.96557958	-106.4378935	3981086	370345	13
Pseudacris	triseriata	35.96048799	-106.724464	3980940	344493	13
Pseudacris	triseriata	36.04154033	-106.846466	3990133	333660	13
Rana	blairi	33.08536369	-107.1769619	3662858	296813	13
Rana	blairi	36.06718853	-104.3719092	3991583	556560	13
Rana	pipiens	36.60703523	-106.3821288	4052170	376390	13
Rana	pipiens	36.6079357	-106.3813104	4052269	376464	13
Rhinocheilus	lecontei	34.392656	-106.899701	3807330	325366	13
Rhinocheilus	lecontei	34.351031	-106.879667	3802679	327122	13
Rhinocheilus	lecontei	34.389004	-106.905131	3806934	324859	13
Rhinocheilus	lecontei	34.381703	-106.919722	3806149	323502	13
Rhinocheilus	lecontei	34.335055	-106.696256	3800610	343963	13
Rhinocheilus	lecontei	31.96724522	-108.3377586	3539901	751592	12
Rhinocheilus	lecontei	31.95989639	-108.6848479	3538331	718799	12
Rhinocheilus	lecontei	31.9573446	-108.70896	3537999	716526	12
Rhinocheilus	lecontei	31.9747316	-108.579207	3540194	728749	12

Rhinocheilus	lecontei	32.42872682	-104.2724722	3588191	568397	13
Rhinocheilus	lecontei	32.31306645	-107.8158476	3578621	234889	13
Rhinocheilus	lecontei	34.50723924	-106.7678536	3819818	337710	13
Rhinocheilus	lecontei	32.40129059	-108.7258592	3587192	713888	12
Rhinocheilus	lecontei	31.88411518	-109.0713214	3529213	682418	12
Rhinocheilus	lecontei	31.46762151	-109.4526297	3482464	647003	12
Rhinocheilus	lecontei	31.87074185	-109.0469681	3527771	684748	12
Rhinocheilus	lecontei	31.88737281	-109.0766544	3529565	681907	12
Rhinocheilus	lecontei	31.89149394	-109.0832548	3530011	681274	12
Rhinocheilus	lecontei	32.05718338	-109.00724	3548510	688126	12
Rhinocheilus	lecontei	32.03583651	-109.0277633	3546108	686232	12
Rhinocheilus	lecontei	32.04979171	-109.0144411	3547678	687461	12
Salvadora	deserticola	32.94890623	-107.2463824	3647862	290009	13
Salvadora	grahamiae	32.52867096	-107.1974126	3601166	293620	13
Salvadora	grahamiae	35.61346689	-106.1732599	3941711	393740	13
Salvadora	grahamiae	35.61332876	-106.1736313	3941696	393707	13
Salvadora	grahamiae	35.57674854	-106.1807673	3937646	393012	13
Scaphiopus	couchi	34.95385629	-104.6133711	3867994	535300	13
Scaphiopus	couchi	34.95457856	-104.5818707	3868085	538176	13
Scaphiopus	couchi	33.20258427	-106.8070459	3675200	331568	13
Scaphiopus	couchi	33.13154672	-107.1002814	3667833	304074	13
Scaphiopus	couchi	33.57948015	-107.1860725	3717672	297112	13
Scaphiopus	couchi	33.93316051	-106.8323076	3756257	330646	13
Scaphiopus	couchi	32.40538255	-108.7257448	3587646	713889	12
Sceloporus	clarkii	32.09448804	-108.9752734	3552703	691067	12
Sceloporus	clarkii	32.09674923	-108.9747512	3552954	691111	12
Sceloporus	clarkii	32.09502834	-108.9704172	3552771	691524	12
Sceloporus	jarrovi	31.51948605	-109.0039257	3488902	689534	12
Sceloporus	jarrovi	31.91785796	-109.2744943	3532630	663139	12
Sceloporus	magister	34.10454118	-106.8216045	3775245	331974	13
Sceloporus	magister	34.2042984	-106.8175349	3786301	332547	13
Sceloporus	magister	34.20444894	-106.8176245	3786318	332539	13
Sceloporus	magister	34.16228411	-106.8036242	3781619	333746	13
Sceloporus	magister	34.15662959	-106.7154793	3780852	341861	13
Sceloporus	magister	33.96024252	-106.7597726	3759142	337403	13
Sceloporus	magister	33.97629303	-106.7621484	3760926	337214	13
Sceloporus	magister	34.14427316	-106.9678317	3779902	318569	13
Sceloporus	magister	34.14427316	-106.9678317	3779902	318569	13
Sceloporus	magister	34.14449427	-106.9679952	3779926	318554	13
Sceloporus	magister	34.14599438	-106.9924854	3780137	316299	13
Sceloporus	magister	34.44237554	-106.9104108	3812862	324485	13
Sceloporus	magister	34.00301177	-106.9912146	3764277	316108	13
Sceloporus	magister	34.00251573	-106.9913039	3764222	316098	13
Sceloporus	magister	34.14551703	-106.817158	3779782	332465	13
Sceloporus	magister	33.83493718	-106.6813045	3745125	344426	13
Sceloporus	magister	33.82361859	-106.7026699	3743902	342428	13
Sceloporus	magister	33.85256113	-106.6965431	3747103	343048	13
Sceloporus	magister	33.95653353	-106.925136	3759006	322114	13
Sceloporus	magister	33.90964248	-106.9542931	3753856	319321	13
Sceloporus	magister	33.90983569	-106.9540221	3753877	319346	13

Sceloporus	magister	33.91156856	-106.9647646	3754088	318356	13
Sceloporus	magister	34.14429797	-106.9673573	3779904	318613	13
Sceloporus	magister	34.2402488	-107.0060796	3790615	315252	13
Sceloporus	magister	34.24022407	-107.00638	3790612	315224	13
Sceloporus	magister	34.23845666	-107.0071454	3790418	315150	13
Sceloporus	magister	34.23902471	-107.0068468	3790480	315178	13
Sceloporus	magister	33.91274563	-106.9286293	3754156	321700	13
Sceloporus	magister	33.91105483	-106.9308288	3753972	321493	13
Sceloporus	magister	33.90823759	-106.9384212	3753673	320785	13
Sceloporus	magister	33.91070371	-106.9411046	3753951	320542	13
Sceloporus	magister	33.90982085	-106.9532057	3753874	319421	13
Sceloporus	magister	33.90907436	-106.9555948	3753796	319199	13
Sceloporus	magister	33.90111364	-106.9819646	3752960	316744	13
Sceloporus	magister	34.10795328	-106.8216597	3775623	331976	13
Sceloporus	poinsetti	33.86737757	-107.5330195	3750338	265689	13
Sceloporus	poinsetti	33.85303278	-107.5503159	3748787	264049	13
Sceloporus	poinsetti	33.84371881	-107.5619524	3747780	262946	13
Sceloporus	poinsetti	33.84308338	-107.5626582	3747712	262879	13
Sceloporus	poinsetti	33.7148442	-107.5247178	3733401	266042	13
Sceloporus	poinsetti	33.71489273	-107.5247014	3733406	266043	13
Sceloporus	poinsetti	33.71454857	-107.523858	3733366	266121	13
Sceloporus	poinsetti	33.81556517	-107.5780435	3744695	261379	13
Sceloporus	poinsetti	33.81066268	-107.5870281	3744172	260533	13
Sceloporus	poinsetti	33.81928171	-107.5741262	3745098	261752	13
Sceloporus	poinsetti	33.71743413	-107.5174153	3733672	266726	13
Sceloporus	poinsetti	33.7172022	-107.5190182	3733650	266576	13
Sceloporus	poinsetti	33.71481931	-107.5246316	3733398	266050	13
Sceloporus	poinsetti	33.80849504	-107.4244748	3743565	275578	13
Sceloporus	poinsetti	33.80876779	-107.4249123	3743596	275538	13
Sceloporus	poinsetti	33.80961277	-107.424115	3743688	275614	13
Sceloporus	poinsetti	33.71729147	-107.5189882	3733659	266580	13
Sceloporus	poinsetti	33.78603749	-107.4933188	3741227	269143	13
Sceloporus	poinsetti	33.79069397	-107.4882334	3741732	269627	13
Sceloporus	poinsetti	33.79069397	-107.4882334	3741732	269627	13
Sceloporus	poinsetti	33.57774829	-107.4074014	3717936	276561	13
Sceloporus	poinsetti	33.5775695	-107.4072992	3717916	276571	13
Sceloporus	poinsetti	33.57753698	-107.407155	3717912	276584	13
Sceloporus	poinsetti	33.49851256	-107.4178143	3709170	275390	13
Sceloporus	poinsetti	33.56266589	-108.1140781	3717399	767911	12
Sceloporus	poinsetti	33.56307015	-108.1164455	3717437	767689	12
Sceloporus	poinsetti	33.56296018	-108.1148381	3717429	767839	12
Sceloporus	poinsetti	33.56270294	-108.1129822	3717406	768012	12
Sceloporus	poinsetti	33.56388361	-108.112107	3717539	768090	12
Sceloporus	poinsetti	33.78571906	-107.492772	3741190	269193	13
Sceloporus	poinsetti	33.92963802	-107.3388966	3756818	283807	13
Sceloporus	poinsetti	33.88027221	-107.4058986	3751486	277484	13
Sceloporus	poinsetti	33.88014439	-107.4059873	3751472	277475	13
Sceloporus	poinsetti	33.88214657	-107.4056288	3751693	277514	13
Sceloporus	poinsetti	33.86777999	-107.4073672	3750103	277315	13
Sceloporus	poinsetti	33.86618659	-107.4065863	3749925	277384	13

Sceloporus	poinsetti	33.86668196	-107.4066345	3749980	277380	13
Sceloporus	poinsetti	33.8666434	-107.4066881	3749976	277375	13
Sceloporus	poinsetti	33.86944774	-107.4068284	3750287	277370	13
Sceloporus	poinsetti	33.91328459	-107.3917439	3755117	278879	13
Sceloporus	poinsetti	33.94366035	-107.4382095	3758587	274662	13
Sceloporus	poinsetti	33.82057638	-107.5733551	3745240	261827	13
Sceloporus	poinsetti	33.82337376	-107.571287	3745545	262026	13
Sceloporus	poinsetti	33.85818464	-107.5832072	3749434	261019	13
Sceloporus	poinsetti	33.95172508	-106.9689368	3758549	318056	13
Sceloporus	poinsetti	33.95180304	-106.9692408	3758559	318028	13
Sceloporus	poinsetti	33.95085546	-106.9685043	3758452	318094	13
Sceloporus	poinsetti	33.95085546	-106.9685043	3758452	318094	13
Sceloporus	poinsetti	33.90994859	-106.954729	3753891	319281	13
Sceloporus	poinsetti	33.90979612	-106.9546139	3753874	319291	13
Sceloporus	poinsetti	33.9098703	-106.9540598	3753881	319343	13
Sceloporus	poinsetti	34.23258036	-106.9849538	3789726	317181	13
Sceloporus	poinsetti	33.87854185	-107.4056424	3751293	277503	13
Sceloporus	poinsetti	33.67227235	-107.5881064	3728825	260048	13
Sceloporus	poinsetti	33.67227235	-107.5881064	3728825	260048	13
Sceloporus	poinsetti	33.66971838	-107.5918637	3728550	259692	13
Sceloporus	poinsetti	33.669537	-107.5919472	3728530	259684	13
Sceloporus	poinsetti	33.66941337	-107.5920496	3728517	259674	13
Sceloporus	poinsetti	33.91869192	-107.080907	3755090	307633	13
Sceloporus	poinsetti	33.92274977	-107.0835466	3755545	307398	13
Sceloporus	poinsetti	33.925349	-107.0856024	3755837	307214	13
Sceloporus	poinsetti	33.92533542	-107.085532	3755836	307221	13
Sceloporus	poinsetti	33.92554111	-107.0857091	3755859	307205	13
Sceloporus	poinsetti	33.92532938	-107.0855055	3755835	307223	13
Sceloporus	poinsetti	33.91753497	-107.0810631	3754962	307616	13
Sceloporus	poinsetti	34.07671326	-107.152547	3772753	301378	13
Sceloporus	poinsetti	34.07678643	-107.1527099	3772761	301363	13
Sceloporus	poinsetti	34.07643733	-107.1548459	3772726	301165	13
Sceloporus	poinsetti	34.07623993	-107.1554996	3772706	301104	13
Sceloporus	poinsetti	34.18837069	-107.2231035	3785276	295136	13
Sceloporus	poinsetti	34.18849901	-107.2246892	3785293	294990	13
Sceloporus	poinsetti	34.18826792	-107.2244816	3785267	295009	13
Sceloporus	poinsetti	34.18813096	-107.223725	3785251	295078	13
Sceloporus	poinsetti	34.28606009	-107.2738526	3796214	290700	13
Sceloporus	poinsetti	34.28606009	-107.2738526	3796214	290700	13
Sceloporus	poinsetti	34.28597393	-107.2762726	3796210	290477	13
Sceloporus	poinsetti	34.28597703	-107.2764544	3796211	290461	13
Sceloporus	poinsetti	34.28615715	-107.2787322	3796235	290251	13
Sceloporus	poinsetti	34.28606546	-107.2789656	3796226	290230	13
Sceloporus	poinsetti	34.28619948	-107.2792575	3796241	290203	13
Sceloporus	poinsetti	34.00191751	-107.144025	3764441	301990	13
Sceloporus	poinsetti	34.00190938	-107.1436904	3764439	302021	13
Sceloporus	poinsetti	34.00173269	-107.1437589	3764420	302015	13
Sceloporus	poinsetti	33.97751335	-107.2575077	3761959	291448	13
Sceloporus	undulatus	32.64168651	-104.2756631	3611797	567937	13
Sceloporus	undulatus	33.69288144	-105.92731	3728490	414056	13

Sceloporus	undulatus	35.264842	-105.3368406	3902465	469362	13
Sceloporus	undulatus	35.826427	-106.6399954	3965938	351861	13
Sceloporus	undulatus	35.86107275	-106.2162654	3969222	390186	13
Sceloporus	undulatus	35.86036624	-106.2222412	3969150	389645	13
Sceloporus	undulatus	35.76119215	-106.2597359	3958193	386118	13
Sceloporus	undulatus	33.58120901	-107.4111902	3718328	276219	13
Sceloporus	undulatus	33.57923297	-107.4105925	3718107	276269	13
Sceloporus	undulatus	35.82749954	-106.6400698	3966057	351856	13
Sceloporus	undulatus	35.82729444	-106.6407058	3966035	351798	13
Sceloporus	undulatus	35.82700283	-106.6404493	3966002	351821	13
Sceloporus	undulatus	35.82560289	-106.6392627	3965845	351926	13
Sceloporus	undulatus	35.82305647	-106.6372891	3965560	352099	13
Sceloporus	undulatus	35.82417034	-106.6373319	3965683	352097	13
Sceloporus	undulatus	35.82684433	-106.6438104	3965990	351517	13
Sceloporus	undulatus	36.04796279	-104.3769096	3989447	556123	13
Sceloporus	undulatus	35.54700879	-106.7827318	3935168	338404	13
Sceloporus	undulatus	32.81951127	-106.2753473	3631998	380616	13
Sceloporus	undulatus	35.08003981	-106.4796685	3882920	365104	13
Sceloporus	undulatus	36.7833546	-105.0704831	4070842	493710	13
Sceloporus	undulatus	33.85519951	-107.5460628	3749017	264448	13
Sceloporus	undulatus	34.0181349	-107.1339537	3766220	302958	13
Sceloporus	undulatus	34.0181349	-107.1339537	3766220	302958	13
Sceloporus	undulatus	34.0188757	-107.1337421	3766301	302979	13
Sceloporus	undulatus	34.73678981	-107.9730692	3847881	227793	13
Sceloporus	undulatus	34.94433864	-107.8388624	3870551	240737	13
Sceloporus	undulatus	35.49900522	-106.9238204	3930084	325509	13
Sceloporus	undulatus	35.50110354	-106.9234088	3930316	325551	13
Sceloporus	undulatus	35.83865644	-104.2940356	3966283	563756	13
Sceloporus	undulatus	33.79415452	-107.6040244	3742381	258913	13
Sceloporus	undulatus	35.88428048	-106.6637541	3972391	349824	13
Sceloporus	undulatus	35.88258918	-106.6642925	3972205	349772	13
Sceloporus	undulatus	33.81545286	-107.5808298	3744689	261120	13
Sceloporus	undulatus	33.79900714	-107.6014111	3742913	259169	13
Sceloporus	undulatus	33.9473825	-107.5026212	3759143	268718	13
Sceloporus	undulatus	36.07067733	-104.334677	3991992	559910	13
Sceloporus	undulatus	36.07083005	-104.3347654	3992009	559902	13
Sceloporus	undulatus	36.07084262	-104.354366	3991998	558137	13
Sceloporus	undulatus	36.04767756	-104.3706981	3989419	556683	13
Sceloporus	undulatus	36.07175943	-104.3532976	3992101	558233	13
Sceloporus	undulatus	36.07080599	-104.3525942	3991995	558297	13
Sceloporus	undulatus	33.79078341	-107.4880788	3741741	269641	13
Sceloporus	undulatus	33.79081517	-107.4879731	3741745	269651	13
Sceloporus	undulatus	33.5776078	-107.4071791	3717920	276582	13
Sceloporus	undulatus	34.75122496	-107.3282767	3847924	286879	13
Sceloporus	undulatus	34.13974877	-106.8205767	3779148	332138	13
Sceloporus	undulatus	33.60009503	-108.0583378	3721696	772969	12
Sceloporus	undulatus	34.22230524	-107.4406802	3789499	275172	13
Sceloporus	undulatus	34.23291036	-107.4615511	3790721	273277	13
Sceloporus	undulatus	34.23296174	-107.4614682	3790727	273285	13
Sceloporus	undulatus	34.2348812	-107.4672982	3790953	272753	13

Sceloporus	undulatus	34.23538486	-107.4800639	3791037	271578	13
Sceloporus	undulatus	34.23558335	-107.4794427	3791058	271636	13
Sceloporus	undulatus	33.82388882	-106.70339	3743934	342362	13
Sceloporus	undulatus	36.31395176	-106.5823145	4019933	357951	13
Sceloporus	undulatus	36.31384112	-106.5793145	4019916	358220	13
Sceloporus	undulatus	36.31167809	-106.5833031	4019682	357858	13
Sceloporus	undulatus	35.41682778	-106.2888341	3920032	382988	13
Sceloporus	undulatus	35.41369085	-106.3377805	3919743	378539	13
Sceloporus	undulatus	35.41366135	-106.3382214	3919740	378499	13
Sceloporus	undulatus	35.41371156	-106.3382823	3919746	378493	13
Sceloporus	undulatus	35.4141625	-106.3385158	3919796	378473	13
Sceloporus	undulatus	35.41453793	-106.3385816	3919838	378467	13
Sceloporus	undulatus	35.38993092	-106.2829012	3917041	383487	13
Sceloporus	undulatus	34.13874429	-108.4961063	3780372	730879	12
Sceloporus	undulatus	34.13820969	-108.4982374	3780308	730684	12
Sceloporus	undulatus	35.25341185	-107.1587679	3903282	303602	13
Sceloporus	undulatus	35.2573992	-107.1541574	3903715	304031	13
Sceloporus	undulatus	35.24969942	-107.1496794	3902852	304420	13
Sceloporus	undulatus	35.22139189	-106.4840561	3898604	364938	13
Sceloporus	undulatus	33.91357234	-106.9452033	3754276	320169	13
Sceloporus	undulatus	35.61277212	-106.1734689	3941634	393721	13
Sceloporus	undulatus	35.61346069	-106.1731927	3941710	393746	13
Sceloporus	undulatus	35.6138595	-106.1730844	3941754	393757	13
Sceloporus	undulatus	35.55745122	-106.1681703	3935492	394128	13
Sceloporus	undulatus	35.55772849	-106.1693707	3935524	394019	13
Sceloporus	undulatus	35.55770444	-106.1718214	3935524	393797	13
Sceloporus	undulatus	34.01809593	-107.1432787	3766233	302097	13
Sceloporus	undulatus	34.01800674	-107.1457313	3766228	301870	13
Sceloporus	undulatus	34.01693135	-107.1435452	3766105	302070	13
Sceloporus	undulatus	34.01687996	-107.1425811	3766097	302159	13
Sceloporus	undulatus	35.03600422	-106.3463807	3877864	377190	13
Sceloporus	undulatus	35.60864143	-106.1339187	3941134	397297	13
Sceloporus	undulatus	35.60789511	-106.1346128	3941052	397234	13
Sceloporus	undulatus	35.59171636	-106.1688101	3939294	394115	13
Sceloporus	undulatus	35.59156188	-106.1687465	3939276	394120	13
Sceloporus	undulatus	35.6142589	-106.1290258	3941752	397748	13
Sceloporus	undulatus	35.60863984	-106.1338729	3941134	397302	13
Sceloporus	undulatus	35.60497141	-106.1391666	3940732	396817	13
Sceloporus	undulatus	35.60494551	-106.1392846	3940730	396807	13
Sceloporus	undulatus	35.59377411	-106.1605752	3939513	394863	13
Sceloporus	undulatus	35.5937431	-106.1606027	3939510	394861	13
Sceloporus	undulatus	35.61856301	-106.16365	3942266	394617	13
Sceloporus	undulatus	35.61810452	-106.1642331	3942215	394564	13
Sceloporus	undulatus	35.57752403	-106.1790541	3937730	393168	13
Sceloporus	undulatus	35.5776304	-106.1789385	3937742	393178	13
Sceloporus	undulatus	35.56803161	-106.1849478	3936684	392621	13
Sceloporus	undulatus	35.61238873	-106.1806971	3941599	393065	13
Sceloporus	undulatus	35.60997063	-106.1816208	3941332	392978	13
Sceloporus	undulatus	35.59792517	-106.1705549	3939984	393965	13
Sceloporus	undulatus	35.60951357	-106.1744007	3941274	393632	13

Sceloporus	undulatus	35.61623552	-106.1904836	3942037	392184	13
Sceloporus	undulatus	33.8766089	-106.5756623	3749591	354273	13
Sceloporus	virgatus	31.87409059	-109.2327064	3527841	667169	12
Senticolis	triaspis	31.93270264	-109.1785684	3534424	672182	12
Sistrurus	catenatus	34.330802	-106.728928	3800189	340949	13
Sistrurus	catenatus	34.342318	-106.723422	3801457	341478	13
Sistrurus	catenatus	34.334671	-106.632823	3800472	349798	13
Sistrurus	catenatus	34.338826	-106.629074	3800927	350151	13
Sistrurus	catenatus	34.338702	-106.629181	3800913	350141	13
Sistrurus	catenatus	34.399421	-106.678368	3807721	345727	13
Sistrurus	catenatus	34.384243	-106.931581	3806452	322417	13
Sistrurus	catenatus	34.330603	-106.729867	3800168	340863	13
Sistrurus	catenatus	34.334552	-106.723932	3800597	341416	13
Sistrurus	catenatus	34.34515527	-106.6951315	3801728	344085	13
Sistrurus	catenatus	34.378228	-106.932407	3805786	322328	13
Sistrurus	catenatus	34.339087	-106.629415	3800956	350120	13
Sistrurus	catenatus	34.34207132	-106.6231142	3801278	350705	13
Sistrurus	catenatus	34.406934	-106.877296	3808875	327455	13
Sistrurus	catenatus	34.344401	-106.621226	3801534	350882	13
Sistrurus	catenatus	34.39266	-106.656422	3806938	347732	13
Sistrurus	catenatus	34.365151	-106.684535	3803930	345097	13
Sistrurus	catenatus	34.396797	-106.678294	3807430	345729	13
Sistrurus	catenatus	34.307497	-106.692043	3797547	344300	13
Spea	bombifrons	34.95468996	-104.58783	3868095	537632	13
Spea	multiplicata	34.9546519	-104.6064166	3868084	535935	13
Spea	multiplicata	35.1314301	-106.7856103	3889077	337312	13
Tantilla	nigriceps	34.40208	-106.605461	3807907	352434	13
Tantilla	nigriceps	36.92676963	-103.4688358	4087843	636372	13
Tantilla	nigriceps	35.10549121	-106.7977604	3886220	336153	13
Tantilla	nigriceps	32.09896574	-108.3225463	3554543	752668	12
Terrapene	ornata	34.4072113	-106.6890554	3808601	344759	13
Terrapene	ornata	34.3725853	-106.6806997	3804748	345463	13
Terrapene	ornata	34.3719233	-106.6811518	3804675	345421	13
Terrapene	ornata	34.392828	-106.6566169	3806957	347715	13
Terrapene	ornata	34.3695067	-106.6824447	3804409	345297	13
Terrapene	ornata	34.3915509	-106.6785176	3806848	345699	13
Terrapene	ornata	34.40663	-106.6783958	3808520	345738	13
Terrapene	ornata	34.4039733	-106.674282	3808219	346111	13
Terrapene	ornata	34.3934094	-106.6571403	3807022	347668	13
Terrapene	ornata	34.4045296	-106.6765379	3808285	345905	13
Terrapene	ornata	34.3823858	-106.6785311	3805832	345681	13
Terrapene	ornata	34.3651164	-106.6852589	3803927	345030	13
Terrapene	ornata	34.3649642	-106.6847849	3803909	345074	13
Terrapene	ornata	34.3937538	-106.6786252	3807093	345693	13
Terrapene	ornata	34.3760448	-106.6788991	3805129	345635	13
Terrapene	ornata	34.3822247	-106.6785136	3805814	345682	13
Terrapene	ornata	34.3944456	-106.6579331	3807138	347597	13
Terrapene	ornata	34.3976471	-106.6604451	3807497	347371	13
Terrapene	ornata	34.3551395	-106.6899184	3802827	344583	13

Terrapene	ornata	34.3868147	-106.6785221	3806323	345690	13
Terrapene	ornata	34.3711662	-106.681475	3804592	345389	13
Terrapene	ornata	34.3477536	-106.6937636	3802014	344216	13
Terrapene	ornata	34.3961813	-106.659285	3807333	347475	13
Terrapene	ornata	34.3370482	-106.699445	3800836	343674	13
Terrapene	ornata	34.3979064	-106.6784507	3807553	345717	13
Terrapene	ornata	34.37308101	-106.6801437	3804802	345515	13
Terrapene	ornata	34.35861787	-106.6880756	3803210	344759	13
Terrapene	ornata	34.34155131	-106.6970195	3801331	343905	13
Terrapene	ornata	34.34654516	-106.6944347	3801881	344152	13
Terrapene	ornata	34.3930571	-106.6784908	3807015	345704	13
Terrapene	ornata	34.39740378	-106.6784487	3807497	345716	13
Terrapene	ornata	34.40467819	-106.6772215	3808302	345842	13
Terrapene	ornata	34.40251448	-106.6684315	3808049	346646	13
Terrapene	ornata	34.38531708	-106.6784756	3806157	345691	13
Terrapene	ornata	34.34671951	-106.694308	3801900	344164	13
Terrapene	ornata	34.34671196	-106.6943122	3801900	344164	13
Terrapene	ornata	34.36441806	-106.6851411	3803849	345040	13
Terrapene	ornata	34.38707267	-106.6785048	3806352	345692	13
Terrapene	ornata	34.3726428	-106.6809175	3804755	345443	13
Terrapene	ornata	34.37238908	-106.6789815	3804724	345621	13
Terrapene	ornata	34.33920622	-106.6982178	3801073	343790	13
Terrapene	ornata	34.06924272	-106.865976	3771404	327809	13
Terrapene	ornata	33.26098049	-106.8417861	3681732	328444	13
Terrapene	ornata	33.19907863	-106.9267435	3675011	320403	13
Terrapene	ornata	35.28256662	-104.2450479	3904640	568653	13
Terrapene	ornata	35.37934835	-103.4981378	3916148	636417	13
Thamnophis	cyrtopsis	33.90483261	-107.397761	3754192	278300	13
Thamnophis	cyrtopsis	31.9319336	-109.1850577	3534328	671570	12
Thamnophis	cyrtopsis	35.5775641	-106.1790531	3937735	393168	13
Thamnophis	elegans	36.52783161	-106.2369974	4043206	389257	13
Thamnophis	elegans	35.98501017	-106.4847046	3983305	366157	13
Thamnophis	elegans	36.03856266	-106.8478488	3989805	333529	13
Thamnophis	elegans	35.95097043	-106.7452164	3979918	342602	13
Thamnophis	elegans	36.03873692	-106.847231	3989823	333585	13
Thamnophis	elegans	35.99737977	-106.8071715	3985168	337110	13
Thamnophis	elegans	35.95097043	-106.7452164	3979918	342602	13
Thamnophis	elegans	36.03873692	-106.847231	3989823	333585	13
Thamnophis	elegans	35.99737977	-106.8071715	3985168	337110	13
Thamnophis	elegans	36.02540893	-104.3613402	3986955	557542	13
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Thamnophis	elegans	36.02782887	-106.8466786	3988612	333612	13
Thamnophis	elegans	34.87104736	-106.1419679	3859337	395627	13
Thamnophis	marcianus	34.417408	-106.842015	3809977	330719	13
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Tropidoclonion	lineatum	35.50110949	-103.4992381	3929651	636111	13
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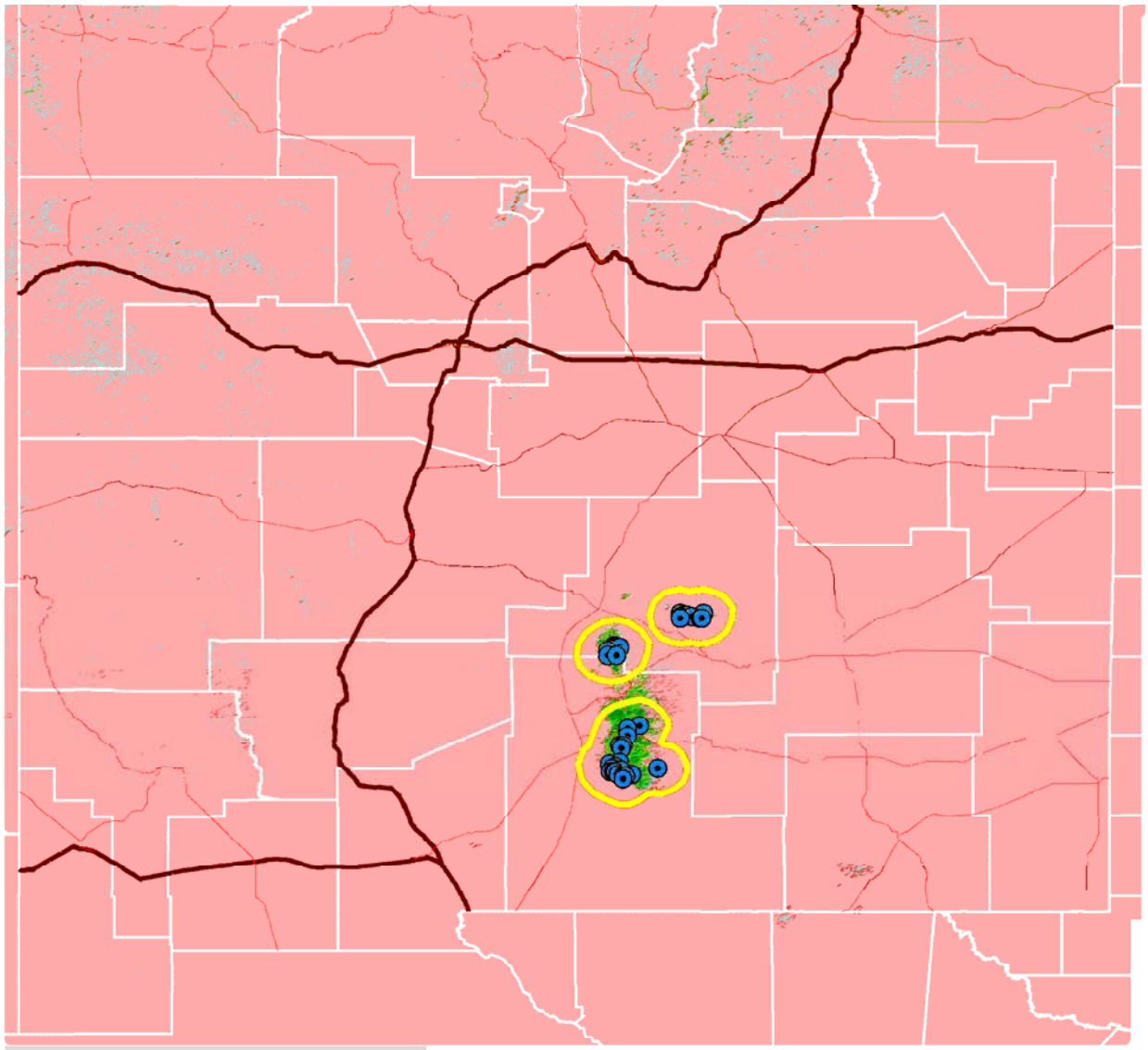
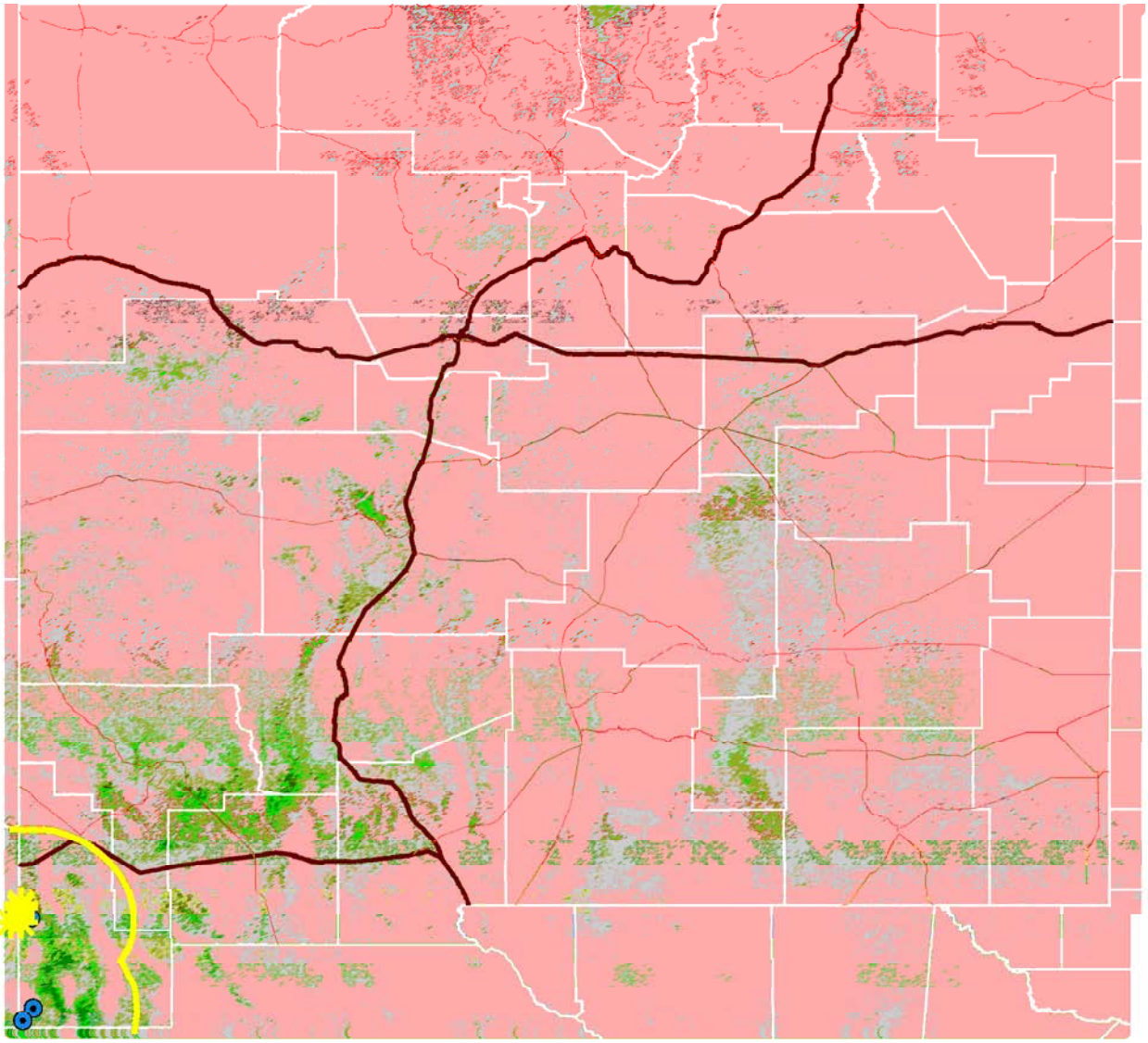
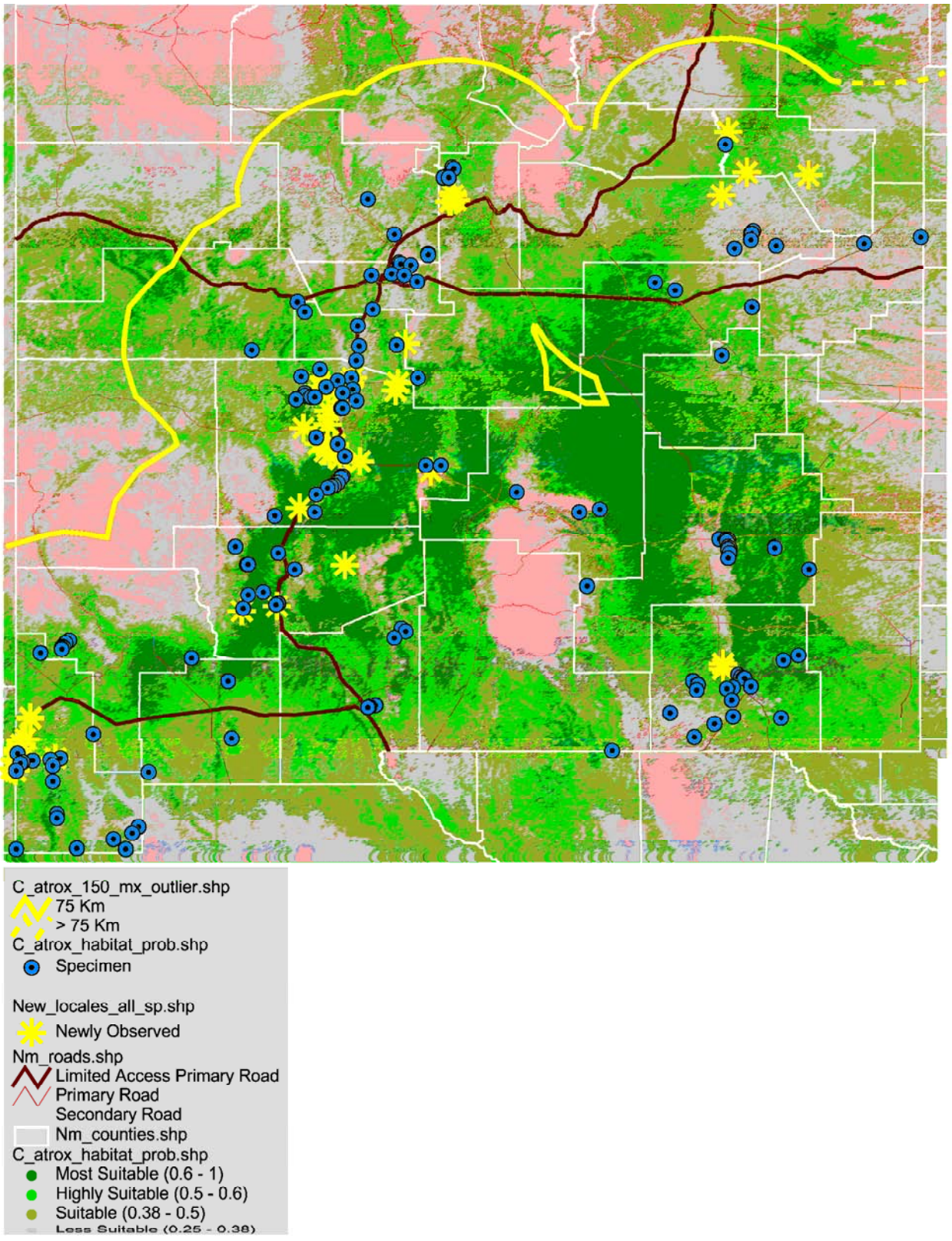
Appendix 6. Examples of individual maps of potential species distribution (Maps for all species of interest are available as electronic images and also in a common GIS format on the enclosed DVD)



Aneides hardii
Sacramento Mountains salamander



Bufo alvarius
Colorado River toad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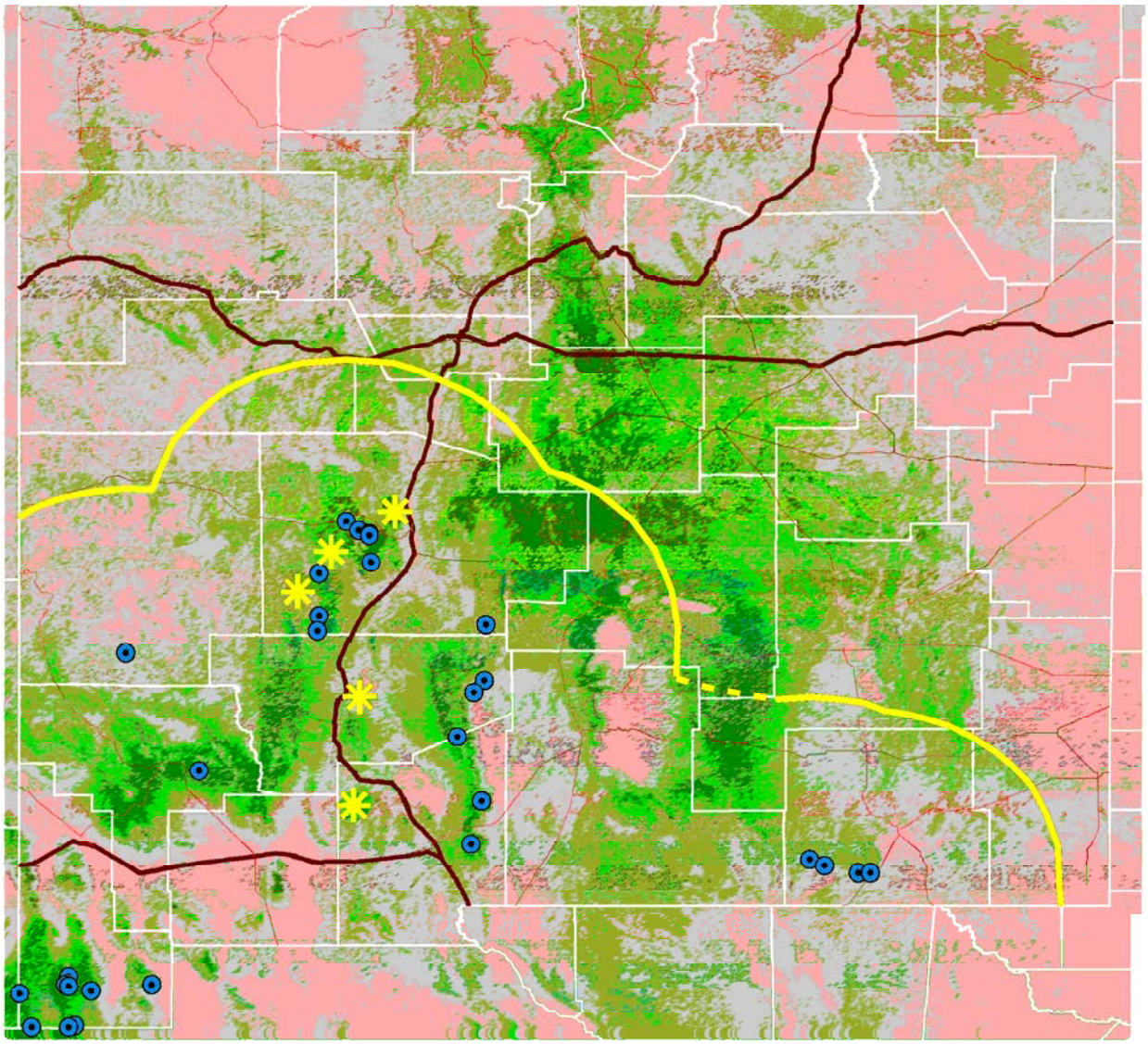
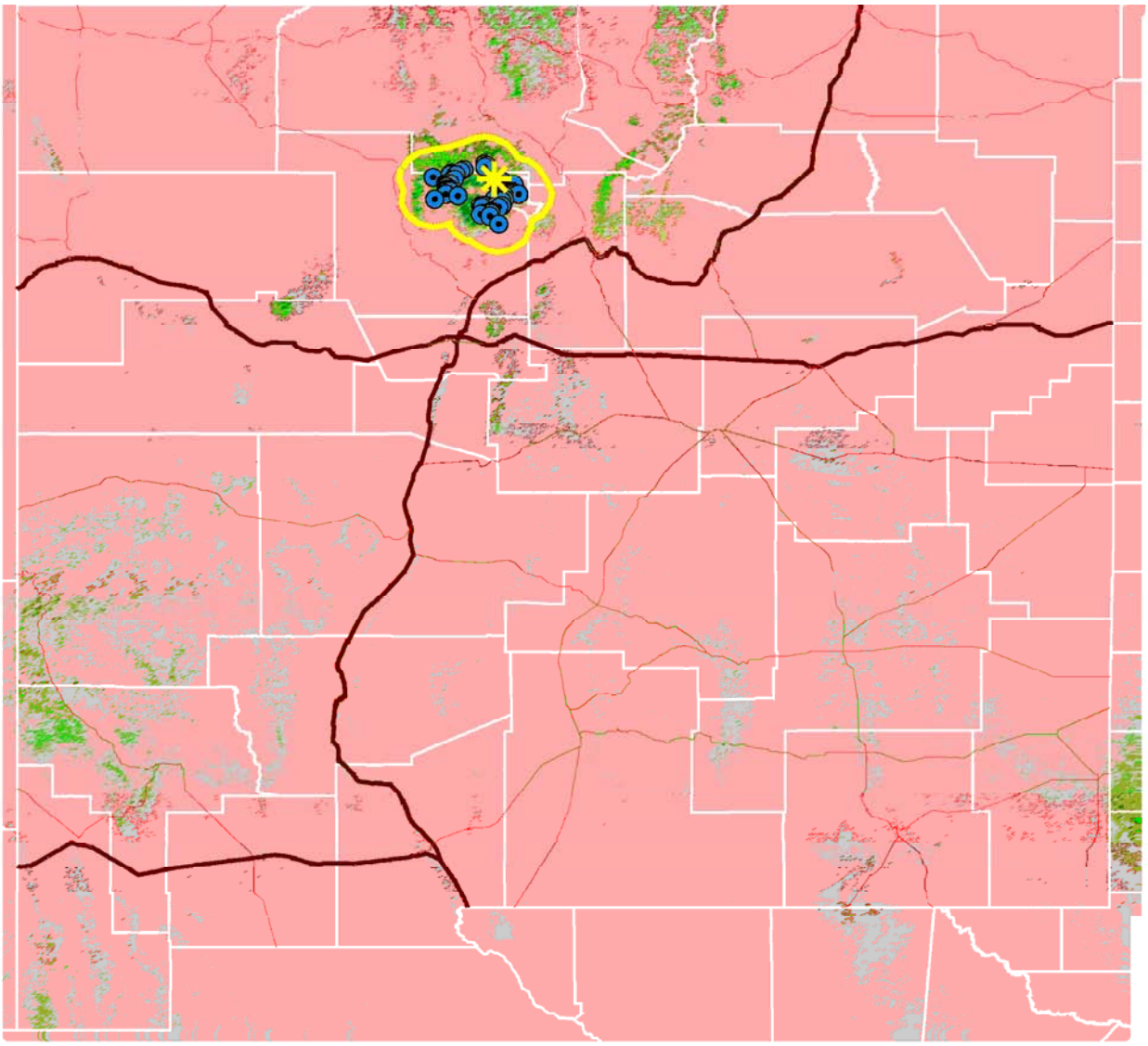
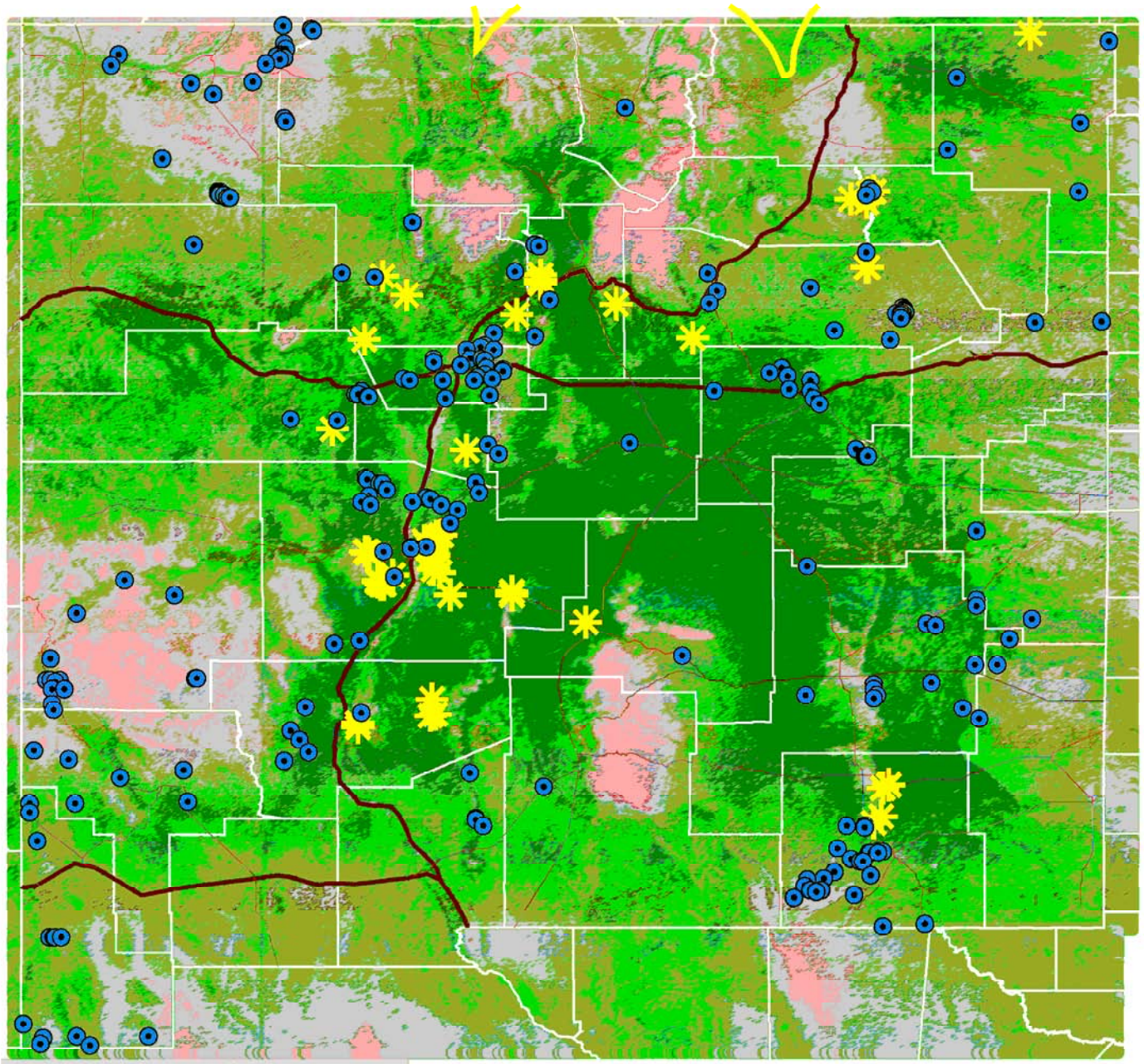
Specimen
New_locales_all_sp.shp
Newly Observed
Nm_roads.shp
Limited Access Primary Road
Primary Road
Secondary Road
Nm_counties.shp
C_atrox_habitat_prob.shp
Most Suitable (0.6 - 1)
Highly Suitable (0.5 - 0.6)
Suitable (0.38 - 0.5)
Less Suitable (0.25 - 0.38)



Crotalus lepidus
Mottled rock rattlesnake



Plethodon neomexicanus
Jemez Mountains salamander



Crotaphytus collaris
Western collared lizard