



Genetic variation in a desert aquatic snail (*Nymphophilus minckleyi*) from Cuatro Ciénegas, Coahuila, Mexico

Angela B. Moline^{1,2}, Stephen M. Shuster², Dean A. Hendrickson³ & Jane C. Marks²

¹Graduate Degree Program in Ecology, Colorado State University, E330 Anatomy-Zoology Building, Fort Collins, CO 80523, U.S.A.

Tel: 970-491-2329. Fax: 1 970-491-0649. E-mail: amoline@lamar.colostate.edu

²Department of Biological Sciences and Merriam-Powell Center For Environmental Research, Northern Arizona University, Flagstaff, AZ 86011, U.S.A.

³Texas Memorial Museum and Section of Integrative Biology, University of Texas, 1 Texas Longhorns #C0930, Austin, TX 78712, U.S.A.

Received 26 November 2002; in revised form 18 November 2003; accepted 7 December 2003

Key words: Allozymes, Wright's *F*-statistics, desert spring, hydrologic connectivity, population genetics, endangered species, management

Abstract

Nymphophilus minckleyi is a hydrobiid snail endemic to the freshwater spring ecosystem of Cuatro Ciénegas, Mexico. We used seven allozyme loci to examine the genetic substructure of *N. minckleyi* from 14 sites (sub-populations) in the basin and to test the hypothesis that spring pools in Cuatro Ciénegas are separated into seven hydrologically distinct drainages. Hierarchical *F*-statistics suggest significant population structure exists among the fourteen populations but not among the seven proposed drainages. Cluster analysis of Nei's genetic distance did not show populations grouping according to drainages, although it did reveal alternative clusters. We found two distinct morphotypes that were supported as genetically distinct groups by the allozyme data. Genetic studies of vagile species in desert spring ecosystems can be used to reveal hydrologic connections and identify genetically unique sub-populations.

Introduction

Desert spring ecosystems are havens of endemism because of their stable environmental conditions and long-term geographic isolation from other aquatic systems (Shepard, 1993; O'Brien & Blinn, 1999). Cuatro Ciénegas, Mexico, has an especially rich endemic fauna when compared to other similar-sized desert spring systems (Minckley, 1984b). Ash Meadows, Nevada, U.S.A. (Deacon & Williams, 1991), supported five endemic fishes (one extinct), nine mollusks, and two insects (Williams et al., 1985). Dalhousie Springs, Australia, has four fishes, six mollusks, and a frog (Zeidler & Ponder, 1989; Crowley & Ivantsoff, 1990). In contrast, Cuatro Ciénegas supports twelve endemic fishes (Minckley, 1984a), nine mollusks (Hershler, 1985) and four reptiles (McCoy, 1984).

Cuatro Ciénegas was designated a Natural Protected Area by the Mexican government in 1994. However, managers lack much of the basic scientific data required to make informed conservation decisions (Secretaria de Medio Ambiente, 1999). In addition to species inventories (Minckley, 1984a; Dinger, 2001), managers require information about the dispersal abilities (Barr & Holsinger, 1985; Bohonak, 1999) and population genetic structure of native species (Meyers et al., 2001). Population genetics are especially important in desert springs where the arid environment limits aquatic animal dispersal and leads to isolated populations. Although a number of descriptive genetic projects are underway on hydrobiid snails, pupfish, and amphipods from Cuatro Ciénegas, no published

studies of genetic population structure exist for any species in the basin.

Cuatro Ciénegas is located in the Chihuahuan desert in northern Mexico. The 840 km² Natural Protected Area is enclosed in an intermontane basin in the Sierra Madre Oriental Mountains (Secretaria de Medio Ambiente, 1994). The surficial geology of the valley is characterized by carbonate rich alluvial material (Meyer, 1973). Due to the extreme faulting and karst geology of the Cuatro Ciénegas area, there are over 200 freshwater pools (pozas), abundant springheads, and streams in the basin as well as sinkholes and underground caves (Secretaria de Medio Ambiente, 1999).

The first biologists to visit Cuatro Ciénegas outlined discrete drainages based on their observations of surface water connections within the valley (Taylor, 1966; Minckley, 1969). A set of aerial photographs was commissioned in 1968, which allowed researchers to refine drainage descriptions (Minckley, 1969). Seven epigeal drainages, which did not precisely correlate to Taylor's drainages, were identified from topographic maps and the aerial photos (Fig. 1).

Identifying Evolutionarily Significant Units (geographically discrete populations that differ in molecular and non-molecular traits (e.g. morphology or behavior)) is a high priority for maximizing biodiversity conservation (Moritz, 1994). Conserving genetic variation within a species may provide some resistance to extinction (Avise, 1994). In this study, we used starch gel electrophoresis to define population genetic structure for the endemic spring snail, *Nymphophilus minckleyi*. We then used the genetic data to test the hypothesis that seven hydrologically distinct drainages exist within the Cuatro Ciénegas basin (Minckley, 1969). Hierarchical population genetic and gene flow data from aquatic organisms can be useful in determining biologically important hydrologic connections, especially in areas characterized by complex hydrogeology, such as Cuatro Ciénegas. Traditional hydrologic mapping techniques, such as dye tracing, can be unpredictable in karst regions and many dyes are toxic to some degree (Field et al., 1995). In addition, traditional surface water mapping techniques yield hydrologic maps that may or may not outline biologically important pathways for dispersal. Mapping aquatic connections with genetic divergence data from non-vagile aquatic organisms has the advantage of identifying biologically important hydrologic connections. Genetic studies have been used previously to outline biologically important drainages even

when there is no genetic isolation by distance (Ross, 1999). Understanding both the hydrological connections among sites and the genetic structure of endemic taxa will help managers identify which sites need the most protection to maintain genetic diversity.

Materials and methods

Previously hypothesized drainages

Minckley (1969) outlined seven drainages in an attempt to explain surficial hydrologic connections in Cuatro Ciénegas (Fig. 1). Canals now connect a few of the previously distinct drainages (Secretaria de Medio Ambiente, 1999), and the karstic geology of the basin strongly suggests the importance of underground hydrologic connections that could link drainages that, based on surface topography, appear to be isolated (Minckley, 1969). Unfortunately the groundwater hydrology of the basin has not been explored in detail to date (Tafelski, 1998). Nevertheless, alternatives to the surficial isolation hypothesis have not been proposed. Because hydrologic connections within the basin allow dispersal and thus gene flow among populations, determining biologically important hydrologic connections is important for conservation (Hershler & Ponder, 1998), both in identifying genetically distinct populations or subpopulations, and in describing potential dispersal routes for invasive species.

N. minckleyi is an aquatic snail, so gene flow is facilitated by hydrologic connections between spring pools. The influence of passive dispersal during floods or by birds (Darwin, 1878, 1882; Rees, 1965; Jarne & Delay, 1991) is discounted because both flooding and wading birds are rare in Cuatro Ciénegas (Contreras-Balderas, 1984). Therefore, if the proposed surficial drainages constrain gene flow, we would expect the hydrologic drainage pattern to be reflected in population genetic structure, with high levels of gene flow within surficial drainages, but low levels among them. In contrast, if dispersal is not limited by surface connections (i.e. there are underground connections or other modes of dispersal), we would not expect to see correlations in allele frequencies among sub-populations within surface drainages. *N. minckleyi* dispersal through underground connections is unlikely because there are no underground food resources for adults (R. Hershler, pers. comm.).

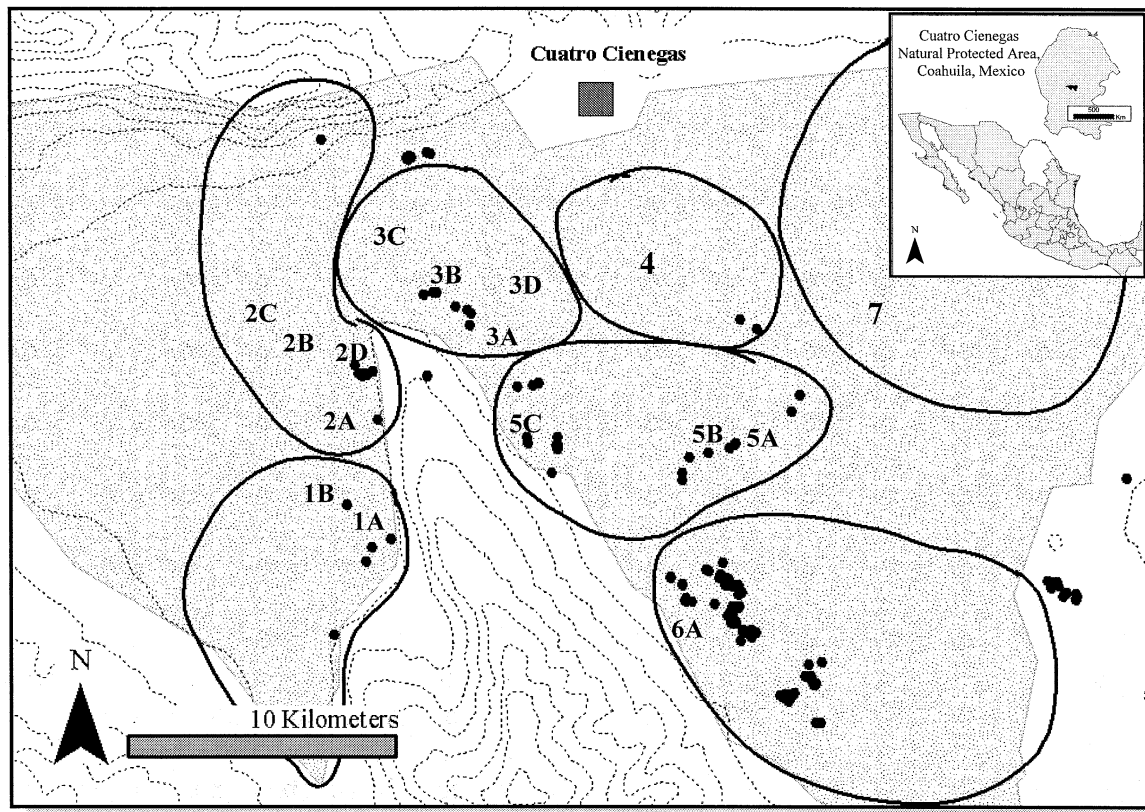


Figure 1. Map of collection locations within seven hypothesized drainages (Taylor, 1966; Minckley, 1969) in the Cuatro Ciénegas Basin. A short description of each site as well as geographic coordinates are given in Appendix A. Drainages (.sites) are: 1.A Churince, 1.B Laguna Grande, 2.A La Becerra, 2.B Garabatal 1, 2.C Garabatal 2, 2.D Juan Santos, 3.A Los Remojos, 3.B Mojarral East, 3.C Rio Mesquites A, 3.D Rio Mesquites B, 4.0 Charcos Prietos drainage (not sampled), 5.A La Maroma, 5.B Los Hundidos, 5.C Tio Candido, 6.A Pozas Azules, 7.0 Rio Salado de Nadadores drainage (not sampled).

Biology of *Nymphophilus minckleyi*

There are two described species within the genus *Nymphophilus*, both endemic to Cuatro Ciénegas (Hershler, 1985). *N. minckleyi* is abundant throughout most of the basin in pools with aquatic vegetation; *N. acarinator* is allopatric to *N. minckleyi* and found only in the far southeastern portion of the basin Santa Tecla area (Hershler, 1985). For this research, we sampled only snails that matched the morphological description of *N. minckleyi*.

Nymphophilus minckleyi (Taylor, 1966) is readily discerned from other Cuatro Ciénegas hydrobiids by its large size (9–13 mm) and generally triangular shell morphology. The shells of the species are translucent, with flattened to slightly rounded whorls with a strong spiral keel (Hershler, 1985). Bodies are darkly pigmented.

Two morphotypes of *Nymphophilus minckleyi* were identified based on shell morphology. The primary morph fits the type description of *N. minckleyi* given by Hershler (1985). The secondary (and far less frequent) morphotype has curved (rather than flattened) whorls and lacks a peripheral keel like *N. acarinator* (Hershler, 1985). Snails of this type were limited to the southeastern lobe of the basin (Los Hundidos, La Maroma and Pozas Azules). Dr R. Hershler examined specimens of both morphotypes and concluded that based on characteristic morphological traits, such as the large shell size, globose shell shape and carinate whorls, that both morphotypes met the description of *N. minckleyi* (Hershler, pers. comm.). The morphotypes were therefore combined for this study.

Collection methods

Hershler sampled over 100 sites in the Cuatro Ciénegas Basin (Hershler, 1985) and catalogued *N. minckleyi* from 19 locations, most of which were large springs and a few streams. We revisited eight of these sites (Churince, Laguna Grande inlet, Becerra, Rio Mesquites A, Mojarral East, Los Remojos, Juan Santos, and Tio Cándido) and sampled six novel habitats (Fig. 1). Some of the original sites were not resampled due to difficulty in locating or accessing them. The geographic range of sampling locations for this study spans the known distribution of *N. minckleyi* and includes 5 of the 7 proposed drainages

Most sites were spring-fed pools or streams with abundant aquatic vegetation, generally either *Nymphaea* or *Utricularia*; see Appendix A for habitat descriptions and geographic coordinates. In most cases, snails were collected by hand from submerged aquatic vegetation. All snails were cryogenically preserved in liquid nitrogen in the field, usually within one hour of collection, and were returned to Northern Arizona University in liquid nitrogen and stored at -80°C until they were processed for electrophoresis. For each site voucher specimens were preserved in 90% ethanol and deposited at the University Autonoma of Mexico.

Electrophoresis

Individual snails were prepared for electrophoresis by thawing and removing soft body parts with forceps. Each whole snail was placed in a microtiter plate with 100 μl of solution (0.05 M Tris-HCl, pH 7.0) and homogenized by hand with a glass rod. Twenty-five μl of the snail extract was placed in a 10% starch (Sigma) gel. Two different buffer systems were used for electrophoresis: TBE (Tris-borate-EDTA, pH 7.0 (Acquaah, 1992) and CT (citrate-aminopropylmorpholine system at pH 7.2 (Clayton & Tretiak, 1972). In both the gel buffer was a 1:10 dilution of the running buffer (Johnson, 2000).

Twenty-five individuals were run together on a gel, providing a comparison of 2 to 4 populations on any one gel. Gels were run for 3 hours at a constant potential drop of 30 milliamps between electrodes. Gels were sliced horizontally to allow for double staining. Stains were prepared using the tetrazolium method (Acquaah, 1992) and immediately applied to the gels. Gels were incubated at 37°C until a scorable stain became visible (15–60 min). Most gels were digitized

on a desktop scanner to provide a permanent record. Some gels were not scanned due to breakage.

Allozyme phenotypes were scored directly from the gel or digital image. Only presumptive loci that were consistently scorable are reported here. Where more than one locus was present on any one gel, each was designated in order of increasing mobility (e.g. PGM-1, PGM-2). Data were obtained for six enzymes and seven loci. Enzymes, buffers, abbreviations, and numbers assigned by the International Union of Biochemistry are as follows: alkaline phosphatase (CT, ALP, 3.1.3.1), hexokinase (TBE, HEX, 2.7.1.1), malate dehydrogenase (CT, MDH, 1.1.1.37), 6-phosphogluconate dehydrogenase (CT, 6PGDH, 1.1.1.44), and phosphoglucomutase (TBE, PGM, 5.4.2.2). An additional six enzymes were tested (FUM, PGI, AAT, AAM, ADH, GOT) but were not used in this analysis because of poor staining or because of uninterpretable results. Sample sizes are given in Appendix A.

Data analysis

Each of the 14 sites was considered a subpopulation; subpopulations were combined into 5 drainages following the surface drainage definitions of Minckley (1969). Descriptive statistics, including heterozygosity and percent polymorphic loci, were calculated with BIOSYS-2 (Swofford et al., 1997). Observed and Hardy-Weinberg expected (HWE) heterozygote frequencies were calculated and tested for conformance to HWE with TFPGA (Miller, 1997).

A Mantel test was performed in TFPGA to test for a correlation between genetic isolation (F_{ST} values) and Euclidian distance among sub-populations (Sokal & Rohlf, 1995). Pairwise F_{ST} values for the Mantel test were generated with FSTAT (Goudet, 2001).

F -statistics were calculated to determine population structure among pools with FSTAT according to the methods described in Weir & Cockerham (1984). Standard errors for the F -statistics were calculated at each locus by jackknifing over all populations in FSTAT.

To test the hypothesis proposed by Minckley (1969) that seven isolated drainages exist, four-level hierarchical F -statistics were calculated with BIOSYS-2 to describe genetic structure among and within drainages (Weir & Cockerham, 1984). The four levels were: total basin (F_{IT}), drainage (F_{DT}), sub-population (F_{ST}), and individual (F_{IS}). Confidence intervals were generated for each statistic from the

jackknifed average and standard error. Standard errors for F_{SD} were calculated by jackknifing over drainages. The variance of F_{ST} was decomposed into the variance due to F_{SD} and F_{DT} . These variance contributions were calculated from four-level hierarchical F -statistics calculated with the Wright78 step in BIOSYS-2. To estimate gene flow among subpopulations and within and among drainages, the number of migrants per generation (N_m) was calculated according to Weir (1996).

UPGMA dendrograms were created in TFPGA for five measures of genetic distance (Roger's original, Roger's modified (Wright, 1978), Nei's original (1972), Nei's modified (1978), and the coancestry distance (Reynolds et al., 1983)) in order to test whether populations clustered within drainages or if an alternative pattern of genetic relationships exists. For each node of the UPGMA dendrograms, TFPGA calculates confidence levels by bootstrapping over loci (Sokal & Rohlf, 1995).

Tied trees, which occur when two or more topologies exist for the same set of allozyme data, can be a problem in cluster analysis (Backeljau et al., 1996). Tied trees occur relatively frequently for UPGMA topologies that are calculated with small sample sizes (Takezaki, 1998). Generally, bootstrap support at tied nodes is low but occasionally is high (e.g., 70–80%). Therefore confidence levels at each node that are generated by bootstrapping should not be used as p-values but rather as indicators of repeatability (Van Dongen, 1995).

Bootstrapping with small sample sizes (e.g. fewer than 20 samples) can have peculiar properties when calculating confidence levels for topologies, because the number of different resamples is limited (Van Dongen & Backeljau, 1995). Van Dongen (1995) suggests bootstrapping over individuals rather than bootstrapping over loci for allozyme data because of the larger sample sizes and greater independence afforded by individuals. Unfortunately, no computer program exists that bootstraps over individuals for cluster analysis of genetic distance, so we generated confidence levels by bootstrapping over loci in TFPGA.

Results

In general, *N. minckleyi* subpopulations met Hardy-Weinberg expectations (HWE). When variable loci within subpopulations were tested, only 21% (19/89) of the cases did not meet HWE ($\alpha = 0.05$). Most

departures from HWE were due to heterozygote deficiency (16/19), which could be an indicator of inbreeding or selection (Appendix A). Much of the genetic differentiation was found in the PGM loci, which may be subject to selection. The average direct count heterozygosity in subpopulations of *N. minckleyi* was 0.36 (\pm standard error 0.09), higher than most reported values for gastropods. For seven gastropods, the average heterozygosity was 0.06 (± 0.03) (Bandoni et al., 1990; Dillon & Lydeard, 1998; Hodges, 1998; Rankevich et al., 1996; Woodruff et al., 1985). The overall level of polymorphism in *N. minckleyi* was 91%, which is slightly higher than other published values for freshwater snails (e.g. overall polymorphism in *Biomphalaria pfeifferi* is 80% (Bandoni et al., 1990).

Population structure and gene flow

Wright (1978) suggested that $F_{ST}(\theta)$ values be interpreted along the following lines: 0–0.05 indicates little genetic differentiation, 0.05–0.15 indicates moderate genetic differentiation, 0.15–0.25 indicates great genetic variation, and F_{ST} values above 0.25 indicate very great genetic differentiation (Hartl & Clark, 1997). F -statistics jackknifed over populations (Table 1) show slight, but significant, levels of population subdivision within the Cuatro Ciénegas basin. Most loci showed little to moderate genetic differentiation among sites ($0 > F_{ST}(\theta) > 0.15$; average $F_{ST} \pm SE = 0.111 \pm 0.033$), while PGM-2 showed very great genetic differentiation ($F_{ST} = 0.259 \pm 0.078$).

When F -statistics were jackknifed over populations and over loci, F_{IT} and F_{ST} were significantly different from zero ($f = F_{IS}$, $\theta = F_{ST}$ and $F = F_{IT}$, Table 1). The value of $F(0.192 \pm 0.096)$ was greater than $\theta(0.111 \pm 0.033)$, which was greater than $f(0.096 \pm 0.082)$. This result indicates that there is genetic differentiation among subpopulations (sites) but that each subpopulation is in HW equilibrium. Pairwise F_{ST} values over loci were calculated to determine the degree of genetic structure among the 14 subpopulations (Table 2). Numbers of migrants were calculated from F_{ST} (Weir, 1996). This calculation assumes that the populations are at equilibrium and that selection is not an important evolutionary influence. More than two migrants per generation between populations are considered sufficient to prevent genetic divergence between populations (Wright, 1973).

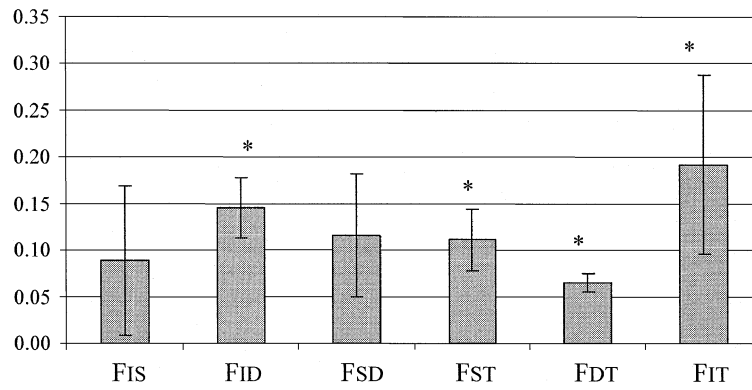


Figure 2. Hierarchical F -statistics calculated according to (Wright, 1978). Error bars are standard errors. F_{IS} = individuals to subpopulation; F_{ID} = individuals to drainage; F_{SD} = subpopulations to drainage; F_{ST} = subpopulations to total; F_{DT} = drainages to total; F_{IT} = individuals to total. *(asterisks) indicate values that are significantly different from zero ($\alpha = 0.05$).

Table 1. F -statistics for all alleles jackknifed over populations (Weir & Cockerham 1984). Each value is \pm standard error. Weir and Cockerham's equivalent in Wright's notations are as follows: $F = F_{IT}$, $\theta = F_{ST}$, $f = F_{IS}$

Locus	f (SE)	θ (SE)	F (SE)
ME	0.342 ^a	0.106	0.405 ^a
	0.120	0.064	0.072
6PGDH	-0.090	0.052	-0.032
	0.152	0.032	0.154
MDH	0.046	0.085 ^a	0.128
	0.118	0.027	0.114
ALP	0.090	0.119	0.199 ^a
	0.062	0.065	0.084
PGM1	0.171 ^a	0.045 ^a	0.208 ^a
	0.043	0.022	0.040
PGM2	0.401 ^a	0.259 ^a	0.557 ^a
	0.053	0.078	0.067
HEX	-0.248	0.043	-0.195
	0.069	0.030	0.075
All loci	0.089	0.111 ^a	0.192 ^a
	(0.081)	(0.033)	(0.096)

^aValues are significant at the $\alpha = 0.05$ level.

Drainage structure

Hierarchical F -statistics (Fig. 2) did not show significant subdivision among drainages (average $F_{DT} = 0.030 \pm 0.082$) but subpopulations within drainages were significantly subdivided ($F_{SD} = 0.149 \pm 0.049$). The average number of migrants among drainages for Cuatro Ciénegas is 8.1-migrants/generation, while the average number of migrants among subpopulations

within drainages is 1.4/generation. This result does not agree with the prediction made for distinct drainages, which suggested that surficial drainages would confine *N. minckleyi* migration and limit gene flow across drainage boundaries.

The majority of the genetic variation is found within subpopulations. The variance partitioning analysis of F_{ST} found that 84% of the variance can be attributed to subpopulations within drainages, whereas only 17% of the variation is attributable to drainages (Preziosi & Fairbairn, 1992). This reinforces the idea that the subpopulation, rather than the drainage, is the genetically important unit.

Genetic isolation by distance

Comparing genetic differentiation and geographic distance provides a picture of dispersal patterns within a given area (Ponder et al., 1995). A simple, straight line relationship between distance and differentiation indicates that genetic exchange among populations is highly correlated to their proximity; a scattered relationship indicates that dispersal is more sporadic (Wright, 1978 *sensu* Ponder et al., 1995).

The Mantel test (999 randomizations) for pooled *N. minckleyi* populations showed a significant ($p < 0.01$), but scattered (correlation coefficient, $r = 0.46$), relationship between F_{ST} and geographic distance. Individual Mantel tests were performed for the drainages that had sufficient sample sizes (drainage 2 and drainage 3). Neither of these tests was significant ($p > 0.4$) and there was considerable scatter in the plots ($r = 0.29$ and $r = -0.36$, respectively). This indicates that gene flow and geographic distance are not tightly coupled.

Table 2. Number of migrants (N_m , below the diagonal) and F_{ST} values (above the diagonal) for all pairs of populations. F_{ST} values between 0–0.15 indicate little to moderate genetic differentiation

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1 La Becerra		0.0091	0.0481	0.0605	0.1359	0.0289	0.1586	0.1834	0.1250	0.0922	0.0657	-0.0144	0.1465	0.1179
2 Churince	27.22		0.0986	0.0680	0.1910	0.0838	0.1154	0.2763	0.1837	0.0971	0.0743	0.0785	0.1111	0.2346
3 Garabatal 1	4.95	2.29		0.0824	0.1171	0.0195	0.1533	0.1840	0.0751	0.1794	0.0843	0.0412	0.1441	0.0325
4 Garabatal 2	3.88	3.43	2.78		0.1518	0.0916	0.0223	0.1893	0.0882	0.1215	-0.0351	-0.0174	0.0184	0.1059
5 Los Hundidos	1.59	1.06	1.88	1.40		0.3486	0.1283	0.2051	0.0416	0.0195	0.0929	0.1660	0.3282	0.1166
6 Juan Santos	8.40	2.73	12.57	2.48	0.47		0.1698	0.3788	0.1976	0.2336	0.1281	0.0574	0.1499	0.1831
7 Laguna Grande	1.33	1.92	1.38	10.96	1.70	1.22		0.1459	0.1133	0.0457	0.0136	0.0457	0.0561	0.1815
8 La Maroma	1.11	0.65	1.11	1.07	0.97	0.41	1.46		0.1977	0.1164	0.1741	0.1982	0.2826	0.2665
9 Mojarral East	1.75	1.11	3.08	2.58	5.76	1.02	1.96	1.01		0.1270	0.0557	0.0954	0.2144	0.0303
10 Pozas Azules	2.46	2.32	1.14	1.81	12.57	0.82	5.22	1.90	1.72		0.0860	0.1385	0.2039	0.2122
11 Los Remejos	3.56	2.93	2.72	0	2.44	1.70	18.13	1.19	4.24	2.66		-0.0154	0.0408	0.0898
12 Río Mesquites A	0	2.93	5.82	0	1.26	4.11	5.22	1.01	2.37	1.56	0		0.0418	0.0810
13 Río Mesquites B	1.46	2.00	1.48	13.34	0.51	1.42	4.21	0.63	0.92	0.98	5.88	5.73		0.2582
14 Tío Candido	1.87	0.82	7.44	2.11	1.89	1.13	1.13	0.69	8.00	0.93	2.53	2.84	0.72	

Genetic distance cluster analyses

Cluster analyses performed on a various genetic distance metrics (Roger's modified genetic distance, Nei's genetic distance, F_{ST}) showed that populations did not cluster according to their drainages nor did they cluster strictly by geographic proximity. We calculated confidence levels for each node of the dendrograms by bootstrapping over loci (100 replicates). Although the five dendrograms were similar with identical nodes appearing in most topologies, bootstrap support was generally low (<60%), which suggests that alternate topologies are viable. Two nodes consistently received high bootstrap support (65–85%), which suggests that an alternative drainage structure to the one being tested for this paper (Fig. 1) exists in Cuatro Ciénegas. The dendrogram that resulted from Nei's genetic distance is shown in Figure 3. This topology illustrates the two nodes that consistently grouped together: the first node includes three sites, Garabatal 2, Los Remojos, and Rio Mesquites A (67–85% bootstrap support), and the second node includes Mojarral East and Tio Cándido (67–83% support). Neither of these two nodes group populations strictly by geographic proximity nor by drainage; for example, Mojarral East lies between the Rio Mesquites A and Los Remojos (Fig. 1).

The dendrogram of Nei's genetic distance (Fig. 3) shows a phylogeographic break that separates the two previously mentioned *N. minckleyi* morphotypes. The cluster of atypical *Nymphophilus* includes the Pozas Azules, Los Hundidos and La Maroma populations in the southeastern lobe of the basin. The divergence point occurred at $D = 0.131$ and was supported by 27% of bootstrap randomizations. For context, interspecific values of Nei's genetic distance are typically greater than 0.5 (range 0.20–0.60), whereas intraspecific comparisons are usually less than 0.10 (Ponder et al., 1995). Although this study shows only moderate support for this phylogeographic break characterized by a difference in allelic frequencies (as opposed to fixed differences) and the two morphotypes probably represent natural phenotypic plasticity within the species, it warrants further investigation with a more sensitive technique.

Discussion

Inbreeding coefficients (F_{IS} and F_{IT}) for *N. minckleyi* are comparable to values observed for other freshwater gastropods. The overall inbreeding coefficient for

N. minckleyi ($F \pm SE$) was 0.192 ± 0.096 compared to the average value of 0.413 ± 0.10 for freshwater snails (Table 1). The mean within-population inbreeding coefficient (f) was 0.089 ± 0.081 for *N. minckleyi* compared to 0.165 ± 0.043 for other aquatic gastropods. Significant inbreeding coefficients have been observed in other freshwater snail species, such as *Biomphalaria*, which has a high number of homozygotes relative to heterozygotes due to the slower growth rate and longer life span of homozygotes (Falniowski & Szarowska, 1999).

Levels of overall population differentiation as indicated by F_{ST} are similar for *N. minckleyi* and other freshwater snails (Table 3). There is a general expectation, particularly for non-vagile species, that population differentiation increases with increasing geographic distance between populations because dispersal, and thus gene flow, is distance limited. Population differentiation as calculated by F_{ST} does not take into consideration the geographic distance separating sampled populations, which can make comparisons among studies difficult. To make cross study comparisons easier, we suggest a normalized genetic differentiation index where the mean F_{ST} is divided by the distance between the two most distant sampling sites in the study ($F_{ST}/scale$). When this index was applied to values for various freshwater snails (Table 3), we find that population substructure in *N. minckleyi* is comparable to *Fluvidona* sp., which is a hydrobiid with 'very restricted gene flow' that is endemic to Wilsons Promontory in southern Australia (Colgan & Ponder, 1994).

Refuting the distinct drainage hypothesis

Our results did not support the drainage hypothesis, indicating that drainages do not restrict gene flow. Other studies have examined levels of genetic divergence among freshwater snail populations within and among drainages (Colgan & Ponder, 1994). *Goniobasis*, for example, showed a high degree of genetic diversity between populations in the same drainage system, which indicated low levels of gene flow; inter-drainage gene flow levels were even lower (Chambers, 1980). The Australian hydrobiids of the genus *Fluvidona* show lower levels of gene flow within drainages than among drainages (Ponder, 1994; Colgan & Ponder, 1994).

In Cuatro Ciénegas, gene flow for *Nymphophilus minckleyi* is not constrained by the seven hypothesized drainages (Minckley, 1969; Taylor, 1966; Hershler &

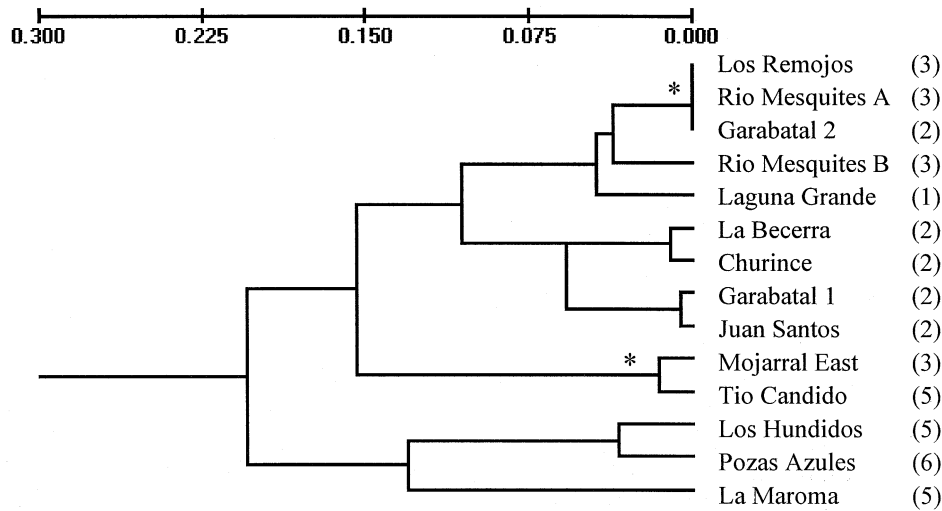


Figure 3. UPGMA dendrogram of Nei's genetic distance (Nei, 1978) between populations. Drainage numbers for each site are in parenthesis. *(asterisks) designate the two nodes with consistently high bootstrap values (65–85%) that are discussed in the text.

Table 3. Average F_{ST} and N_m (number of migrants) for various freshwater mollusks. F_{ST}/scale is the normalized genetic differentiation to aid in comparing levels of population substructure across studies with different geographical distances between sites

Species	No. loci	No. samples	Scale (km)	F_{ST} (mean)	N_m (mean)	Reference	F_{ST}/scale
<i>Goniobasis</i> (2 sp.)	14	12	1000	0.408	0.36	Chambers, 1980	0.0004
<i>Lymnaea peregra</i>	6	4	50	0.018	13.64	Jarne & Delay, 1990	0.0004
<i>Biomphalaria glabrata</i>	13	6	1000	0.805	0.06	Mulvey et al., 1998	0.0008
<i>Biomphalaria pfeifferi</i>	7	12	500	0.589	0.17	Bandoni et al., 1990	0.0012
<i>Fluvidonia</i> sp. Straight-s	22	8	7.8	0.130	1.67	Coglan & Ponder 1994	0.0167
<i>Fluvidonia</i> sp. 3	22	12	7.8	0.086	2.66	Coglan & Ponder 1994	0.0110
<i>Fluvidonia</i> sp. 4	22	26	9.4	0.075	3.08	Coglan & Ponder 1994	0.0080
<i>Fluvidonia</i> sp. 5	22	14	17.8	0.161	1.30	Coglan & Ponder 1994	0.0090
<i>Fonsochela accepta</i>	24	12	250	0.116	1.91	Coglan & Ponder 1994	0.0005
<i>Fonsochela aquatica</i>	24	16	150	0.110	2.02	Coglan & Ponder 1994	0.0007
<i>Fonsochela zeidlereri</i>	23	16	205	0.360	0.44	Coglan & Ponder 1994	0.0018
<i>Fonsochela variabilis</i>	27	19	55	0.196	1.03	Coglan & Ponder 1994	0.0036
<i>Trochidrobia punicea</i>	24	17	112.5	0.143	1.50	Coglan & Ponder 1994	0.0013
<i>Trochidrobia smithi</i>	18	7	150	0.426	0.34	Coglan & Ponder 1994	0.0028
<i>Trochidrobia minuta</i>	18	3	25	0.086	2.66	Coglan & Ponder 1994	0.0034
<i>Bythinella</i>	7	20	300	0.490	0.26	Falniowski & Szarowska, 1999	0.0016
<i>Nymphophilus minckleyi</i>	7	14	17	0.111	2.00	present study	0.0065
Average	17.65	12.82	226.90	0.25	2.06		0.0041
St. Deviation	7.18	6.04	319.56	0.22	3.13		0.0046

Hayek, 1988). First, if the drainages were isolated, one would expect to see very few snails migrating across the drainage boundaries; however the migration rate among drainages is relatively high. Second, the majority of the genetic variance is found within subpopula-

tions rather than within drainages, which indicates that genetic significance of the drainages may be an artifact of pooling subpopulations. Third, the dendrograms of genetic distances between *N. minckleyi* populations do not cluster by drainage (Fig. 3).

The *N. minckleyi* gene flow data corroborates evidence from *Mexipyrigus churinceanus* shell morphology and *Astyanax mexicanus* dispersal. Hershler & Hayek (1988) tested the hypothesis that geographic patterns in *Mexipyrigus* shell morphology derived from the seven evolutionarily distinct drainages; however they failed to find a correlation between the two. The population density of the Mexican tetra (*A. mexicanus*) fluctuates from one pool to another on a very rapid basis, suggesting that individuals move readily among drainages (Minckley, 1984a). The groundwater hydrology of the basin has not been studied so we are unable to determine whether dispersal occurs through underground connections, although the possibility exists (Tafelski, 1998).

Alternative drainages

N. minckleyi migration rates and genetic distance dendrograms suggest that alternative drainages may be structuring gene flow. Although the *Nymphophilus* data do not support the drainage hypothesis proposed by Minckley (1969), the pairwise F_{ST} values show heterogeneous gene flow among populations indicating that corridors for and barriers against snail migration exist in Cuatro Ciénegas. The cluster analysis for each of the five genetic distance measures included two nodes with high bootstrap support: (1) the Mojarral East-Tio Candido cluster, (2) the Garabatal 2-Rio Mesquites A-Los Remojos cluster. Genetic data from additional aquatic organisms, or direct hydrologic data, are needed to confirm or refute the existence of alternative drainages at Cuatro Ciénegas. In addition, the genetic data support the presence of an evolutionarily significant unit in the southeast portion of the basin where *N. minckleyi* populations are geographically isolated and have a distinct morphology.

Managing naturally fragmented populations

Desert springs are habitats for endemic species in a variety of groups which have presumably speciated in relatively stable and isolated conditions. This study shows how identifying genetically distinct subpopulations on an endemic snail provides insight into the underlying hydrological structure of a complex spring ecosystem. This is an important first step in helping scientists and managers understand dispersal patterns of a suite of endemic taxa which can be used to design management plans to protect sites which harbor genetically unique taxa.

Acknowledgements

The authors would like to thank Dr Francisco Garcia de León of Instituto Tecnológico de Cd. Victoria for sharing permits with us, the Área Protegida (SEMARNAT) staff at Cuatro Ciénegas for logistical support Heidi Kloeppel, Biol. Aldo Guevara Carrizales, Tim McBride, Paul Anthony, and others for help in the field, Kevin Johnson for help in the lab. Philip Service, Thomas Sisk, Bruce Hungate, Robert Hershler and two anonymous reviewers provided helpful comments on the manuscript. This research was funded by The Nature Conservancy Ecosystem Science Program to JCM and DAH, The National Science Foundation (POWRE program award to JCM), Sigma Xi Grants-in-Aid-of-Research to ABM, and the North American Benthological Society Conservation Committee graduate student award to ABM. This research was conducted under comisión nacional de acuacultura y pesca, permiso de fomento 180202-613-050 and amendments.

References

- Acquaah, G., 1992. Practical Protein Electrophoresis for Genetic Research. Dioscorides Press, Portland, OR.
- Avise, J. C., 1994. Molecular Markers, Natural History, and Evolution. Chapman & Hall, New York, NY.
- Backeljau, T., L. De Bruyn, H. De Wolf, K. Jordaens, S. Van Dongen & B. Winnepeninckx, 1996. Multiple UPGMA and Neighbor-joining trees and the performance of some computer packages. *Molecular Biology and Evolution* 13: 309–313.
- Bandoni, S. M., M. Mulvey, D. K. Koech & E. S. Loker, 1990. Genetic structure of Kenyan populations of *Biomphalaria pfeifferi* (Gastropoda: Planorbidae). *Journal of Molluscan Studies* 56: 383–391.
- Barr, T. C., Jr. & J. R. Holsinger, 1985. Speciation in cave faunas. *Annual Review of Ecology and Systematics* 16: 313–337.
- Bohonak, A. J., 1999. Dispersal, gene flow and population structure. *The Quarterly Review of Biology* 74: 21–45.
- Chambers, S. M., 1980. Genetic divergence between populations of *Goniobasis* (Pleuroceridae) occupying different drainage systems. *Malacologia* 20: 63–81.
- Clayton, J. W. & D. N. Treliak, 1972. Amine-citrate buffers for pH control in starch gel electrophoresis. *Journal of the Fisheries Research Board of Canada* 29: 1169–1172.
- Colgan, D. J. & W. F. Ponder, 1994. The evolutionary consequences of restrictions on gene flow: Examples from hydrobiid snails. *The Nautilus*, Supplement 2: 25–43.
- Contreras-Balderas, A. J., 1984. Birds from Cuatro Ciénegas, Coahuila, México. *Journal of the Arizona-Nevada Academy of Science* 19: 77–79.
- Crowley, L. E. L. M. & W. Ivantsoff, 1990. A second hardy-head, *Craterocephalus gloveri* (Pisces: Atherinidae), from Dalhousie Springs, central Australia. *Ichthyological Exploration of Freshwaters* 1: 113–122.
- Darwin, C., 1878. Transplantation of shells. *Nature* 18: 120–121.

- Darwin, C., 1882. On the dispersal of fresh-water bivalves. *Nature* 25: 529–530.
- Deacon, J. E. and C.D. Williams, 1991. Ash Meadows and the legacy of the Devils Hole pupfish. In Minckley, W. L. & J. E. Deacon (eds), *Battle Against Extinction: Native Fish Management in the American West*. University of Arizona Press, Tucson, AZ.: 69–87.
- Dillon, R. T. J. & C. Lydeard, 1998. Divergence among mobile populations of the pleurocerid snail genus, *Leptoxis*, estimated by allozyme electrophoresis. *Malacologia* 39: 113–121.
- Dinger, E. C., 2001. Aquatic Invertebrates of Cuatro Ciénegas, Coahuila, Mexico and Effects of Fish on Stromatolite Invertebrate Assemblages. Department of Biology, Northern Arizona University, Flagstaff, AZ.
- Falniowski, A. M. & K. M. Szarowska, 1999. Homozygote excess and gene flow in the spring snail *Bythinella* (Gastropoda: Prosobranchia). *Journal of Zoological Systematics and Evolutionary Research* 37: 165–175.
- Field, M. S., R. G. Wilhelm, J. F. Quinlan & T. J. Aley, 1995. An assessment of the potential adverse properties of fluorescent tracer dyes used for groundwater tracing. *Environmental Monitoring and Assessment* 38: 75–96.
- Goudet, J., 2001. FSTAT, a program to estimate and test gene diversities and fixation indices. Updated from Goudet (1995). Available from <http://www.unil.ch/izea/software/fstat.html>.
- Hartl, D. L. & A. G. Clark, 1997. *Principles of Population Genetics*. Sinauer Associates, Inc., Sunderland, MA.
- Hershler, R., 1985. Systematic revision of the Hydrobiidae (Gastropoda: Rissoacea) of the Cuatro Ciénegas basin, Coahuila, Mexico. *Malacologia* 26: 31–123.
- Hershler, R. and L. C. Hayek, 1988. Shell variation of springsnail populations in the Cuatro Ciénegas Basin, Mexico: Preliminary analysis of limnocene fauna. *The Nautilus* 102: 56–64.
- Hershler, R. & W. F. Ponder, 1998. A review of morphological characters of hydrobioid snails. *Smithsonian Contributions to Zoology* 600: 55.
- Hodges, M. A., F. W. Allendorf, 1998. Population Genetics and Pattern of Larval Dispersal of the Endemic Hawaiian Freshwater Amphidromous Gastropod *Neritina granosa* (Prosobranchia: Neritidae). *Pacific Science* 52: 237–249.
- Jarne, P. & B. Delay, 1990. Population genetics of *Lymnaea peregra* (Mueller) (Gastropoda: Pulmonata) in Lake Geneva. *Journal of Molluscan Studies* 56: 317–321.
- Jarne, P. & B. Delay, 1991. Population genetics of freshwater snails. *Trends in Ecology and Evolution* 6: 383–386.
- Johnson, K. M., 2000. An Analysis of the Genetic Population Structure of *Paracerceis sculpata* in the Gulf of California. Department of Biology, Northern Arizona University, Flagstaff, AZ.
- Kimura, M. and J. F. Crow, 1964. The number of alleles that can be maintained in a finite population. *Genetics* 49: 725–738.
- McCoy, C. J., 1984. Ecological and zoogeographic relationships of amphibians and reptiles of the Cuatro Ciénegas Basin. *Journal of the Arizona-Nevada Academy of Science* 19: 49–60.
- Meyer, E. R., 1973. Late-Quaternary paleoecology of the Cuatro Ciénegas basin, Coahuila, México. *Ecology* 54: 983–995.
- Meyers, M. J., F. A. H. Sperling & V. H. Resh, 2001. Dispersal of two species of Trichoptera from desert springs: Conservation implications for isolated vs. connected populations. *Journal of Insect Conservation* 5: 207–215.
- Miller, M. P., 1997. Tools for population genetic analyses (TFPGA) 1.3: A Windows program for the analysis of allozyme and molecular population data. Computer software distributed by the author.
- Minckley, W. L., 1969. Environments of the Bolsón of Cuatro Ciénegas, Coahuila, Mexico, with special reference to the aquatic biota. Texas Western Press., El Paso, Texas. Science Series 2: 1–65.
- Minckley, W. L., 1984a. Cuatro Ciénegas fishes: Research review and a local test of diversity versus habitat size. *Journal of the Arizona-Nevada Academy of Science* 19: 13–21.
- Minckley, W. L., 1984b. Three decades near Cuatro Ciénegas, Mexico: Photographic documentation and a plea for area conservation. *Journal of the Arizona-Nevada Academy of Science* 26: 89–118.
- Moritz, C., 1994. Defining 'Evolutionarily Significant Units' for conservation. *Trends in Ecology and Evolution* 9: 373–375.
- Mulvey, M., M. C. Newman & D. S. Woodruff, 1998. Genetic differentiation among West Indian populations of the shistosom-transmitting snail *Biomphalaria glabrata*. *Malacologia* 29: 309–317.
- Nei, M., 1972. Genetic distance between populations. *American Naturalist* 106: 283–292.
- Nei, M., 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics* 89: 583–390.
- O'Brien, C. & D. W. Blinn, 1999. The endemic spring snail *Pyrgulopsis montezumensis* in a high CO₂ environment: importance of extreme chemical habitats as refugia. *Freshwater Biology* 42: 225–234.
- Ponder, W. F., 1994. Australian freshwater Mollusca: conservation priorities and indicator species. *Memoirs of the Queensland Museum* 36: 191–196.
- Ponder, W. F., P. Egger & D. J. Colgan, 1995. Genetic differentiation of aquatic snails (Gastropoda: Hydrobiidae) from artesian springs in arid Australia. *Biological Journal of the Linnean Society* 56: 553–596.
- Preziosi, R. F. & D. J. Fairbairn, 1992. Genetic population structure and levels of gene flow in the stream dwelling waterstrider, *Aquarius* (= *Gerris remigis*) (Hemiptera: Gerridae). *Evolution* 46: 430–444.
- Rankevich, D. L., B. E. Nevo, A. Beiles & Z. Arad, 1996. Genetic and physiological adaptations of the prosobranch landsnail *Pomatias olivieri* to microclimatic stresses on Mount Carmel, Israel. *Israel Journal of Zoology* 42: 425–441.
- Rees, W. J., 1965. The aerial dispersal of mollusca. *Proceedings of the Malacological Society of London* 36: 269–282.
- Reynolds, J., B. S. Weir & C. C. Cockerham, 1983. Estimation of the coancestry coefficient: basis for a short-term genetic distance. *Genetics* 105: 767–779.
- Ross, T. K., 1999. Phylogeography and conservation genetics of the Iowa Pleistocene snail. *Molecular Ecology* 8: 1363–1373.
- Secretaría de Medio Ambiente, R. N. y. P. S., 1994. Decree of the Cuatro Ciénegas Natural Protected Area.
- Secretaría de Medio Ambiente, R. N. y. P. S., 1999. Programa de Manejo del Área de Protección de Flora y Fauna Cuatro Ciénegas. Instituto Nacional de Ecología, Tlaxcopac, México.
- Shepard, W. D., 1993. Desert springs – both rare and endangered. *Aquatic Conservation: Marine and Freshwater Ecosystems* 3: 351–359.
- Sokal, R. R. & F. J. Rohlf, 1995. *Biometry: the Principles and Practice of Statistics in Biological Research*. W. H. Freeman and Co., New York.
- Swofford, D. L., R. B. Selander & W. C. Black IV, 1997. BIOSYS-2: A Computer Program for the Analysis of Allelic Variation in Genetics, Ft. Collins, CO.

- Tafelski, R. D., 1998. Unpublished report to the Nature Conservancy, 'Groundwater reconnaissance of the Cuatro Ciénegas area.' HRS Consultants, Inc. Lakewood, CO.
- Takezaki, N., 1998. Tied trees generated by distance methods of phylogenetic reconstruction. *Molecular Biology and Evolution* 15: 727–737.
- Taylor, D. W., 1966. A remarkable snail fauna from Coahuila, Mexico. *The Veliger* 9:152–223.
- Van Dongen, S., 1995. How should we bootstrap allozyme data? *Heredity* 74: 445–447.
- Van Dongen, S. & T. Backeljau, 1995. One- and two-sample tests on single locus inbreeding coefficients using the bootstrap. *Heredity* 74: 127–133.
- Weir, B. S., 1996. *Genetic Data Analysis II: Methods for Discrete Population Genetic Data*. Sinauer Associates, Inc. Publishers, Sunderland, MA.
- Weir B. S. and C. C. Cockerham, 1984. Estimating F -statistics for the analysis of population structure. *Evolution* 38: 1358–1370.
- Williams, J. E., D. B. Bowman, J. E. Brooks, A. A. Echelle, R. J. Edwards, D. A. Hendrickson & J. J. Landye, 1985. Endangered aquatic ecosystems in North American deserts with a list of vanishing fishes of the region. *Journal of the Arizona-Nevada Academy of Science* 20: 1–61.
- Woodruff, D., M. Mulvey & M. Yipp, 1985. Population genetics of *Biomphalaria straminea* in Hong Kong. *Journal of Heredity* 76: 355–360.
- Wright, S., 1973. *The Origin of the F -statistics for Describing the Genetic Aspects of Population Structure*. University of Hawaii Press, Honolulu.
- Wright, S., 1978. *Evolution and the Genetics of Populations*. University of Chicago Press, Chicago.
- Zeidler, W. and W. F. Ponder (eds), 1989. *Natural History of Dalhousie Springs*. South Australian Museum, Adelaide.

Appendix A. Genetic characteristics for each locus in each population. N is population size, n_a is the actual number of alleles, n_e is the effective number of alleles (Kimura & Crow, 1964), H_{obs} is the direct count heterozygosity, H_{exp} is the Hardy–Weinberg expected heterozygosity (Nei, 1972), p -values are the Chi-squared results. HWE is yes if the population $p > 0.025$ and $p < 0.975$, meaning that the locus meets Hardy-Weinberg expectations.

		N	n_a	n_e	% Het	H_{obs}	H_{exp}	p -value	HWE
Poza la Becerra	26.8800, 102.1384								
	<i>ME</i>	0	–	–	–	–	–	–	
	<i>6PGDH</i>	30	3	2.01	0.53	16.00	20.20	0.183	Yes
	<i>MDH</i>	34	3	2.17	0.62	21.00	16.99	0.168	Yes
	<i>ALP</i>	47	3	2.02	0.57	27.00	21.97	0.116	Yes
	<i>PGM-1</i>	30	3	2.07	0.40	12.00	15.00	0.273	Yes
	<i>PGM-2</i>	20	2	1.88	0.45	9.00	14.47	0.035	Yes
	<i>HEX</i>	3	2	2.00	0.33	1.00	1.50	0.564	Yes
Poza Churince	26.8397, 102.1341								
	<i>ME</i>	5	2	1.47	0.40	2.00	1.60	0.576	Yes
	<i>6PGDH</i>	17	3	2.10	0.12	2.00	8.47	0.002	No
	<i>MDH</i>	19	2	1.95	0.63	12.00	9.26	0.198	Yes
	<i>ALP</i>	19	2	2.00	0.63	12.00	10.00	0.371	Yes
	<i>PGM-1</i>	17	2	1.84	0.47	8.00	7.77	0.901	Yes
	<i>PGM-2</i>	13	3	1.59	0.31	4.00	4.62	0.631	Yes
	<i>HEX</i>	10	2	1.83	0.50	5.00	4.55	0.754	Yes
El Garabatal 1	26.8952, 102.1419								
	<i>ME</i>	20	2	1.47	0.30	6.00	6.40	0.780	Yes
	<i>6PGDH</i>	22	3	1.39	0.32	7.00	5.89	0.375	Yes
	<i>MDH</i>	21	2	1.69	0.29	6.00	8.57	0.169	Yes
	<i>ALP</i>	13	2	1.74	0.31	4.00	5.54	0.317	Yes
	<i>PGM-1</i>	10	2	1.98	0.50	5.00	4.95	0.975	Yes
	<i>PGM-2</i>	0	–	–	–	–	–	–	
	<i>HEX</i>	0	–	–	–	–	–	–	
El Garabatal 2	26.8896, 102.1580								
	<i>ME</i>	6	2	1.95	0.17	1.00	2.92	0.107	Yes
	<i>6PGDH</i>	32	4	2.28	0.63	20.00	15.75	0.127	Yes
	<i>MDH</i>	36	3	2.02	0.56	20.00	17.78	0.453	Yes
	<i>ALP</i>	28	2	1.69	0.36	10.00	11.43	0.508	Yes
	<i>PGM-1</i>	37	4	2.02	0.30	11.00	17.64	0.022	No

Continued on p. 191

Appendix A. Continued

		<i>N</i>	<i>na</i>	<i>ne</i>	% Het	H_obs	H_exp	<i>p</i> -value	HWE
		<i>N</i>	<i>na</i>	<i>ne</i>	% Het	H_obs	H_exp	<i>p</i> -value	HWE
	<i>PGM-2</i>	33	3	2.05	0.36	12.00	16.12	0.142	Yes
	<i>HEX</i>	32	2	1.98	0.53	17.00	15.86	0.684	Yes
		<i>N</i>	<i>na</i>	<i>ne</i>	% Het	H_obs	H_exp	<i>p</i> -value	HWE
Los Hundidos	26.8665, 102.0321								
	<i>ME</i>	0	–	–	–	–	–	–	–
	<i>6PGDH</i>	29	2	1.92	0.48	14.00	14.40	0.879	Yes
	<i>MDH</i>	19	2	1.99	0.63	12.00	9.47	0.245	Yes
	<i>ALP</i>	30	3	2.27	0.37	11.00	14.98	0.145	Yes
	<i>PGM-1</i>	6	2	1.80	0.00	0.00	2.67	0.014	No
	<i>PGM-2</i>	0	–	–	–	–	–	–	–
	<i>HEX</i>	0	–	–	–	–	–	–	–
Juan Santos	26.8979, 102.1462								
	<i>ME</i>	26	2	1.30	0.27	7.00	6.06	0.428	Yes
	<i>6PGDH</i>	30	3	2.02	0.80	24.00	14.73	0.001	No
	<i>MDH</i>	34	2	1.23	0.09	3.00	6.28	0.002	No
	<i>ALP</i>	12	2	1.95	0.50	6.00	5.83	0.921	Yes
	<i>PGM-1</i>	2	2	2.00	1.00	2.00	1.00	0.157	Yes
	<i>PGM-2</i>	0	–	–	–	–	–	–	–
	<i>HEX</i>	13	2	1.74	0.62	8.00	5.54	0.109	Yes
La Maroma	26.8704, 102.0205								
	<i>ME</i>	2	2	1.60	0.00	0.00	1.00	0.157	Yes
	<i>6PGDH</i>	30	3	2.18	0.10	3.00	6.18	0.005	No
	<i>MDH</i>	28	3	2.08	0.54	15.00	13.84	0.657	Yes
	<i>ALP</i>	26	3	2.36	0.27	7.00	7.44	0.762	Yes
	<i>PGM-1</i>	31	2	1.95	0.39	12.00	11.87	0.952	Yes
	<i>PGM-2</i>	14	3	2.91	0.00	0.00	1.86	0.000	No
	<i>HEX</i>	4	2	2.00	0.75	3.00	1.88	0.230	Yes
Laguna Grande	26.8513, 102.1487								
	<i>ME</i>	4	1	1.00	0.50	2.00	1.50	0.505	Yes
	<i>6PGDH</i>	20	3	1.27	0.25	5.00	9.78	0.029	Yes
	<i>MDH</i>	25	3	2.21	0.60	15.00	12.50	0.317	Yes
	<i>ALP</i>	21	2	1.40	0.33	7.00	10.50	0.127	Yes
	<i>PGM-1</i>	30	3	1.66	0.43	13.00	14.58	0.552	Yes
	<i>PGM-2</i>	28	2	1.15	0.04	1.00	13.55	0.000	No
	<i>HEX</i>	29	2	1.88	0.62	18.00	14.48	0.191	Yes
Mojarral East	26.9228, 102.1189								
	<i>ME</i>	57	2	1.98	0.28	16.00	28.28	0.001	No
	<i>6PGDH</i>	101	2	1.98	0.73	74.00	49.90	0.000	No
	<i>MDH</i>	102	4	1.69	0.23	23.00	40.17	0.000	No
	<i>ALP</i>	6	3	2.57	0.33	2.00	3.00	0.414	Yes
	<i>PGM-1</i>	21	3	2.71	0.43	9.00	10.41	0.536	Yes
	<i>PGM-2</i>	20	2	1.28	0.05	1.00	4.38	0.001	No
	<i>HEX</i>	64	2	1.84	0.64	41.00	29.18	0.001	No
Pozas Azules	26.8140, 102.0197								
	<i>ME</i>	0	–	–	–	–	–	–	–
	<i>6PGDH</i>	18	3	2.11	0.33	6.00	9.00	0.157	Yes
	<i>MDH</i>	22	2	1.94	0.36	8.00	10.64	0.245	Yes
	<i>ALP</i>	10	2	1.60	0.50	5.00	3.75	0.292	Yes

Continued on p. 192

Appendix A. Continued

		<i>N</i>	<i>na</i>	<i>ne</i>	% Het	<i>H_obs</i>	<i>H_exp</i>	<i>p</i> -value	HWE
Los Remojos	<i>PGM-1</i>	22	2	1.90	0.41	9.00	10.43	0.520	Yes
	<i>PGM-2</i>	21	3	1.98	0.29	6.00	9.33	0.102	Yes
	<i>HEX</i>	21	3	2.36	0.81	17.00	10.50	0.005	No
	26.9126, 102.1072								
	<i>ME</i>	5	3	1.92	0.40	2.00	2.40	0.709	Yes
	<i>6PGDH</i>	20	2	2.06	0.60	12.00	9.60	0.264	Yes
	<i>MDH</i>	18	2	1.99	0.50	9.00	8.97	0.990	Yes
	<i>ALP</i>	7	2	1.69	0.57	4.00	2.86	0.290	Yes
	<i>PGM-1</i>	20	3	2.18	0.55	11.00	9.98	0.646	Yes
<i>PGM-2</i>	21	3	2.19	0.33	7.00	10.50	0.127	Yes	
<i>HEX</i>	16	2	1.93	0.44	7.00	7.72	0.710	Yes	
Rio Mesquites A	26.9300, 102.1274								
	<i>ME</i>	0	–	–	–	–	–	–	–
	<i>6PGDH</i>	22	3	2.07	0.59	13.00	10.43	0.248	Yes
	<i>MDH</i>	23	2	1.94	0.74	17.00	11.15	0.012	No
	<i>ALP</i>	23	3	1.68	0.43	10.00	8.87	0.541	Yes
	<i>PGM-1</i>	18	3	1.98	0.50	9.00	8.31	0.723	Yes
	<i>PGM-2</i>	18	3	2.07	0.33	6.00	8.89	0.168	Yes
	<i>HEX</i>	15	3	2.07	0.60	9.00	7.37	0.390	Yes
Rio Mesquites B	26.9333, 102.1276								
	<i>ME</i>	7	2	1.69	0.29	2.00	2.86	0.427	Yes
	<i>6PGDH</i>	32	3	2.13	0.25	8.00	15.00	0.008	No
	<i>MDH</i>	29	2	2.00	0.62	18.00	14.48	0.191	Yes
	<i>ALP</i>	22	3	2.29	0.45	10.00	10.91	0.696	Yes
	<i>PGM-1</i>	28	2	1.62	0.36	10.00	11.43	0.508	Yes
	<i>PGM-2</i>	19	3	1.17	0.16	3.00	2.76	0.709	Yes
	<i>HEX</i>	20	2	2.00	0.70	14.00	10.00	0.074	Yes
Tio Candido	26.8701, 102.0784								
	<i>ME</i>	32	2	1.64	0.28	9.00	12.48	0.114	Yes
	<i>6PGDH</i>	43	3	1.88	0.72	31.00	19.83	0.000	No
	<i>MDH</i>	44	3	1.43	0.36	16.00	13.09	0.140	Yes
	<i>ALP</i>	20	3	2.12	0.20	4.00	9.60	0.009	No
	<i>PGM-1</i>	17	2	1.94	0.35	6.00	8.24	0.263	Yes
	<i>PGM-2</i>	16	2	1.44	0.13	2.00	4.88	0.018	No
	<i>HEX</i>	22	2	1.37	0.32	7.00	5.89	0.375	Yes
		<i>N</i> ± SE	SE	<i>na</i>	% Het	<i>ne</i>			
Over all Populations									
	<i>ME</i>	12	4.44	3	0.29	2.18			
	<i>6PGDH</i>	32	5.65	3	0.46	2.02			
	<i>MDH</i>	32	5.73	3	0.48	1.96			
	<i>ALP</i>	20	2.89	2	0.42	1.69			
	<i>PGM-1</i>	21	2.69	4	0.43	2.03			
	<i>PGM-2</i>	16	2.68	4	0.22	2.10			
	<i>HEX</i>	18	4.47	4	0.57	2.13			