

*City of San Diego*

# *Vernal Pool Inventory*



*2002-2003*







## THE CITY OF SAN DIEGO

The City of San Diego is pleased to provide you with a copy of its 2002-2003 Vernal Pool Inventory. This inventory builds off of seminal work completed by R. Mitchel Beauchamp (1979) and Dr. Ellen Bauder (1986), as well as over 2500 hours of City staff conducting site specific vernal pool surveys.

This inventory was the product of a grant from the U.S. Fish and Wildlife Service to improve understanding of the current distribution and conservation status of vernal pools within the jurisdiction or ownership of the City of San Diego. The inventory will serve as the foundation for the **Citywide** Vernal Pool Management Plan currently underway.

While the inventory focused on identifying the location and size of vernal pool basins, and five sensitive vernal pool plants, it is my hope that it will serve as the basis for future monitoring and research efforts. Because all of the information was collected with a sub-meter differential Global Positioning System and stored in a Geographic Information System, the data can be easily aggregated with other vernal pool inventories currently underway by the County of San Diego and Marine Corps Air Station Miramar. This will allow a regional perspective on the status of these unique ecosystems.

It is my sincere belief that through proper management, vernal pool habitat can be protected, enhanced and restored. While we cannot undo the tremendous loss of vernal pool habitat that has occurred over the last century, we can strive to maintain and manage what remains. It is in this light that the Inventory and the pending Citywide Vernal Pool Management Plan are presented for your use.

Sincerely,

A handwritten signature in cursive script that reads "Keith A. Greer".

Keith A. Greer, Deputy Planning Director



### Planning Department

202 C Street, MS 5A • San Diego, CA 92101-3865

Tel (619) 236-6479 Fax (619) 236-6478

## **ACKNOWLEDGEMENTS**

### **City Staff**

Keith Greer, Deputy Planning Director  
Holly Cheong, Environmental Biologist  
Randy Rodriguez, Associate Planner  
Melanie Johnson, Associate Planner  
Chad Kane, Assistant Planner  
Richard Brown, Cover Designer  
Betsy Miller, Biologist Intern  
Khalil Martinez, GIS Intern  
David Rousso, Planning Intern

### **Consultants**

Dr. Andrew Bohonak, San Diego State University  
Dr. Marie Simovich, University of San Diego  
Dr. Bonnie Ripley, University of San Diego

Dr. Robert Fisher, USGS-B.R.D.  
Brian Yang, USGS-B.R.D.

Larry Sward, Helix Environmental  
Greg Mason, Helix Environmental  
Keli Balo, Helix Environmental

Christina Schaffer, EDAW

Robert MacAller, RECON

This information is available in alternative formats upon request.



Printed on recycled paper.

## Table of Contents

Section	Page
<b>1. Introduction</b> .....	1
1.1 Background .....	1
1.2 Purpose of Project .....	3
<b>2. Methods</b> .....	4
2.1 Research on Existing Vernal Pool Inventories .....	4
2.2 Field Data Collection .....	4
2.3 Limitations .....	6
<b>3. Results</b> .....	8
3.1 Inventory Summary .....	8
3.2 Results by Site .....	12
3.2.1 Del Mar Mesa .....	13
3.2.1.a Li Collins (H 40) .....	13
3.2.1.b Greystone Torrey Highlands (H 39) .....	14
3.2.1.c Rhodes (H 18-23) .....	15
3.2.1.d Del Mar Mesa (H series, H 1-15) .....	17
3.2.1.e Shaw Texas (H 17) .....	20
3.2.2 Carmel Mountain (H 31-32, H 38) .....	22
3.2.3 Mira Mesa .....	24
3.2.3.a Mesa Norte (B 11) .....	24
3.2.3.b Tierra Alta (B 5-6) .....	25
3.2.3.c Lopez Ridge (B 7-8) .....	26
3.2.3.d Crescent Heights (B 7-8) .....	27
3.2.3.e Fieldstone (C 17-18) .....	28
3.2.3.f Winterwood (C 10-16) .....	30
3.2.3.g Mira Mesa Market Center (C 27) .....	31
3.2.3.h Maddox (C 28) .....	32
3.2.3.i Parkdale Carroll Canyon (D 5-8) .....	34
3.2.3.j Carroll Canyon Preserve (D 5-8) .....	35
3.2.3.k Arjons (I 1) .....	37
3.2.4 Nobel Drive .....	39
3.2.4.a Pueblo Lands (I 12) .....	39
3.2.4.b Bob Baker (I 6 B) .....	40
3.2.4.c Bob Baker 2 (I 6 C) .....	41
3.2.4.d Nobel Research Park (X 7) .....	43
3.2.4.e Nobel Drive (X 5) .....	45
3.2.5 Kearny Mesa .....	47
3.2.5.a Cubic (U 19) .....	48
3.2.5.b Miramar (EE, FF, GA, GG, HH, RR) .....	49
3.2.5.c Magnatron (U 15) .....	49

	3.2.5.d Sander (U 15) .....	50
	3.2.5.e General Dynamics (N 8) .....	52
	3.2.5.f Montgomery Field (N 1-6) .....	54
	3.2.5.g Serra Mesa Library (N 7) .....	57
3.2.6	Mission Trails Regional Park .....	59
	3.2.6.a Mission Trails Regional Park (Q 2) .....	59
	3.2.6.b Murphy Canyon (G 1) .....	63
3.2.7	Urban San Diego .....	63
	3.2.7.a Kelton (S 4) .....	63
	3.2.7.b Chollas Lake .....	64
3.2.8	Otay Lakes .....	64
	3.2.8.a Proctor Valley (R 1) .....	64
	3.2.8.b Otay Lakes (K 3, 5, 10, 13) .....	65
3.2.9	Otay Mesa .....	67
	3.2.9.a Robinhood Ridge (J 4-5) .....	68
	3.2.9.b J 4 .....	69
	3.2.9.c Hidden Trails (J 2 W, J 31) .....	71
	3.2.9.d J 2 W .....	72
	3.2.9.e J 3 .....	73
	3.2.9.f Sweetwater High School (J 33) .....	75
	3.2.9.g West Otay A + B (J 32) .....	77
	3.2.9.h J 34 .....	80
	3.2.9.i Recon South (J 14) .....	81
	3.2.9.j 905 (J 14) .....	82
	3.2.9.k J 11 East .....	84
	3.2.9.l J 11 West .....	86
	3.2.9.m J 12 .....	87
	3.2.9.n J 13 East .....	88
	3.2.9.o J 13 North .....	90
	3.2.9.p J 13 South .....	92
	3.2.9.q J 14 .....	94
	3.2.9.r Arnie's Point (J 15) .....	95
	3.2.9.s J 16-18 .....	96
	3.2.9.t Wruck Canyon (J 16-18) .....	97
	3.2.9.u J 21 .....	98
	3.2.9.v J 27 .....	99
	3.2.9.w J 28 East .....	101
	3.2.9.x J 29-30 .....	102
	3.2.9.y Brown Field (J 35) .....	103
	3.2.9.z Otay Mesa Road Helix (J 2 S) .....	104
	3.2.9.aa Otay Mesa Road Recon (J 2 W) .....	106
	3.2.9.bb Otay Mesa Road Pardee (J 2 S, J 2 W) ...	108
	3.2.9.cc Recon Cal Terraces (J 2 N, J 2 S, J 2 W) .	110
3.2.10	Marron Valley (MM 1) .....	112
3.3	<i>B. sandiegonensis</i> Genetic Research .....	114

<b>4.0</b>	<b>Synopsis</b> .....	114
<b>5.0</b>	<b>References</b> .....	122

## List of Figures

Figure		Page
1.	Regional Distribution of San Diego Vernal Pools .....	2
2.	Precipitation in San Diego County for the 2002-2003 Rainfall Year ..	6
3.	Histogram of Vernal Pool Basin Area .....	8

## List of Appendices

### Appendix

- A. Survey Dates and Staff
- B. Fairy Shrimp Protocol Surveys
- C. Lambert Coordinate Maps
- D. Vernal Pool Indicators by Site
- E. Facultative Wetland Species by Site
- F. Upland Species by Site
- G. Sensitive Species by Site
- H. Preliminary Results of Fairy Shrimp Genetics Study

**APPENDIX H**  
**PRELIMINARY RESULTS OF FAIRY SHRIMP**  
**GENETICS STUDY**



**MSCP vernal pool inventory**  
**City of San Diego (USFWS)**  
**Conservation genetics of the endangered fairy shrimp species Branchinecta sandiegonensis**

Andrew J. Bohonak, Department of Biology, San Diego State University  
**August 12, 2005**

This is the final report for the contract “*Genetic testing of the endangered fairy shrimp species Branchinecta sandiegonensis*” to Andrew J. Bohonak from the City of San Diego. This contract was set up in late 2002 and work for the project officially began January 1, 2003. The contract ended in June 2005. Marie A. Simovich (University of San Diego), a subcontractee and full collaborator on this project. Simovich is permitted by USFWS for work on *B. sandiegonensis*, and Bohonak is listed under that permit.

A scientific publication based on the data summarized here will be submitted for publication. A copy of this manuscript will be provided to Keith Greer (City of San Diego) and Jonathan Snapp-Cook (U.S. Fish and Wildlife Service).

### Summary

A genetic study based on mtDNA sequencing of *B. sandiegonensis* from across its range found two evolutionary significant units “ESUs” that should be strongly considered for unique conservation status. Pool complexes that are in undisturbed areas are often genetically unique.

### Motivation

Worldwide changes in land use (primarily agriculture and urbanization) have led to a global loss of temporary wetlands. In southern California, it is estimated that 95% of the vernal pools have been lost (Bauder 1998 and references therein). The threats to these naturally fragmented habitats are compounded by their inherent natural isolation at both local and regional scales. (Local metapopulations of ponds are found in areas where hydrologic conditions facilitate pool formation. Regionally, these pool complexes are separated kilometers or tens of kilometers by geologically unfavorable terrain.) Contemporary and historical connectivity between pools at these two scales is largely a matter of speculation (Bohonak & Jenkins, 2003). Because the continued loss of vernal pools may interact in complex ways with future climate change, there are many uncertainties concerning the persistence of vernal pool habitats, their associated ecosystem services and the endangered species they maintain (Pyke 2004).

Fairy shrimp (Crustacea: Branchiopoda: Anostraca) are relatively large crustacean zooplankton (> 10 mm) restricted almost entirely to temporary wetlands worldwide. At least five Anostracan species are listed on the U.S. Endangered Species list, with more under consideration. Over 30 fairy shrimp are considered threatened or endangered worldwide. This project examined population genetic structure in the federally endangered fairy shrimp *Branchinecta sandiegonensis* in order to gain insight into contemporary and historical connectivity among pools and pool complexes, and make conservation recommendations.

Prior to this study, only allozymes had been used to study genetic structure in this species (Davies et al. 1997), and there are no DNA-level population genetic studies for any fairy shrimp. Davies et al. (1997) found significant genetic differentiation among 10 pools for *B. sandiegonensis* using allozymes, and evidence for a “temporal Wahlund effect” within pools. (The importance of overlapping generations created by the fairy shrimp cyst bank may be reflected in heterozygote deficiencies within each pond.) The goal of this study was to expand coverage to include the majority of the species range, including all pool complexes on City of San Diego property. The choice of mitochondrial DNA sequence variation over allozymes for this study reflects the higher degree of precision that can be obtained with mtDNA sequencing. Also, sequence-level variation permits a wider range of analyses that can be used to separate contemporary and historical processes such as allopatric isolation and gene flow.

## Methods

Fairy shrimp were collected as adults or cysts, or hatched from sediment samples by Marie A. Simovich. Individuals were collected from across southern California, identified to species according to Eriksen and Belk (1999), and stored in 95% ethanol or at -80° C until analysis. A map containing the collection locations (City and non-City) is provided in Figure 1. We chose to sample additional ponds not specifically located on City of San Diego property, so that our results represent the dispersal biology and evolutionary history of this species across its entire range. These additional samples were analyzed using funds obtained by Bohonak and Simovich from other sources.

Protocol for amplifying a 658 bp portion of the mitochondrial gene cytochrome oxidase I (COI) was adapted from existing lab protocol for arthropods. (Bohonak has developed universal primers similar to LCO-1490 and HCO-2198 of Folmer et al. 1994). PCR products were cycle sequenced using BigDye v. 3 termination (Perkin-Elmer) and sequenced on an ABI 377 automated sequencer or and ABI 3100 sequencer. Sequence alignments were conducted by eye using the program Sequencher. (Alignment is largely trivial, since COI is a protein-coding gene, and no insertions or deletions were detected.) Some individuals were cycle sequenced in both directions.

Evolutionary relationships among haplotypes were determined using maximum parsimony with PAUP 4.0 (Swofford 2001), and with network parsimony reconstruction as implemented in TCS (Clement et al. 2000). General population genetics summary statistics were calculated using PAUP.

## Results

### *General summary statistics*

DNA was analyzed from 316 individual *B. sandiegonensis* from 75 pools in 30 “pool complexes”. (A pool complex is a local metapopulation of hydrologically linked pools). An additional 31 fairy shrimp from other species (*B. coloradensis*, *B. lynchi*, *B. lindahli*) were also sequenced for use in comparative studies and as outgroups. From the 316 *B. sandiegonensis* sequenced, 50 unique haplotypes (“alleles”) have been found. (Each allele is a sequence that differs from all other alleles by one or more base pairs.) The average divergence between all

alleles is 1.65%, and the maximum divergence is 3.04%. Of 657 bp sequenced from the CO I gene, 478 are constant, 132 are parsimony informative, and 47 are parsimony uninformative.

### *Haplotype distributions*

Table 1 summarizes allele distributions within and among pools, pool complexes and geographic regions. (Note: Although the City's original labeling scheme called geographic regions "Complexes" and local metapopulation of hydrologically connected pools "Sites", I refer to a local hydrologically linked set of pools a "complex" in this report.) For clarity, Table 1 lists pools nested within complexes, nested within regions.

There are two dominant features in this data set. First, the numbers generally fall out along a diagonal, indicating that pool complexes are often fixed for unique haplotypes found nowhere else in the species. There is a high degree of endemism apparent within local groups of hydrologically linked pools, and genetic differentiation among regions is high. This is particularly obvious in areas such as Ramona, Otay Mesa, Otay Lakes and Marron Valley, which have less influence from development and recreation than sites in Mira Mesa and Del Mar.

Second, two groups of haplotypes can be distinguished: "A" and "B". Alleles within group A or B differ from each other by relatively few mutational differences (avg. 0.78% divergence, maximum 1.52%). Divergence between A and B is much more pronounced (avg. 2.52% between pairs of alleles, maximum 3.04%). This indicates that individuals from Group A and B have been isolated from one another biologically for many thousands (or perhaps millions) of years with little or no dispersal or hybridization.

Pools in the Nobel, Mira Mesa, Del Mar and the Montgomery Field/General Dynamics areas tend to have more alleles than pools in areas that are relatively pristine (e.g., Otay Lakes, Marron Valley, Ramona, Murphy Canyon: see Table 1).

### *Geographic and phylogenetic analysis*

A maximum parsimony analysis was conducted with PAUP (100 bootstraps, heuristic search), using 6 sequences from *B. lynchi*, *B. lindahli* and *B. coloradensis* as outgroups. The consensus tree and bootstrap values are presented in Figure 2. *B. sandiegonensis* is monophyletic in 100% of the bootstraps, supporting the designation of this species as it is currently recognized. Clades A and B are monophyletic 91% and 92% of the time, respectively, indicating that these are also likely to be real evolutionary units. The sister species to *B. sandiegonensis* cannot be determined with this particular analysis; it is unclear whether the addition of more genes or the use of a model-based analysis (e.g., Bayesian estimation of the phylogeny) would be needed to resolve this question.

### Specific conclusions

These analyses indicate that:

- 1) *B. sandiegonensis* represents a monophyletic taxon (i.e., a "good species" from an evolutionary perspective) in this data set. It is monophyletic in 100% of the bootstraps conducted. Additional genetic and morphological analyses of the genus will be needed to resolve additional taxonomic issues. I recommend maintaining the current nomenclature at this time.

- 2) There is considerable genetic variation within this species.
- 3) There is high mtDNA divergence among vernal pool “complexes” that are, in some cases, only tens of kilometers apart.
- 4) It is obvious that gene flow between pool complexes is lower in areas that are less impacted by development and recreation (e.g., vernal pool complexes in Ramona, Otay Mesa, Otay Lakes and Marron Valley). The simplest conclusion is that human activities tend to artificially homogenize natural populations of *B. sandiegonensis* and increase (rather than decrease) the genetic variation in any particular pool. Consequently, local adaptation to the unique hydrological, biological and chemical aspects of each pool complex may be hindered in these areas.
- 5) There is a deep split between clades “A” and “B”. The clades are reciprocally monophyletic on most trees.
- 6) Clades A and B have unusual allopatric distributions (outlined in Figure 1), which do not correspond to any known current or past geologic features.
- 7) Only 4 individual fairy shrimp of 316 analyzed violate the generalized distributions of clade A and B in Figure 1. (Note the outlying “1”s in Table 1.) These appear to represent very recent introductions of shrimp:
  - a) from {Nobel Drive, Del Mar, Mira Mesa or Carmel Mountain} into {Ramona}
  - b) from {Nobel Drive, Del Mar, or Mira Mesa} into {Sander}
  - c) from {Marron Valley} into {Mission Trails}We recommend that all vernal pool researchers and consultants thoroughly clean their boots and nets after visiting each site.
- 8) There is some phylogenetic structure within clades A and B that indicates long-standing geographic isolation. For example, haplotypes A16 and A26, restricted to the border region, form a monophyletic group. The same is true for:  
{A17, A18, A23} restricted to Marron Valley and Otay Mesa,  
{A19, A20, A21, A22} restricted to Del Mar,  
{B5, B17} found only in Ramona and Pendleton  
{B21, B14, B15, B16}. B21 is found only San Onofre; the others are restricted to Miramar.
- 9) Haplotype A25, found only in Costa Mesa, is most similar to haplotypes found in Otay Mesa, possibly indicating a long distance dispersal event.
- 10) Evolutionary significant units “ESUs” that should be considered for conservation include the two major clades (A and B) and many individual pool complexes. According to some interpretations of the ESU concept, every pool complex that is genetically unique could be considered an ESU worthy of separate consideration. Full scientific acceptance of this would likely require additional genetic analyses with other markers and studies demonstrating morphological, physiological and/or ecological divergence as well.

### Caveats

The taxonomic status of *Branchinecta sandiegonensis* is outside the scope of this study.

Literature cited

- Avice, JC. 2000. Phylogeography: the history and formation of species. Harvard University Press.
- Bauder, ET & S McMillan. 1998. Current distribution and historical extent of vernal pools in southern California and northern Baja California, Mexico. pp. 56-70 *in* Witham, CW *et al.*, eds. Ecology, conservation and management of vernal pool ecosystems. California Native Plant Society.
- Bohonak, A. J. 2002. IBD (Isolation By Distance): a program for analyses of isolation by distance. *Journal of Heredity* 93: 153-154.
- Bohonak, AJ & DG Jenkins. 2003. Ecological and evolutionary significance of dispersal by freshwater invertebrates. *Ecol. Letters* 6: 782-796.
- Clement, M, D Posada & KA Crandall. 2000. TCS: a computer program to estimate gene genealogies. *Mol. Ecol.* 9: 1657-1659.
- Davies, CP, MA Simovich & SA Hathaway. 1997. Population genetic structure of a California endemic branchiopod, *Branchinecta sandiegonensis*. *Hydrobiol.* 359: 149-158.
- Eriksen, CH & D Belk. 1999. Fairy shrimps of California's puddles, pools, and playas. Mad River Press.
- Folmer, O, M Black, W Hoeh, R Lutz & R Vrijenhoek. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Mol. Mar. Biol. Biotechnol.* 3: 294-299.
- Huelsenbeck, JP & F Ronquist. 2004. MrBayes: Bayesian inference of phylogeny.
- Posada, D., and K. A. Crandall. 1998. MODELTEST: Testing the model of DNA substitution. *Bioinformatics* 14: 817-818. v.3.7.
- Posada, D, KA Crandall & AR Templeton. 2000. GeoDis: A program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. *Mol. Ecol.* 9: 487-488.
- Pyke, CR. 2004. Habitat loss confounds climate change impacts. *Frontiers Ecol. Env.* 2: 178-182.
- Schneider, S, J-M Kueffer, D Roessli & L Excoffier. 1998. Arlequin: a software for population genetic data analysis. v. 1.1
- Swofford, DL. 2002. PAUP: phylogenetic analysis using parsimony. v. 4.0b10
- Templeton, AR. 1998. Nested clade analyses of phylogeographic data: testing hypotheses about gene flow and population history. *Mol. Ecol.* 7: 413-418.

Table 1: Haplotype distributions within and among pool “complexes” (local metapopulations of hydrologically linked pools).

Figure 1: Geographic distribution of samples, with the primary distributions of clades A and B circled. Only 4 individuals violate these primary distributions (see Table 1). Black dots indicate ponds sampled.

Figure 2: mtDNA gene tree for *Branchinecta sandiegonensis*. (Maximum parsimony tree, 50% majority consensus, nodes indicate bootstrap support).



Region	Complex	Pond	Haplotype																												
			A07	A08	A10	A01	A02	A21	A22	A12	A14	A20	A11	A04	A19	A13	A15	A06	A03	A29	A05	A25	A16	A26	A09	A24	A27	A18	A23	A28	A17
Nobel drive	Nobel drive	1	1	1		1	7																								
		2				4																									
		3		1		2																									
	Eastgate	1			1	1	1																								
		2				4																									
		4?				2																									
Del Mar	Bowtie	1			1	2	1	1																							
		2				2	2																								
		3				1		2	1																						
	Del Mar Mesa North	1			1	1					1																				
		2				1	1																								
Del Mar Mesa East		2				1			1																						
		3							1																						
	4											3	1																		
	RR1	5							2			1	1																		
						1		1	1	1					1																
Mira Mesa	Cousins	1				5																									
		2					4																								
		3				1	3																								
	Winterwood	1				3										2															
		2					1			1		1										1									
		3																													
		4								2																					
Brown	1				2							2																			
	2					3																									
	3					1					1										2										
Maddox		1				17														1	1										
		2				3			1																						
		4				3																									
		7				1																									
Carmel Mountain	Carmel Mountain	1				5																									
Costa Mesa	Costa Mesa	D																			1	2									
Otay Lakes	Otay Lakes	1																			7	1									
Otay Mesa	Snake Cholla	1																					2								
		2																				5		1							
	Arnie's Point	1																									3	2			
		2																										2	1		
J16-18																										1	1			2	
Goat Mesa																												5			
Marron Valley	Marron Valley	3																													
		5																													
Ramona	Ramona	7				1																									
		17B W6																													
Pendleton	DZ Tank Park	DZTP																													
Miramar	AA10	68.3E																													
		MC5																													
		MC6																													
	AA9	K4																													
		MC4																													
	A4	103.5																													
		105 MC9																													
Mission Trails	Mission Trails	1																													
		3																													
MFGD	General Dynamics	1																													
		2																													
		3																													
	Sander	1																													
		4																													
Montgomery Field		3																													
		5																													
		6																													
Chollas	Chollas	2																													
Murphy Canyon	Murphy Canyon	A2																													
		A5																													
		B1 B3																													
San Onofre	San Onofre	A																													
		C																													
Grand Total			1	1	1	60	30	11	4	13	1	1	8	2	1	3	1	2	2	1	4	1	14	3	1	4	2	8	1	2	11





