Metacommunity Dynamics of Gila River Fishes (R11AC81531)

Final Report

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Executive Summary

Our project combined field surveys of fish communities and habitat characteristics with estimates of population genetic structure to identify and evaluate critical factors influencing fish communities in the Gila River basin of New Mexico. Fish communities were structured along a strong habitat gradient associated with stream size, with distinct differences in the distribution of native and nonnative fishes. Nonnative warm-water species generally occurred in mainstem habitats, whereas coldwater nonnative salmonids occurred in high elevation tributaries. Habitat affinities of native species varied, with some occurring in mainstem habitats and others in tributaries. Several native species, such as desert sucker *Pantosteus clarkii*, Sonora sucker *Catostomus insignis*, and longfin dace *Agosia chrysogaster*, were abundant across a broad range of habitats. Characterizing differences of dispersal among species was attempted with tagging studies (via passive integrated transponder PIT tagging) and otolith microchemistry. Contrasting movement patterns among species with different life history traits was hampered by low abundances and limited recaptures of most species. Unexpected variability in otolith crystalline structure also confounded the use of otoliths to identify differences in natal and adult habitat. Nevertheless, we were able to make inferences on dispersal by investigating patterns of genetic structure. For our genetic analyses, we first used the conceptual framework developed by Winemiller and Rose (1992) to classify fishes based on key ecological traits and then matched those trait classifications with patterns of genetic diversity. Genetic assays identified different patterns of genetic structure and diversity that were somewhat related to species life history characteristics. These patterns ranged from moderate levels of spatial structure in small-bodied, short-lived species indicating dispersal limitation to almost no spatial structure in large-bodied species without dispersal limitation. Nonnative equilibrium strategists had limited distributions, indicating limited dispersal, strong habitat preference, or both. Finally, we used Bayesian networks to visualize the associations between the persistence of federally endangered species and measures of nonnative predator biomass, system productivity, wildfire and distance from source populations. Both distance from source populations and the presence of nonnative predators could negatively influence the persistence of these species. Combined, the experiments conducted during this project emphasize the importance of both habitat heterogeneity and dispersal processes as major structuring factors of Gila River fish communities. Conservation actions should aim to maintain connectivity among diverse habitats within the upper Gila River basin.

Background

The upper Gila River in New Mexico is one of the last unobstructed rivers in the Colorado River basin with a largely intact native fish fauna, including four federally listed and one state listed species. Understanding factors that allow persistence of native species faced with threats of predation by nonnatives, water development plans that would fragment habitats, and increased frequency and severity of disturbances associated with climate change will help reveal the consequences of those stressors. We used a multi-scale and synthetic approach to quantify dispersal patterns, species interactions, and habitat attributes within the Gila River stream ecosystem. This approach tested the importance of these factors in shaping community dynamics of this unique and highly threatened fish fauna. Our approach used a metacommunity framework and considered multiple fish communities in discrete habitats (reaches within tributaries or between tributary confluences) connected by dispersal. The overarching question addressed in the research was: How does habitat connectivity influence community dynamics (e.g., predation by nonnatives) and species persistence in arid-land stream networks? Within this broad question we had three main tasks: (1) Test the relative importance of dispersal factors, spatial factors, habitat, and biotic interactions on metacommunity dynamics; (2) Evaluate variation in dispersal patterns (tendency and symmetry) of species having three different life history strategies; and (3) Develop a predictive model for conservation of native fish communities in fragmented stream networks.

Our study began in Spring 2012 and through a no-cost extension terminated on 30 September 2014. Several extreme events occurred during our study period that influenced our findings. First, in summer 2012 there were severe drought conditions that contributed to the Whitewater-Baldy Fire, which burned 79,854 ha of our study area between 9 May and 23 July. Ash flows following this fire and the smaller Miller Fire (35,950 ha) in 2011 greatly reduced the abundance of many fish species in the Gila River (Whitney 2014). Although this limited our ability to rigorously complete some aspects of this study (e.g., recapture of PIT tagged fish), it did provide baseline data that will be used in a current study funded by the New Mexico Department of Game and Fish to characterize the recovery of the Gila River ecosystem from wildfire.

Below, we outline the findings of our research organized by the three main objectives (tasks) of the research.

Task 1: Test the relative importance of dispersal factors, spatial factors, habitat, and biotic interactions on metacommunity dynamics.

Occupancy sampling - Sixteen sites in the upper Gila River basin (Fig. 1) were selected to evaluate native and nonnative metapopulation dynamics, which when combined among species, can be used to infer metacommunity dynamics. Sites ranged from small tributaries in relatively pristine areas to mainstem habitats that are influenced by irrigation returns and agriculture in the flood plains (sites 1, 3, 4, and 5). By sampling these sites multiple times to determine the presence or absence of each species (Appendix I) we calculated the metapopulation probabilities of occupancy (p_o: number of samples occupied/total number of samples), colonization (p_c: number of colonization events/number of colonization opportunities), and local extinction (p_e: number of extinction events/number of extinction opportunities) (Gotelli and Taylor 1999). A colonization event was defined as a site going from unoccupied to occupied between two consecutive time periods, and an extinction event occurred when a site went from occupied to unoccupied between two consecutive time periods. By definition, colonization events cannot occur if the site is always occupied, and extinctions cannot occur if the site is never occupied. Colonization and extinction opportunities were the number of times a site was unoccupied or occupied, respectively.

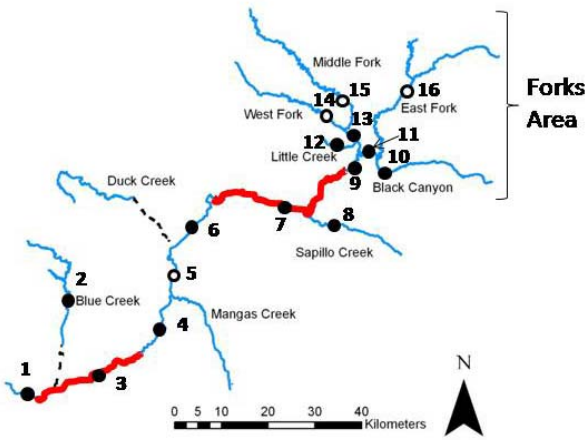

Figure 1. Map of the Gila River in New Mexico. Points represent sampling locations for occupancy, abundance, genetic tissues and otolith microchemistry. Open points indicate long-term monitoring sites. Reaches in bold red indicate canyons and dashed lines are ephemeral streams.

In general, occupancy was higher and extinction lower for natives (mean $p_o = 0.36$; mean $p_e = 0.15$) compared to nonnatives (mean $p_o = 0.25$; mean $p_e = 0.34$). Among native species, longfin dace *Agosia chrysogaster*, Sonora sucker *Catostomus insignis*, and desert sucker *Pantosteus clarkii* had the highest occupancy and lowest extinction, whereas western mosquitofish *Gambusia affinis*, red shiner *Cyprinella lutrensis*, and yellow bullhead *Ameiurus natalis* represented nonnatives with the highest occupancy and lowest extinction (Table 1). Sites above the lower canyon in the Cliff-Gila valley (4 and 5) and one site in the upper forks area (13) had the highest native occupancy and lowest extinction, whereas sites in the modified Redrock Valley (sites1 and 3) or the unmodified East Fork tributary (sites 11 and 16) had high nonnative occupancy and the lowest extinction for nonnatives (Table 2). Both groups had low colonization probabilities (native $p_c = 0.05$; nonnative $p_c = 0.06$) (Table 1). Higher occupancy and lower extinction of natives generally suggest they are better adapted to habitats and disturbance regimes of the upper Gila River compared to nonnatives. By extension, maintaining the current character of the upper Gila River Basin may help ensure high occupancy and low extinction of

native fishes continues into the future. However, nonnatives occur often at both sites with modified flow regimes and habitat in the Redrock Valley and sites with few modifications in the East Fork tributary. Both of these habitats could provide a source of nonnative colonists that might continually influence the success of native species in the system (Table 2). Sites of high occupancy and low extinction did not generally coincide between natives and nonnatives, suggesting differential habitat preferences or negative biotic interactions (competition and predation) limiting co-occurrence between natives and nonnatives. Finally, these results suggested that dispersal aptitude inferred from colonization probabilities did not differ between natives and nonnatives despite their difference in ecological traits.

Table 1. Metapopulation probabilities of occupancy (p_o), colonization (p_c), and extinction (p_e) of native and nonnative fishes in the upper Gila River Basin during March 2012-June 2013.

Origin	Scientific Name	Species Code	Common Name	p_o	p_c	p_e
Native	*Agosia chrysogaster*	AGOCHR	Longfin dace	0.75	0.36	0.14
	Pantosteus clarkii	PANCLA	Desert sucker	0.73	0.17	0.13
	Catostomus insignis	CATINS	Sonora sucker	0.65	0.04	0.05
	Rhinichthys osculus	RHIOSC	Speckled dace	0.41	0.11	0.19
	Tiaroga cobitis	TIACOB	Loach minnow	0.30	0	0.15
	Meda fulgida	MEDFUL	Spikedace	0.19	0.04	0.31
	Gila nigra	GILNIG	Headwater chub	0.11	0.03	0.5
	Pantosteus plebius	PANPLE	Rio Grande sucker	0.06	0	0
	Oncorhynchus gilae	ONCGIL	Gila trout	0.01	0.02	1
Nonnative	*Gambusia affinis*	GAMAFF	Western mosquitofish	0.58	0.11	0.14
	Ameiurus natalis	AMENAT	Yellow bullhead	0.34	0.09	0.14
	Cyprinella lutrensis	CYPLUT	Red shiner	0.34	0	0.18
	Pylodictis olivaris	PYLOLI	Flathead catfish	0.29	0.09	0.47
	Micropterus dolomieu	MIDCOL	Smallmouth bass	0.26	0.04	0.28
	Pimephales promelas	PIMPRO	Fathead minnow	0.24	0.04	0.33
	Ictalurus punctatus	ICTPUN	Channel catfish	0.21	0.1	0.63
	Cyprinus carpio	CYPCAR	Common carp	0.16	0.11	0.56
	Lepomis cyanellus	LEPCYA	Green sunfish	0.16	0.1	0.58
	Oncorhynchus mykiss	ONCMYK	Rainbow trout	0.16	0.06	0.67
	Micropterus salmoides	MICSAL	Largemouth bass	0.03	0	1

Table 2. Metapopulation probabilities of occupancy (p_o), colonization (p_c), and extinction (p_e) of native and nonnative fishes across 16 sites in the upper Gila River Basin during March 2012-June 2013. Site numbers refer to those given in Fig. 1.

			p_o		p_c		p_e	
Site Name	Site Code	Site #	Native	Nonnative	Native	Nonnative	Native	Nonnative
Sunset Canal	SUN	1	0.22	0.36	0.00	0.07	0.00	0.24
Blue Creek	BLU	2	0.27	0.00	0.00	0.00	0.10	—
Middle Box	MB	3	0.31	0.45	0.00	0.12	0.08	0.11
Bird Area	BA	4	0.56	0.35	0.00	0.10	0.00	0.27
Riverside	RS	5	0.51	0.29	0.06	0.16	0.11	0.46
Gila Farm	GF	6	0.11	0.36	0.03	0.07	0.50	0.50
Turkey Creek	TC	7	0.16	0.31	0.07	0.17	0.50	0.47
Sapillo Creek	SAP	8	0.27	0.09	0.04	0.00	0.20	0.00
Grapevine	GV	9	0.36	0.36	0.18	0.17	0.29	0.60
Black Canyon	BLA	10	0.44	0.02	0.00	0.00	0.00	1.00
Lower East Fork	LEF	11	0.20	0.44	0.00	0.08	0.29	0.22
Little Creek	LC	12	0.38	0.00	0.09	0.00	0.08	—
Removal Reach	RR	13	0.60	0.18	0.07	0.14	0.14	0.67
West Fork	WF	14	0.53	0.00	0.00	0.00	0.11	—
Middle Fork	MF	15	0.42	0.38	0.14	0.07	0.20	0.41
Upper East Fork	UEF	16	0.38	0.42	0.14	0.00	0.36	0.15

Metacommunity analysis

Another way of evaluating processes structuring communities is to classify patterns of species occurrence into different elements of metacommunity structure (Leibold and Mikkelson 2002; Presley et al. 2010). This is a hierarchical analysis that sequentially examines patterns of coherence, turnover, and boundary clumping. A species' range is perfectly coherent when occurrences along a gradient are not interrupted by embedded absences. For example, a metacommunity with a "random distribution" would have species with many embedded absences in their distribution and thus have very low coherence. Turnover is a tendency for species to replace each other along environmental gradients. Finally, boundary clumping is the degree to which different species ranges are clustered together. Identifying these patterns in a metacommunity can help infer mechanisms structuring the metacommunity. For example, a lack of coherence in metacommunity structure suggests that species are randomly distributed across the landscape, whereas highly coherent structure suggests the presence of a strong environmental gradient that species are responding to. If metacommunity structure is coherent it might have high turnover, suggesting species are responding differently to the environmental gradient. In contrast, they may be highly nested, suggesting some sites along the gradient are of poor quality and only support the most common species. Finally, high levels of boundary clumping suggest that groups of species are responding similarly to environmental gradients. We used data on the presence and absence of species across our 16 sample sites to quantify metacommunity structure

in the Gila River using the methods described in Leibold and Mikkelson (2002) and Presley et al. (2010).

Fish communities in the Gila River were found to be highly coherent ($z = 3.43$; $P < 0.001$) suggesting they responded strongly to environmental gradients (Fig. 2). Arranging species and sites along these latent environmental gradients indicated that gradient is associated with stream size, with certain species associated with larger, mainstem habitats with greater discharge and others associated with small tributaries with low discharge. Several species were ubiquitous (e.g., desert sucker, Sonora sucker and longfin dace). These communities also exhibited significant turnover ($z = -4.10$; $P < 0.001$), illustrating species replacements along this gradient of stream size. Finally, there was also significant boundary clumping, indicating groups of species responded similarly to these gradients. Results from this analysis are relevant to the conservation of fishes in the Gila River. Specifically, patterns of metacommunity structure indicate the importance of mainstem and tributary systems as containing unique assemblages. However, many of the unique species to mainstem habitats are nonnative fishes such as channel catfish *Ictalurus punctatus*, red shiner and common carp *Cyprinus carpio* (Fig. 2). Federally endangered loach minnow *Tiaroga cobitis* and spikedace *Meda fulgida* are intermediate along these gradients and occur at some mainstem and large tributary sites. Unique assemblages in tributaries include native speckled dace *Rhinichthys osculus* and nonnative rainbow trout *Oncorhynchus mykiss*. Overall, this analysis indicates potentially different response of native and nonnative fishes to environmental gradients in the Gila River and is consistent with the metapopulation results presented above.

Figure 2. Presence – absence matrix of fishes collected across 16 sites on the Gila River, NM. Sites and species are arranged through reciprocal averaging to highlight patterns of species turnover and boundary clumping across sites. Species (column) and site (row) abbreviations are given in Tables 1 and 2, respectively. Embedded absences are filled in to highlight patterns of turnover. Rare species, occurring at < 3 sites are omitted were omitted from the analysis.

Fish marking – In June 2011 we began tagging fishes > 120 mm with passive integrated transponder (PIT) tags, which continued through October 2013. Tagging occurred across the 16 study locations, in addition to other opportunistic locations coinciding with sampling associated with other projects (see Propst et al. 2014). Determination of movement distances was accomplished by either recapturing individuals with electrofishing or seining or with the use of antenna arrays deployed on the West Fork, Middle Fork, and East Fork Gila River tributaries near their confluences with the mainstem. Antenna arrays employed a "pass-through" design, which recorded timing and tag number of individuals as they swam through the array (Fig. 3). Arrays were deployed between March and July of 2013. Movement distance was the watercourse distance between a marking location and the recapture location or antenna array.

In total we tagged 983 individuals (4 native species and 9 nonnative species), with 552 individuals tagged across the 16 sites and 431 individuals tagged at opportunistic locations (Appendix II). Sonora sucker (n = 658), desert sucker (n = 116), and yellow bullhead (n = 76) accounted for 89% of tagged individuals. As mentioned above, large wildfires and subsequent ash flows greatly reduced densities of fishes in the Gila River, thus our ability to detect movement patterns was limited to the most common species. We recaptured 154 individuals using manual methods for 4 native and 5 nonnative species, with 137 (89%) of those individuals represented by Sonora sucker. The antenna arrays provided an additional 386 re-encounters from 2 native and 4 nonnative species, 326 (84%) of which came from Sonora sucker. Recapture data indicated a mean dispersal distance for Sonora sucker of 383 m (min = 0m; max = 5,978m), and antenna array re-encounters provided a similar mean dispersal distance of 404 m (min = 0m; max = 7,942m) (Appendix II). We present mean dispersal distance based on both recapture methods for other species in Appendix II, but suggest cautious interpretation of those results given the limited number of recaptures.

Figure 3. Antenna arrays deploy on the West, Middle, and East Forks Gila River to record movement of individuals tagged with passive integrated transponder (PIT) tags. The antenna consists of red power battery cable, which is configured in a loop perpendicular to flow running

along the bottom and top of the stream. As a tagged individuals swim through the antenna loop a signal is transferred from the loop to a multiplexer that records and stores the data from each antennae, which is located in the box with the yellow lid. The blue boxes attached to each antenna loop contain the antenna tuners, which ensure the loop is properly tuned to receive signals from the PIT tags. The array is powered by a 6V deep cycle battery located in the box with the yellow lid, which is recharged by a solar panel. The antenna arrays were deployed between March and July 2013, until monsoonal flooding forced their removal.

Otolith microchemistry – Water samples were collected in June 2011, March, June, and October 2012, and June and October 2013 to evaluate spatiotemporal variability in water chemistry among sites. Water samples were sent to Dr. Gwen Macpherson at the University of Kansas Department of Geology to evaluate differences in magnesium (Mg), manganese, (Mn), strontium (Sr), and barium (Ba) among sites, and identify specific elements that could be used to differentiate otolith signatures across sites (Fig. 4). This was a necessary first step prior to identifying sites we could select to test dispersal aptitude using this method. Results indicated that the multi-elemental signatures for site 2 (higher Mg and Sr) and 10 (higher Mn and Sr) differed from all other sites (arrows in Fig. 4), and could be used to look for dispersal from the mainstem to tributaries and vice versa.

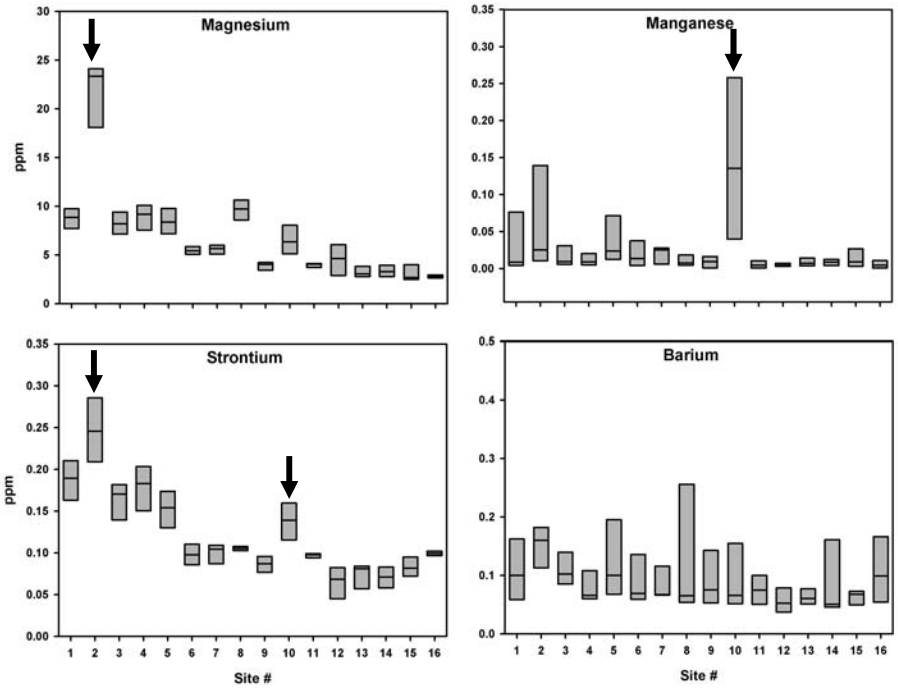

Figure 4. Spatial variation in concentrations of elements used in fish otolith microchemistry analysis. Boxes represent the 25 and 75th percentiles, with the horizontal line within the box representing the site median. Arrows identify sites with unique water chemistry relatively to surrounding sites.

To evaluate if differences in water chemistry among tributary and mainstem locations translated to differences in otolith microchemistry, we compared the multi-elemental concentrations of longfin dace otolith core and edge signatures between sites 1 (mainstem) and 2 (tributary) during June and October 2013, and between site 10 (tributary) and site 13 (mainstem) during June 2013

(n=15-20 individuals per site per sample period). Core signatures represent the water chemistry conditions a fish experienced soon after hatching, whereas otolith edge signatures represent the water chemistry conditions a fish experienced when captured. If among-site differences in water chemistry are temporally stable, large differences between otolith core and edge concentrations within an individual are suggestive of movement between locations with differing water chemistry conditions. We predicted that edge signatures from site 2 would be distinct from those of site 1 because of greater magnesium and strontium concentrations, and that edge signatures from site 10 would be distinct from those of site 13 as a result of greater manganese and strontium (based on results presented in Fig. 4). If individuals had not dispersed between tributary and mainstem locations, we predicted that the core signatures would resemble edge signatures in tributary or mainstem locations, but would be distinct between locations. If dispersal had occurred between the tributary and mainstem, we predicted a mainstem-captured individual would have high elemental concentrations in the core with lower concentrations in the edge, or a tributary-captured individual would have low concentrations in the core and higher concentrations in the edge. Given our multivariate response (4 elemental concentrations) for the core and edge of multiple individuals we used the multivariate indirect ordination technique of principal component analysis (PCA) to visualize results (Fig. 5). Using singular value decomposition of the covariance matrix of individual multi-elemental concentrations PCA arranges individuals along 4 axes (the number of elements) so that all axes are uncorrelated and that individuals with similar multi-elemental concentrations are positioned near one another in multivariate space. The first axis (PC1) represented the dominant gradient of variation in multi-elemental concentrations, with each subsequent axis (PC2-PC4) representing secondary gradients. For all three analyses, negative PC1 scores represented high concentrations of Sr, and positive scores represented high concentrations of Mn and Mg. Similar to Sr, Ba also had negative PC1 scores, except when comparing site 1 vs. 2 in October 2013. This first axis, however, did not reflect differences among sample sites, as predicted. In June 2013, it appeared that individuals captured in the same location had different calcium carbonate otolith structures, including aragonite, vaterite, or calcite. Individuals with an aragonite otolith structure have greater uptake of Sr and Ba, whereas individuals with vaterite or calcite otoliths have greater uptake of Mg and Mn (Melancon et al. 2005). It appears that intra-population variation in otolith calcium carbonate structure confounded our ability to examine movement, as calcium carbonate differences might confound effects of water chemistry. Of those fish with apparent aragonite otolith structure (negative PC1 scores), fish from Blue Creek appeared to have higher concentrations of Sr, relative to Sunset Canal, as indicated by positive scores on PC2. Note, one individual had a core otolith signature of Blue Creek and an edge signature of Sunset Canal, which does not make sense, as we would expect the edge signature to reflect that water chemistry of the site it was captured. Data from June 2013 indicated high overlap in otolith chemistry between sites 10 and 13, regardless of site differences in water microchemistry. Finally, data from October 2013 again indicated higher Sr concentrations in Blue Creek fishes with a few outlier edge samples that did not conform to predictions based on water chemistry. In

summary, otolith edge and core microchemistry indicated differences between Blue Creek and Sunset Canal, but not between Black Canyon and Removal Reach (Fig. 5). Moreover, the grouping of core and edge signatures at Blue Creek and Sunset Canal indicate limited movement, but the presence of several outliers suggested caution is necessary when interpreting these data. Further use of otolith microchemistry methods to infer movement in the upper Gila River may require methodological controls that separate the effects of water chemistry from those of calcium carbonate structure. X-ray diffraction or Ramen spectroscopy is required to confirm that calcium carbonate structures of our fishes' otoliths are actually different.

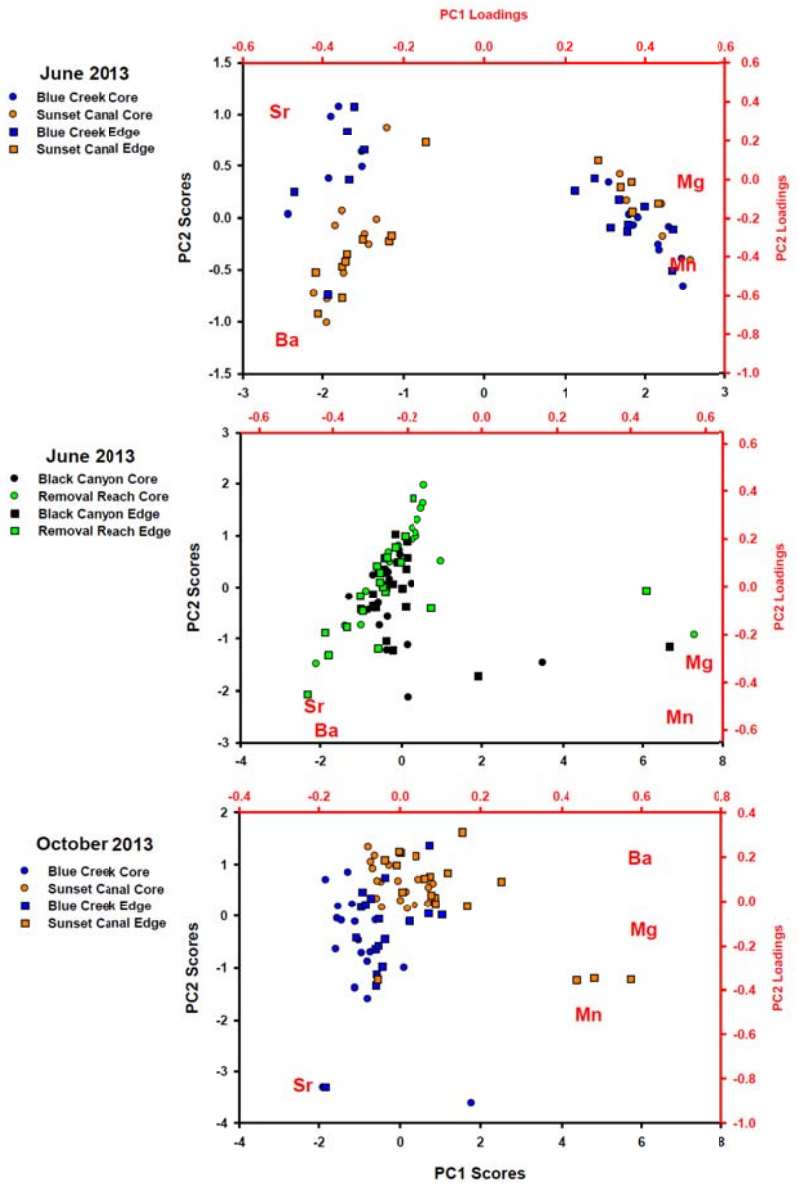

Figure 5. Principal component analysis (PCA) biplots describing variation in longfin dace core and edge chemical signatures during June 2013 for Sunset Canal and Blue Creek (top panel) and Removal Reach versus Black Canyon (middle panel), and during October 2013 for Sunset Canal versus Blue Creek (bottom panel). PCA loading abbreviations are: Mg= magnesium; Mn= manganese; Sr=strontium; Ba=barium.

Task 2: Evaluate variation in dispersal patterns (tendency and symmetry) of species having three different life history strategies (opportunistic, periodic, and equilibrium strategists).

Evaluating different dispersal patterns among species is critical to understanding metacommunity dynamics. It is also likely that dispersal patterns can be predicted by key life history characteristics. Using the trilateral life history theory of Winemiller and Rose (1992) we classified Gila River fishes into life history categories based on fecundity, investment per progeny, and length at maturity as well as other associated traits according to Olden et al. (2006). To visualize differences among species, we used principal components analysis to visualize differences in species traits in two-dimensional space (Figure 6). Spikedace and longfin dace were classified as opportunistic species, Sonora sucker as periodic strategists, and smallmouth bass *Micropterus dolomieu* was classified as an equilibrium species. Desert sucker and yellow bullhead were intermediate between periodic and equilibrium strategists. Small-bodied, short lived opportunistic species are predicted to show less dispersal and more asymmetry (i.e., a difference in the magnitude of dispersal between upstream and downstream directions) in dispersal patterns than large-bodied, long lived periodic species. We also predicted equilibrium strategists to have less dispersal than periodic species because these species are predicted to have specific habitat requirements (i.e., specialists). Gene flow was used to estimate dispersal because it provides a composite measure of local abundance (i.e., local abundance is tied to levels of diversity as measured by allelic richness) and migration rate (i.e., degree of genetic differentiation as measured by F_{ST}).

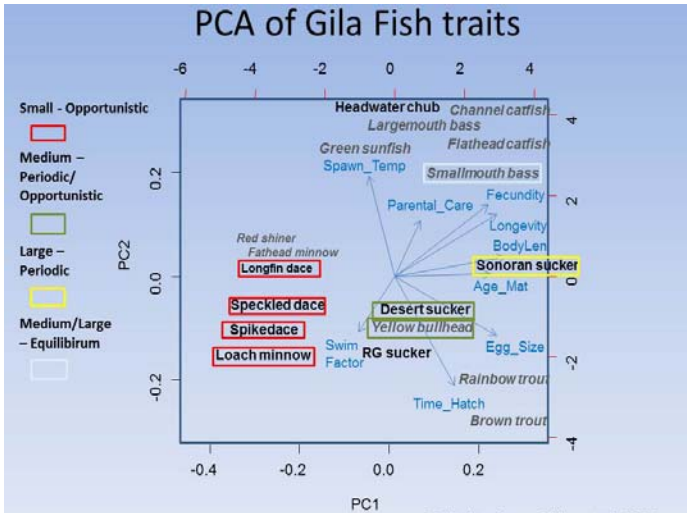

Figure 6. Principal component analysis illustrating variation in life history traits among Gila River fish species. This analysis was used to classify species and test for differences in patterns of gene flow and diversity.

<u>Microsatellite DNA analysis</u> – We assayed genetic diversity via nuclear DNA encoded microsatellite markers. Specifically, we expected spatial patterns of genetic diversity and allelic differentiation to reflect differences in genetically effective dispersal (i.e. gene flow) among species with different life-history strategies. Fin clips were collected from the six species listed above at the 16 sites from October to December 2010 (Appendix III). Protocols for DNA extraction, microsatellite amplification, genotyping, and preliminary analyses are provided in Pilger and Turner (2012). We used mean allelic richness (A_R) as a measure of genetic diversity (which accounts for differences in sample sizes among samples) and F_{ST}, calculated globally for each species and in pairwise fashion across sites, as a measure of allelic differentiation. Comparing global F_{ST} values among species can provide an indication of the level of gene flow occurring, and thus a degree of dispersal for each species. Additionally, comparison of A_R among sites can provide an indication of symmetry in gene flow because if gene flow is

symmetric, then all sites are expected to have the same level of diversity, whereas, asymmetric gene flow should result in differences in diversity among sites.

Analyses of microsatellite data from each species provided evidence for differential dispersal tendencies related to life history. Global F_{ST} values were variable among species and not entirely useful for comparing among life history strategies (Appendix IV). However, most opportunistic species, except loach minnow, and the equilibrium strategist, smallmouth bass, had slightly higher global F_{ST} values relative to periodic species or intermediate periodic/equilibrium strategists. Speckled dace, an opportunistic strategist exhibited the highest observed F_{ST} values indicating very little gene flow between the Forks Area and Blue Creek. Unfortunately, variability within groups was too high to make rigorous conclusions between the relationship between life history strategy and gene flow (F_{ST}). Comparisons of pairwise F_{ST} values among species and life history strategies allowed us to further analyze spatial structuring of each species. Three opportunistic species (spikedace, loach minnow and speckled dace) and one intermediate strategist (desert sucker) showed a correlation between pairwise F_{ST} and stream distance indicating some degree of dispersal limitation (Fig. 7; Appendix IV). Most opportunistic species had high F_{ST} values across a canyon-bound reach of the Gila River mainstem (between sites 6 and 9 in Fig. 1), indicating diminished gene flow. This pattern was most pronounced for spikedace, speckled dace, and longfin dace. Spatial genetic patterns not related to life history strategy were also observed. For instance, tributaries appeared to influence spatial genetic structuring for longfin dace and Sonora sucker as indicated by higher pairwise F_{ST} values over relatively short distances in the isolation-by-distance plots (red ovals in Fig. 7).

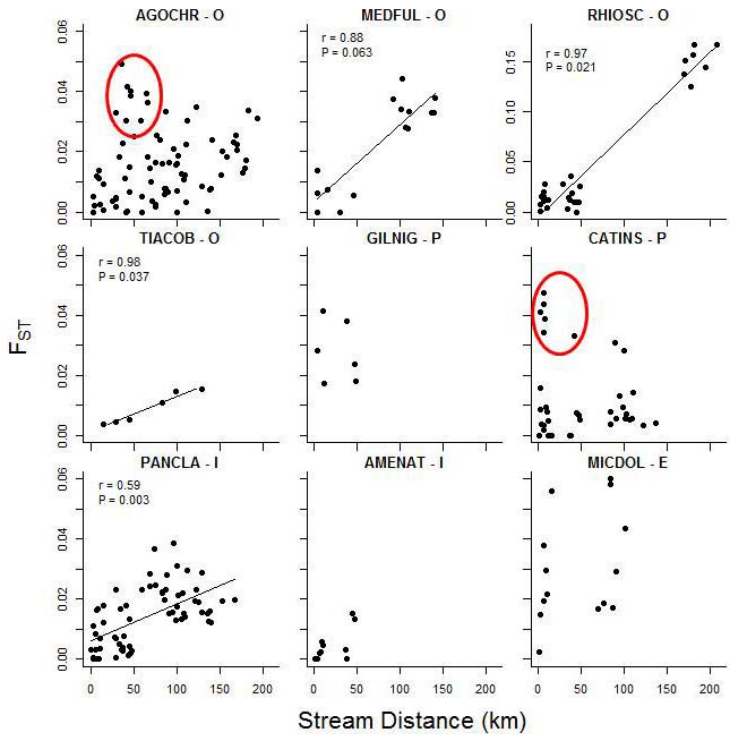

Figure 7. Plots of pairwise F_{ST} versus stream distance among sites for Gila River species representing each life history strategy. Life history strategies indicated by code following species code: E = equilibrium, O = opportunistic, P = periodic, I = intermediate. Mantel r and P values are provided for significant correlations and in Appendix IV. All axes identical except for RHIOSC y-axis.

Although patterns of genetic differentiation based on global F_{ST} were qualitatively similar among species, the distribution of allelic richness (A_R) differed substantially (Fig. 8). For example, we observed a strong trend of increasing A_R at downstream sites for longfin dace and spikedace. Conversely, A_R was greater upstream and diminished slightly downstream for desert sucker. This pattern might suggest longfin dace and spikedace have restricted upstream movement through the canyon-bound reach, limited perhaps by velocity gradients (e.g., Grossman et al. 2010) and/or the occurrence of predatory fishes (e.g., smallmouth bass and flathead catfish *Pylodictis olivaris*). Such limitation in upstream movement results in asymmetric gene flow, and consequently, lowered diversity at upstream sites and higher diversity downstream (e.g. Morrisey & deKerchove 2009), is consistent with a mass-effects dynamic that predicts dispersal of individuals should be greatest in a downstream direction. Over several generations, asymmetric dispersal and gene flow and high extinction/colonization rates could lead to precipitous loss of diversity in upstream sites following broad-scale disturbance of severe magnitude.

In contrast to longfin dace, desert sucker exhibits relatively high A_R in upstream tributary localities suggesting that gene flow is asymmetrical in the opposite direction. Downstream movement and gene flow is probably facilitated by large numbers of drifting larval fishes (Remington 2007), and upstream movement may be facilitated by fewer (but larger) juveniles or mature adults that are invulnerable to predation by piscivores in the canyon-bound reach. In general, genetic data are consistent with a mass-effects model of distribution throughout the catchment. Local extinction downstream is probably replenished by a genetically diverse pool of larval fishes drifting from sites upstream, whereas upstream localities are replenished by larger fishes colonizing open habitat.

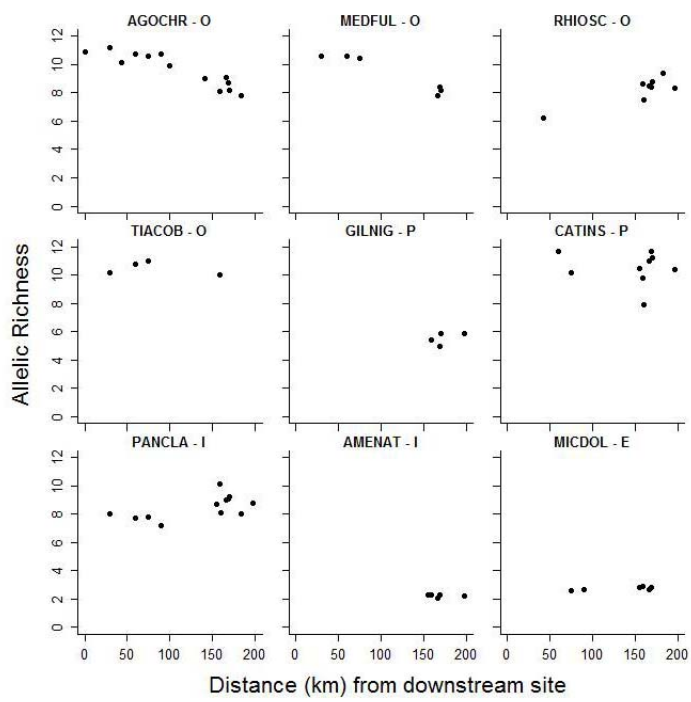

Figure 8. Plots of allelic richness vs distance for Gila River species representing each life history strategy. Life history strategies indicated by code following species code: E = equilibrium, O = opportunistic, P = periodic, I = intermediate. Distance of each site is measured from the most downstream sample location (site 1), therefore, points to the left on each plot are downstream and points to the right are upstream sites. All axes are identical.

Non-native equilibrium strategists, smallmouth bass,

and intermediate strategist, yellow bullhead, posed a problem for direct comparison of A_R across sites. Because these species were introduced within the last century, and the possibility of founder effects, these species showed relatively low A_R at all sites (Fig. 8). Genetic diversity levels did not differ among sites which could be a result of a founder effect and symmetrical gene flow. Seasonal population sampling suggests stable populations of smallmouth bass at sites 9 and 11 (Appendix I), which also appear to have a relatively high degree of gene flow and slightly higher A_R. Lower relative A_R at other sites with ephemeral populations might indicate at least some of these might have originated outside of sites we sampled (e.g., we did not have genetic data from site 16 that also had a stable, but small population of adult smallmouth bass).

Task 3: Develop a predictive model for conservation of native fish communities in fragmented stream networks.

We developed several Bayesian networks using the Netica software (http://www.norsys.com/) to synthesize our data and predict how factors that might be influenced by management actions; specifically, biomass of nonnative species or fragmented populations. Bayesian networks provide a graphical and probabilistic representation of correlative and causative variables (Cain 2001) that are useful when applied to natural resource management (McCann et al. 2006). These "causal networks" consist of a set of variables (nodes) and directed links between variables. Variables represent events with two or more mutually exclusive states (e.g., a species is present/absent, or stream discharge is high/medium/low). Causal nodes are called "parent" nodes and effect nodes are called "child" nodes. Parentless nodes are described by marginal probabilities (e.g., ''Discharge"), which are obtained by observations. A conditional probability is the probability of the state of each child node, given the states of its parent variables (Cain 2001).

Figure 9 illustrates potential causal factors that influence the presence or absence of two federally endangered fishes in the Gila River, loach minnow (Figure 9a) and spikedace (Figure 9b). Each node (boxes) represents variables that we measured at each of our 16 sites. We added a "wildfire" node to indicate how the Miller fire in summer 2011 and Whitewater Baldy fire in summer 2012 might have influenced the probability of occurrence of these species. The other causal nodes included (1) biomass of nonnative predators as a measure of predation effects; (2) stream discharge as a measure of habitat effects; (3) algal biomass as a measure of the productivity of basal resources, and (4) distance to source populations, which is the distance along the stream course to locations that had the most consistent populations of each species (for loach minnow that was site #4 and for spikedace it was sites #4 and #14). Combined, these variables account for a range of ecological factors including biotic interactions, habitat quality and dispersal processes. Probabilities for each node were generated from data collected during this study and continuous variables were classified into two categories based on the distribution of values and our estimation of the range of values that might elicit a response. The software then evaluated the conditional probabilities for each node. To evaluate the importance of the

different nodes on the persistence of these species, we conducted a sensitivity analysis with each of the fish species occurrences as the target node. This analysis evaluates the expected reduction in variance in species occurrence attributed to each variable. Finally, we were able to manipulate variables to evaluate the estimated influence on the probability of occurrence of each species. The variable with the strongest influence on the occurrence of loach minnow was discharge (~6% variable reduction) and for spikedace distance from source (~5% variable reduction; Table 3). Simulating the influence of distance from source populations illustrates the persistence of these species at sites away from core population centers. For example, loach minnow occurred in 50.0% of samples taken from sites within 50 km of the source population (at site #4) but only occurred in 22.5% of samples taken at sites > 100 km from the source population (Figure 9a). Similarly, spikedace occurred in 36.0% of samples taken within 20 km of the source populations (at sites #4 and #14) but only 18.3% of samples taken at sites > 40 km from the sources (Figure 9b). The occurrence of nonnative predators had less of an impact on loach minnow (0.24% variance reduction) than spikedace (2.5% variance reduction; Table 3). The probability of occurrence of loach minnow only decreases from 36.7% at sites with < 1 g/m^2 of nonnative predators to 32.2% at sites with > 1 g/m^2 of nonnative predators. In contrast, probability of occurrence of spikedace shifts from 27.3% to 13.7% in the presences of > 1 g/m^2 of nonnative predators. There are a large number of simulations that could be conducted that are not described here. However, our intention is to share this tool with resource managers and continually update based on new data or potential driver variables.

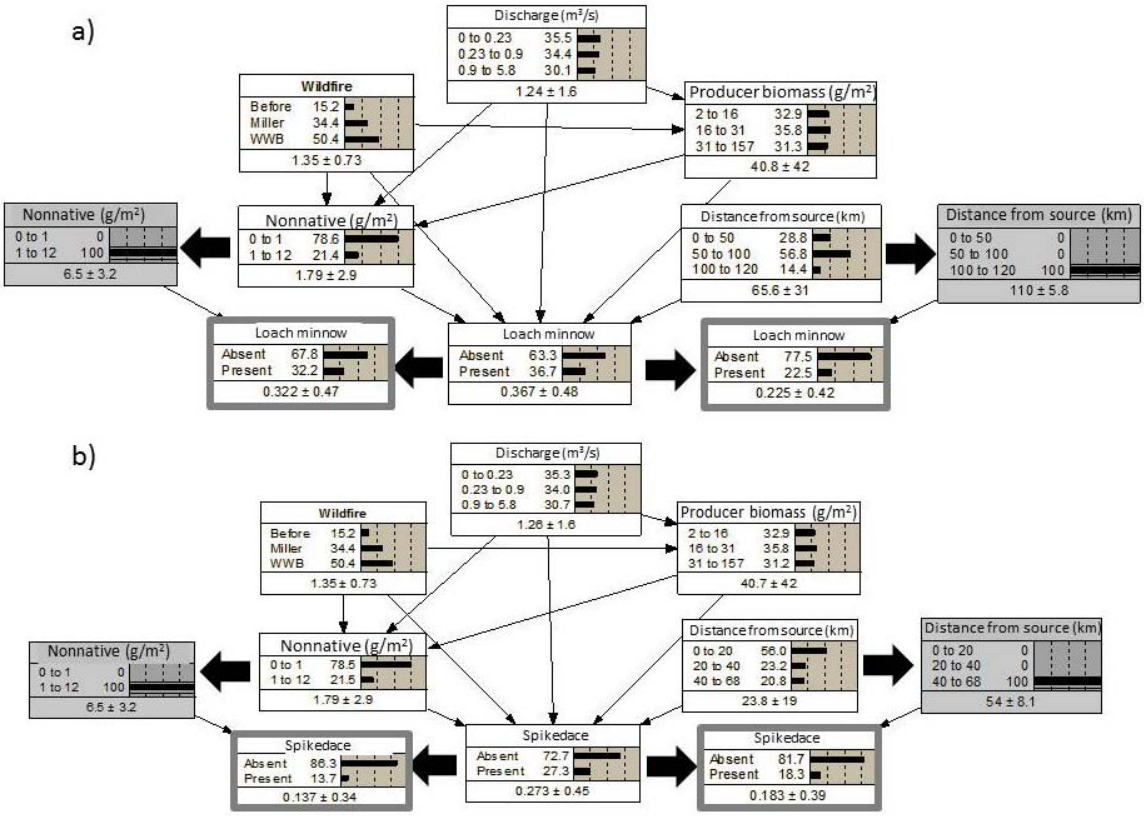

Figure 9. Bayesian networks illustrating the influence of causal variables on the presence of federally endangered loach minnow (a) and spikedace (b) in the upper Gila River, New Mexico. Sensitivity analysis (Table 3) was performed to identify those variables in which the probabilities of occurrence are most associated. Nodes (white boxes) are variables measured across the 16 sites in Figure 1. Grey nodes connected to the original network with thick arrows represent simulations

Table 3. Sensitivity analysis of variables potentially influencing the occurrence of loach minnow and spikedace in reaches of the upper Gila River, New Mexico.

Node	Variance Reduction	Percent
Loach_minnow	0.2324	100.00
Disch_m^3/s	0.0141	6.08
Source_distance_km	0.0085	3.66
Algal_biomass_mg_ m^2	0.0027	1.15
Wildfire	0.0018	0.73
NN_g_per_m^2	0.0006	0.24
Spikedace	0.1984	100.00
Source_distance_km	0.0098	4.94
Algal_biomass_mg_ m^2	0.0061	3.06
NN_g_per_m^2	0.0051	2.55
Wildfire	0.0034	1.72
Disch_m^3/s	0.0008	0.39

Summary and Conservation implications

Metacommunity analysis indicated that communities are arranged along a habitat gradient of streams size and that native and nonnative species have different response to these gradients. Native species have source populations in both mainstem reaches (e.g., loach minnow and spikedace) and tributaries (e.g., speckled dace and headwater chub). Other natives, such as longfin dace and the two native sucker species are more ubiquitous. When viewed across species, our data suggest that maintaining different habitats within the Gila River is necessary for maintenance of the entire native community. Patterns of genetic structure supplemented by limited movement data also provided insights into the importance of dispersal among habitats. The two sucker species appear to have high rates of gene flow and disperse broadly among habitats in the upper Gila River with, at least for desert sucker, upstream reaches potentially acting as source populations. Other native species have more limited dispersal along the mainstem, such as spikedace and loach minnow, which are potentially more vulnerable to

population declines associated with disturbances. Finally, speckled dace have genetically distinct populations in headwaters that are separated by large spans of mainstem habitat. It is likely that extirpation of those populations would result in loss of genetic diversity that would take long periods of time to recolonize.

Based on these findings and our observations in the system over the past two decades (Propst et al. 2008, Stefferud et al. 2011, Whitney et al. 2014), we developed Bayesian networks that illustrate potentially important associations among environmental factors and the persistence of two federally endangered fish species. This exercise is meant to be an adaptable framework for predicting how probabilities of occurrence might be influenced by management actions (e.g., nonnative removal), natural disturbances (e.g., wildfire) or habitat alteration (e.g., fragmentation). Specifically, data from ongoing sampling can be included in the analysis and additional nodes can be generated as we learn more about the system. The current network supports conclusions from community monitoring and genetic studies, indicating that both spatial heterogeneity (i.e., of source populations) and dispersal processes should be maintained. Modifications to the upper Gila River that block migration or benefit nonnative fishes are likely to have a negative influence on native fishes in this system.

Manuscripts and reports associate with project R11AC81531

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Appendix I. Number of individuals caught for each species across sites and sample periods. Species going from present (# caught >0) to absent (# caught =0) between consecutive time periods represents extinction events, whereas colonization events are the opposite. Dashes indicate a site was not sampled during that time period. Species codes can be found in Table 1, and site codes can be found in Table 2.

Site	Year	Month	AGO CHR	AME NAT	CAT CLA	CAT INS	CAT PLE	CYP CAR	CYP LUT	GAM AFF	GIL NIG	ICT PUN	ICT SPP	LEP CYA	MED FUL	MIC DOL	ONC GIL	ONC MYK	ONC SPP	PIM PRO	PYL OLI	RHI OSC	SAL TRU	TIA COB	Spp. Rich.
1	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Oct	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	2012	Mar	9	0	10	0	0	0	61	1	0	1	0	0	0	0	0	0	0	8	1	0	0	0	7
		Jun	2445	0	44	0	0	0	85	56	0	0	0	0	0	0	0	0	0	2	3	0	0	0	6
		Oct	248	1	10	0	0	0	11	1051	0	3	0	0	0	0	0	0	0	4	0	0	0	0	7
	2013	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	4301	0	314	0	0	0	4	92	0	0	0	0	0	0	0	0	0	19	0	0	0	0	5
2	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Oct	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	2012	Mar	171	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55	0	0	3
		Jun	820	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69	0	0	3
		Oct	239	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	2
	2013	Mar	46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78	0	0	2
		Jun	2021	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	352	0	0	2
3	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Oct	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	2012	Mar	103	0	21	0	0	0	366	0	0	2	0	0	0	0	0	0	0	6	1	0	0	6	7
		Jun	810	0	1	0	0	0	47	40	0	2	0	0	0	0	0	0	0	0	5	0	0	30	7
		Oct	2	0	6	0	0	1	27	4	0	18	0	0	0	0	0	0	0	2	11	0	0	2	9
	2013	Mar	5	0	2	0	0	1	10	3	0	10	0	0	0	0	0	0	0	5	0	0	0	5	8
		Jun	4	0	0	0	0	3	29	44	0	10	0	0	0	0	0	0	0	85	2	0	0	1	8
4	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	1717	1	337	50	0	0	9	34	0	0	0	0	314	0	0	0	0	0	1	0	0	40	9
		Oct	390	1	32	77	0	0	5	94	0	0	0	0	89	0	0	0	0	18	3	0	0	59	10
	2012	Mar	99	0	11	22	0	0	9	4	0	1	0	0	24	0	0	0	0	2	0	0	0	48	9
		Jun	539	1	369	309	0	0	7	98	0	0	0	0	155	0	0	0	0	0	0	0	0	32	8
		Oct	36	1	15	27	0	0	2	75	0	0	0	0	1	0	0	0	0	4	0	0	0	14	9
	2013	Mar	15	1	19	30	0	0	0	16	0	1	0	0	1	0	0	0	0	6	0	0	0	15	9
		Jun	92	7	35	38	0	0	0	45	0	0	0	0	11	0	0	0	0	5	1	0	0	53	9
5	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	1235	0	918	4289	0	0	1	3	0	0	0	1	12	0	0	0	0	0	0	0	0	44	8
		Oct	173	0	62	116	0	2	4	87	0	0	0	0	12	0	0	0	0	1	0	0	0	75	9
	2012	Mar	15	0	13	8	0	0	2	4	0	0	0	0	17	2	0	0	0	0	0	0	0	30	8
		Jun	29	0	1051	3073	0	0	1	57	0	0	0	1	5	0	0	0	0	0	0	0	0	98	8
		Oct	2	0	24	20	0	1	6	40	0	0	0	0	0	0	0	0	0	0	1	0	0	33	8
	2013	Mar	3	0	10	11	0	0	0	8	0	1	0	0	1	2	0	0	0	0	0	0	0	12	8
		Jun	5	0	119	463	0	0	0	8	0	0	0	0	0	1	0	0	0	0	0	0	0	32	6
6	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	42	0	6	1	0	6	0	0	0	2	0	4	0	12	0	0	0	0	2	0	0	0	8
		Oct	12	0	4	0	0	2	13	13	0	0	0	7	0	4	0	0	0	0	3	0	0	0	8
	2012	Mar	0	0	0	1	0	0	10	5	0	1	0	5	0	1	0	0	0	0	1	0	0	0	7
		Jun	2	0	0	7	0	3	7	19	0	0	0	1	0	1	0	0	0	0	3	0	0	0	8
		Oct	1	0	0	0	0	0	1	21	0	8	0	0	0	0	0	0	0	0	2	0	0	0	5
	2013	Mar	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		Jun	0	0	0	1	0	3	2	45	0	0	0	0	0	0	0	0	0	0	3	0	0	0	5

Site	Year	Month	AGO CHR	AME NAT	CAT CLA	CAT INS	CAT PLE	CYP CAR	CYP LUT	GAM AFF	GIL NIG	ICT PUN	ICT SPP	LEP CYA	MED FUL	MIC DOL	ONC GIL	ONC MYK	ONC SPP	PIM PRO	PYL OLI	RHI OSC	SAL TRU	TIA COB	Spp. Rich.
7	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Oct	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	2012	Mar	8	0	1	0	0	0	17	0	0	4	0	0	0	0	0	0	0	1	0	0	0	0	5
		Jun	22	0	14	0	0	0	65	24	0	0	0	6	0	0	0	0	0	6	3	0	0	0	7
		Oct	0	0	0	0	0	0	17	4	0	0	0	1	0	0	0	0	0	0	1	0	0	0	4
	2013	Mar	1	0	1	0	0	1	3	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	5
		Jun	0	0	1	0	0	0	22	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
8	2011	Mar	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Jun	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
		Oct	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
	2012	Mar	21	0	0	0	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	4
		Jun	105	0	0	0	219	0	0	0	0	0	0	0	0	0	3	4	0	0	0	0	0	0	4
		Oct	86	0	0	0	62	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	3
	2013	Mar	37	0	0	0	53	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	3
		Jun	102	0	0	0	93	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	3
9	2011	Mar	22	7	26	43	0	0	0	1	0	0	0	0	0	6	0	0	1	0	1	10	0	83	10
		Jun	80	10	10	48	0	0	0	16	0	0	0	0	0	1	0	0	0	2	0	22	0	69	9
		Oct	60	4	2	3	0	0	15	18	0	0	0	2	0	13	0	0	0	1	1	3	0	14	12
	2012	Mar	0	3	0	4	0	0	0	12	0	0	0	0	0	13	0	1	0	0	0	0	0	9	6
		Jun	0	3	0	258	0	0	0	2	0	0	0	2	0	8	0	0	0	0	1	0	0	3	7
		Oct	3	2	1	6	0	4	0	9	0	0	0	0	0	1	0	0	0	0	0	3	0	2	9
	2013	Mar	1	0	1	1	0	0	0	0	0	0	0	1	3	0	0	1	0	0	0	0	0	1	7
		Jun	0	4	4	213	0	3	1	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	7
10	2011	Mar	6	0	29	13	0	0	0	0	0	0	0	0	0	0	0	38	0	0	0	359	9	0	6
		Jun	42	0	25	8	0	0	0	0	0	0	0	0	0	0	26	0	0	0	0	369	6	0	6
		Oct	0	0	15	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	132	1	0	4
	2012	Mar	3	0	5	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	103	0	0	5
		Jun	60	0	3	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	529	0	0	4
		Oct	27	0	14	21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	508	0	0	4
	2013	Mar	21	0	18	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	290	0	0	4
		Jun	157	0	11	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	918	0	0	4
11	2011	Mar	1	6	30	36	0	0	0	7	0	0	0	0	0	9	0	0	0	0	0	0	0	0	6
		Jun	0	12	57	89	0	0	0	46	0	0	0	0	0	5	0	0	0	0	0	0	0	1	6
		Oct	0	10	3	26	0	0	0	1	2	0	0	0	0	5	0	0	0	0	4	0	0	0	7
	2012	Mar	0	5	4	21	0	0	0	1	0	0	0	0	0	1	0	2	0	0	1	0	0	2	8
		Jun	0	19	2	56	0	0	0	1	0	0	0	0	0	4	0	0	0	0	1	0	0	0	6
		Oct	0	22	0	15	0	0	0	5	0	0	0	1	0	4	0	0	0	0	2	0	0	0	6
	2013	Mar	0	4	0	18	0	0	0	7	0	0	0	0	0	1	0	7	0	0	0	0	0	0	5
		Jun	0	25	6	544	0	1	0	22	0	0	0	2	0	4	0	0	0	0	4	0	0	0	8
12	2011	Mar	0	0	143	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1012	0	0	3
		Jun	0	0	59	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1013	2	0	4
		Oct	0	0	49	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	267	1	0	4
	2012	Mar	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	168	0	0	3
		Jun	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	352	0	0	2
		Oct	7	0	15	91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	513	0	0	4
	2013	Mar	1	0	5	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	202	0	0	4
		Jun	3	0	7	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	419	0	0	4
13	2011	Mar	5	4	12	46	0	0	0	15	2	0	0	0	16	5	0	0	0	14	0	17	0	0	10
		Jun	49	1	31	108	0	0	0	0	7	0	0	0	8	3	0	0	0	0	0	92	0	0	8
		Oct	7	2	5	5	0	3	0	11	2	0	0	0	0	0	0	0	0	6	0	22	0	2	10
	2012	Mar	1	0	6	4	0	0	0	0	0	0	0	0	5	0	0	1	0	1	0	13	0	7	8
		Jun	6	1	4	26	0	0	0	3	1	0	0	0	0	1	0	0	0	1	0	8	0	1	10
		Oct	14	0	1	6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	27	0	1	6

Site	Year	Month	AGO CHR	AME NAT	CAT CLA	CAT INS	CAT PLE	CYP CAR	CYP LUT	GAM AFF	GIL NIG	ICT PUN	ICT SPP	LEP CYA	MED FUL	MIC DOL	ONC GIL	ONC MYK	ONC SPP	PIM PRO	PYL OLI	RHI OSC	SAL TRU	TIA COB	Spp. Rich.
	2013	Mar	1	1	2	7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	9	0	0	6
		Jun	3	4	4	16	0	0	0	0	4	0	0	0	4	0	0	0	0	0	0	11	0	2	8
14	2011	Mar	43	0	111	17	0	0	0	0	1	0	0	0	49	0	0	3	3	0	0	568	2	0	9
		Jun	49	0	83	35	0	0	0	0	2	0	0	0	31	0	0	4	0	0	0	681	10	0	8
		Oct	9	0	1	12	0	0	0	0	2	0	0	0	6	0	0	0	0	0	0	103	0	0	6
	2012	Mar	28	0	12	7	0	0	0	0	1	0	0	0	8	0	0	0	0	0	0	98	0	0	6
		Jun	10	0	4	113	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	121	0	0	5
		Oct	18	0	0	12	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	175	0	0	4
	2013	Mar	11	0	0	1	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	44	0	0	4
		Jun	3	0	4	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	107	0	0	4
15	2011	Mar	46	24	54	63	0	0	4	2	13	0	0	0	5	2	0	0	1	7	0	37	1	0	13
		Jun	34	31	107	64	0	0	1	5	46	0	0	0	16	1	0	0	0	5	0	147	3	0	12
		Oct	4	35	8	16	0	1	2	9	0	0	0	0	0	2	0	0	0	0	0	11	3	0	10
	2012	Mar	8	9	5	17	0	0	1	23	0	0	0	0	0	1	0	1	0	1	0	7	0	0	10
15		Jun	0	15	3	23	0	1	0	30	0	0	0	0	0	3	0	0	0	0	1	2	0	0	8
		Oct	16	15	2	6	0	1	0	5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	7
	2013	Mar	2	3	1	5	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	7
		Jun	0	10	59	213	0	0	0	6	1	0	0	0	0	3	0	0	0	1	1	1	0	0	8
16	2011	Mar	0	7	45	57	0	0	0	12	2	0	2	0	0	11	0	0	0	0	0	1	1	0	9
		Jun	0	10	8	21	0	0	0	14	2	0	2	3	0	7	0	0	0	0	0	5	0	0	9
		Oct	0	10	3	5	0	0	0	34	2	4	0	2	0	6	0	0	0	0	0	1	0	0	9
	2012	Mar	9	11	5	25	0	0	0	68	1	2	0	1	0	12	0	0	0	0	0	0	0	0	9
		Jun	2	9	5	13	0	0	0	26	1	1	0	1	0	5	0	0	0	0	0	1	0	0	10
		Oct	0	16	0	12	0	0	0	31	1	10	0	2	0	6	0	0	0	0	0	0	0	0	7
	2013	Mar	0	31	5	14	0	0	0	32	0	0	1	1	0	6	0	0	0	0	0	1	0	0	8
		Jun	0	13	2	4	0	0	0	144	1	0	2	0	0	3	0	0	0	0	0	0	0	0	7
	Total		16885	411	4592	11284	431	38	867	2642	95	87	7	44	810	175	29	77	5	213	67	10080	39	826	

Appendix II. Number of individuals tagged between June 2011 and October 2013 as well as number of individuals recaptured using manual (June 2011-October 2013) or antenna array methods (March-July 2013). Dashes indicate a species was not recaptured with a particular method. See Table 1 for species' codes. Mean dispersal distance (meters) is calculated as the mean of watercourse distance between marking and recapture locations or between marking locations and an antenna array. The minimum and maximum of these values are also reported. See Table 1 for species codes.

Origin	Species	# Tagged	# Recaptured	Mean Distance (Min-Max)	Antenna Re-encounters	Mean Distance (Min-Max)
Native	CATCLA	116	5	0	3	1,011 (0-2,478)
	CATINS	658	137	383 (0-5,987)	326	404 (0-7,942)
	GILNIG	19	1	856	0	—
	ONCGIL	10	1	3,976	0	—
Nonnative	AMENAT	76	2	0	11	1,052 (0-9,431)
	CYPCAR	20	2	0	3	531 (197-698)
	ICTPUN	2	0	—	0	—
	LEPCYA	8	0	—	0	—
	MICDOL	34	1	0	14	0 (0-0)
	MICSAL	2	0	—	0	—
	ONCMYK	7	0	—	0	—
	PYLOLI	24	4	40 (0-90)	29	197
	SALTRU	7	1	26	0	—
	Total	983	154	—	386	—

Appendix III. Species and localities where fin clips were collected and preserved in 95% EtOH for genetic analysis from October and November of 2010. The number of individual fishes sampled at each locality is reported.

Site	AGOCHR	AMENAT	CATINS	GILNIG	MEDFUL	MICDOL	PANCLA	RHIOSC	TIACOB	Total
Bird Area	32	4	31		31	5	31		34	168
Black Canyon	30		10				35	30		105
Blue Creek	30							30		60
East Fork		32	33	20		5	33	21		144
Gila Farm	31		7			30	14		1	83
Grapevine	28	21	28	12		29	30	30	30	208
Heart Bar	30	12	30	3	30	26	31	30		192
Little Creek			31				31	32		94
Lower East Fork		16	30			30	30			106
Middle Box	29		3		17		20		19	88
Middle Fork	30	37	32	19	35	35	32	30		250
Riverside	30		29		29	31	30		30	179
Sapillo Creek	30									30
Sunset Canal	31									31
Turkey Creek	30					3				33
West Fork	36		30	26	30	2	30	28		182
Totals	397	122	294	80	172	196	347	201	114	1953

Appendix IV. Global F_{ST} values and Mantel correlation for each species based on multilocus microsatellite data. F_{ST} 95% confidence intervals were estimated using a bootstrapping approach. Life history categories are indicated for each species. Mantel correlation (r) and associated *P*-values for each species analyzed the correlation between pairwise F_{ST} and pairwise stream distance among sites. The number of sites (N) that a species occurred at with sufficient numbers of individuals (> 10) for genetic analysis is also indicated.

Life History	Species	N	Global F_{ST}	95% CI	Mantel r	*P*
Opportunistic	AGOCHR	13	0.016	0.012-0.020	0.18	0.114
	MEDFUL	6	0.021	0.015-0.026	0.88	0.063
	RHIOSC	8	0.042	0.027-0.062	0.97	0.021
	TIACOB	4	0.005	0.003-0.012	0.98	0.037
Periodic	GILNIG	4	0.015	0.012-0.044	-0.24	0.743
	CATINS	9	0.014	0.01-0.02	-0.21	0.762
Intermediate (Per./Equ.)	PANCLA	12	0.013	0.009-0.016	0.59	0.003
	AMENAT	5	0.006	-0.004-0.024	0.66	0.020
Equilibrium	MICDOL	6	0.028	0.015-0.042	0.30	0.170