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Evaluation of Sampling Precision for Native and Nonnative Fish in the Gila River Basin, New Mexico

Zach Klein [1,*] and Matt Zeigler [2]

[1] Department of Fish, Wildlife and Conservation Ecology, New Mexico State University, 2980 South Espina, Las Cruces, NM 88033, USA
[2] New Mexico Department of Game and Fish, Fisheries Management Division, 1 Wildlife Way, Santa Fe, NM 87505, USA; matthew.zeigler@dgf.nm.gov
* Correspondence: zklein@nmsu.edu

Abstract: Biologists commonly use standard sampling protocols to ensure that data are comparable spatiotemporally. Data also need to be precise to allow for statistically meaningful comparisons. However, the effort needed to precisely sample desert fishes is unclear. We used a resampling approach to evaluate the effort requirements needed to precisely sample fishes among six wadeable rivers in the Gila River basin, New Mexico. We evaluated the number of samples that are necessary to obtain relative density estimates that had 25% relative standard error 80% of the time. We also estimated the effort needed to precisely characterize species richness. Our results indicate that precisely sampling fish in the Gila River basin is difficult. Sonora Sucker *Catostomus insignis*, Desert Sucker *C. clarkii*, Longfin Dace *Agosia chrysogaster*, and Speckled Dace *Rhinichthyes osculus* were generally the only species that could be precisely sampled. Characterizing the native species assemblage in the Gila River basin required between two and seven reaches, whereas the entire species assemblage could only be characterized in 50% of the study systems. The challenge of precisely sampling fish in the Gila River basin suggests that alternative sampling methods may be required to characterize changes in density or species distribution in desert Southwest systems.

Keywords: sampling precision; desert fish; southwest USA

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1. Introduction

Establishing standardized monitoring protocols is an important consideration for natural resource management agencies [1,2]. Standard protocols help to reduce bias by ensuring that data collection is consistent [1]. Consistent data can then be compared through space and time [3]. However, spatiotemporal data need to be relatively precise to ensure that comparisons and conclusions are reliable [4,5]. The statistical power necessary to detect trends through time and space may still be lacking even when fish are monitored using standard protocols [4,6]. The effort used to sample freshwater fishes in Kansas impoundments generally did not provide precise enough estimates for temporal trend analysis [6]. Therefore, estimating the amount of effort needed to precisely sample fish populations is a prudent step to ensure that data collected by natural resource management agencies are reliable and can be used to make sound management decisions.

Data precision is an especially important consideration for freshwater fishes in the American Southwest. Arid and semi-arid regions have relatively depauperate species assemblages [7]. These fishes are commonly species of conservation concern and are

negatively affected by various anthropogenic influences such as dewatering, habitat degradation, and nonnative species [8–10]. The conservation of native desert fishes is therefore a primary focus of natural resource management agencies. Although conservation goals vary, managers are frequently interested in understanding how conservation efforts (e.g., habitat restoration and nonnative species removal) influence the population dynamics and demographics of species of conservation concern [11–13]. Data precision is therefore of paramount concern for maximizing managers' ability to detect changes in population status and making informed management decisions. Unfortunately, the amount of effort needed to obtain precise data is not available for most desert fishes.

The importance of considering effort when sampling fish is typified in New Mexico where the New Mexico Department of Game and Fish (NMDGF) dedicates considerable effort monitoring the population status of native species [14]. For the past 20 years, the NMDGF and their partners have sampled native fishes using a habitat-based sampling approach, whereby river reaches were separated into mesohabitats (e.g., pool, riffle, and run) and the fish assemblage and habitat characteristics of each mesohabitat were sampled separately. Questions have recently been raised as to the value of the habitat-based sampling approach given the logistic challenges (e.g., time and personnel) of sampling a suite of species and their habitats throughout the state. We evaluated the effort needed to precisely sample fishes in the Gila River basin of southwestern New Mexico. Specifically, we evaluated the number of samples that would be needed to obtain relative density estimates that had 25% relative standard error 80% of the time. We also estimated the effort needed to characterize the species assemblage of the Gila River basin at various levels of precision. Although this study focused on the Gila River basin, the results are likely applicable in rivers with similar habitat characteristics and species assemblages.

2. Materials and Methods

2.1. Site Selection and Sampling

In 1988, the NMDGF monitored the fish assemblage of the Middle Fork Gila River. In 2005, a more intensive sampling design was employed, whereby fish assemblages were sampled annually in the Tularosa, San Francisco, Gila, West Fork Gila, East Fork Gila, and Middle Fork Gila rivers (Figure 1). Five permanent reaches (150–230 m) were sampled in the Gila River, whereas one permanent reach was sampled in the Tularosa River (155 m), San Francisco River (174 m), West Fork Gila River (166 m), East Fork Gila River (145 m), and Middle Fork Gila River (183 m; Figure 1). In the summers of 2006 to 2022, the NMDGF and their partners sampled a 4 km reach of the West Fork Gila River (Heart Bar hereafter). This sampling design resulted in 18 years of sampling data for the Middle Fork Gila River, 17 years of data for the Tularosa River, San Francisco River, Gila River, West Fork Gila River, and East Fork Gila River, and 16 years of sampling data for the Heart Bar.

The habitat characteristics and species assemblages of the study systems were similar. Stream flow in these systems had high inter-annual variability and are characterized by winter–spring snowmelt and summer monsoons [15]. Among the rivers, the average wetted width varied from 2.03 to 3.45 m, the mean depth was between 0.2 and 0.4 m, and the average water velocity was between 0.31 and 0.42 m s^{-1}. Native species included Desert Sucker *Catostomus clarkii*, Gila Trout *Oncorhynchus gilae*, Loach Minnow *Tiaroga cobitis*, Longfin Dace *Agosia chrysogaster*, Roundtail Chub *Gila robusta*, Sonora Sucker *Catostomus insignis*, Speckled Dace *Rhinichthyes osculus*, and Spikedace *Meda fulgida*. Nonnative species included Bullhead Catfish *Ameiurus* spp., Bluegill *Lepomis macrochirus*, Brook Stickleback *Culaea inconstans*, Brown Trout *Salmo trutta*, Channel Catfish *Ictalurus punctatus*, Common Carp *Cyprinus carpio*, Fathead Minnow *Pimephales promelas*, Flathead Catfish *Pylodictus olivaris*, Green Sunfish *L. cyanellus*, Largemouth Bass *Micropterus salmoides*, Rainbow Trout

O. mykiss, Red Shiner *Cyprinella lutrensis*, Smallmouth Bass *M. dolomieu*, and Western Mosquitofish *Gambusia affinis*.

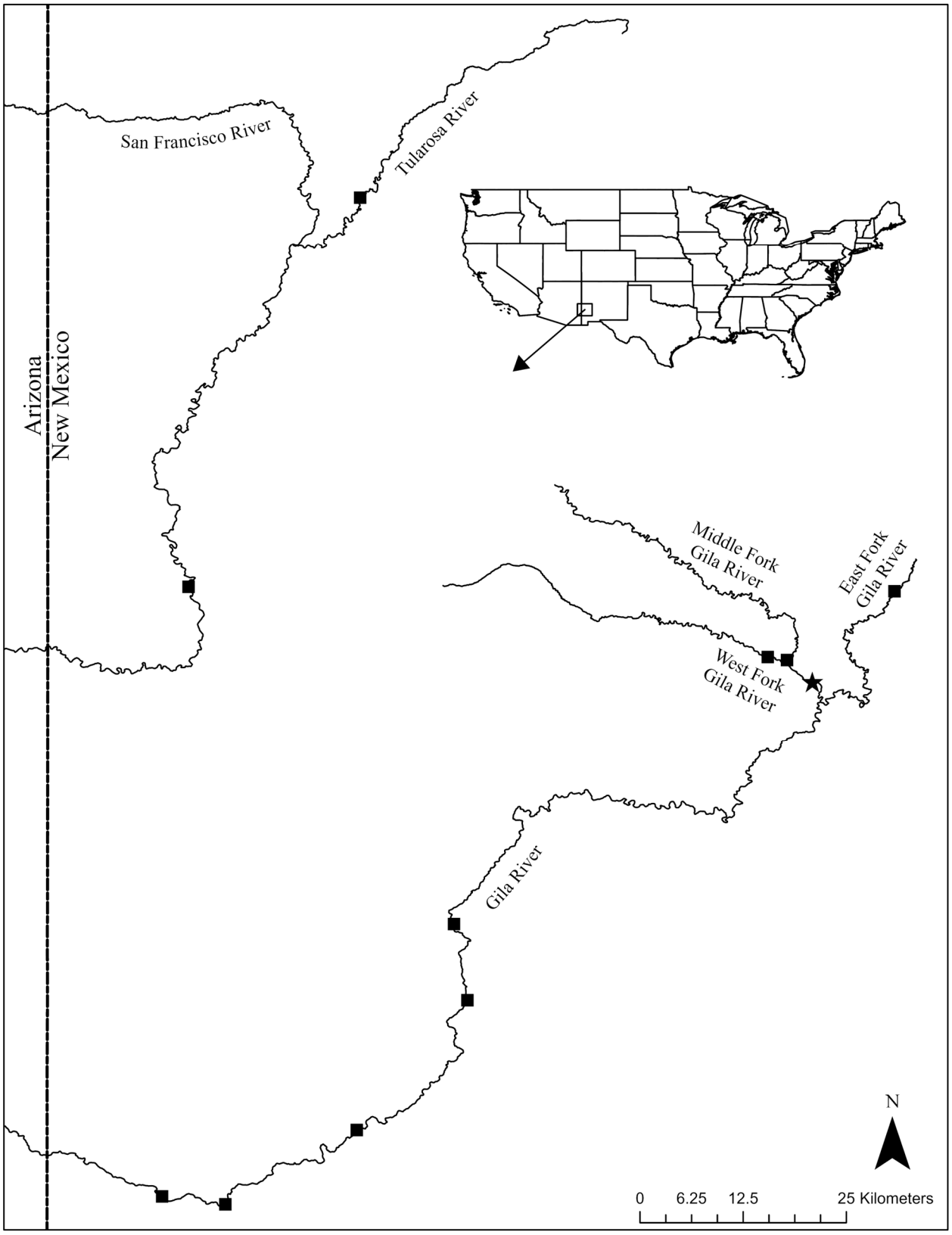

Figure 1. The location of permanent sampling sites (squares) and the Heart Bar sampling site (star) in the Gila River basin, southwestern New Mexico.

Regardless of the system, the mesohabitats (e.g., riffle, run, and pool) of each reach were sampled separately using backpack electrofishing, seining, or backpack electrofishing into a seine. Nine to sixteen different mesohabitats were sampled at each reach with riffles and runs being the most common. Each mesohabitat was sampled with a single gear. Runs were sampled using electrofishing with a crew consisting of one backpack unit and two netters. At the Heart Bar reach, two crews (6 people in total) worked in tandem and electrofished in a single, upstream pass due to stream width. Seines were constructed of 3.0 mm mesh and measured 3.0 m × 1.8 m. Seining was conducted in pool margins by two individuals in a single downstream pass. Seines were also used in conjunction with electrofishing to sample riffle habitat. For this method, one individual would electrofish a riffle downstream while two individuals simultaneously "kicked" the substrate, with the goal of "pushing" benthic-oriented species into a stationary seine. Regardless of the sampling method, fish were identified to species, measured (TL), and weighed (g). All native species were returned to their point of capture. Nonnative species were euthanized with an overdose of MS-222 in the Middle Fork Gila, San Francisco, Tularosa, and West Fork Gila rivers because these reaches are solely managed for native species. Following fish sampling, the length and width (three to five measurements) of each mesohabitat were measured (m) and used to estimate species-specific relative densities (number of fish divided by the mesohabitat area [m^2]).

2.2. Analysis

We used a resampling approach to evaluate the effort requirements needed to precisely estimate species-specific relative densities (fish/m^2; [4,6,16]. Sampling data from the Gila River basin and Heart Bar (S1) were analyzed separately to account for differences in sampling time (summer vs. autumn). We analyzed sampling data by individual gear type because mesohabitats were not sampled with multiple gears. For the resampling analysis focused on relative density, data from a single gear-specific sampling event in a mesohabitat served as the sample unit. For each gear type, catch data from two through *n* sampling events were randomly resampled with replacement 1000 times [4,6]. We then calculated the relative standard error for each of the 1000 iterations [4]. For example, catch data from two river-specific sampling events were randomly selected and the relative standard error was calculated. We repeated this process 1000 times to provide 1000 equally probable catch distributions and associated relative standard error estimates. We repeated the resampling process iteratively (four sampling events, five sampling events, . . .*n* sampling events) up to 100 sampling events. For each number of sampling events (i.e., 2–100), we calculated how many sampling events achieved an RSE_{25}. If RSE_{25} was achieved 80% or more of the time, we assumed the associated level of effort precisely represented the relative density for a given species [4,6,17,18]. The upper bound of 100 sampling events was based on personal experience, whereby a crew could realistically sample 100 mesohabitats in five days. If fewer than 100 sampling events occurred over the study period, the maximum number of sampling events served as the upper bounds [4]. For instance, only 59 mesohabitats were sampled with a backpack electrofisher in the Gila River over the study period; therefore, the upper bound for the analysis was 59 sampling events. The analysis focused on the effort requirements needed to precisely sample all native species and select nonnative species (i.e., Bullhead Catfish, Channel Catfish, Smallmouth Bass, Flathead Catfish, Brown Trout).

We used a similar resampling procedure to understand the effort requirements needed to characterize species richness in the Gila Basin at various precision levels [16]. The Gila River basin was historically sampled at the mesohabitat scale, but mesohabitats are a poor sampling unit to characterize species assemblages because of species-specific habitat use. Therefore, we used mesohabitat data to create "reaches". We assumed that a sampling

reach was a contiguous stretch that equaled roughly 30 times the mean wetted width of a given river (mean length = 232 m; [1]. A reach thus represented the catch data from a series of adjoining mesohabitats that equaled about 30 times the mean wetted width of a given river. Because a reach encompassed numerous mesohabitats and associated sampling methods, reach-specific data used for resampling represented pooled data from all gear and mesohabitat types. Two to twenty-five river-specific sampling events were resampled with replacement 1000 times. We calculated species richness for each of the 1000 iterations. We then estimated the mean proportion of the total available species (based on historical catch data) sampled. This process was repeated for two through twenty-five reaches. We selected 25 reaches to represent a realistic number of "reaches" that a crew could sample in five days. We analyzed species richness sampling requirements for native species and all species (native and nonnative).

3. Results

Over the sampling period, 364 mesohabitats were sampled in the Gila River basin, whereas 1868 mesohabitats were sampled in the Heart Bar from 2006 to 2022 (Tables 1–3). About 74,000 fish representing 21 species were sampled from the Gila River basin over the sampling period. Roughly 64,000 fish from 18 species were sampled from the Heart Bar from 2006 to 2022. Regardless of the system, Longfin Dace, Desert Sucker, and Sonora Sucker were the most abundant species (16–34% of total). Nonnative species tended to be rare among systems (<6% of total).

Table 1. The median number of backpack electrofishing samples (and 25 and 75 percentiles) needed to obtain an RSE_{25} 80% or more of the time for native and select nonnative species in the Gila River basin. Dashes indicate that the species was not sampled over the study period.

Species	Heart Bar	Gila River	WF Gila River	MF Gila River	EF Gila River	San Francisco River	Tularosa River	Overall
				Native				
Agosia chrysogaster	>100	58 (57, 59)	>17	>18	>18	>16	>18	>100
Catostomus clarkii	>100	>59	>17	>18	>18	>16	>18	84 (75, 92)
Catostomus insignis	83 (75, 92)	>59	>17	>18	>18	14 (13, 16)	>18	68 (52, 84)
Gila robusta	>100	>59	>17	>18	>18	—	—	>100
Meda fulgida	>100	>59	>17	>18	>18	>16	—	>100
Oncorhynchus gilae	>100	—	>17	—	—	—	—	>100
Rhinichthyes osculus	>100	—	>17	>18	>18	>16	>18	80 (70, 90)
Tiaroga cobitis	>100	>59	>17	>18	>18	>16	>18	>100
				Nonnative				
Ameiurus spp.	>100	>59	>17	>18	>18	—	—	95 (92, 97)
Ictalurus punctatus	—	>59	—	—	>18	—	—	>100
Micropterus dolomeiu	>100	>59	>17	>18	>18	>16	—	96 (93, 98)
Pylodictus olivaris	>100	>59	—	>18	—	—	—	>100
Salmo trutta	>100	—	>17	>18	—	—	—	>100

The effort needed to precisely sample relative density by gear varied by species and river (Tables 1–3). Backpack electrofishing was the most effective method for precisely sampling relative density. For instance, the relative density of Desert Sucker, Sonora Sucker, Speckled Dace, Bullhead Catfish, and Smallmouth Bass could all be precisely sampled in the Gila River basin using backpack electrofishing. However, the ability to obtain precise estimates of relative density using backpack electrofishing was highly variable among rivers. Longfin Dace and Sonora Sucker were the only species that achieved an RSE_{25} 80% or more of the time among the sampled rivers (Table 1). Backpack electrofishing into a seine also yielded precise and reliable estimates of relative density (Table 2). The relative density of Desert Sucker, Loach Minnow, Longfin Dace, and Speckled Dace could all be sampled precisely, but precise estimates of relative density were limited to select rivers. For instance, Heart Bar was the only river where the relative density of Longfin

Dace, Speckled Dace, and Loach Minnow could be estimated precisely (i.e., RSE_{25} 80% or more of the time). Precise estimates of species-specific relative density were only achieved for Longfin Dace using seines (Table 3). Regardless of gear type, a large number of sampling events needed to occur to obtain precise estimates of relative density (Tables 1–3). Between 14 and 83 sampling events were needed to obtain precise estimates of relative density using backpack electrofishing (Table 1). Similarly, 13 to 96 sampling events were needed to obtain precise estimates of relative density using the backpack electrofishing–seine combination (Table 2).

Table 2. The median number of backpack electrofishing–seine samples (and 25 and 75 percentiles) needed to obtain an RSE_{25} 80% or more of the time for native and select nonnative species in the Gila River basin. Dashes indicate that the species was not sampled over the study period.

Species	Heart Bar	Gila River	WF Gila River	MF Gila River	EF Gila River	San Francisco River	Tularosa River	Overall
				Native				
Agosia chrysogaster	96 (93, 98)	>45	>13	>14	>12	>13	>10	>100
Catostomus clarkii	>100	>45	>13	13 (12, 14)	>12	>13	>10	>100
Catostomus insignis	>100	>45	>13	>14	>12	>13	>10	>100
Gila robusta	>100	>45	>13	>14	>12	—	—	>100
Meda fulgida	>100	>45	>13	>14	>12	>13	—	>100
Oncorhynchus gilae	>100	—	>13	—	—	—	—	>100
Rhinichthyes osculus	91 (87, 96)	—	>13	>14	>12	>13	>10	90 (85, 95)
Tiaroga cobitis	69 (54, 85)	>45	>13	>14	>12	>13	>10	>100
				Nonnative				
Ameiurus spp.	>100	>45	>13	>14	>12	—	—	>100
Ictalurus punctatus	—	>45	—	—	>12	—	—	>100
Micropterus dolomeiu	>100	>45	>13	>14	>12	>13	—	>100
Pylodictus olivaris	>100	>45	—	>14	—	—	—	>100
Salmo trutta	>100	—	>13	>14	—	—	—	>100

Table 3. The median number of seine samples (and 25 and 75 percentiles) needed to obtain an RSE_{25} 80% or more of the time for native and select nonnative species in the Gila River basin. Dashes indicate that the species was not sampled over the study period.

Species	Heart Bar	Gila River	WF Gila River	MF Gila River	EF Gila River	San Francisco River	Tularosa River	Overall
				Native				
Agosia chrysogaster	>100	58 (57, 58)	>14	>15	>12	>9	>3	>100
Catostomus clarkii	>100	>58	>14	>15	>12	>9	>3	>100
Catostomus insignis	>100	>58	>14	>15	>12	>9	>3	>100
Gila robusta	>100	>58	>14	>15	>12	—	—	>100
Meda fulgida	>100	>58	>14	>15	>12	>9	—	>100
Oncorhynchus gilae	>100	—	>14	—	—	—	—	>100
Rhinichthyes osculus	>100	—	>14	>15	>12	>9	>3	>100
Tiaroga cobitis	>100	>58	>14	>15	>12	>9	>3	>100
				Nonnative				
Ameiurus spp.	>100	>58	>14	>15	>12	—	—	>100
Ictalurus punctatus	—	>58	—	—	>12	—	—	>100
Micropterus dolomeiu	>100	>58	>14	>15	>12	>9	—	>100
Pylodictus olivaris	>100	>58	—	>15	—	—	—	>100
Salmo trutta	>100	—	>14	>15	—	—	—	>100

In general, the effort needed to characterize species richness in systems in the Gila River basin were relatively low (Figures 2 and 3). On average, between 2 and 10 reaches were needed to detect 75% or more of the species in a given system. However, total species richness (i.e., 100% of species) could only be detected in the Gila River, East Fork Gila River, and West Fork Gila River in 25 or fewer reaches (Figure 2). Considerably less effort was needed to detect native species (Figure 3). An average of two to four reaches were needed to detect 75% or more of the native fish in a given system. Among the rivers, all of the native species could be detected in an average of 25 or fewer reaches.

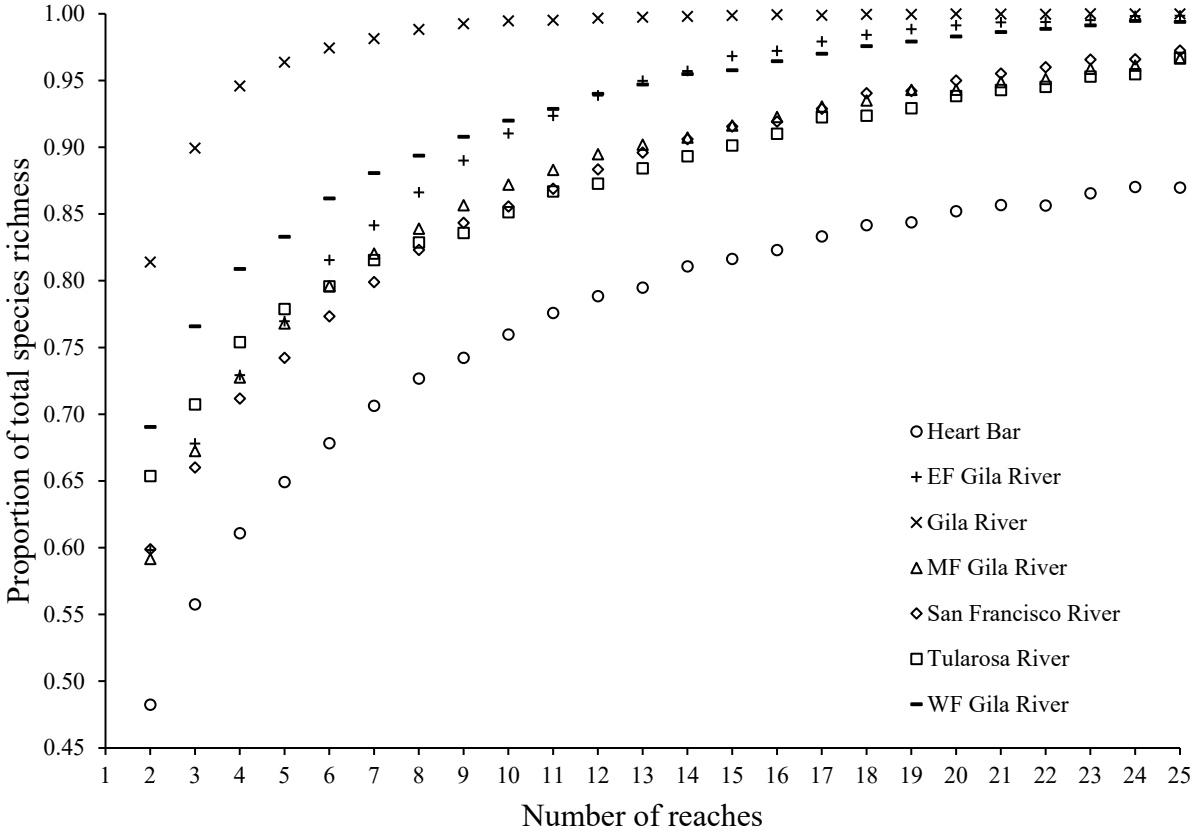

Figure 2. The proportion of total species richness by the number of sampling reaches for all species in the Gila River basin.

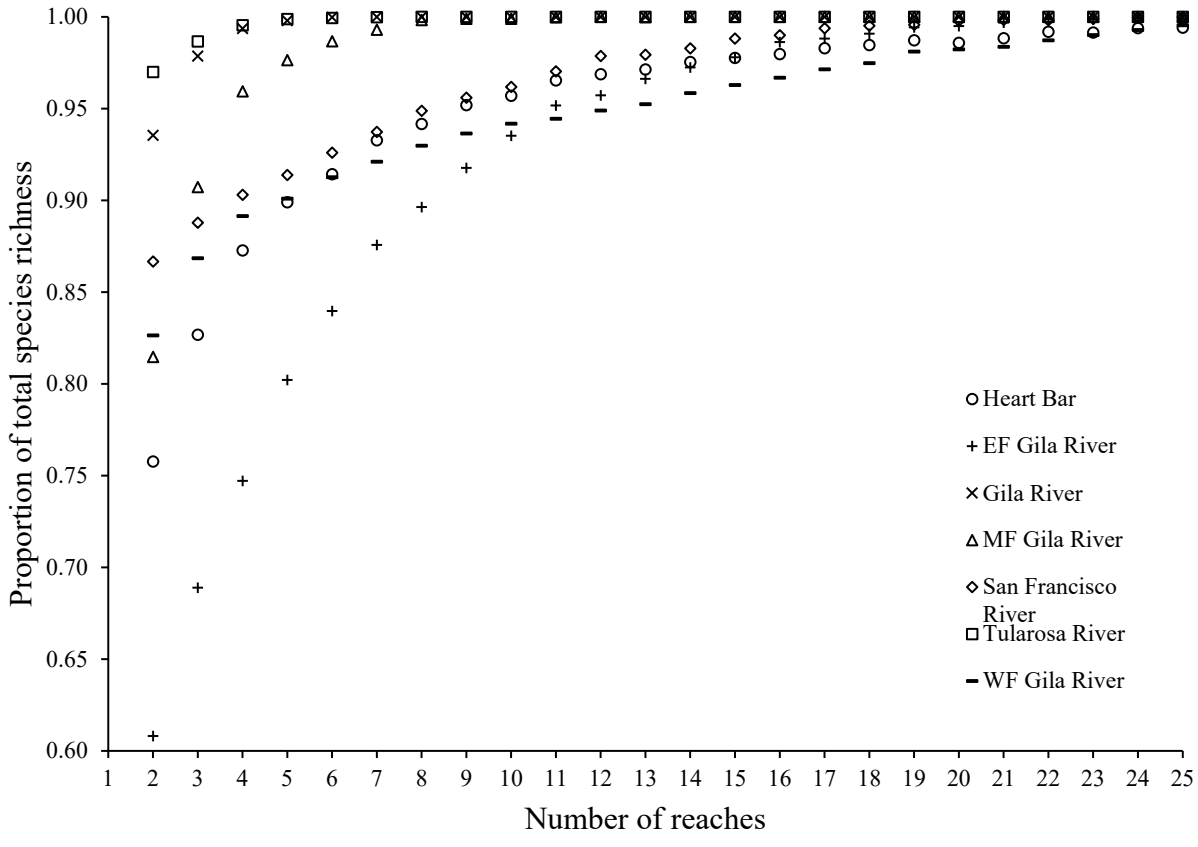

Figure 3. The proportion of total species richness by the number of sampling reaches for all native species in the Gila River basin.

4. Discussion

Our results suggest that the effort requirements needed to precisely sample fish in rivers is frequently logistically untenable for most natural resource management agencies [19–22]. More than 400 randomly sampled reaches were needed to detect a 10% change in catch-per-unit effort for Speckled Dace in Muddy Creek, Wyoming [21]. About 2900 random mesohabitat samples were needed to detect a 25% change in Flannelmouth Sucker *Catastomus latipinnis* relative abundance using electrofishing in the Colorado River [20]. In the current study, most species could not be precisely sampled in fewer than 100 sampling events. Although we did not estimate the total number of sampling events that needed to occur to achieve precise density estimates, sampling more than 100 mesohabitats is likely unrealistic for routine monitoring. The inability to precisely sample fishes characteristic of the desert Southwest may require managers to consider alternative sampling approaches.

Establishing permanent sampling sites has the potential to reduce the amount of effort that is needed to precisely sample fishes in the Gila River basin [4,18,20]. Sampling permanent sites increased the ability to detect changes in species-specific catch-per-unit effort by as much as 45% in Muddy Creek, Wyoming, compared to a random sampling approach [21]. Although fixed-site sampling may be more appropriate for assessing temporal trends, it is important to note that random samples are often more suitable for identifying spatial variability [19–21]. However, if species change habitat use through time, the advantages of a fixed-site sampling approach may be limited due to high variation in abundance through time [19–21]. This concern is especially germane in highly dynamic systems such as in the Gila River basin where variable precipitation patterns result in large variations in habitat availability [23–25]. If neither fixed-sites or random-sites satisfy the objectives of a natural resource management agency, managers may decide to focus effort on alternative estimation techniques. For instance, population abundance could be estimated using mark-recapture or depletion methods if trends in population abundance were of interest and relative density estimates were unreliable [20,21,26]. Managers may also consider a periodic sampling approach, whereby larger portions of specific rivers are intensively sampled on a rotating basis [6,19,27]. This approach may alleviate time constraints and allow managers the ability to obtain precise estimates of relative density or abundance.

The effort required to estimate species richness is often reported to be lower than those needed to precisely estimate relative abundance or density [19,22]. Fewer samples were needed to precisely estimate species richness compared to precisely estimating relative abundance among four streams in Nebraska and Kansas [22]. In the current study, 75% of the total native species richness could be estimated in fewer than 10 reaches, whereas species-specific density was rarely precise in 25 or fewer reaches. Although estimating species richness required relatively little effort in the Gila River basin, our results may not be applicable in systems with highly disparate species diversity and/or a complex habitat [22,28,29]. The higher effort requirements needed to estimate species richness in side-channel habitat was hypothesized to be due to differences in habitat characteristics and species richness between main channels and side channels in the Kootenai River, Idaho [30]. Habitat complexity (e.g., depth, water velocity, and substrate type) was correlated with species richness in two Panama streams [23]. Our results are likely similar to other systems in the Southwest, but large differences in habitat characteristics or species richness may change the required effort needed to characterize species assemblage.

Our results highlight the common challenge of precisely sampling fish [6,21,27,31]. Therefore, it is prudent to carefully consider sampling objectives when developing sampling designs [3]. If study objectives are focused on evaluating temporal trends, natural resource management agencies may struggle to collect data that are precise enough to detect

meaningful changes in species abundance [4]. Imprecise data will likely lead to tenuous conclusions and may lead to inappropriate management decisions [32]. If collecting precise data is challenging, managers may need to consider alternative sampling approaches that specifically address their objectives [27]. For instance, if temporal trends in abundance are of interest, managers may employ mark-recapture or depletion methods to reliably estimate species abundance [20,21]. Managers may also be interested in characterizing species richness. Our results suggest that such an objective could be accomplished in 25 or fewer reaches typical of the Gila River basin. Although 25,200 m reaches represents a considerable amount of effort (i.e., 5 km), managers could potentially employ a rotating sampling design to allow more effort to be exerted on a single system, annually [6]. Combining traditional sampling methods with newer techniques such as environmental DNA metabarcoding could also allow managers to increase samples across space while maintaining the ability to determine abundance [33–35]. Precisely sampling freshwater fishes is clearly challenging. However, the development of clear objectives and subsequent implementation of appropriate sampling approaches is an important consideration for enhancing the conservation of fishes in the Southwest.

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References

1. Bonar, S.A.; Hubert, W.A.; Willis, D.W. (Eds.) *Standard Methods for Sampling North American Freshwater Fishes*; American Fisheries Society: Bethesda, MD, USA, 2009.
2. Pope, K.L.; Lochmann, S.E.; Young, M.K. Methods for assessing fish populations. In *Inland Fisheries Management in North America*, 3rd ed.; Hubert, W.A., Quist, M.C., Eds.; American Fisheries Society: Bethesda, MD, USA, 2010; pp. 325–345.
3. Hansen, M.J.; Douglas Beard, T.; Hayes, D.B., Jr. Sampling and experimental design. In *Analysis and Interpretation of Freshwater Fisheries Data*; Guy, C.S., Brown, M.L., Eds.; American Fisheries Society: Bethesda, MD, USA, 2007; pp. 51–120.
4. Dumont, S.C.; Schlechte, W. Use of resampling to evaluate a simple random sampling design for general monitoring of fishes in Texas reservoirs. *N. Am. J. Fish. Manag.* **2004**, *24*, 408–416. [CrossRef]
5. Radinger, J.; Britton, J.R.; Carlson, S.M.; Magurran, A.E.; Alcaraz-Hernández, J.D.; Almodóvar, A.; Benejam, L.; Fernández-Delgado, C.; Nicola, G.G.; Oliva-Paterna, F.J.; et al. Effective monitoring of freshwater fishes. *Fish Fish.* **2019**, *20*, 729–747. [CrossRef]

6. Koch, J.D.; Neely, B.C.; Colvin, M.E. Evaluation of precision and sample sizes using standardized sampling in Kansas reservoirs. *N. Am. J. Fish. Manag.* **2014**, *34*, 1211–1220. [CrossRef]
7. Harms, T.K.; Sponseller, R.A.; Grimm, N.B. Desert streams. In *Encyclopedia of Ecology*; Jørgensen, S.E., Fath, B.D., Eds.; Elsevier: Oxford, UK, 2008; pp. 871–879.
8. Olden, J.D.; Poff, N.L. Long-term trends of native and non-native fish faunas in the American Southwest. *Anim. Biodivers. Conserv.* **2005**, *28*, 75–89. [CrossRef]
9. Jelks, H.L.; Walsh, S.J.; Burkhead, N.M.; Contreras-Balderas, S.; Díaz-Pardo, E.; Hendrickson, D.A.; Lyons, J.; Mandrak, N.E.; McCormick, F.M.; Nelson, J.S.; et al. Conservation status of imperiled North American freshwater and diadromous fishes. *Fisheries* **2008**, *33*, 372–407. [CrossRef]
10. Pool, T.K.; Olden, J.D. Taxonomic and functional homogenization of an endemic desert fish fauna. *Divers. Distrib.* **2012**, *18*, 366–376. [CrossRef]
11. Rinne, J.N.; Minckley, W.L. *Native Fishes of Arid Lands: A Dwindling Resource of the Desert Southwest*; USDA Forest Service General Technical Report RM-206; U.S. Forest Service: Fort Collins, CO, USA, 1991.
12. Paroz, Y.M.; Propst, D.L. *Distribution of Spikedace, Loach Minnow, and Chub Species in the Gila River Basin, New Mexico, 1908–2007*; New Mexico Department of Game and Fish: Santa Fe, NM, USA, 2007.
13. Propst, D.L.; Gido, K.B.; Stefferud, J.A. Natural flow regimes, nonnative fishes, and persistence of native fish assemblages in arid-land river systems. *Ecol. Appl.* **2008**, *18*, 1236–1252. [CrossRef]
14. Propst, D.L. *Threatened and Endangered Fishes in New Mexico*; Technical Report No. 1; New Mexico Department of Game and Fish: Santa Fe, NM, USA, 1999.
15. Gido, K.B.; Propst, D.L.; Whitney, J.E.; Hedden, S.C.; Turner, T.F.; Pilger, T.J. Pockets of resistance: Response of arid-land fish communities to climate, hydrology, and wildfire. *Freshw. Biol.* **2018**, *64*, 761–777. [CrossRef]
16. Quist, M.C.; Bruce, L.; Bogenschutz, K.; Morris, J.E. Sample size requirements for estimating species richness of aquatic vegetation in Iowa lakes. *J. Freshw. Ecol.* **2007**, *22*, 477–491. [CrossRef]
17. Robson, D.S.; Reiger, H.A. Sample size in Peterson mark-recapture experiments. *Trans. Am. Fish. Soc.* **1964**, *93*, 215–226. [CrossRef]
18. Wilde, G.R.; Fisher, W.L. Reservoir fisheries sampling and experimental design. In *Multidimensional Approaches to Reservoir Fisheries Management*; Miranda, L.E., DeVries, D.R., Eds.; Symposium 16; American Fisheries Society: Bethesda, MD, USA, 1996; pp. 397–409.
19. Peterson, J.T.; Rabeni, C.F. Optimizing sampling effort for sampling warmwater stream fish communities. *N. Am. J. Fish. Manag.* **1995**, *15*, 528–541. [CrossRef]
20. Paukert, C.P. Comparison of electrofishing and trammel netting variability for sampling native fishes. *J. Fish Biol.* **2004**, *65*, 1643–1652. [CrossRef]
21. Quist, M.C.; Gerow, K.G.; Bower, M.R.; Hubert, W.A. Random versus fixed-site sampling when monitoring relative abundance of fishes in headwater streams of the upper Colorado River basin. *N. Am. J. Fish. Manag.* **2006**, *26*, 1011–1019. [CrossRef]
22. Fischer, J.R.; Paukert, C.P. Effects of sampling effort, assemblage similarity, and habitat heterogeneity on estimates of species richness and relative abundance of stream fishes. *Can. J. Fish. Aquat. Sci.* **2009**, *66*, 277–290. [CrossRef]
23. Angermeier, P.L.; Schlosser, I.J. Species-area relationships for stream fishes. *Ecology* **1989**, *70*, 1450–1462. [CrossRef]
24. Winemiller, K.O.; Tarim, S.; Shormann, D.; Cotner, J.B. Fish assemblage structure in relation to environmental variation among Brazos River oxbow lakes. *Trans. Am. Fish. Soc.* **2000**, *129*, 451–468. [CrossRef]
25. Eby, L.A.; Fagan, W.; Minckley, W.L. Variability and dynamics of a desert stream community. *Ecol. Appl.* **2003**, *13*, 1566–1579. [CrossRef]
26. Hayes, D.B.; Bence, J.R.; Kwak, T.J.; Thompson, B.E. Abundance, biomass, and production. In *Analysis and Interpretation of Freshwater Fisheries Data*; Guy, C.S., Brown, M.L., Eds.; American Fisheries Society: Bethesda, MD, USA, 2007; pp. 327–374.
27. Wagner, T.; Irwin, B.J.; Bence, J.R.; Hayes, D.B. Detecting temporal trends in Freshwater fisheries surveys: Statistical power and the important linkages between management questions and monitoring objectives. *Fisheries* **2013**, *38*, 309–319. [CrossRef]
28. Dauwalter, D.C.; Pert, E.J. Electrofishing effort and fish species richness and relative abundance in Ozark Highland streams of Arkansas. *N. Am. J. Fish. Manag.* **2003**, *23*, 1152–1166. [CrossRef]
29. Patton, T.M.; Hubert, W.A.; Rahel, F.J.; Gerow, K.G. Effort needed to estimate species richness in small streams on the Great Plains in Wyoming. *N. Am. J. Fish. Manag.* **2000**, *20*, 394–398. [CrossRef]
30. Watkins, C.J.; Quist, M.C.; Shepard, B.B.; Ireland, S.C. Electrofishing effort requirements for estimating species richness in the Kootenai River, Idaho. *Northwest Sci.* **2016**, *90*, 315–327. [CrossRef]
31. Neebling, T.E.; Quist, M.C. Comparison of boat electrofishing, trawling, and seining for sampling fish assemblages in Iowa's nonwadeable rivers. *N. Am. J. Fish. Manag.* **2011**, *31*, 390–402. [CrossRef]
32. Brown, M.L.; Allen, M.S.; Beard, T.D., Jr. *Fisheries Techniques*, 3rd ed.; Zale, A.V., Parrish, D.L., Sutton, T.M., Eds.; American Fisheries Society: Bethesda, MD, USA, 2012; pp. 15–79.

33. Shaw, J.L.A.; Clarke, L.C.; Wedderburn, S.D.; Barnes, T.C.; Weyrich, L.S.; Cooper, A. Comparison of environmental DNA metabarcoding and conventional fish survey methods in a river system. *Biol. Conserv.* **2016**, *197*, 131–138. [CrossRef]
34. Hallam, J.; Clare, E.L.; Jones, J.I.; Day, J.J. Biodiversity assessment across a dynamic riverine system: A comparison of eDNA metabarcoding versus traditional fish survey methods. *Environ. DNA* **2021**, *3*, 1247–1266. [CrossRef]
35. Andres, K.J.; Lambert, T.D.; Lodge, D.M.; Andres, J.; Jackson, J.R. Combining sampling gear to optimally inventory species highlights the efficiency of eDNA metabarcoding. *Environ. DNA* **2023**, *5*, 146–157. [CrossRef]